

11th INTERNATIONAL CONFERENCE:

ACHIEVEMENTS & CHALLENGES IN BIOLOGY

DEVOTED TO 120TH ANNIVERSARY OF PROFESSOR MIRALI AKHUNDOV

13-14 OCTOBER, 2022

BAKU STATE UNIVERSITY BAKU, AZERBAIJAN

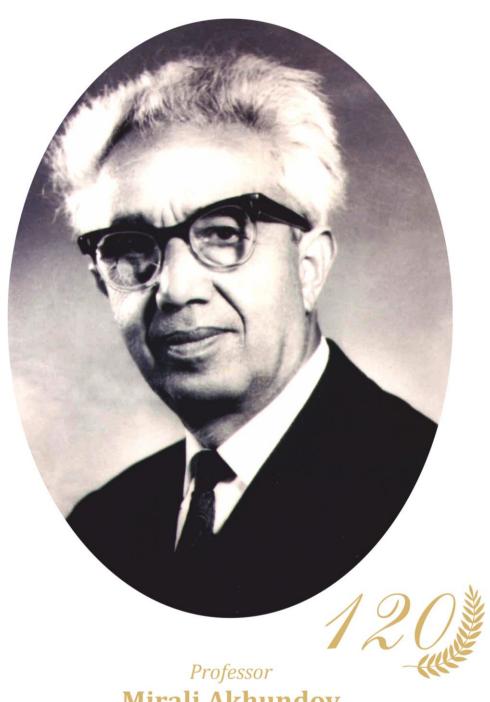
ABSTRACT BOOK

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Mirali Akhundov (1902-1992)

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FOREWORD

The 11th International Conference ""ACB-2022": Achievements and Challenges in Biology" is organized by Baku State University and is devoted to 120th anniversary of eminent professor Mirali Akhundov.

The prominent representative of the Azerbaijani scientific community professor Mirali Akhundov devoted himself to the development of education and science, to the formation of highly-skilled and qualified biologists in the country.

Mirali Abdulla oghlu Akhundov was born in 1902 on February 22 (March 5) in Sheki city. Having received his primary education in Sheki, in 1919 he entered Baku Teachers Seminary, and in 1923 he was one of the first graduates of this school. In the same year, he was sent as a teacher to the Zagatala region, and at the age of 21, he was appointed as head of a five-year primary school. At the same time (within 1923-1926) M.A.Akhundov worked as a teacher at the Industrial and Agricultural Technical School. In 1926-1930, M.A.Akhundov received his higher education at the Faculty of Biology of Azerbaijan State University (currently – Baku State University).

In 1932 he entered the postgraduate course of the Pedagogical Institute in Moscow on the subject "Genetics" and under the guidance of famous scientists A.S.Serebrovsky and N.K.Koltsov studied the crossing-over phenomenon on chromosomes, and in 1935, he defended his Thesis and received the scientific degree of Candidate of Biological Sciences (Ph.D.). From 1935 until the last days of his life, he worked continuously at Azerbaijan State University, and for a while at Azerbaijan Pedagogical Institute and the Institute of Zoology of Academy of Sciences.

M.A.Akhundov organized regular expeditions to the regions of the country, and studied species and breed composition of domestic birds in Azerbaijan. M.A.Akhundov also studied the effect of biologically active substances on the growth and development of various animals.

M.A.Akhundov founded the Department of Genetics and Darwinism at Baku State University and the only Museum of "Evolutionary Training" in Transcaucasia in 1937.

M.A.Akhundov's scientific activity was very extensive. He carried out researches in the field of teaching of biological sciences in Azerbaijan and had a significant impact on improving the education of this branch of science. His research in this area is reflected in more than 30 scientific-methodical papers and 3 books.

M.A.Akhundov wrote a number of textbooks and teaching materials for higher schools in the Azerbaijani language. He is the author of such textbooks and teaching materials as "Genetics" (1966, 1981), "Essentials of Darwinism" (1954), "Darwinism" (1961), "Introduction to Biology" (1965), "Resources from Biology" (1974), "Evolutionary Training" (1989), etc.

M.A.Akhundov published about 40 scientific papers in a number of books and various journals. He was the author of some popular scientific books.

The main pearls of his scientific creativity are the works he wrote by studying the development of biological ideas that existed in Azerbaijan in the XI-XIX centuries. Based on facts, the author proved that classics such as Nizami, Fizuli, Khagani, Hasan Bay Zardabi, M.F.Akhundov were ahead of their time with many biological ideas. About 20 scientific papers and 3 monographs were published by M.A.Akhundov in this field: "Our classics about nature" (1980), "Ahead of Time" (1990), "Our classics ahead of time about nature" (2015).

M.A.Akhundov had different positions in education and cultural sphere in the country. He was the Chairman of the Baku Branch of the Republican Society of Geneticists and Selectionists, The Chairman of the Republican Council on the History of Biological Sciences under the Academy of Sciences. He was entrusted with the management of the Educational Methodical Council of the Faculty. M.A.Akhundov was one of the first compilers of the compendium "Study of Chemistry and Biology", which is an invaluable resource for biology teachers. He was the editor of this collection for many years. M.A.Akhundov made a great contribution to the education of Biology in our schools. In 1943, he was awarded the title of "Honored Teacher" for his activities in this field. The government highly valued his pedagogical, scientific and public activity, and he was awarded the title of "Honored Scientist" by the Supreme Council of the Azerbaijan SSR in 1972.

M.A.Akhundov also worked extensively as a lecturer in "Bilik" society. For more than 35 years, he delivered interesting lectures on scientific and scientific-methodological topics to large audiences of workers and collective farmers, educational and medical workers, institutes and scientific organizations. His voice was regularly heard on radio and television. His speeches were highly appreciated by a wide audience.

This year we celebrate the 120th anniversary of the birth of the prominent scientist, educator, honored scientist and honored teacher,

the founder of genetics in Azerbaijan, Doctor of Biological Sciences, professor Mirali Abdulla oghlu Akhundov.

In connection with the 120th anniversary of M.A.Akhundov, one of the streets in his hometown of Sheki was named after him in order to perpetuate his memory.

More than 300 conference papers from 20 countries will be presented at the 11th International Conference ""ACB-2022": Achievements and Challenges in Biology" devoted to the 120th anniversary of the birth of professor Mirali Akhundov in sections "Genetics, Molecular Biology, Microbiology", "Biophysics, Biochemistry, Physiology", "Nanobiotechnology, Botany, Flora Conservation", "Zoology and Aquaculture" and "Systems' Ecology" during two days.

We wish for successful conference days.

Prof. Afat Mammadova Chairman of Organizing Committee

I. GENETICS, MOLECULAR BIOLOGY, MICROBIOLOGY

POWER OF GENOMICS: PERSPECTIVE AND FUTURE POTENTIAL

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Keywords: genome; healthcare; multi-omics platform.

Advanced genome technologies driven genomic research has revolutionized the advancements in different areas including agriculture, environmental sustainability and most importantly human healthcare system. The cost effective and fast generation of genomic data has been instrumental in the identification of underlying disease causative factors and understanding pathological mechanisms. Thus, genomics is serving remarkably in solving some of the most challenging health problems around the globe including inherited disorders, complex medical conditions, cancer progression as well as in tracking disease outbreaks. In developed countries healthcare professionals are using genomic data to diagnose and clinically manage their patients, however, despite the advancement in genomics, there remains a constrain in effective utilization of genomic data in health care systems of low- and middle-income countries. In a low to middle income country like Pakistan, in different disease focused areas in healthcare specialties including ocular, neurological and cardiovascular diseases, we have demonstrated how genomics can help in accurate diagnosis of diseases and in developing effective and targeted treatment strategies. In addition, we have also demonstrated how international and national collaborations are effective in attaining the objectives of evidence-based medicine using new genomic technologies in transforming healthcare by highlighting the role of genomics in health and disease in facilitating future research.

Genomics being the first discipline in omics, was followed by transcriptomics, epigenomics, proteomics, metabolomics and microbiomics, and presently revolutionizing into single cell omics approaches, the application of genomic data in present and future health care has become enormous. The time has come to think about establishing a "global genomics" based "global omics hub" an integrated multi-omics platform which will have the potential of massive advancements in new drug discovery for the treatment of communicable and non-communicable diseases. The genomic based integrated omics data hub can serve to remove the inequality between developing and industrialized nations, where the data

generated by developed countries can provide a platform for developing countries to invest further in data analysis instead of data generation (which requires more financial and physical resources) and transform it into translational research having the potential of implementation of genomics or on broader scale "omic medicine" in countries worldwide. The "global genomics" based "global omics hub" can pave the way for improvement in not only population and subpopulation level medicine but also personalized medicine. The "global genomics" based "global omics hub" model will revolutionize into "theraomics" a dimension yet to establish for betterment of new and better drug discovery for the management and treatment of diseases across the globe.

MOLECULAR AND CELLULAR MECHANISMS OF RADON-INDUCED LUNG CANCER

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Keywords: lung cancer; radon; microRNA; mitomiR; fc-mtDN.

Radon-induced lung cancer is a significant problem of biomedicine worldwide. Radon is a chemically inert radioactive gas that occurs naturally as an indirect decay product of uranium. World Health Organization identified exposure to radon and its decay products as the second leading cause of lung cancer after tobacco use and a major risk factor in the non-smoking population. Despite the fact that the WHO has determined the permissible radon standards to be $100~\text{Bq/m}^3$, the risk of lung cancer increases from $50~\text{Bq/m}^3$. Prolonged exposure to radon causes damage to cellular components, mitochondria, and oxidative stress, which leads to damage to lung tissue.

For the moment, the association of radon and the risk of lung cancer is not in doubt, but the molecular and cellular mechanisms of how radon induces malignant cell transformation remains unclear. In recent years, significant progress has been made in studying the interactions between genes and their products, epigenetic mechanisms and environmental factors. Several studies have shown that the epigenetic basis of lung cancer is associated with changes in the microRNAs expression profile and emerging evidence has been accumulated about the involvement of microRNAs in the carcinogenesis of various malignant neoplasms, including lung can-

cer [Wang *et al.,* 2018; Bersimbaev *et al.,* 2020]. microRNAs are small noncoding RNAs that are involved in the regulation of target genes at the post-transcriptional level. microRNAs are known to control many cellular processes, such as proliferation, differentiation, and cell death.

Mitochondrial microRNA (MitomiR) is a class of microRNA molecules that can regulate the expression of mitochondrial proteins and control the functional activity of mitochondria. It was shown that various mitomiRs are involved in the pathogenesis and progression of lung cancer acting as regulators of mitochondrial processes. As a result, it is possible to state the study of mitomiRs as new biomarkers of radoninduced lung cancer is a relevant and promising area.

Free-circulating mitochondrial DNA (fc-mtDNA) can serve as a kind of trigger for the transduction of pro-inflammatory signals in animal cells. The fc- mtDNA mediated via toll-like receptors the synthesis of pro-inflammatory cytokines by activating the NF-K β signaling pathway. It plays a key role in the development of an inflammatory response. Any ionizing radiation contributes to the promotion of cell death, both due to ROS, and non-reparable damage to the genetic material, which makes further cell life impossible. In addition, radon can alter the expression profile of miRNAs, which can activate apoptosis and inflammation. The effect of radon leads to the death of cells of the bronchial epithelium, which is accompanied by the release of a large amount of mtDNA, which, due to the activation of the NF-K β signaling pathway, mediates the synthesis of pro-inflammatory cytokines. As a result of this activation, inflammation develops, which is one of the key factors in lung cancer oncogenesis. miRNAs can contribute to this process.

ASSESSMENT OF GENETIC DIVERSITY IN AEGILOPS TAUSCHII COLLECTION USING GBS-BASED SNP MARKERS

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Keywords: single nucleotide polymorphisms; genetic variation; unique alleles; transition; transversion.

Genotyping by sequencing (GBS) is a high-throughput, NGS-based multiplex genotyping technique and is the most successful genotyping method applied to plant breeding [Poland and Rife, 2012]. Genomic da-

ta obtained during genotyping by sequencing are equivalent to the information provided by thousands of molecular markers from the whole genome and all chromosomes [Elshire et al., 2011]. In the current study the genetic diversity of 106 Aegilops tauschii accessions of Azerbaijan and Georgian origin was investigated using the GBS method. As a result of GBS analysis, a total of 348 high quality single nucleotide polymorphisms (SNP) were obtained with a minor allele frequency of higher than 10%. The number of unique alleles per genotype varied from 1 to 12, the total for the collection was 19. All types of single nucleotide substitutions (4 transitions and 8 transversions) were found among Aeailops genotypes, which indicate the higher variability of the Ae, tauschii genome. Of a single nucleotide mutations detected in the Ae. tauschii collection, 2/3 were transition-type (Ts) and 1/3 - transversion-type (Tv) with a Ts/Tv ratio of 2.1. $A \leftrightarrow G$ and $C \leftrightarrow T$ mutations were the most common transitions, while most transversions were of the $C \leftrightarrow G$ type. Only one out of the 348 markers was T↔A transversion type. The average PIC and GDI for the collection based on GBS data were 0.303 and 0.386, respectively. Since South Caucasus and Azerbaijan are considered one of the origin centers of Ae. tauschii, high diversity was expected [Abbasov et al., 2019]. Nei genetic distance index among accessions varied between 0-1 and averaged 0.64. Cluster analysis grouped accessions into 3 main clusters with sharply differentiated subclusters. A genotype of Azerbaijan origin (TA1662) formed an independent cluster. Within the cluster, the relationship between the grouping and the origin country, geographical region and coordinates has been identified. The first 3 axes in PCoA analysis explained 88% of genome variation. The cluster, PCoA, and STRUCTURE analyzes revealed a sharp genetic differentiation between the Ae. tauschii collections of Azerbaijan and Georgia. In addition, within each country subpopulations that differed significantly were identified. The lack of gene flow among Ae. tauschii populations located in different countries, geographical regions and coordinates has led to their isolation from other populations and, ultimately, to such differentiation. The genetic variation, as well as genotypes with unique alleles, identified by GBS analysis in the Ae. tauschii collection can be effectively used in order to create new, higher quality wheat varieties and to enrich the D genome of bread wheat.

GENOME LEVEL EVALUATION OF HCV PREVALENCE VALUES IN SAMSUN REGION IN 2022

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Keywords: hepatitis C virus (HCV); PCR test; HCR RNA concentration.

HCV genotype and subtype distribution differ according to geographic origin and transmission risk category [UNITED NATIONS, World Economic Situation and Prospects, 2018]. The HCV burden in public health is estimated at about 71 million people worldwide by World Health Organization (WHO) with at least 400,000 people that died every year from HCV disease [Global hepatitis report, 2017]. New hepatitis C treatments with oral direct-acting antivirals (DAAs) showing high rates of response, with short treatment duration have been available [Pawlotsky, 2014]. Molecular tests are used to confirm HCV infection. Definitive diagnosis of HCV infection is made quantitatively by HCV RNA PCR test and treatment is started. These tests are indicated to confirm replication in subjects found anti HCV Ab positive or to detect viremia in acute infection, during the window period (when Ab assays are still negative). Commercialized HCV RNA tests are very sensitive and able to detect and quantify less than 30 copies/mL (reference) or <15 IU/mL of HCV RNA or less [Guillou-Guillemette, 2019].

In this study, we planned to retrospectively evaluate the positive case prevalence results, including age and gender, according to the results of HCV RNA tests that came to our hospital in 2022.

HCV RNA test that is a quantitative nucleic acid test was performed on the cobas \$4800 System to diagnose HCV.

The cobas® 4800 System automatically determines the HCV RNA concentration for the samples and controls. The HCV RNA concentration is expressed in International Units per milliliter (IU/mL). The study demonstrates that cobas® HCV detected HCV RNA at a concentration of 9.2 IU/mL in EDTA plasma and 7.6 IU/mL in serum with a hit rate of \geq 95% for the 400 μ L sample processing volume and at a concentration of 15.2 IU/mL in EDTA plasma and 15.3 IU/mL in serum with a hit rate of \geq 95% for the 200 μ L sample processing volume.

SPSS for Windows 22.0 program was used for statistical analysis of the study. Continuous variables obtained from the study were given as mean±standard deviation (X±SD). Categorical variables were expressed as

percentage frequency. P values below 0.05 were considered statistically significant. Categorical variables were compared with chi-square test and continuous variables were compared with independent sample t test.

In our study, HCV RNA (Quantitative) test positive case was found at the lowest age of 20 and the highest at the age of 86 years. In addition, HCV RNA (Quantitative) test positive cases were not found in those aged 35-45 and 45-55. On the other hand, the highest rate of HCV RNA (Quantitative) test positive cases was found in the 25-35 age group. In our study, all 13 individuals with positive HCV RNA (Quantitative) test up to the age of 60 were male. These 13 individuals constitute 72.22% of 18 male individuals with positive HCV RNA (Quantitative) test.

DIAGNOSIS METHOD OF STUDY OF DROUGHT AND SALT STRESSES RESISTANCE OF F₁ HYBRIDS AND PARENTAL FORMS (*ILKIN* AND *SHAKAR*) OF TOMATO

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Keywords: tomato; hybrid; chlorophyll; durability.

All living organisms, including plants, are constantly exposed to the environmental factors in which they live [Aliyev *et al.*, 2014].

One of the methods used to assess stress tolerance is the study of changes in the amount of chlorophyll (a+b). Under the influence of stress factors, green plastids break down, which leads to a decrease in the amount of chlorophyll. However, the less the pigments changes under stress, the more stable the specimens [Smolnikova *et al.*, 2011; Udovenko *et al.*, 1988].

Based on this indicator, the resistance of the F_1 hybrids and their parent forms (*Ilkin* and *Shakar*) to salt and drought was studied. It was determined that the amount of chlorophyll (a+b) in one of the parent forms, *Ilkin* tomato, was significantly destroyed (15-16%) under the impact of drought and salt. According to the results, the *Ilkin* variety was assessed as a medium resistant to both salt and drought.

Shakar, another parent form, was more resistant to salt and drought stresses than the *Ilkin* variety, where 8 percent of chlorophyll

(a+b) was destroyed by drought and 6 percent by salt. The study found that hybrids were more resistant to stress factors than parental forms due to changes in the amount of chlorophyll (a+b). Thus, the amount of chlorophyll (a + b) in the hybrid forms did not change under the influence of both drought and salt.

In both parent forms, chlorophyll "a" is more variable than chlorophyll "b". In the *Ilkin* variety, this indicator was 4.157 mcg under control, 3.96 mcg after drought stress and 4.5 mcg after salt stress. Also, the amount of chlorophyll (a+b) in the control of the *Shakar* variety was 5.30 mcg, in drought - 5.03 mcg, and after salt stress - 5.22 mcg. In the F₁ hybrid forms of *Ilkin* and *Shakar*, the amount of chlorophyll (a+b) in the control was 4.92 mcg. This indicator is higher than that of the mother's form *Ilkin*, and less than that of the father's form *Shakar*. This event is probably the result of the fact that this hereditary indicator manifests itself in a codominant way in the first generation.

The hybrid forms are also not susceptible to diseases such as viruses, mounds, leaf rot, which are characteristic for the tomato plant.

The study showed that the F_1 hybrid of *Ilkin* and *Shakar* was more resistant to drought, salinity and a number of diseases than the parent forms during adaptation to stressors. Unlike their parents, the positive traits of the hybrid form can be considered the result of adaptive heterosis.

IDENTIFICATION OF GALT GENE MUTATIONS FROM DIFFERENT ETHNIC GROUPS OF THE AZERBAIJAN POPULATION

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Keywords: galactosemia; gene; disease; ethnic groups; mutation.

Galactosemia is a rare autosomal recessive metabolic disease caused by mutations in the galactose-1-phosphate uridyl transferase (GALT) gene. This study aims to identify pathogenic mutations underlying galactosemia in four families from different ethnic groups in the Azerbaijan population.

Blood samples were collected from four families in the Azerbaijan population and extracted genomic DNA. High-throughput sequencing (Sanger sequencing analysis) was used for detection of single nucleotide substitutions of the *GALT* gene.

In 2018-2021 genetic screening of the *GALT* gene was conducted among 218 newborns and 412 child including different ethnic groups from different regions of Azerbaijan. Genome DNA was obtained by automatic isolation from 200 ml of venous blood. The DNA concentration was measured by the Digital spectrometer. Integrity and quantity of genomic DNA and polymerase chain reaction (PCR) products were identified by electrophoresis on 2% agarose gels. The genome DNA underwent the PCR procedure for every protein-encoding exon of the GALT gene. The nucleotide sequence of purified fragments was studied in GENOME Lab GeXP™ Sequencing. Purified product was dyed with fluorescent dve by BigDve Terminator V.3.1, and processed by Cycle Sequencing PCR. Positive Cycle Sequencing PCR samples, controlled by electrophoresis in agarose gels, were extracted from the BigDye XT with a dve-purifying agent. The obtained nucleotide chains were identified through SeqScape® version 2.7 software program, then compared by means of the National Center for Biotechnology Information (NCBI) Blast Ce, to normal *GALT* nucleotide chains and only then were the substitutions identified [Timson, 2016; Bosch, 2006].

A heterozygous form of the P325L (C>T) mutation was found in the 9th exon of the *GALT* gene in the newborn son of the Udin ethnic group from the Shaki hospital. The mother's parents are cousins. The other two daughters of the family are healthy.

A heterozygous form of the H132Q (C>G) mutation was found in the 5th exon of the GALT gene in the newborn son of the Avar ethnic group in the Balakan region. The patient's parents are cousins. The first two daughters of this family died in the first months of their lives with similar symptoms.

A heterozygous form of the Q97R (A>G) mutation was found in the 6th exon of the *GALT* gene in an Azerbaijani newborn boy in Gabala. The other children in this family are healthy.

Another newborn girl with a heterozygous form of the Q97R (A>G) mutation was born in Gusar and belongs to the Lezgi ethnic group. The other children of this family are healthy.

The present study identified the *GALT* mutations in the four families from different ethnic groups in Azerbaijan population with galactosemia and expanded the phenotypic and mutational spectrum of *GALT*. High-throughput sequencing conducted in our study is a convenient and useful tool for clinical diagnosis of galactosemia and other associated genetic disorders.

OPTIMIZATION OF PLASMID DNA CO-TRANSFECTION CONDITIONS TO OBTAIN SARS-COV-2 SPIKE GLYCOPROTEIN PSEUDOTYPED LENTIVIRAL PARTICLES

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Keywords: SARS-CoV-2 spike pseudotyped virus; lentiviral vectors; transfection.

The recent emergence and rapid global spread of SARS-CoV-2 and outbreak of COVID-19 have created a pandemic situation all over the world. This necessitated the research to understand the multistep virus entry process for subsequent disease prevention and control.

Owing to its high infectivity and pathogenicity, SARS-CoV-2 has to be handled in biosafety level 3 laboratories. Pseudotyped virus particles are useful virological tools that can effectively replace the need for live SARS-CoV-2 for a broad range of applications and can be investigated in biosafety level 2 laboratories [Chen *et al.*, 2021; Fu *et al.*, 2021; Yang *et al.*, 2021]. To date several SARS-CoV-2 pseudovirus particle production and infection systems have been successfully generated [Hoffmann *et al.*, 2020; Nie *et al.*, 2020; Ou *et al.*, 2020]. However, the importance of applying an empirical approach to optimizing the production efficiency has been well demonstrated [Toon *et al.*, 2020].

The aim of the present study was to determine the optimal conditions of the lentiviral vector system plasmid DNA co-transfection for effective SARS-CoV-2 pseudovirus production in HEK 293T cells.

To obtain the recombinant virus particles pseudotyped with SARS-CoV-2 spike glycoprotein lentiviral packaging system was used. It consisted of three different plasmids: pLPSARS-S, coding full-length spike glycoprotein of SARS-CoV-2; psPAX2, containing gag-pol genes, and pWPXL, the self-inactivated lentiviral vector, carrying a reporter $\it egfp$ (enhanced green fluorescence protein) gene under control of promoter region of the human elongation factor 1 alpha-encoding gene (hEF1 α). To produce the recombinant virus particles human cell line HEK 293T was used. Cells were cultured in Dulbecco's modified Eagle's medium supplemented with 10% fetal bovine serum, 2 mM L-glutamine, 100 units/mL penicillin, 100 µg/mL streptomycin and incubated at 37 °C in a humidified atmosphere saturated with 5% CO₂.

Experimental studies were performed to evaluate the impact of several factors on pseudovirus production efficiency: ratio between the lentiviral

vectors pLPSARS-S, psPAX2 and pWPXL; total amount of plasmid DNA; type and quantity of the transfection reagent. To estimate the transfection efficiency the number of the reporter gene *egfp* copies was evaluated in supernatants collected 48 hours post transfection by real-time PCR using a standard curve based on serial dilutions of backbone plasmid pWPXL. It was shown that the best ratio of plasmids pLPSARS-S, psPAX2 and pWPXL for co-transfection (with an absolute amount of DNA equal to 2.9 μ g) was 1:2:3. The highest pseudovirus titer was achieved with polyethyleneimine used as a transfection reagent in 1:1 ratio with the amount of DNA.

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MOLECULAR STUDY OF LYSOSOMAL STORAGE MUCOPOLYSAC-CHARIDOSIS DISORDER IN AZERBAIJAN

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Keywords: enzyme; mps types; mucopolysaccharidosis; fluorometry.

Modern classification distinguishes several basic types of MPS's depending on the character of enzymatic deficiency: type I-Hurler syndrome, Scheie syndrome, Hurler-Scheie syndrome; type II-Hunter syndrome; type III-Sanfillipo syndrome (A, B, C and D types); type IV-Morquio syndrome (A and B types); type VI-Maroteaux-Lamy syndrome; type VII-Sly syndrome.

All MPS's have autosomal recessive inheritance type except MPS type II, which has X-linked recessive inheritance.

MPS frequencies in different populations in the world vary from 66000 to 450000.

For the first time in Azerbaijan, were carried out population genetic studies to identify MPS disorders by means of modern molecular diagnostic methods.

Material was collected during 2018-2022 years in specialized children's medical centers in Baku city as well as in expedition studies

in regions of the Republic. Patients were selected during clinic examinations of doctor-pediatrician and doctor-geneticist.

56 patients were identified with an age range between 6 months and 28 years of age. The division by genders was as follows: 15 males and 11 females. Blood samples from patients for studies were collected on DBS (Dry Blood Sample) cards.

All patients' samples have undergone enzymatic analysis on all MPS types. The following enzymes were involved: α -L-iduronidase (MPS I), iduronate-2-sulfatase (MPS II), heparan N-sulfatase (MPSIIIA), α -N-acetylglucosaminidase (MPS IIIB), heparan- α -glucosaminide N-acetyltransferase (MPS IIIC), N-acetylglucosamine 6-sulfatase (MPS IIID), N-acetylgalactosamine-6-sulfate sulfatase (MPS IVA), β -galactosidase (MPS IVB), arylsulfatase B (MPS VI).

Fluorometry method was used to identify enzymes' activities and mutations' testing was done with the NGS method.

Enzyme analysis has shown activity deficiencies of the following enzymes: α -L-iduronidase, iduronate-2-sulfatase, heparan- α -glucosaminide N-acetyltransferase, N-acetylgalactosamine-6-sulfate sulfatase and arylsulfatase B.

N-acetylgalactosamine-6-sulfate sulfatase enzyme levels were sharply lowered in 26 patients and varied in the range <0,1(LOD)µmol/L/h-<0,6(LOD)µmol/L/h, that is specific for homozygous and heterozygous states when normal one was \geq 2,0 µmol/L/h.

Molecular-genetic analysis made it possible for us to identify 7 types of *GALNS* gene (MPS IVA) mutations that had only nucleotide substitutions as: c.553C>T, c.439T>A, c.1283A>G, c.157G>A, c.463G>T, c.1018G>T and c.443A>G. These mutations were found in homozygous, double heterozygous (compound) and heterozygous states. *GALNS* gene mutations were for the first time identified in patients from our Republic. All of them are described in scientific articles and not novels.

It should be mentioned that MPS type IV frequency in Azerbaijan Republic prevailed over other MPS types: MPS IV - 46,4%, MPS III - 13%, MPS VI - 9%, the rest was MPS II and MPS I 0%. These results greatly differ from previously presented in the scientific study results in different populations throughout the world where MPS I keeps the first place [Terzioglu *et al.*, 2002; Chkioua *et al.*, 2014, 2015; Jurecka *et al.*, 2015; Khan *et al.*, 2017; Puckett *et al.*, 2021].

We also identify and study other MPS mutations and discuss disorder prophylaxis ways in the families of reproductive ages.

ULTASTRUCTURE OF THE FERRITIN MOLECULES IN THE NUCLEO-PLASM OF GINGIVAL CELLS IN PATIENTS WITH β-THALASSEMIA

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Keywords: β -thalasemia; gingival; ferritin molecule; transmission electron microscope.

There is still no consensus on the presence and possible mechanism of entry of the ferritin molecule into the nucleoplasm of cells through nuclear pores. The aim of this study is to detect the ferritin molecule in the nucleoplasm of gingival cells in patients with β -thalassemia at the ultrastructural level.

An electron microscopic study of gingival biopsies (in 18 patients) obtained under medical indications under conduction anesthesia was carried out. The materials for electron microscopy were fixated in a solution containing 2% paraformaldehyde, 2% glutaraldehyde and 0.1% picric acid prepared in a phosphate buffer (pH=7.4). The postfixation procedures and Araldite-Epon blocks were prepared according to general methods accepted in electron microscopy [Ellias, 2014]. Ultrathin sections (50-70 nm) were obtained by the aid of Leica EM UC7 ultramicrotome (Germany) and examined under the TEM JEM-1400 (JEOL Japon) at an accelerating voltage of 80-100 kV. Digital image files were obtained with a Veleta - side-mounted TEM CCD camera (Olympus-Soft Imaging Solutions, Münster, Germany).

The structures involved in the formation of individual ferritin molecules are detected only at high magnifications (> 100,000) of an electron microscope and consist of two components: in comparison with the surrounding elements of the cytosol, an electron-light protein shell-apoferritin and an electron-dense crystalline core-colloidal iron hydroxide.

At the ultrastructural level, were found ferritin molecules in the cytoplasm, near the outer nuclear membrane, in the lumen of the nuclear pores and in the nucleoplasm of all cell types involved in the formation of the epithelial cover and the lamina propria of the gingival mucosa in patients with β -thalassemia. Despite the fact that in all cases the number of ferritin molecules was greater in the cytosol of cells than in the nucleoplasm, the presence in the nucleoplasm of structures with an electron-light circle on the periphery and an electron-dense glandular core in the center, characteristic of ferritin molecules, is beyond any

doubt. Both in the cytoplasm and in the nucleoplasm, the number of ferritin molecules is much greater in the cellular elements taken from patients with the exudative phase of exacerbation of chronic catarrhal-sclerosing gingivitis in patients with β -thalassemia.

Elucidation of the molecular mechanisms of the passage of ferritin molecules through nuclear pores is of not only theoretical but also important practical interest in the design of new types of chelators.

IF 1 IN EVERY 8 CANCER IS HEREDITARY, SHOULD ALL CANCER PATIENTS TO BE SCREENED WITH GENETIC TESTS?

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Keywords: cancer; mutations; treatment; genomic evaluation.

It has been reported that 5% to 10% of all cancers are hereditary [Hodgson, 2008], as well as, inherited mutations cause 1 out of every 8 cancers [Walter Alexander, 2022].

A study of approximately 3000 patients with a wide variety of cancer stages and types, including breast, colon, lung, ovarian, pancreatic, bladder, prostate and uterine cancers, reported that current clinical guidelines are not very sensitive in understanding hereditary cancers [Samadder *et al.*, 2020]. However, finding an inherited mutation in a cancer patient or family members can change the perspective on the treatment of that cancer.

In a study published in the journal *JAMA Oncology*, it was reported that *BRCA1* and *BRCA2* genetic tests should be screened not only in breast and ovarian cancer, but also in a wider group of patients such as biliary tract cancer, esophageal cancer and stomach cancer [Breast Cancer Association Consortium, 2022]. Finding BRCA mutations in a patient makes that person more susceptible to a next-generation class of cancer drugs called PARP inhibitors.

PARP inhibitors have so far been found to have significant efficacy in the presence of pathogenic *BRCA1* and *BRCA2* variants in ovarian, breast, prostate and pancreatic cancers. According to the results of this study, the importance of testing hereditary cancer genes in more patients is emphasized, and it is reported that PARP inhibitor drugs may be beneficial for more patients. These tests should be considered especially for patients with a family history of cancer of the biliary tract,

cervical cancer, colon and rectum cancer, endometrial cancer, esophageal cancer, and stomach cancer [Breast Cancer Association Consortium, 2022; Momozawa *et al.*, 2022].

In a study evaluating the use of inherited genetic testing in 55,595 patients with colorectal cancer, pathogenic/possibly pathogenic genetic changes in genes including *MSH2*, *MLH1*, *PMS2*, *MSH6*, *CHEK2*, *APC*, *BRCA2*, *ATM*, and *MUTYH* were detected in 143 (18%) of 788 patients [Nelson, 2021]. According to the results of this study, it was reported that 44% of patients may potentially be suitable for sensitive therapies such as PD1 and PD-L1 inhibitors based on pathogenic variants in repair genes such as Lynch syndrome [Nelson, 2021].

In a recent separate study, 2984 cancer patients treated for various solid tumor cancers were tested for a multi-gene panel using next-generation sequencing [Samadder $et\ al.$, 2020]. Of the participants, 13.3% (n = 397) tested positive for pathogenic mutations. Of these, approximately 70% (282 of 397 patients) carried genes with medium and high penetrance that increases cancer risk.

Cancer genetics studies are increasingly used in modern medical oncology practice. Testing for inherited cancer genes is underutilized in cancer care for both patients and their families due to outdated guidelines that often limit testing to a narrow group of high-risk patients. All cancer patients should have access to complete genetic information that can guide their care and inform their family's health. Genomic evaluation, including genetic testing, should be offered to every cancer patient to determine if they have an underlying inherited mutation that predisposes them to their cancer and how to incorporate this information into designing the best surgical and treatment options for that patient.

EVALUATION OF COTTON GENOTYPES RESISTANT TO VERTICILLIUM WILT

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Keywords: Verticillium dahlia Kleb; cotton collection; resistance; disease index.

One of the most devastating diseases of cotton is Verticillium wilt disease caused by the Verticillium dahlia Kleb. fungus. In addition to causing severe economic damage to farms each year, the disease also

reduces the quality of raw cotton. The use of fungicides is ineffective and also seriously affects the environment. Tissue of diseased plants, irrigation canals, etc. can be easily spread to surrounding areas by irrigation system. The fungus has about 450 host plants, including trees, shrubs and economically important plants such as cotton, tomato, pepper etc. Using of susceptible crop varieties leads to the formation of more resistant pathogens and more severe soil contamination. The most effective way to control the disease is to create resistant varieties for utilization in agriculture.

The main purpose of the study is to characterize local and introduced collection samples of cotton for resistance to Verticillium wilt disease, to study the genetic basis of resistance to Verticillium wilt disease, to identify disease-resistant genotypes and to recommend them for future breeding programs. Experiments were carried out at an artificially inoculated field located in Absheron Experimental Station of Genetic Resources Institute. 29 cotton collection varieties of different origin were used as plan material: local varieties – Ganja-195, Ganja-110, Ganja-114, Ganja-182, Ganja-160, Ganja-200, Karabakh -11, Karabakh-12, AP-317, Agdash-3, Zafar, Bayragdar, Barakat; Greek varieties - Assos, Prime, Select, Edessa; Uzbek varieties – Tashkent-1, Tashkent-2, Tashkent-3; Kyrgyzstan varieties – Navai, Kyrgyzstan-179; Turkish varieties – Flash, Lima, Beyaz altun, Carisma, PG, CSN-12.

During the assessment of the disease by cross-section of the stem, after harvesting, the root collar part of the plants was cut and the degree of stains on the xylem tubes was evaluated as 0-4 (0-no color change in the cross-section of the stem; 1-25%; 2 - 26-50%; 3-51-75%; 4-76-100% of the cross-section of the stem was brown). The values of disease index were calculated using formula: disease index = 0a+1b+2c+3d+4e/n, whereas '0, 1, 2, 3, 4' – the ranking number according to the assessment scale, 'a, b, c, d, e' – the number of plants according to each scale, 'n' – the number of total plants. Variation of the values of disease index between 0-2 shows resistance, 2-4 susceptible genotypes.

Among local genotypes, the Karabakh-12 genotype had a higher disease index than other local genotypes [Table 1]. Greek genotype Edessa showed high susceptibility compared to other genotypes. Local Barakat, Ganja-200, Zafar, Ganja-114, AP-317, Ganja-182, Ganja-160, Tashkent-2 of Uzbek origin, Assos of Greek origin, Prime, Select, Flash, and Lima genotypes of Türkiye origin showed resistance to the disease.

Thus, the most susceptible varieties were Edessa (0.348), Carisma (0.259) and Karabakh-12 (0.216).

Table 1. The values of disease index of cotton genotypes artificially inoculated
by Verticillium wilt

Genotype	Index	Genotype	Index	Genotype	Index
Barakat	0	Karabkh-11	0.097	Navai	0.148
Ganja-200	0	Karabagh-12	0.216	Kyrgyzstan -179	0.053
Zafar	0	Bayragdar	0.033	Flash	0
Ganja-114	0	Assos	0	Lima	0
AP-317	0	Prime	0	Beyaz altun	0.045
Ganja-182	0	Select	0	Carisma	0.259
Ganja-160	0	Edessa	0.348	PG	0.136
Agdash-3	0.129	Tashkent-1	0.167	CSN-12	0.188
Ganja-195	0.038	Tashkent-2	0		
Ganja-110	0.182	Tashkent-3	0.059		

Currently, one of the most effective ways to increase resistance to Verticillium wilt disease in cotton is to develop sustainable cotton genotypes. In this regard, the selection of resistant forms by evaluating resistant genotypes in an artificial inoculation environment, in addition to enriching the characteristics of resistant genotypes, plays the role of a scientific basis for breeding programs for the creation of complex resistant forms. Screening with specific primers and the use of biochemical markers to genetically justify the resistance of immune varieties will allow the selection of varieties with complex resistance.

NEW SAMPLES OF POLONICUM WHEAT (T.POLONICUM L.) OF AZERBAIJAN

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Keywords: varieties; lifestyle; components of yield.

Rare, but similar in genomic composition, wheat species that occupied different areas in the past have a great potential for enrichment of wheat intraspecific polymorphism. By involving rare species, distant spontaneous hybrids of wheat in interspecific crossing, it is possible to enrich durum and bread wheat varieties with new genes and gene blocks [Rustamov, 2014, 2016].

Long-term observations show that in non-isolated, mixed crops in tetra- and hexaploid species, the frequency and diversity of spontaneous hybrids increase. With the help of direct individual selection, it is possible to enrich the gene pool of any species with new varieties and forms in a short time. Polonicum wheat (*Triticum polonicum* L.) is rare naked specie of the genus *Triticum* L. New *T. polonicum* accessions were selected in hybrid and breeding nurseries of Terter ZES of Research Institute of Crop Husbandry from the founders - polonicum forms and evaluated for morphometric and agronomical traits during the 2012-2021 years. The study of new samples showed, that the growth habit, earing time, plant height, lodging and disease resistance, shape and density of the spike show a very high variability and a wide intraspecific polymorphism.

As a result of the study, samples of *T. polonicum* belonging to 16 varieties were selected, which were transferred to the National Gene Bank. Most of them are the varieties of subsp. *polonicum*: var. *chrysospermum*, var. *pseudolevissimum*, var. *skalasubovii*, var. *pseudochrysospermum*, var. *pissarevii*, var. *rufescens*, var. *pseudocaryopsirubrum*, var. *polonicum*, var. *rubrosemineum*, var. *caryopsirubrum*, var. *heydelbergi*, var. *abyssinicum* and var. *levissimum*. In addition, were found three new varieties (var. *pseudoabyssinicum* var. nova, var. *pseudorubrosemineum* var. nova and var. *azerpseudocaryopsirubrum* var. nova) belonging to *T. polonicum* subsp. *abyssinicum*.

The majority of samples from the world collection of VIR have a spring lifestyle. The new samples transferred to the Gene Bank differ in their lifestyle; almost half of the samples (47.5%) are winter lifestyle. The new accessions also significantly differed in plant height: the minimum height (semi-dwarf forms) was 70.0 cm, while the maximum height was 177.0 cm. In samples belonging to subsp. abyssinicum, the height of the plants was in the range of 70-95 cm. The new samples differ in spike density and awning: the ears are awnless with short and ordinary awns; ears are short, medium length and long; ears are loose, medium density and ultra-dense; spikes are fan-shaped. In favorable years, samples with truebranched ears were also identified. In new samples, the grain shapes is mainly elongated (7-12 mm), but in undersized ones are found genotypes with oval grains. Most of the polonicum samples were proved to be resistant to lodging and diseases. Selected accessions are proposed to be used as a raw material for creating low- and medium height, high-yielding durum wheat varieties with high grain quality and resistance to diseases.

ANTIMUTAGENIC ACTIVITY OF AN ANTIOXIDANT OF DIFFERENT CONCENTRATIONS ON WHEAT SEED ROOTS BEFORE AND AFTER EXPOSURE TO ELECTROMAGNETIC WAVES

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Keywords: mutation; chromosomes; mutagenesis; antioxidant; wheat.

The data obtained experimentally by numerous researchers testify to the specific effect of electromagnetic waves on biological objects. The fields of application of modern genetics are very diverse. One of these areas is antimutagenesis, which is widely studied in plants, animals, microorganisms and humans [Apasheva *et al.*, 2006].

Dry seeds of soft wheat variety "Absheron" (*Triticum aestivum* L.) were used as an object of study, 0.1 and 1.0% solutions of chromium salt of 2,6-dichloro ethyl-1-phenyl propionic acid, synthesized at Baku State University, were used as an antioxidant. Dry wheat seeds were exposed to 50 and 100 MHz doses of electromagnetic waves. The duration of EMW exposure to objects for each dose was 5, 10 and 15 minutes.

In the first variant, the seeds were exposed to a dose of electromagnetic radiation of 100 MHz. At the same time, the frequency of induced mutations increased to $10.65 \pm 1.48\%$. In other variants of the study, the frequency of induced mutations in the roots of wheat seeds treated with antioxidants before EMW was reduced to $4.39 \pm 0.90\%$. In this variant, seeds (dry seeds) were exposed to EMW for 5 minutes. However, in later versions of the study, in which the seeds were kept in the EMW environment for 10 and 15 minutes, the frequency of induction mutations increased to some extent depending on the time of exposure. So, in the roots of seeds treated with a 1.0% antioxidant solution before exposure to EMW, i.e. AO (1.0%) + EMW - in the 10-minute version, this figure was $5.25 \pm 0.44\%$, whereas in aged for 15 minutes and then germinated seeds - the frequency of induced mutations increased to $6.15 \pm 1.15\%$.

Modified anaphases in preparations from seed roots, which were first exposed to EMW for 5 minutes and then treated in a 1.0% antioxidant solution, were $5.38 \pm 0.98\%$. At the same time, altered anaphases increased to 5.58 ± 1.04 percent in preparations obtained from seed roots kept in the EMW medium for 10 minutes. Finally, we determined that the altered anaphases in seed roots exposed to EMW for 15 minutes and then treated with antioxidants were 6.64 ± 1.19 percent.

The frequency of chromosomal changes in seed roots exposed to EMW at a dose of 50 MHz, but not treated with an antioxidant, in the control variant was $7.62 \pm 1.17\%$. However, the frequency of chromosomal changes in seed roots, first treated with an antioxidant and then exposed to EMW for 5 minutes, decreased to $4.51 \pm 0.94\%$. Our results showed that the treatment of dry wheat seeds with an antioxidant of a certain exposure and dose before exposure to EMW shows the best antimutagenic effect. It was found that 0.1% concentration of the antioxidant has a higher antimutagenic effect.

COMPARATIVE PROMOTER ANALYSIS OF PROTEIN GENES IN POMEGRANATE VARIETIES

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Keywords: Punica granatum L.; architecture of promoters; Head-to-Head gene; bidirectional promoters.

To date, the nuclear genomes of thousands of different organisms, in particular over 180 garden plants have been sequenced and annotated. Large differences in the genome sizes of different species and the number of annotated genes were found, and this is considered natural. However, according to these indicators, it seems surprising that there are sharp differences between the varieties of the same species. Existing annotations of various plant genomes contain large gaps in the structure of genomes and in the structure of genes encoded by them, elements that control genome expression, as well as in the architecture of promoters, which are key "players" in the regulation of transcription [Shahmuradov *et al.*, 2017].

In this study, potential promoter maps of the promoters of annotated protein genes in the nuclear genomes of three varieties (Guloysha, Dabenzi and Tunisia) of pomegranate (*Punica granatum* L.) species were identified and compared. Nearly hundreds of neighboring Head-to-Head gene pairs with potential bidirectional promoters between them has been found [Dhadi *et al.*, 2009]. For the first time, some common and distinctive features of these pomegranate varieties were identified. Based on the results of comparative analysis, it has been hypothesized that Guloysha and Tuni-

sia are closer to each other among the three varieties of pomegranate. The results obtained are of practical importance both in terms of improving the annotation of the nuclear genomes of the pomegranate variety Guloysha, Dabenzi and Tunisia, and for elucidating the architecture of promoters, one of the main regulators of pomegranate genome expression, and their application in practice.

GENETIC DIVERSITY FOR MORPHOLOGICAL TRAITS, ISSR MARKERS AND ANTHRACNOSE RESISTANCE GENES IN COMMON BEAN COLLECTION

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Keywords: common bean; anthracnose; ISSR; resistance; genetic diversity.

Common bean (*Phaseolus vulgaris* L.) is one of the most important legume crops for human consumption with high nutritional value and taste quality [Gonçalves-Vidigal et al., 2013]. Biomorphological traits, genetic diversity and anthracnose (C. lindemuthianum) resistance of 37 local and introduced common bean accessions were studied using molecular marker technology to identify promising donor materials for breeding programs. There was considerable variation among genotypes for all studied traits, 8 genotypes distinguished with high productivity were selected. In our study, productivity per 1 m² was shown to depend only on the plant height and the number of pods per plant. The number of pods per plant accounted for 17% of the variance and was the main factor affecting yield per 1m² as a result of the regression analysis. Cluster analysis could classify genotypes according to their productivity. A total of 39 bands were amplified using 5 ISSR primers in 37 common bean accessions, of which 13 were polymorphic. The averages for polymorphism rate, genetic diversity coefficient and PIC in the whole collection were 33%, 0.56 and 0.36, respectively. UBC828 has been found to be more informative in determining genetic diversity in common bean collection. Accessions were scattered on the PCoA plot; the first axis explained 36.1% of the variation, while the first three accounted for 56%, and the first five for 68.7% of the variation. Polymorphism was also noted for anthracnose resistance genes in common bean genotypes. Molecular marker analysis showed that the coupling marker OAS13 for the Co-4² gene was present in a majority of accessions. However, SCAR markers SZ04₅₆₇ and SZ20₈₄₅ [Queiroz *et al.*, 2004] linked with the *Co-6* gene were only present in eleven and four genotypes, respectively. In total *Co-6*, providing resistance to 23, 31, 69, 453 (61) 73, 81, 89 and 64 (21) races of the pathogen, was found in 40.5% of studied *Ph. vulgaris* genotypes. Breeders can accelerate the creation of new productive and resistant varieties suitable for local agro-climatic conditions by selecting accessions with the desired loci, low genetic similarity and positive biomorphological traits, such as in K-13044, K-13038, AzePHA-36, as well as can directly use them on farms and breeding programs as donors of valuable genes and traits. In addition, a low diversity in common bean accessions of Mesoamerican gene pool for ISSR loci can be increased by including Andean genotypes in breeding programs.

COMPARATIVE ANALYSIS OF MEIOSIS IN DIFFERENT WHEAT-ALIEN SPECIES DERIVATIVES

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Keywords: wheat-alien hybrids; Triticeae tribe; genetic diversity; meiosis; meiotic irregularities.

Hordeum, Secale, Aegilops, Thinopyrum (syn. Agropyron) and other alien species belonging to the *Triticeae* tribe have large genetic diversity and serve as a valuable genetic reservoir for wheat improvement. Many of these species have been used for more than a century for the production of wheat × alien hybrids and introgression lines [Molnár-Láng et al., 2014; Kai et al., 2021]. The study of wheat-alien lines is of great theoretical interest for elucidating the evolutionary relationships between chromosomes, including the study of the degree of homology of wheat chromosomes and genomes to those of other cereal species [Efremova et al., 2018]. Meiotic pairing regularization ensures a high degree of fertility of new allopolyploids, whose genomic integrity may persist through generations [Blasio et al., 2022]. The study of meiosis in the hybrids provides a valuable method for estimating the level of genetic transfer and recombination between the chromosomes of cultivated and wild species [Fernandez-Calvin et al., 1994]. The aim of our study was the comparative analysis of meiosis in totally 10 wheat-alien accessions (2 Elymus-wheat, 3 Hordeum-wheat and 5 wheat - Agropyron species derivatives) obtained from scientific centers (WGGRC, CIMMYT, IAS and IPK) of different countries (USA, Mexico, Spain and Germany) and during the several years reproduced in the conditions of Absheron (Azerbaijan). Meiotic irregularities observed in all wheatalien species derivatives were chromosome luggages in anaphase I and II (recorded for 2 *Elymus*-wheat, 2 *Hordeum*-wheat and 2 wheat - *Agropyron* species derivatives), chromosome bridges in anaphase I (noticed in 2 *Hordeum*-wheat and 3 wheat - *Agropyron* species derivatives) and micronuclei in anaphase I and II (revealed for 2 *Elymus*-wheat species derivatives). The main chromosomal configurations at metaphase I for all wheatalien species derivatives were bivalents, quadrivalent and trivalent chromosomal configurations at late diakinesis and early metaphase I were observed in 2 wheat - *Agropyron* species derivatives - *T. aestivum / Ag. ponticum* and *T. aestivum / Ag. intermedium*. Results indicated that meiotic irregularities were characteristic for all of the studied wheat-alien species derivatives.

PROTEIN CODING CAPACITY OF HUMAN GENOME

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Keywords: long noncoding RNA; open reading frame (ORF); CAP-dependent scanning mechanism.

When the first variants of the human genome were presented to the scientific community in 2001 [International Human Genome Sequencing Consortium, 2001; Venter *et al.*, 2001], it was not known how many genes we had. It was thought to be found out soon. Although twenty years have passed, since 2000, the questions "How many genes do we have?" and "How many different proteins are synthesized in our cells?" are unanswered. An alternative splicing, altogether with an alternative initiation and termination of transcription, can generate many different transcripts and proteins from the same eukaryotic gene. Moreover, introns and long noncoding RNAs can also contain protein genes. The initiation points for the synthesis of most eukaryotic proteins are determined by a CAP-dependent scanning mechanism located at the beginning of the mRNAs and near the CAP. However, due to the Internal Ribosome Entry Sites (IRES), translation can also begin at points of mRNAs far from the CAP.

To explore the protein coding capacity of human genome, in 106143 known mRNAs collected in human GENCODE resources (https://www.gencodegenes.org/pages/gencode.html), we performed a search for additional (unknown) potential open reading frames (ORFs) encoding polypeptides composed of at least 200 amino acids. The search revealed 1896 novel ORFs/proteins capable of encoding polypeptides different from known human proteins. A comparison of these putative proteins with known protein sets in mice and rats, as well as with 477,985 proteins in Swiss-Prot resources, showed that the absolute majority of 1896 "novel" proteins (about 1800) could be classified as "unknown proteins". These results suggest that the human genome is capable of encode many unknown proteins not presented in our current proteome annotated.

MOLECULAR AND GENETIC MECHANISMS EFFECT OF NANOGRAPHENE-NEURO-PEPTIDE-OLEOCANTHAL (NONA) FOR INHIBITION OF ALZHEIMER IN RAT MODEL

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Keywords: Alzheimer; oleocanthal; gene expression; rat.

Alzheimer disease (AD) is one of the most comman human health problems. AD is a complex progressive neurodegenerative disorder affecting humans mainly through the deposition of amyloid-beta and accumulations on the neurons of the hippocampus and cortex of the brain. Oleocanthal from olive oil has anti-inflammatory, anti-cardiovascular, anti-malignancy, and anti-AD characteristics. The main problem with Alzheimer's is that the drug is not delivered to the brain due to a blood-brain barrier. A neuropeptide isolated from scorpion venom easily crosses the blood-brain border. This study investigates histopathology and network expression of genes affecting Alzheimer's changes.

In this study, a nanocomposite of graphene dot was synthesized with the hydrothermal method, and oleocanthal and scorpion neuropeptide were banded to that particle with the shaking process, and synthesis of nanographene dot oleocanthal–neuropeptide (NONP) were

tested by FT-IR, XRD, VSM, SEM, EDX and TEM methods. The male rats were injected with nano-manganese-Alzheimer's injection. In this research, 30 rat with an average weighted 250 g were divided into three groups: control group, Alzheimer's group, and Alzheimer's group treated with NONP (treatment group). When Alzheimer's state was confirmed, the treatment group was treated subcutaneously with a standardized extract of NONP (3 mg per 1 cc) with three doses 2 cc, 1 cc, and 0.5 cc daily for a week. After the 10 days of the treatment, the rats received behavior tests to evaluate treatment effectiveness in MRI scanning results, hematoxylin-eosin histochemistry staining, and expression of AD-related genes.

Treatment with 30 mg NONP per kg body weight improved amnesia behavior, histopathological images, and MRI scans. Also, the expression of genes of the apolipoprotein pathway (*APOE*, *APO*), secretase *ABCA1*, *ABCA7*, *SORL1*, and *MPO* had changed significantly (P<0.01).

Scorpion neuropeptides can transport substances to the brain through the blood-brain barrier by the mechanism of blocking sodium and potassium channels. Oleocanthal had amyloid beta clearance potential in the neuron. These findings provide experimental support that the potentially reduced risk of AD associated with NONA could be mediated by the enhancement of A β clearance from the brain.

GENETIC VARIANTS OF THE SPECTRUM OF α - AND β -GLOBIN CLUSTERS IN PATIENTS WITH HEMOGLOBINOPATHY IN THE REPUBLIC OF AZERBAIJAN

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Keywords: hemoglobinopathies; thalassemia; mutation, deletions, genetics.

Hemoglobinopathies are the most common autosomal recessive monogenic disorders worldwide. Among them, thalassemias are distinguished, caused by a violation of the synthesis of polypeptide chains that make up normal hemoglobins, and abnormal hemoglobins, caused by violations of the primary structure of hemoglobin [Goss *et al.*, 2014]. According to WHO, from 300,000 to 500,000 homozygous carriers of this pathology are born annually, of which most are sickle cell disease caused by abnormal hemoglobin S (*HbS*) [Rumyantsev, 2015].

It has been proven that hemoglobinopathies are region-specific disorders; each population has its own characteristic spectrum of genetic variants. In Azerbaijan, the disease is spread mainly in the southern regions of the republic, but due to migration of the population and an increase in the number of mixed marriages, the frequency of β -thalassemia in a heterozygous state among various nationalities inhabiting the country is about 1%.

The main cause of β-thalassemia is point mutations in the promoter region, coding sequence, splicing sites and polyadenylated sites of the HBB gene located on the short arm of the 11th chromosome, leading to splicing disorders, reading frame shift or the formation of a premature termination codon. Longer deletions involving the genes of the β-globin cluster and βLRS (long-read sequencing) regulatory sequences occur with a lower frequency. The most common cause of α thalassemia is extended deletions affecting one or both of the a-globin genes (HBA1, HBA2) located on the short arm of the 16th chromosome. The material for the study was collected from 82 residents of the northern regions of Azerbaijan (which make up the Siyazan, Shabran, Guba, Gusar and Khachmas regions) in 2021. Patients were aged 2 to 15 years, in whom, according to the results of a consultation with a hematologist, hemoglobinopathy was suspected. The legal representatives of all patients signed a voluntary informed consent to conduct a molecular genetic study of α - and β -globin clusters. EDTA tubes were used to collect whole blood samples. The DNA extraction procedure from the samples was carried out using the AmpliPrime DNA-sorb B commercial reagent kit at the genetic laboratory of the Republican Diagnostic Center according to the manufacturer's instructions.

Fifty-six genetic variants were found, of which 62.5% (n = 35) lead to b-thalassemia, and to the occurrence of abnormal *HbS*. All these variants, according to the latest data, have a very high prevalence in Azerbaijan (31%, 9%, 34%, 39% and 7%), respectively. Among all the republics of the former USSR, Azerbaijan was recognized as the most endemic in terms of the spread of hemoglobinopathies. The results of a study of the molecular spectrum of genetic disorders of the globin cluster will optimize the provision of not only specialized assistance by the hematological service, but also medical genetic consultations in the region.

STUDY OF THE SIGNIFICANCE OF DIFFERENT TRAITS IN CHICKPEA (CICER ARIETINUM L.) GENOTYPES

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Keywords: chickpea; productivity; PCA.

Chickpea, used as food in our country and cultivated since ancient times, is rich in carbohydrates, proteins, and essential amino acids [Amirov *et al.*, 2016]. After wheat, barley, and corn, chickpea is very important in ensuring food security in the country. It is used not only as food but also as a precursor in crop rotation [Mirzayev, 2019]. At present, creating new high-quality varieties of chickpea is one of the urgent issues.

Biomorphological and economic indicators were studied in 76 chickpea genotypes. The studied samples are of ICARDA origin. Productivity indicators in the samples were conducted at the Genetic Resources Institute, technological analyzes, like the cooking time [Williams, 1988] and the ratio of the shell to the kernel [Sayar *et.al.*, 2017] were carried out at the Agricultural Research Institute. Statistical analysis was performed with the SPSS statistical computer program. The Principal Component Analysis (PCA) was used to study the significance of different traits in genotypes. This analysis showed high variability between different groups and within each group [Table 1]. According to our results, the sum of the variation of 6 components was 74.88%. The first three PCs, which accounted for 48.379% of the observed variability, were 19.97%, 15.19%, and 13.22%, respectively. The number of beans, productivity per plant, and productivity per 1m² of the field were evaluated based on these components (PC1, PC2, and PC3).

Table 1. Results of the PCA

	Components					
	1	2	3	4	5	6
NBP	0.821	-0.123		-0.367	-0.101	0.104
PP	0.775			-0.409		0.272
SMP	0.676	-0.126	-0.292	0.176	0.300	0.217
PH	0.647	0.534		0.369		
BW		0.778	0.122	-0.235	-0.117	
BL	-0.122	0.556			-0.438	
CT			0.902	0.131		
KSR	0.220		0.844	0.139		-0.117
FBH	0.285	0.556	-0.150	0.661	0.227	
Total	2.795	2.127	1.851	1.409	1.279	1.022
Dispersion%	19.968	15.192	13.219	10.067	9.135	7.299
Summary%	19.968	35.160	48.379	58.446	67.582	74.880

According to PC1, the number of beans per plant (NBP), productivity per plant (PP), productivity per square meter (SMP), and plant height (PH) showed a variation of 19.968%, and the number of beans per plant was the most important indicator. Bean width (BW), bean length (BL), and the height of the first bean (FBH) varied by 15.192%, appearing as significant traits for the second factor. The most important of these traits was the width of the bean. PC3, which accounts for 13.219% of the total variation, has traits such as cooking time (CT) and kernel to shell ratio (KSR).

The genotype variation of the studied chickpea genotypes has been effectively explained in 6 indicator elements in the screen plot [Figure 1]. It showed relative stability from indicator element 7 to 8, and after indicator 8, this variation began to decline sharply. As a result, all analyses were performed based on 6 selected indicator elements. Because PCA minimizes multidimensional data, it allows the visualization of data.

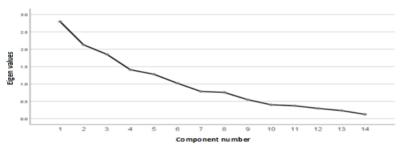


Figure 1. Screen plot of PCA

GLIADIN POLYMORPHISM IN DURUM WHEAT LANDRACES

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Keywords: electrophoresis; cluster analysis; Jaccard similarity coefficient; genetic diversity.

In this research 30 tetraploid durum wheat (*T. durum* Desf.) genotypes obtained from the Azerbaijan National Gene Bank were evaluated by A-PAGE method of Zillman and Bushuk [1978] modified by Poperelya [1989]. The research material consisted of 20 durum wheat varieties

(var.alborovinciale, var.apulicum, var.boeufii, var.hordeiforme, var.leucomelan, var.leucurum, var.melanopus, var.niloticum, var.obscurum and v.reichenbachii), and 10 released varieties (Agh bughda, Shirvan and Sharq folk varieties, and selective breeding varieties - Garagilchig 2, Tartar, Mughan, Mirbashir 50, Vugar, Barakatli 95, Shiraslan 23). During the analysis, a total of 53 different spectra and 96 patterns were identified in 4 zones (ω-, γ-, β-, and α-zones). Between them 20 different spectra (bands) and 30 different patterns were found in the ω-zone, whereas 12 spectra and 19 different patterns were revealed in the γ-zone of gliadin proteins. In ω-zone the spectrum Nº4 and in γ-zone the spectrum Nº7 were identified as high-frequency spectra, which were detected in 25 and 27 genotypes, respectively. Also spectra Nº6 and Nº1 were identified as high-frequency spectra, which were observed in 33.3% and 30% of the samples, accordingly. The lowest frequencies were revealed for spectra Nº4 and Nº9. Nei's genetic diversity index [Nei, 1973] calculated for the β-zone was 0.891.

The values of Jaccard's similarity coefficient between genotypes were determined by UPGMA cluster analysis method, and the wheat genotypes were grouped into 6 clusters. The first cluster includes four genotypes: v.obscurum, Tartar variety, v.alborovinciale and v.melanopus. In this group, v.melanopus and v.apilucum samples are connected by pattern Nº4 in the ω -zone, however Tartar and v.alborovinciale genotypes by pattern Nº2 in the γ -zone. 8 samples were grouped in the second cluster, and pattern Nº5 of the γ -zone was found in each of them.

Pattern Nº4 was detected in the β -zone of Mirbashir 50 and Garagylchig 2.

Pattern Nº15 of the γ -zone was observed in v.leucomelan (Yevlakh) and v.murciense (Saatli) accessions, which were grouped into the third cluster. Inside of this cluster v.leucomelan and v.hordeiforme samples characterized by the pattern Nº2 in the β -zone, v.apulicum (Nakhchivan), v.niloticum and v.leucomelan genotypes – by the pattern Nº13 in the β -zone. The Agh bughda landrace was located in the fourth group. This genotype was distinguished by pattern Nº4 in the γ -gliadin zone. 4 samples were grouped into the fifth cluster. Pattern Nº8 was monitored in the γ -gliadin zone in each of the samples of this group, with the exception of the V. melanopus-Gazakh genotype. Two samples: v.leucurum (Shamakhi) and Shirvan variety were grouped into the sixth cluster. The genetic distance between these samples was recorded as 0.122.

Electrophoresis of gliadin proteins confirms the high genetic diversity among the studied durum wheat samples and the significance of raw material for future breeding programs.

ASSESMENT OF DROUGHT AND SALINITY RESISTANCE OF DIFFERENT LOCAL DURUM WHEAT (*T. DURUM* DESF.) ACCESSIONS

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Keywords: high temperature; salinity; drought; resistance; durum wheat.

The aim of the study was to assess the resistance to drought, salinity and high temperature of 19 durum wheat (T.durum Desf.) samples, belonged to 14 botanical varieties by their seed germination. To determine the resistance of wheat samples to drought, heat and salinity stresses were used different methods in water, sugar solution (20 atm.), after impact of heat factor and 0.3 M saline solution, by which high-resistance, medium and low-resistance samples were selected. The heat resistance of the embryos was revealed by the ability of their seed germination after incubation during 25 minutes at the 54° C temperature in a thermostat (in water) by comparison with control.

The values of general drought tolerance index were calculated based on the formula L=2a+b, whereas L - the total drought tolerance index, a - percentage of seed germination in sucrose solution, b - percentage seed germination after impact of the heat factor [Goncharova *et al.*, 1988; Osipov *et al.*, 1980].

Among the studied accessions 8: K-26 *Niloticum,* K-19 *Obscurum,* K-60 *Hordeiforme,* K-55 *Erythromelan,* K-12 *Murciense,* K-58 *Hordeiforme,* K-33 *Mut. Lubicum, Barakatli 95 were* selected as resistant to both - drought and heat stresses. The range of the sustainability indices of these samples varied from 180 to 220.

Since 7 wheat varieties: K-1 *Mutico Leucurum*, K-55 *Erythromelan Host*, K-99 *Coerulescens*, K-15 *Mutico Provinsale*, K-59 *Leucomelan Host*, K-5 *Mutico Hordeiforme*, and K-52 *Niloticum* had different resistance to drought and heat stresses (some were resistant to drought and some others - to heat stress), they were assigned into the second group, with the range of value of the sustainability index from 128 to 175. The two accessions - K-6 *Murceiense* and K-24 *Africanum* were classified as unstable.

Inside of 19 durum wheat varieties 7 (K-18 *Aleksandrina*, K-55 *Erythromelan Host*, K-26 *Niloticum Feaks*, K-15 *Mutico Provinsale*, K-60 *Hordeiforme*, K-49 *Murciense*, and K-58 *Hordeiforme*) were resistant to salinity, whereas 6 (K-1 *Mutico Leucurum*, K-6 *Murciense*, K-24 *Africanum*, K-59 *Leucomelan*, K-62 *Mut. Aleksandrina*, K-5 *Mutico Hordeiforme*)

– unsustainable and 4 others (K-99 *Coerulescen,* K-19 *Obscurum Feaks,* K-33 *Mut. Lubicum,* K-52 *Niloticum*) were belonged to the group of medium-resistant.

In order of investigated samples 5 were detected as resistant to each of 3 stresses, which are: *Barakatli* 95, K-26 *Niloticum*, K-49 *Murciense*, K-58 *Hordeiforme* and K-60 *Hordeiforme*.

Four samples: K-5 *Erythromelan*, K-11 *Hordeiforme*, K-16 *Mut. Lubicum*, and *Barakatli* 95 were resistant to both - drought and salt stresses.

Selected high resistance samples can be planted in suitable areas and used as a donor in breeding programs in the field of resistance to drought, heat and salinity.

COMPARISON OF HUMAN AND MOUSE TYROSINE KINASE GENES

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Keywords: human; mouse, protein kinase; tyrosine kinase; promoter analysis.

Protein kinases (PK) make up the largest superfamily of eukaryotic proteins. Phosphorylation of proteins through kinases is one of the mechanisms for the regulation of intracellular signaling and cell activity. PKs are assumed to be functionally related to about 30% of all human proteins. The human PK family has at least 568 members and they constitute more than 2% of the annotated proteins in the human genome [Manning et al., 2002]. PKs transfer the phosphate group to the amino acids serine, threonine or tyrosine. Tyrosine kinases (TK) are a relatively small but very important subclass of the PK class. TKs activate or stop a number of "normal" cell functions. They are involved in the development of many forms of cancer. In the human and mouse genomes, 88 and 80 TK genes were annotated, respectively. Orthologs of the vast majority of human TK genes were found in the mouse genome. Although the structural and functional properties of tyrosine kinases have been extensively studied, many questions related to the regulation of their organization and expression in the genome, various normal processes, and diseases remain unanswered.

In this study, we performed a comparative bioinformatics analysis of promoter regions of all annotated tyrosine kinase genes of humans and mice. It was found that after the human and the mouse diverged from their

common ancestor (65-80 million years ago), the DNA sequences encoding almost all of the TK genes remained conservative, but fundamental changes took place in the promoter regions. It is thought that the main interspecific difference in TK proteins occurred in the promoter regions that control the transcription of TK genes.

EXOSOMAL NANOPARTICLES IN CANCER DRUG DELIVERY Foruzandeh Zahra

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Keywords: exosomal nanoparticles; cancer; immunotherapy.

Due to recent breakthroughs in nanotechnology, various exosomal nanoparticles have shown considerable potential in diagnostics and therapies. To fully realize nanoparticle capabilities, however, a safe, efficient, biocompatible, stable, tissue-specific, and non-immunogenic delivery mechanism is required. Exosomal natural nanoscale vesicles are cell-derived nano-sized vesicles in the size range of 30-150 nm that are implicated in intercellular communication through transmitting molecular information between cells. Recently, exosomes have been assessed for exploitation as novel drug delivery techniques due to their distinctive properties for carrying specific molecules and surface proteins. As a result, based on the therapeutic purpose, diverse kinds of exosomes can be correlated with particular drugs and employed as delivery systems to meet the demands of customized medicine. Exosomal nanoparticles have both stimulatory and suppressor activity on immune responses in cancer. As a result, they can be involved in immunotherapy procedures. They can even transport chemotherapeutic drugs directly to the target location, reducing targetability complications. Chemoimmunotherapy is a supplementary treatment approach that combines chemotherapy and immunotherapy. Exosomal nanoparticles are essential for delivering chemoimmunotherapy drugs into tumor tissues. Exosomes produced by mesenchymal stem cells (MSCs) and dendritic cells (DCs) are commonly utilized in immunotherapy, and their aid may be useful in chemoimmunotherapy for a variety of reasons. MSCs are pluripotent stem cells with self-renewal capacity originating from bone marrow, umbilical cord, pulp, fat, menstrual blood, and other sources, which they use to evoke healing process through direct recruitment into damaged tissue including the liver, kidney, heart, lung, and so on. MSC-derived exosomes upregulate the expression of the immunomodulatory molecules, such as proteins and miRNAs, implicated in the immunoregulatory axis. This study focuses on exosomes, including their biogenesis, intracellular trafficking, transportation abilities, and functions, with a particular emphasis on next-generation drug delivery mechanisms that incorporate nanoparticle size with a non-cytotoxic impact, target specificity, and a high drug-carrying capacity, driving them valuable in the therapy of a sort of disorders.

STUDY OF CROSS ABILITY BETWEEN BREAD WHEAT (T. AESTIVUM L.) AND WHEAT-RYE SUBSTITUTION LINES

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Keywords: bread wheat; substitution line; wide hybridization; cross ability; seed setting.

Improving and increasing the genetic diversity of common wheat (*Triticum aestivum* L.) is possible due to introgressive wide hybridization, leading to the transfer of beneficial traits from wild relatives to wheat. Since weedy rye (*Secale sereale* L.) is resistant to some abiotic (drought, frost, etc.) and biotic (diseases and pests) stresses, different wheat-rye substitution, addition, and translocation lines obtained from the crosses among wheat accessions and weedy rye are widely used in various breeding programs as a donor for producing both triticale and wheat-rye hybrids possessing different genomic composition.

As far as a long-term goal of this research is to enrich the genome of common wheat with useful rye genes and increase the stress resistance of common wheat, and an immediate goal is a comparative study of meiosis and fertility in newly obtained wheat-rye hybrids, hybridization was mainly carried out between common wheat and wheat-rye substitution lines. The cross ability of parental forms involved in hybridization was studied taking into account the hybrid seed set for each combination, germination ability of F_0 grains and viability of F_1 hybrid plants.

Wheat-rye substitution lines 375SD, 378/3SD, 383/1SD, 384/1D and 384/2D [Aliyeva *et al.*, 2020] were used as donors in crosses, bread wheat cultivars and lines Absheron (Azerbaijan), Rumeli (Türkiye), Bezostaya-100 (Russia), Chinese Spring (China), 171ACS, 172ACS, 626AO, TG-3, 225KX-86 – as recipients.

Seed setting success ranged from 0-67.57% in the 20 hybrid combinations studied. A total of 1424 spikelets were pollinated, and 351 hybrid grains were obtained. Thus, the success of seed setting (F_0) in the hybrid combination averaged 24.65%. Only 183 grains germinated of these, and the germina-

tion ability of hybrid grains averaged 52.14%. According to the number of hybrid plants planted in the experimental plot and completed their growing season, it was determined that the average viability of hybrid plants was quite high and amounted to 89.07%.

As a result of studying the success of seed-setting and germination abilities of seeds, as well as the viability of hybrid plants, it was found that the cross ability between the wheat-rye substitution lines and bread wheat accessions is much higher than in direct crosses between wheat and rye. So, it was considered expedient to involve hexaploid wheat-rye lines, such as 375SD, 378/3SD, 383/1SD, 384/1D and 384/2D, containing 1-6 pairs of rye chromosomes in their genomic composition, into the appropriate breeding programs.

Thus, the results of our study are of particular practical importance in future studies on the enrichment of the common wheat genome with useful rye genes.

ASSESSMENT OF SALT STRESS TOLERANCE OF DIFFERENT SOYBEAN GENOTYPES

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Keywords: soybean genotypes; salinity tolerance, germination index.

Soil salinity is one of the important stress factors that reduce plant growth and productivity. Salt stress prevents or delays germination, and disrupts a number of physiological and biochemical processes in plants.

Soybean is one of the oldest agricultural crops [Yusifov, 2020], which occupies one the main places among cereals and legumes. Soybean oil is used to make butter, margarine, confectionery, vitamin preparations, lecithin concentrates, canned food, diet drinks, dairy substitutes and other products [Hajiyev *et al.*, 2012; Humbatov *et al.*, 2016].

Soybeans have been found to be more sensitive to several abiotic stresses than some other legumes. Salinity tolerance of soybeans during the germination phase has been found to be an important factor for use in saline soils, and there is a strong correlation between environmental factors and seed germination. One of the most important issues facing soybean selection, which is currently important in agriculture, is the creation, identification and recommendation of future genotypes re-

sistant to biotic and abiotic stress factors, along with the creation of high-yielding varieties. For this reason, the main purpose of the study is to assess the resistance of geographically distant soybean genotypes to salt stress, to select tolerant genotypes and to recommend them for future selection programs.

The researches were carried out in the department of Technical and Forage Plants of the Genetic Resources Institute. Genotypes Cukurova-5, Cukurova-12, Cukurova-13 of Türkiye origin, Regale of German origin, Canada-3, Canada-4 of Canadian origin, Krasnodar-68, Umanskaya of Russian origin, Bravo of Ukrainian origin were used as research material. 10 seeds of each genotype were placed in a thermostat in 3 repeats Petri dishes, and the number of seedlings per day was calculated according to the Al-Mudarris method [Al-Mudarris, 1998]. In all studied genotypes a lower salinity rate was observed compared to controls.

According to the results of the study, in Chukurova-5 genotype the final germination percentage under control conditions was 97%, 93% at 100 mM salt concentration, 73% at 200 mM salt concentration; the final germination percentage of Chukurova-12 genotype was 83% at control, 73% at 100 mM salt concentration, 60% at 200 mM salt concentration; in Chukurova-13 genotype it was 93% under control conditions, 40% at 100 mM salt concentration, 30% at 200 mM salt concentration; final germination under control conditions in Agrovol genotype was 90%, 57% at 100 mM salt concentration, 53% at 200 mM salt concentration; final germination percentage under control conditions was 77% in Regale genotype, 63% at 100 mM salt concentration, 10% at 200 mM salt concentration; in Bravo genotype the final germination percentage under control conditions was 90%, 87% at 100 mM salinity and 47% at 200 mM salinity; in Krasnodar-68 variety the final germination rate under control conditions was 60%, 60% at 100 mM salt concentration and 20% at 200 mM salt concentration. Thus, the final germination percentage of the Chukurova-5 genotype under control conditions, as well as at 100 mM and 200 mM salt solutions, were higher than all other genotypes. The Chukurova-13 genotype had the lowest germination rates at 100 mM and 200 mM salinity and the Regale genotype at 200 mM salinity.

Another important indicator, the germination index, together characterizes the percentage and rate of germination. According to this index, the maximum price is taken for germinated seeds on the first day, and the price decreases for each subsequent day. Among the studied samples, Cukurova-5 genotype also received the highest score on the germination index [Figure 1].



Figure 1. Germination index different soybean genotypes

As a result of the analysis, the Cukurova-5 genotype of Turkish origin was selected as a perspective genotype with high performance on the studied parameter.

PHYTOPATHOLOGICAL ASSESSMENT OF GRAPE GENOTYPES ON A NATURAL BACKGROUND

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Keywords: powdery mildew; phytopathological assessment; resistant grape varieties; cluster analysis.

Grape (*Vitis vinifera* L.) is one of the most widely grown and economically important plant in the world. Currently, viticulture is a threat to the country's economy, and the quality and natural use of grape genetic resources, the creation of new productive and sustainable varieties to ensure the intensive development of this area prevents great harm.

The study of local grape varieties and forms at the molecular level, the assessment their resistance to major diseases at the field, the identification of resistance genes are of great theoretical and practical importance [Shixlinski, 2016; Kozar, 1990].

In recent years, fungal diseases in vineries have become the most important diseases, infecting vine orchards and reducing productivity and quality, especially in newly planted vineyards and seedlings. The most important disease factors limiting viticulture in the world are powdery mildew (*Erysiphe necator* syn. *Uncinula necator*) and downy mildew (*Plasmopara viticola*). Currently, about 800 pests, more than 1,000 pathogens causing fungal, bacterial, viral and mycoplasmal diseases have been registered in the grape plant.

As a result of the research, the resistance of grape varieties and forms to powdery mildew was estimated on a 5-point scale improved by I.N.Naydenova

[Nedov, 1985]. Phytopathological assessment of grape vines was carried out on a natural background. Phytopathological assessment of the infection of 100 grape varieties and forms with the main fungal disease was carried out on a natural background at the Absheron Scientific-Research Center. As a result of phytopathological assessment resistance to powdery mildew disease 11 varieties with immunity (0 points), 14 varieties high resistant (2-2.5 points), 54 varieties tolerant (medium resistant, 3-3.5 points) and 21 varieties low resistant (4-4.5 points) were detected. Very high resistant (1-1.5 points) and non-resistant (5 points) grape varieties were not determined. The immune, resistant and tolerant grape varieties are recommended to use in breeding programs to obtain pathogen-resistant genotypes.

During the study was also done cluster analysis based on the Euclidean distance index by appling UPGMA method of the PAST statistical software package. It is known that cluster analysis is one of the important methods used to reveal the similarities and differences of genotypes. Since the studied genotypes were grouped into 4 main clusters according to their indicated characteristics, the dendrogramme was analyzed by dividing the investigated grape varieties into these clusters respectively. The cluster analysis was useful in separation of the grape varieties depending of their resistance to powdery mildew.

INSIGHT INTO DATE PALM GENETIC DIVERSITY AND SEX DETERMINATION: EXPERIMENTAL AND COMPUTATIONAL APPROACHES

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Keywords: chloroplast genotyping; DNA barcode; molecular markers; Phoenix dactylifera *L.*

Date palm (*Phoenix dactylifera* L., Arecaceae) is one of the most important fruit products (more than 1.3 M tonnes, FAOSTAT, 2019) in Islamic Republic of Iran. Date palm trees are propagated by both offshoots and seeds. Up to now, our date palm cultivation has been based on traditional approaches and therefore we need to move towards modern approaches of molecular breeding and biotechnology. In present study, we used eight different nuclear DNA based markers for DNA barcoding and sex determi-

nation including IRAP, REMAP, SRAP, ISSR, SSR, EST-SSR, SCoT and SCAR as well as three chloroplast regions *rbcL*, *matK*, and *trnH-psbA* sequences. About 113 date palm trees of 13 known cultivars, cultivated in different regions of Islamic Republic of Iran were used. AMOVA for each marker revealed significant genetic difference among date palms, while it showed a higher degree of within cultivar genetic variability compared to that of among population diversity. Some degree of common shared alleles occurred between date palms cultivars. Also, gene flow and genetic admixture were observed among date palm cultivars based on STRUCTURE analysis. Heatmaps of genetic versus morphological/or agronomic characters in date palm cultivars differed from each other showing the cultivars morphological changes are not merely related to their genetic content. It points toward the potential role played either by environmental conditions or local selection practice. ILD (incongruence length difference test) heterogeneity test based on chloroplast region sequences revealed that the genes used are not homogenous and produce different evolutionary signals, and the phylogenetic trees constructed by each of these genes differ in topology. A combined data was used to produce a phylogenetic tree by SVD Quartets method, to consider evolutionary signals of all three genes together. Date palm cultivars were separated in two distinct major clades corresponding to their geographical distribution, Khuzestan province and Sistan and Baluchestan province. In regard to sex determination which is controversial issue in date palm nursery and breeding, multiple correspondence analyses (MCA) biplot also showed genetic difference within male and female trees. We introduced sex specific alleles for Islamic Republic of Iranian male date palm cultivars as a fast track in seedlings. Different association studies performed identified the candidate genetic regions which are significantly associated with sex differentiation in date palm cultivars. The present study produced some new information with regard to potential DNA barcodes for commercial date palms cultivation and threw light on the date of cultivar divergence in this area.

GENERAL SUMMARY OF THE RESEARCH ON IDENTIFICATION OF IDIOPATHIC EPILEPSY IN AZERBAIJAN

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Keywords: idiopathic epilepsy; GBD; molecular genetic analysis.

Epilepsy is a chronic brain disease characterized by repetitive motion, sensory, vegetative, cognitive or mental disorders associated with excessive neuronal irritation in the cerebral cortex. Today, the incidence of epilepsy in the world is 61.4 / 100000 (139.0 / 100000 - 48.9 / 100000) people, the prevalence rate is 7.6 / 1000 (8.75 - 5.18 / 1000 people) [Beghi, 2020]. According to the information of the World Health Organization (February 9, 2020), around 5 million people in the world are diagnosed with epilepsy each year. The figure is 49/100,000 in high-income countries, while it can be up to 139/100,000 in low and middle-income countries. The studies on the epidemiology of diseases include important information about the history of these areas. Thus, the prevalence of epilepsy in developed countries is lower than in other economically poor countries.

First of all some points need to be clarified before clinical and laboratory examination for diagnosing idiopathic epilepsy (generalized in the modern classification provided by ILEA): the period of onset of seizures, age, frequency and duration of seizures, and other noteworthy details. If a patient has symptoms before the age of 10, he or she is more likely to have idiopathic epilepsy. IGE is a common group of epilepsies, accounting for approximately 15% –20% of persons with epilepsy.

The studies conducted by GBD (Global Burden Disease) between 1990 and 2016 showed that idiopathic epilepsy (generalized by a new classification) constitutes 5.0% of all neurological diseases. Globally, idiopathic epilepsy ranks 5th place among neurological diseases after stroke, migraine, dementia and meningitis. DisMod-MR 2.1, which can perform an improved Bayesian meta-analysis for GBD during the research, was used. Due to a systematic study, the data obtained from 89 unique data sources reporting about epilepsy rates caused by genetic or unexplained reasons 18 out of 21 regions of the world were abled to obtain predictions of idiopathic epilepsy rates by location and year using a linear-mixed model. In these reports covering 195 countries and territories, the indicator for Azerbaijan and neighboring countries was

as follows: Russia - 8.7%, Armenia - 7.4%, Azerbaijan - 25.5%, Georgia - 4.5%, Islamic Republic of Iran - 18.1%, Türkiye – 18.4%.

The first research on the epidemiology of epilepsy in Azerbaijan covered the city of Baku, and as a result, it was identified that 'the disease is 2.8 per 1,000, and 2.0 per 1,000 in rural areas' [Rahimov, 1986]. Then, in 2013, epidemiological indicators of epilepsy were studied at the 'national level', which covered children aged 0-14 years, therefore epilepsy was 6.7 per 100,000 children and the prevalence was 1.3 per 1,000 children in 2004 [Ahmedov, 2013].

Currently, the existing results on the diagnosis and simultaneous etiology of epilepsy in Azerbaijan are possible through EEG and MRI which makes it difficult to study the disease from a genetic point of view. The research conducted recently has been relatively effective. Thus, as a result of molecular genetic analysis it was found out that a patient who was heterozygous for the *CHRNA2* gene was homozygous or compound heterozygous for the *KCTD7 gene*. Using a set of modern molecular genetic methods, a missense mutation of the *SPTAN1* gene was identified in a 9-month-old child diagnosed with early epileptic encephalopathy (*SPTAN1*, 2908G>A) [Nasibova *et al.*, 2020]. Also for the first time, five mutations of the *CFTR* gene were identified: Phe508del, 965 (T>C), 1000 (G>T), 1210-1211 (T>G), and 328 (G>C) [Huseynova *et al.*, 2020].

STUDY OF LOCAL AND INTRODUCED LENTIL SAMPLES USING ISSR MOLECULAR MARKERS

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Keywords: Lens culinaris Medik; genetic parameters; Jaccard similarity index; PCR; cluster analysis.

The study revealed the polymorphism among local and introduced lentil genotypes using ISSR markers.

56 polymorphic amplicons were recorded as the result of PCR analysis in 33 lentil genotypes conducted using 10 ISSR primers. UBC 873 (10 amplicons) and UBC 112 (10 amplicons) primers have demonstrated the highest number of amplicons; the lowest number of amplicons were detected by

UBC 827 and UBC 854 primers (4 amplicons by each). The average number of amplicons was 6.9 (per primer).

The GD (genetic diversity) mean was 0.82. High genetic diversity was determined by UBC 854 (0.97) and UBC 811 (0.94) primers, whereas low genetic diversity - by UBC 873 (0.66) primers.

EMR (Effective Multiplex Ratio) and MI (Marker Index) values varied between 6.45-11.34 and 1.28-3.41, respectively. The highest value of the marker index (3.41) was observed with the UBC 873 primer, producing 10 bands and the lowest value (1.68) by the UBC 827 primer, producing 4 bands. GDI (genetic diversity index) and PIC (polymorphism information content) values among these samples were 0.82 and 0.74, respectively.

A cluster analysis of the lentil genotypes was performed using the SPSS software [Nie *et al.*, 1968], at that values of Jaccard similarity index [Gilbert, 1884] ranged from 0.21 to 0.93.

The 33 studied lentil genotypes were grouped into 5 different clusters. Four of the 7 samples grouped into the first cluster were introduced from ICARDA, and 3 samples were of Azerbaijani origin. The minimum and maximum GSI (genetic similarity index) values among these samples were 0.19 and 0.95, respectively.

Flip2011-13 and ILC-10940 were the closest genotypes (GDI=0.95), whereas Flip2011-43 and ILC-10946 (GDI=0.19) were the furthest genotypes in the first cluster. The values of genetic similarity coefficient among the 7 samples included into the second cluster were 0.21-0.64. Flip 2011-18, Flip 2011-19 and Flip 2010-101 samples were grouped at close genetic distance from each other. The ILC-10933 (ICARDA) is located at a distance from other samples in this cluster.

The third cluster also consists of 7 samples; the minimum and maximum similarity index values of ILC-10925 grouped in this group with other samples (ICARDA) were calculated as 0.24-0.58.

5 samples were grouped into the fourth cluster. GSI values among these samples were 0.34-0.67. 3 of these samples were introduced from ICARDA.

7 samples were grouped into the fifth cluster. The highest value of GDI (0.76) was recorded between ILC-43 and ILC-26 samples.

Flip2011-51 (ICARDA) and ILC 10946 were the most distant genotypes, and the genetic similarity index value was recorded as 0.11.

Thus, UBC-873, UBC-810, UBC-809, UBC-827, UBC-811, UBC-112, UBC-864 and UBC 859 ISSR primers were considered to be suitable for the study of genetic polymorphism in lentils.

The crossing of genetically divergent forms with positive economic indicators selected from the collection, allows obtaining important hybrids for breeding.

MAIN TRENDS IN THE GENETIC FACTOR OF MALE INFERTILITY Babayev Medjnun, Mammadova Rena, Mardomi Farid

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Keywords: male infertility; spermatozoa; diagnostics; genes; mutation.

Male infertility (MI) is a serious pathological condition that requires complex comprehensive diagnostics, urgent correction, and in some cases prevention. Frequent causes of male infertility are violations of the structure and quantity of spermatozoa, affecting their mobility and ability to fertilize. The main genetic causes of MI development are: 1) deletions (removal of genetic fragments) of the *AZF* locus; 2) polymorphism (an increase in repeats of a genetic fragment - CAG) of the *AR* gene; 3) mutations (violation of the sequence) of the *CFTR* gene. Currently, these markers are an integral part of the standard criteria for the complex diagnosis of the genetic manifestations of MI, occurring in a group of patients in 10-15% of cases [Kumar *et al.*, 2015].

An important role in the development of pathologies such as oligozoospermia and azoospermia is played by deviations in a specific region of the Y chromosome - the *AZF* locus (azoospermia factor). The genes included in it determine the normal course of spermatogenesis, and if the genetic structure of the AZF locus is disturbed, the formation of male germ cells can be seriously impaired. The *AZF* locus is located on the long arm of the Y chromosome (Yq11). Genes located at this locus play an important role in the process of spermatogenesis [Dabaja and Schlegel, 2014]

An important role in the development of pathologies such as oligozoospermia and azoospermia is played by deviations in a specific region of the Y chromosome - the *AZF* locus (azoospermia factor). The genes included in it determine the normal course of spermatogenesis, and if the genetic structure of the AZF locus is disturbed, the formation of male germ cells can be seriously impaired. The *AZF* locus is located on the long arm of the Y chromosome (Yq11). Genes located at this locus play an important role in the process of spermatogenesis [Dabaja and Schlegel, 2014].

The *AZF* locus is divided into 3 regions: AZFa, AZFb, and AZFc. In each of them, genes involved in the control of spermatogenesis have been identified. Deletions at the *AZF* locus can be complete; completely removing one or more of the AZF regions, and partial, when they do not completely capture any of its three regions. Almost all patients with deletions of AZFb or AZFb+c have azoospermia due to severe disorders of spermatogenesis (Sertoli cell-only syndrome). The *SRY* (Sex-determining Region Y) gene is especially important in the genetic control of male-type development. In the absence of a chromosome region containing the SRY gene, the phenotype will be female with a male 46, XY karyotype. This genetic study includes the analysis of the *AZF* locus of the chromosome - 13 clinically significant deletions: sY86, sY84, sY615, sY127, sY134, sY142, sY1197, sY254, sY255, sY1291, sY1125, sY1206, sY242, as well as the determination of the *SRY* gene deletion [Radchenko, 2012].

Another determining factor in male infertility is a violation of the hormonal regulation of spermatogenesis, in which the male sex hormones androgens play a key role. They interact with specific androgen receptors, determining the development of male sexual characteristics and activating spermatogenesis. In men with cystic fibrosis, the vas deferens are most often absent or blocked by thick mucus. At the same time, the disease does not disrupt the production of sex hormones and the function of the sex glands. Sexual development is normal, although it can be slowed down due to lung disease and poor digestion.

Thus, the analysis of the literature data indicates that in our time the diagnosis of male infertility is at a high level and there are many modern, high-tech ways of diagnosis and therapy.

SYNTHESIS OF NANO-GRAPHENE OLEUROPEIN SHUTTLE DRUG AND EFFECTS ON THE ABCA1 AND ABCA7 EXPRESSION ALZHEIMER

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Keywords: Alzheimer's; mouse model; manganese; nano-graphene oleuropein; gene expression.

Alzheimer's is a very important and common progressive neurological disease that is at the top of global health programs. The disease is caused by the formation of amyloid plaques and hyperphosphorylation of

TAO protein. So far, many genes, including the *ABCA7/1* genes, have been reported in Alzheimer's. The identification of medicinal plants and their important compounds, including oleuropein in olives, to control dementia has doubled the importance of the issue.

The aim of this study was to investigate the effect of olive-derived oleuropein and its transfer to the hippocampus of the brain and to produce a shuttle drag based on a nanographene dot magnet and a peptide in scorpion venom (*Centruroides margaritatus*) called margatoxin and to investigate its effects at the molecular level.

In this study, 32 rats were purchased from Tehran Pasteur Institute and produced Alzheimer's model mice using nano-manganese powder. By MRI test, histopathology was confirmed by hematoxylin and eosin and behavioral test. Nanorophene dot oleuropein magnet was synthesized by hydrothermal and shaker methods. Eleuropine, graphene dot and nanographene dot oleuropein magnet were injected subcutaneously at different doses. The brain hippocampus was then sampled and in addition to behavioral testing and histopathology, ABCA1/7 genes were measured by real-time PCR.

Different doses of oleuropein and nano-oleuropein dot magnetic were increased in terms of behavioral test and histopathological results as well as expression of *ABCA7/1* genes in the use of treatments compared to the Alzheimer's group. The expression level of *ABCA1/7* genes in Alzheimer's disease can be a good marker for predicting Alzheimer's. MRI and histopathology (hematoxylin-eosin staining) and behavioral testing confirmed the presence of Alzheimer's. Applications of treatments to improve Alzheimer's symptoms were significant in ANOVA test. The most symptoms of improvement were seen in the use of nano-oleuropein dot magnet cc1 and the eosinization of nerve cells was minimized in these treatments. In these treatments, a significant increase in the expression of *ABCA1/7* genes was observed. In general, treatment with oleuropein and nano-oleuropein dot magnetism reduced Alzheimer's symptoms.

The results of experiments related to the effect of different doses of nano-oleuropein margatoxin showed that there was a significant difference between the different doses in terms of histopathological results, behavioral test and expression of ABCA1/7 genes (P<0.01). Thus, the rate of forgetfulness index in behavioral testing and accumulation in hippocampal neurons decreased with increasing nano-oleuropein, while the expression level of ABCA1/7 genes increased. Therefore, with the use of nano-oleuropein margatoxin, Alzheimer's symptoms and its molecular indices were improved.

APPLICATION OF ISSR MARKERS FOR ESTIMATION OF GENETIC DIVERSITY IN DURUM WHEAT

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Genetic erosion or loss of genetic diversity of crops is one of the global problems of agriculture nowadays. Different methods are currently used for evaluation of genetic polymorphism in plants including various types of markers (morphological, molecular, etc.). Molecular

Keywords: genetic erosion; DNA extraction; molecular markers; polymorphism.

markers are powerful tools in assessment of biodiversity, identification of promising cultivars, quantitative trait loci (QTL) mapping, etc [Anne, 2006]. Different PCR based dominant markers such as ISSR, SCoT, SRAP, etc. have been effectively used for quantification of genetic diversity in different plants [Reddy *et al.*, 2002].

In the present study, ten ISSR markers (UBC-821, UBC-824, UBC-826, UBC-829, UBC-840, UBC-841, UBC-842, UBC-862, UBC-880, and UBC-881) have been employed for analysis of genetic diversity in fifty *Triticum durum* Desf. accessions provided by National Gene Bank. DNA extraction was performed according to the CTAB method with modifications [Doyle and Doyle, 1987]. Purity and quality of DNA specimens were examined on a NanoDrop spectrophotometer. The reproducibility of the ISSR amplifications was assessed using selected primers with different DNA samples isolated independently from the same cultivar and amplified at different times. Under the optimized PCR conditions, the banding profiles were consistent among PCR experiments. Amplification products were separated by electrophoresis in 2% agarose gel, stained with 0.05% ethidium bromide solution, and visualized in UV light using the Bio-Rad gel documentation system.

The bands produced by different ISSR markers following amplification were analyzed and scored as present (1) or absent (0) in agarose gels and entered into a binary matrix representing the ISSR profile of each accession. After examining the banding patterns produced by different ISSR primers, total number of bands, number of polymorphic bands and percentage of polymorphism were determined. Ten ISSR primers used generated 110 loci with an average of 11 loci per primer. The number of polymorphic loci was 100; this comprises 90.9 % of the total number of amplified loci. The percentage of polymorphism ranged from 72.72% (UBC-829) to 100% (UBC-821, UBC-824, UBC-826, UBC-840) with an average of

91.6% polymorphism per primer. Among ISSR markers used in the present study, UBC-862 and UBC-880 have produced the highest total number of bands and the highest number of polymorphic bands.

Examination of the results allows to conclude that the markers generated by the primers UBC-821, UBC-824, UBC-826, UBC-829, UBC-840, UBC-841, UBC-842, UBC-862, UBC-880, UBC-881 are highly efficient for evaluation of genetic diversity in durum wheat.

ANTIMUTAGENIC EFFECT OF AN ANTIOXIDANT ON THE ROOTS OF WHEAT AND ONION SEEDS AT VARIOUS PERIODS OF STORAGE IN OZONE

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Keywords: ozone; antioxidant; wheat; onion; mutagenesis.

In recent years, ozonized air has been increasingly used in various fields of agriculture. Many modern technologies are based on the use of ozone. And this is no coincidence; ozone has many properties, the use of which allows us to solve various problems. It is known from the literature that the normal amount of ozone in the air is 0.01-0.02 mln⁻¹, or 10⁻⁶-2x10⁻⁶%, which is sufficient to initiate *in vitro* autoxidation of unsaturated fatty acids (UFAs) [Bakhshalieva, 2010]. The amount of ozone that accumulates in the air during combustion causes great biological damage to living organisms. This also includes chromosome breaks, which are most likely caused by radiation. To this end, were set the task to study the effect of a 0.1% antioxidant solution on the frequency of chromosomal changes in the wheat roots and onion seeds with different shelf life in the ozone environment.

Seeds of soft wheat of the "Champion" variety (*Triticum aestivum* L.) and onion (*Allium fistulozum* L.) were used as an object, (2E,4E)-1-(2-hydroxyphenyl)-5-phenylpenta-2,4-diene-1-OH - as an antioxidant. The seeds of both objects were kept in ozone for 5, 10, 15, 30, 45, and 60 minutes. In the control variant, the seeds were soaked only with distilled water and germinated. Roots of wheat seeds were fixed when they reached 0.6-0.8 cm (first mitosis) and temporary preparations were made from them. Chromosomal changes were determined by the anaphase method. The frequency of spontaneous mutations in the roots of wheat seeds was $3.10 \pm 0.81\%$, in the roots of onion seeds - $2.77 \pm$

0.64%. However, as the time spent in the ozone layer increases, the frequency of chromosome aberrations also changed. In wheat germ roots (5, 10, 15, 30, 45 and 60 minutes), this indicator was 3.78 ± 0.85 ; 3.84 ± 0.82 ; 4.65 ± 1.04 ; 4.03 ± 0.97 ; 5.09 ± 1.05 ; and 6.38 ± 1.26 percent. In the roots of onion seeds it was 3.68 ± 0.76 ; 3.95 ± 0.80 ; 4.93 ± 0.97 ; 5.36 ± 1.04 ; 6.11 ± 1.10 and 7.40 ± 1.32 percent. However, in the seed roots treated with a 0.1% antioxidant solution, these indicators decreased by almost 1.5-2.0 times.

At the same time, we studied the effect of ozone on the laboratory germination of seeds of wheat and onion and found that with an increase in the time of storage of seeds in an ozone environment, the rate of seed germination decreases. And also, were detected that when seeds are treated with an antioxidant before storage in an ozone environment, seed germination partially increases. Thus, the frequency of chromosomal changes is significantly reduced when treated with antioxidants before storage in an ozone environment. Therefore, in studies conducted in this direction, we recommend pre-treatment of seeds with antioxidants.

Our study shows that plants have sufficient resistance to oxidative damage that occurs when a sudden change in the physiological state of the body. This is due to the existence of effective antioxidants in the plant cell, which are able to provide protection against oxygen radicals.

ANALYSIS GENETIC VARIABILITY IN OLIVE (OLEA EUROPEA L.) BASED ON ISSR AND SCOT MOLECULAR MARKERS

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Keywords: Mission; Zard; salicylic acid; somaclonal variation, PCoA plot.

Olive is one of the economically important horticultural plants throughout the world, which is also cultivated in different regions of Islamic Republic of Iran. Due to continuous artificial selection and cultivation for species desired agronomic features, olive plants in general encounter genetic erosion through the loss of genetic variability. Therefore, it is crucial to have sufficient genetic diversity within olive germplasm, which might be used in future breeding and hybridization of olive cultivars. We aimed to investigate potential genetic diversity and somaclonal variation brought

about by tissue culture of two commercially important olive cultivars namely, Zard and Mission. For this we studied the genetic structure of the mother plants and tissue culture regenerated plants by using both ISSR and SCoT molecular markers. PCoA plot of the olive plants studied based on both ISSR and SCoT data separated plants of both cultivars from each other due to differences in their genetic content. Similarly within each olive cultivar, the control plants differed from treated plants and are placed far from them. This clearly indicated that the treatment used affected the genetic structure of olive plants. In the case of Mission cultivar, the plants treated with 50 mM sodium chloride were placed closer to the control plants due to a lower degree of genetic changes as compared to the other plants. Moreover, plants treated with 100 mM sodium chloride were placed far from plants studied. Therefore, a higher dosage of sodium chloride may bring about a higher degree of genetic changes in Mission olive cultivar. The similar results were obtained with salicylic acid treatments. The economic problem of somaclonal variants in fruit crops and woody plants is high because of their long life cycles. Therefore, the identification of possible somaclonal variants at an early stage of development is critical for quality control during plant tissue culture and transgenic plant production, and for the introduction of variants [Soniya et al., 2001; Sheidai et al., 2008].

PERSPECTIVES, MORAL AND ETHICAL ISSUES OF GENETIC EDIT PERSON

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Keywords: ethics; medicine; genetics; human; editing.

The rapid development of science and technology in the 20th century has led to the fact that science and, in particular, biology and medicine have received tremendous opportunities to interfere in the existence of various biological objects, including humans. Gene modification techniques have been used for several decades and play a large role in biomedical research. New genome editing technologies allow for simple and precise modifications in a wide range of biological species [Gippenreiter, 2002].

There is widespread support for the use of these technologies to better understand the causes of diseases and their treatment; they have significant potential for research in this area and for improving human health. However, their application to human gametes or embryos raises many ethical, social and safety concerns, especially when a given genome modification can be passed on to future generations. As a result, many prominent experts around the world, and not only from the field of biomedicine, are calling for an in-depth analysis of the potential risks of genome editing and for regional discussions regarding the application of these technologies to humans.

Modern genetics has provided new opportunities for studying the activity of an organism: with the help of induced mutations, it is possible to turn off and on almost any physiological process, interrupt the biosynthesis of proteins in the cell, change morphogenesis, and stop development at a certain stage.

In recent years, the rapid development of molecular biological approaches and methods has allowed geneticists not only to decipher the genomes of many organisms, but also to design living beings with desired properties.

It is estimated that every year 7.9 million babies, 6% of all newborns in the world, are born with serious defects of genetic or partially genetic origin. To date, about 10 thousand different human diseases are known, of which more than 3 thousand are hereditary. Mutations have already been identified that are responsible for diseases such as hypertension, diabetes, certain types of blindness and deafness, and malignant tumors. Genes responsible for one of the forms of epilepsy, gigantism, etc. have been discovered. In recent years, the molecular basis of heredity has been discovered, the genetic code has been deciphered; new artificial genes are created; viruses are grown in test tubes; identical twins of frogs and sheep are created from the cells of a mature organism; human cells are fertilized in test tubes; women are transplanted with embryos [Markov, 2010].

Gene editing will become acceptable when the benefits to both individuals and society outweigh the risks. Today, both the possible risks and benefits and the levels of acceptable risk remain uncertain. From the point of view of the philosopher J. Harris (University of Manchester, UK), editing human genes is a means to make evolution "a process more rational and much faster than Darwinian evolution". At some point, he notes, humanity will have to move beyond the fragile planet and nature, and one way to do this is to improve human nature.

STUDY OF GENETIC POLYMORPHISM IN A NEW CHICKPEA COLLECTION

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Keywords: ISSR markers; Cicer arietinum L.; polymorphism.

Inter-Simple Sequence Repeat (ISSR) markers were used to determine the genetic diversity of 32 chickpea (*Cicer arietinum* L.) genotypes during the research. 10 ISSR primers produced a total of 64 fragments, 48 of which were polymorphic. The highest numbers of amplicons were observed by UBC 859 and UBC 808 primers, the lowest numbers - by primers UBC 878 and UBC 809. 78% of the bands synthesized with 10 ISSR primers were polymorphic; the highest polymorphism was recorded through UBC 827 (80%), UBC 869 (75%) and UBC 823 (75%) primers. The genetic diversity index mean ranged from 0.24 to 0.75. A cluster was constructed based on the data obtained with ISSR markers using the SPSS [Nei *et al.*, 1968] software package and the average value of Jaccard's similarity coefficient [Gilbert, 1884] for 32 chickpea genotypes was 0.46.

EMR (Effective Multiplex Ratio) and MI (Marker Index) parameters were studied to assess the discriminating ability of the ISSR marker system in the chickpea crop. EMR and MI values ranged from 3.1-5.4 and 0.43-1.69, respectively. The marker index value was higher in primers with a large number of common and polymorphic alleles; the highest value of this parameter was observed for UBC 859 (1.69) and UBC 808 (1.55), synthesized by 9 bands each, and the lowest value for the UBC 809 primer, synthesized by 3 bands.

In dendrogramme which is the graphical representation of performed cluster analysis all genotypes were grouped into 6 clusters. Cluster I was the largest one having 9 genotypes, whereas cluster II (5 genotypes), cluster III (7 genotypes), clusters IV and V (4 genotypes), and cluster VI (2 genotypes) were smaller groups. Cluster analysis identified most of the studied chickpea genotypes, and the genotypes showing 100% genetic similarity were not revealed. The minimum and maximum values of the genetic similarity index among genotypes were 0.24 and 0.87, respectively.

The average of Jaccard genetic similarity index was 0.36, so Flip 13-52c, Flip 13-53c, Flip 13-54c and Flip 13-55c, as well as F13-48 and Flip 13-50c (genetic similarity index value 0,87) were identified as the nearest genotypes. Flip13-102c and Flip 13-30c, Flip 13-64c and Flip13-

65c, Flip 13-32c and Flip 13-35c, Flip 13-67c and Flip13-74c were identified as the farthest genotypes (genetic similarity index value 0.15). Genetically distant genotypes can be used in breeding programs to achieve high yields.

Involving of Flip13-28c, Flip13-30c, Flip13-31c, Flip13-32c, Flip13-33c, Flip13-35c, Flip13-36c, Flip13-39c, Flip13-43c, Flip13-47c, Flip13-48c, Flip13- 50c, Flip13-52c, Flip13-53c, Flip13-54c with minimal genetic similarity in chickpea improvement programs will help to create varieties with favorable characteristics such as high productivity potential and maximize the parental selection during crossing.

PRODUCTION OF IN VITRO CELL APO-EXOSOME AND MEXOSOME WITH HERBAL FOR DRUG RESISTANT INHIBITION

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Keywords: apo-exosome; mexosome; cancer cell; MDR.

Cancer is the most critical health problem in human society for which no definitive cure has been found yet. Lack of targeted drug delivery to cancer cells and the adverse effect of chemical anticancer drugs on normal cells on the one hand and various reasons as well as activation and deactivation of resistance pathways and lack of specific drugs for all pathways effective in cancer cell proliferation and drug resistance (MDR), on the other hand, requires scientists to always look for methods to solve these problems. Exosomes are vesicles that leave cells at any stage of the cell cycle. It contains function RNA, mRNA, some cytoplasmic proteins and DNA, and even a double-walled cytoplasmic matrix with different contents depending on the cell growth conditions. Exosomes are easily transported into the cell through endocytosis due to the cell membrane's structure without the immune response problem. This study aimed to induce apoptosis using the active ingredients coumarin, quercetin, and oleuropein of plant origin in Wharton's jelly mesenchymal stem cells and sensitive cancer cells and collect active

exosomes. It affects the inhibition of drug-resistant cancer cells and the molecular-genetic mechanism of inhibition in exosome treatment.

First, MCF7, AGS, and HT29 cancer cells were cultured in RPMI culture medium, and mesenchymal cells were cultured from umbilical cord Wharton's jelly in DMEM culture medium. Concentrations of LC50 and LC75 of coumarin, quercetin, and oleuropein of *Melilotus officinalis* (L.) Pall., *Morus alba* L., and *Olea europaea* L. were treated for 48 hours. Exosomes were extracted from the culture medium of cells using 100,000 g by ultracentrifugation and confirmed by Western blotting and DLS. Exosomes were applied to protein-resistant MCF7, AGS, and HT29 drug-resistant cancer cells at different concentrations by Bradford protein-based concentration assay, and the rate of inhibition was estimated at 50%. At the same concentration, in addition to identifying miRNAs of exosome contents in apoptotic cancer cells (Apo-Exo), identify and express apoptotic pathway genes including *Bcl2*, *Bax*, *CASP8*, *CASP9* and *CASP3*, mTOR, and ACT, etc. The use of real-time PCR was measured.

Treatment of induced exosomes to inhibit cancer cells and mesenchymal cells could significantly inhibit drug-resistant cancer cells at LC75 concentration. Its molecular mechanism was more through induction of apoptosis through internal and external pathways. Exosomes of epithelial cell (Apo-Exosome) origin induce internal pathway apoptosis, and exosomes of mesenchymal origin (Mexosome) induce external pathway apoptosis through the death receptor.

Exosomes with apoptotic-induced contents can inhibit and induce apoptosis in resistant cancer cells, without proper response of the carrier immune system into the cells.

OPTIMIZATION OF PROTOCOLS FOR OBTAINING HAPLOID WHEAT PLANTS RESISTANT TO STEM AND LEAF RUST

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Keywords: stem and leaf rust; haploid wheat plants.

The use of doubled haploid (DH) plants has revolutionized modern plant breeding and genetic mapping studies in many important crops, especially maize, oilseed rape, sunflower, wheat, barley, rice, potato, citrus, and apple. The use of DHs may cut in half the time needed to

produce a commercial cultivar in crops such as winter wheat. Doubled haploid technology is useful in plant improvement for gene transfer and production of breeding lines, and in general biology for genome mapping and studies of chromosome behavior and phylogenetic relationships. However, when working with wheat, the yield of haploid plants from the culture of anthers and microspores is low. Optimization of protocols for obtaining haploids and diploids will speed up the process of selecting wheat hybrids based on economically valuable traits.

The aim of the study was to optimize the protocols for obtaining haploid wheat plants in the culture of anthers and microspores of 10 hybrid wheat lines carrying genes for resistance to leaf and stem rust.

5 media of various nutritional components and hormones were used in the work: modified Murashige-Skoog (MS) and Chu (N6) [Ali *et al.*, 2021], C17 [Ponitka *et al.*, 2009] and W14, P-4 mf [Pauk *et al.*, 2003]. The ears were selected at the stage of entering the tube. Cold treatment was carried out for 7-14 days. For callus formation, hormones 0.5-2.5 mg/l 2,4-D, 0.1-0.5 mg/l kinetin were added to nutrient media, MS and 190-2 medium were used for regeneration [Barakat *et al.*, 2017] with the addition of 0.5-1 mg/l of kinetin, 0.5-1 mg/l 6-BAP. Microspores were selected and cultured according to the protocol [Wang *et al.*, 2019] with modifications.

When studying 10 hybrid wheat lines for responsiveness to introduction into culture in vitro and culture of anthers and microspores, the most promising nutrient media in terms of composition turned out to be Murashige-Skoog medium with the addition of 1 mg / g of 2,4-D and 0.1 mg / l of kinetin, this medium showed the highest yield of embryoid structures, which allowed to accelerate the process of obtaining haploid plants, the average value was 0.5%-1.5%. As a medium for regeneration, the MS medium with the addition of 0.5 mg/l of kinetin and 1 mg/l of 6-BAP was also the most effective. During working with wheat microspores at the single core stage or early binuclear stage, anthers were homogenized in a mortar and microspores were purified in a maltose and mannitol gradient. Callusogenesis was observed after 5-7 weeks. Regeneration was in microspore culture on a medium with 1 mg/l of 6-BAP and 0.5 mg/l of kinetin (0.5%), except albino plants.

Thus, these protocols allow obtaining up to 2% of regenerating haploid plants, which is a fairly high indicator for wheat. The resulting haploid plants can be used as donors of resistance genes in further breeding or getting of DH lines.

EVALUATION OF MAGNETIC COUMARIN NANOCOMPOSITE SYNTHESIS AND ITS EFFECT ON APP, MS4A4E, ABCA1 GENES IN ALZHEIMER'S RATS

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Keyword: Alzimer; rat; manganese; coumarin magnetic nanocomposite.

Alzheimer's disease is a multifactorial, progressive and deadly disease and is the main form of dementia which is expressed by functional and structural disorders. Deposition of amyloid beta plaques outside neurons and accumulation of TAO protein inside neurons are the most important known factors in Alzheimer's disease. So far, several genes including *APP*, *MS4A4E*, and *ABCA1* have been reported in Alzheimer's. One of the causes of Alzheimer's disease is a decrease in acetylcholine levels in areas of the brain. A logical way to increase acetylcholine levels is to block the activity of the enzyme responsible for its metabolic breakdown. Phytochemical coumarins have biological activities, including inhibition of AChE, which will also be effective in inhibiting the formation of toxic amyloid beta deposits.

SPIONs – superparamagnetic iron oxide nanoparticles are used in the delivery of magnetic nanoparticle drugs in drug delivery. In this experiment, we encapsulated coumarin on the surface of iron oxide superparamagnetic nanoparticles, and due to the superparamagnetic properties of iron oxide nanoparticles, coumarin was transferred to the rat brain by applying an external magnetic field.

The aim of this study was to investigate the synthesis of magnetic coumarin nanocomposite and its effect on *APP*, *MS4A4E* and *ABCA1* genes at the molecular level in Alzheimer's rats.

Twenty-five male rats weighing approximately 300 g were prepared and divided into three groups: healthy, Alzheimer's and treatment. By injecting 60 mg of manganese nanopowder daily, they became Alzheimer's. Behavioral testing and MRI were used to confirm Alzheimer's disease in rats. Then, 0.5 cc, 1 cc and 2 cc coumarin and magnetic coumarin nanocomposite were treated. After sampling from the brain, part of the hippocampus for histopathological examination and eosin staining was placed in 10% formalin and another part was transferred to the laboratory for molecular tests in liquid nitrogen. A NanoDrop device was used to evaluate the RNA quantity. To assess the expression of genes, cDNA made from real-time PCR reaction was used by SYBR

Green method on the Rotor-Gene Q device. Finally, the data were analyzed using SPSS, ANOVA, Duncan and regression tests.

By injecting manganese nanopowder with Aβ deposition in the hippocampus of rats became Alzheimer's. MRI imaging, histopathology and behavioral testing confirmed that the application of coumarin and magnetic coumarin nanocomposite to improve the symptoms of Alzheimer's disease was significant in the ANOVA test, which was performed on *APP*, *ABCA1* and *MS4A4E* genes. The highest improvement in *ABCA1* gene was related to 1 cc coumarin and 2 cc magnetic nanocomarin. In the *APP* gene, the greatest improvement was in 2 cc coumarin and 2 cc magnetic nanocoumarin, and in the *MS4A4E* gene, the greatest improvement was in 1 cc coumarin and 1 cc magnetic nanocoumarin. Eosinization of nerve cells was minimized in these treatments. According to histopathological results as well as the results of molecular tests (gene expression), it can be stated that injection of coumarin and coumarin nanocomposite can significantly reduce nanomanganese-induced Alzheimer's.

NATURAL COLORED COTTON

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Keywords: Gossypium hirsutum L.; natural color spectrum of the fiber; micronaire; mean length; reflectance.

Colored cottons existed in the 3rd century B.C. in Indo-Pakistan, Egypt and Peru. Natural colors of cotton then were mocha, tan, gray, and red-brown. It was during the industrial revolution that the looms came. Since the colored cotton fibers were short, processing them on the looms became a hindrance. So the long-fibered white cotton slowly and steadily replaced them on the looms and subsequently growing white cotton became an inevitable part of agriculture and the colored cottons grew extinct for a long time [Peng *et al.*, 2020].

Recent concerns about the state of the environment and the desire to get back to all things environmentally friendly like organic farming saw a slow start and revival of the once extinct naturally colored cottons [Vreeland, 1993; 1999].

Cotton lines and varieties with colored fibers exist naturally, but the fiber quality of these varieties is extremely low and does not meet the requirements for use in the textile industry [https://www.unnatisilks.com/blog/naturally-colored-cottons-a-regain-in-popularity/].

The brown fiber AB-25, AB-51, AB-47, AB-48 genotypes belonging to the cotton collection of the Technical and Fodder Plants Department of the Genetic Resources Institute, stored in the National Gen Bank, were taken as research material.

To conduct fiber quality analysis, 10 g of pure cotton was manually separated from the seed. Then, in the Technology laboratory of the Technical and Fodder Crops Department of Genetic Resources Institute, the Statex HVI-Compact equipment was used to analyze a number of fiber parameters: Upper Half Mean Length (UHML); Micronaire (MIC); Fineness (FIN);

Fiber quality indicators of brown cotton are given in table 1. The upper half mean length indicator is lower in brown fiber cotton genotypes. In the AB-25 genotype, the upper half mean length indicator is equal to 25.9 mm. That is, the length of the fiber is of average length. Among the samples of the brown fiber variety, the highest indicator is specific to the AB-25 genotype.

Table 1. Fiber quality indicators of brown fiber genotypes

Nº	Variety examples	Upper Half Man Length (UHLM)	Micronaire (MIC), unit	Fineness (FIN), m/tex	Yield of cotton, g.	Mass of a cone, g.
1.	AB-25	25,9	5,5	208	83,4	4,2
2.	AB-51	22,4	5,2	182	69,0	3,5
3.	AB-47	24,9	5,1	171	84,5	4,2
4.	AB-48	22,2	5,4	198	99,4	5,0

The micronaire index varies in the range of 5.1-5.5. Since brown fiber varieties have a micronaire index higher than the base range, they are considered pre-fiber and unsuitable for producing high-quality products.

In the AB-25 genotype, the fineness indicator was also the maximum, equal to 208 m/tex. The lowest indicator is characteristic of the AB-47 genotype. As can be seen from the table, it is 171 m/tex.

From a plant if we look at the yield of cotton, we see that the yield is low in brown fiber varieties and varies in the range of 69.0-99.4 g. Accordingly, the mass of a cone is also low.

The obtained results show that natural colored cotton is harmless for production. However, by hybridizing white cotton with brown cotton, it is possible to create new genotypes that combine the natural color shades of the fiber and high fiber quality.

INCREASE CYTOTOXIC AND APOPTOTIC EFFECTS OF SIMVAS-TATIN-LOADED PLGA-PEG NANOPARTICLES ON MCF-7 BREAST CANCER CELLS

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Keywords: simvastatin; breast cancer; polymeric nanoparticles; leptin; apoptosis. Recently, in studies on anticancer drugs, simvastatin (SIM) has received more attention due to its anti-cancer properties, however, its molecular mechanisms are not precisely known [Hassanabad, 2019]. On the other hand, the lipophilicity feature of SIM restricted its application as a chemotherapy agent [Jamialahmadi *et al.*, 2021]. This study aimed to investigate the mechanism of action of simvastatin in inhibiting the growth and proliferation of MCF-7 cells and also to increase its efficiency through the use of poly(lactic-co-glycolic acid)–polyethylene glycol (PLGA-PEG) nanoparticles.

Dynamic Light Scattering (DLS), Field Emission Scanning Electron Microscopy (FESEM), and Fourier Transform Infrared Spectroscopy (FTIR) were used to characterize drug-loaded nanoparticles (NPs). MTT assay was used to evaluate the anti-proliferative effects of SIM-loaded NPs compared to control groups. Annexin V/propidium iodide (PI) staining was employed to detect apoptosis of MCF-7 cells and cycle analysis of drug-loaded NPs were evaluated by flow cytometry [Cao *et al.*, 2017]. The real-time PCR method was used to measure the expression of apoptotic genes, leptin (*LEP*), leptin receptor (*LEPR*) and telomerase reverse transcriptase (*hTERT*) genes [Malendowicz *et al.*, 2006].

MTT assay indicated that treatment of cells with SIM-loaded NPs decreased cell viability of MCF-7 cells in 48h compared to control groups (P<0.05) which was accompanied by an accumulation of cells in the sub-G1 phase of the cell cycle. The flow cytometry assay results indicated that SIM-loaded NPs significantly enhanced the apoptotic rates compared to control groups (P<0.05). Gene expression analysis showed up-regulation of Bax, Fas and p53 genes and also a decrease of LEP, LEPR, and hTERT genes in MCF-7 cells treated with drug-loaded NPs.

Taken together, our results suggest that one of the anticancer mechanisms of simvastatin may be due to its effect on the expression of LEP and hTERT genes, thereby limiting cell proliferation. Furthermore, these results demonstrate that PLGA-PEG NPs are an efficient delivery tool for controlling the growth of breast cancer cells.

ETHNO-TERRITORIAL DISTRIBUTION OF THE C677T OF MTHFR GENE IN THE POPULATION OF THE AZERBAIJAN REPUBLIC

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Keywords: single nucleotide polymorphism; allelic frequency; cardiovascular diseases.

The prevention of hereditary diseases associated with gen and chromosomal disorders, in particular multifactorial-polygenic diseases, is one of the actual areas of medical genotyping. It is known that there is an association between C667T *MTHFR* gene polymorphism and cardio-vascular diseases [Gupta, 2012; Yang *et al.*, 2012]. Based on this, for the first time, in the population of the Azerbaijan Republic has identified C677T mutation of the methylenetetrahydrofolate reductase (*MTHFR*) gene both in the control group and among patients with diseases of the cardiovascular system.

Control group was comprised of practically healthy individuals (60 men and 48 women) of 20 to 52 years old. Each individual has been selected empirically, without any relationship with each other. The composition of this group was multinational and corresponded to the main national and ethnic composition of the Republic; they were Azerbaijanis - 58 people (53.7%), Lezgins - 21 people (19.4%), Russians - 9 people (8.3%), Talyshs - 12 people (11.1%) and other nationalities - 8 people (7.4 %).

The 2nd group, which consisted of 72 patients (39 men, 33 women)with cardiovascular diseases (CVD), were contain 43 Azerbaijanis (59.7%), 8 Lezgins (11.1%), 6 Russians (8.3%), 9 Talyshs (12.5%) and 6 people (8.3%) with other nationalities at the age of up to 18 years old.

C677T polymorphism of the *MTHFR* gene inside of control group was identified in heterozygotic state in 24 cases: 13 cases among Azerbaijanis (22.41%), 4 cases among Lezgins (19.05%), 3 cases among Talyshs (25%), 2 cases among Russians (22.22%) and 2 cases among the representatives of other nationalities (25%).

In the group of patients with CVD this polymorphism was identified in 27 cases in heterozygotic state: in 16 cases among Azerbaijanis (37.2%), in 3 cases among Lezgins (37.5%), in 4 cases among Talyshs (44.44%), in 2 cases among Russians (33.33%) and in 2 cases among the representatives of other nationalities (33.33%). This mutation wasn't identified in homozygotic state.

Differing phenotypic frequencies of C667T polymorphism were observed in the control group, ranging from 19.05% (Lezgins - 4 out of 21 people) to 25.0% (Talyshs - 3 out of 12 people and others - 2 out of 8 people) among ethnic groups living in Azerbaijan. The frequencies of C667T mutation among Talyshs and in the group of representatives of other nationalities were the same. The frequencies of that mutation were 22.22% (2 out of 9) and 22.41% (13 out of 58) among Russians and Azerbaijanis, respectively.

The phenotypic frequency of C667T polymorphism among the patients with CVD was distributed in accordance with the increase of phenotypic frequencies in the following manner: among Russians– 2 cases out of 6 (33.33%), among the representatives of other nationalities – 2 cases out of 6 (33.33%), among Azerbaijanis – 16 cases out of 43 (37.2%), among Lezgins – 3 cases out of 8 (37.5%), among Talyshs – 4 cases out of 9 (44.44%).

Based on the results of the study, it can be concluded that the lowest frequency of C667T polymorphism of the *MTHFR* gene was identified among Russians with phenotypic frequency – 55.55%, and the highest frequency – in the group of Talyshs – 69.44%.

Thus, the distribution of identified the C667T polymorphism of the MTHFR gene inside of studied ethnic groups of Azerbaijan Republic population was uneven.

AN INFANT PATIENT WITH COINHERITANCE OF ALPHA – GENE TRIPLICATION AND IVS 1.5 G/C MUTATION OF BETA-THALASSEMIA

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Keywords: thalassemia, intermedia; beta-thalassemia; heterozygous; homozygous.

Few studies deal with the triplications of the alpha-globin gene in b-thalassemia in infants and its effect on the phenotype, which was the main objective of this study. The severity of jaundice was higher in cases of intermediate thalassemia with alpha-triplication and one of the alpha-triplication cases showed a marked increase in serum bilirubin after intercurrent disease. Patients with triplication may develop prominent jaundice with a significant increase in serum bilirubin due to pre-

vious aggravating factors [Panigrahi et al., 2005]. The IVS-I-5 ($G\rightarrow C$) substitution, a severe mutation, is the most common allele in the south of the country. This mutation, defined as "Asian/Indian" defect, is very common in a belt comprising the regions of the Indian subcontinent, the UAE (Emirates), Oman and the south of Islamic Republic of Iran [Diez-Martin et al., 1991]. Alpha-triplication can lead to a-chain, excess leading to a higher chain: b ratio. Rearrangement of the alpha-triplication may exist in two different functional forms; in one form it exacerbates the imbalance of the a : b chain, leading to a more severe presentation in b-heterozygous thalassemia [Bianco et al., 1997]. The purpose of this trial was to determine the clinical relevance of alpha-triplication in Islamic Republic of Iranian thalassemic patients. A one-year-old Islamic Republic of Iranian infant with jaundice referred to the pediatric physician. The patient had performed an electric splenectomy. In laboratory had taken from the patient CBC testing that result as seen below: RBC count=3. 24*106 mcL, Hb=8.5 mg/dL, HCT=25.5 %, MCV= 78 fL, MCH= 23.4 pg, MCHC=29.9 g/dL. Hemoglobin levels and red blood cell scores were estimated using an automated cell counter (Sysmex K-4500). In the peripheral blood smear had seen well anisocytosis, hypochromic, microcytosis, poikilocytosis RBC with target cell and 350 NRBC per 100 WBC Howell-jolly bodies well in circulating red blood cells (that's a Howell-jolly bodies are histopathologically finding of basophilic nuclear).

Patient iron profile result, according to serum ferritin = 239.6. The test for Hemoglobin electrophoresis was performed: Hb A1=92.2%, Hb A2=2.9%, Hb F=4.9. The G6PD enzyme activating was sufficient. So, the patient was diagnosed with thalassemia intermedia. In a molecular genetics study of beta – thalassemia carriers, the patient's father had a heterozygous mutation of the IVS-I-5 ($G\rightarrow C$)/wild type allele.

This study showed that coinheritance of homozygous triplicated $\alpha\text{-gene}$ with heterozygous $\beta\text{-thalassemia}$ can lead to various clinical phenotypes

INVESTIGATION OF GENOFOND TYPES OF PERSIMMON SPECIES (DIOSPYROS L.) SPREAD IN SHAKI-ZAGATALA REGION

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Keywords: persimmon varieties; pomology; maturing time; distribution.

During current research in different regions of Azerbaijan - providing expeditions to widespread persimmon sorts places and location, creations of collection were started by taking first samples, also pomology analysis was completed. The main purpose of research was to reveal different types and sorts of widespread persimmon in Shaki-Zagatala region, to define location and coordinates, and value fruits pomology properties. Special Altimeter GPS programme was used to locate the coordinates of different sorts and forms of persimmon in Shaki-Zagatala district. For research of fruit physical/mechanical properties "Program and methodology sorts variety study of fruits, berries and nuts fruits crops" [Sedova et al., 1999] were used.

Early ripen persimmon sorts mature in the first part of October, whereas medium ripen sorts - at the end of October, late sorts - at the end of November and at the beginning of December [Gu et al., 2008]. During research conducted in the area all three persimmon sorts were found. These persimmon types are oriental, common and growing in wild nature [Azizov et al., 2020]. During research it was defined that in North West region persimmon is mainly found at 200-500 meters above sea level. There are differences according to fruits pomology properties as well. Slightly rounded and elongated fruits are widely spread in that region. Fruits are mainly vellow and orange. Yellow fruits are available in Balakan region, orange are mostly in Shaki and Gakh regions and are found along the roads. In the end of research in the region persimmon sorts and forms, fruits weight, color and forms were explored and analyzed. At the same time, different sorts and forms of persimmon vary in their weights. In the research region big sized persimmon was found in Shaki region (ShG-01 - 308,7 g). Medium sized sorts and forms were mainly found in Gakh and Balakan regions, small sized fruits were found in Balakan, Gakh and Zagatala regions (BG-01-55,7 g; GSh-01- 91,7 g; ZM-02 -4,6 g). Creation of a persimmon collection and selection of varieties of genetic types will be useful for selection works on this plant.

PRENATAL DIAGNOSIS OF THALASSEMIA

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Keywords: prenatal diagnosis, thalassemia, CVS, PGD, amniocenteses, cordocentesis. The increase in the epidemic of thalassemia minor in some societies is cause to the warning of hematology and genetic scientists. Marriage between the minor genotype definitely leads to thalassemia major. Prenatal diagnosis is the best and surest way to prevent genetic diseases and is now widely practiced. Performing this operation on time prevents the birth of infants with various inherited and genetic diseases. Prenatal diagnosis technique is actually examining the condition of the fetus during pregnancy; for example, thalassemia is one of the genetic diseases that prenatal diagnosis allows to born a healthy child for couples who carry the disease genes.

Diagnosis of prenatal thalassemia syndrome is made by both invasive and non-invasive methods, fetal biopsy and various techniques to identify thalassemia mutations. With non-invasive methods such as: examination of maternal blood, examination of free fetal DNA floating in the mother's blood, etc., many suspicious cases can be detected. In invasive methods of prenatal diagnosis, it is necessary to access the embryonic specimen, such as: amniocentesis, cordocentesis, chorionic villus sampling (CVS) and examination of the embryo before implantation (preimplantation genetic diagnosis - PGD) through in vitro fertilization (IVF), which is performed in pregnancies and before pregnancy. Mutation detection methods can also be divided into direct and indirect categories. In the direct method can be used techniques, allele-specific oligonucleotide (ASO) hybridization and, amplification refractory mutation system (ARMS), to find point mutations and Gap-PCR to detect deletion, can be mentioned. And in indirect methods can be applied to techniques, Denaturing Gradient Gel Electrophoresis (DGGE) and, denaturing High-Performance Liquid Chromatography (dHPLC), to find unknown mutations by searching the whole gene, Multiplex Ligation-dependent Probe Amplification (MLPA) and, Quantitative Multiplex PCR of Short Fragments (QMPSF), to find deletions and, real-time PCR and high resolution melting curve analysis (HRM analysis), pointed to find point mutations. These techniques include both screening and diagnostic methods, and depending on the type, have their own specific sensitivity and degree, which have a great impact on the control of inherited diseases such as thalassemia, before birth.

STUDY OF NUCLEOTIDE CONTENT OF cDNAs, CDSs, 3'UTRs AND 5'UTRs IN THE GENOME OF DIFFERENT SPECIES

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Keywords: genome; cDNA; CDS; 3'UTR; 5'UTR; nucleotide.

An untranslated region (or UTR) refers to either of two sections, one on each side of a coding sequence on a strand of mRNA. Depending on their positions (5' or 3' side) around the genes they are called 5' UTR or 3' UTR, respectively. mRNAs have some regulatory codes which can define the fate of an individual mRNA in translation [Sadovskaya *et al.*,2021].

The identification of coding sequences (CDSs) is an important step in the functional annotation of genes. In genetics, complementary DNA (cDNA) is DNA synthesized from a single-stranded RNA template in a reaction catalyzed by the enzyme reverse transcriptase.

Comparative analysis of the nucleotide content of cDNAs, CDSs, 3'UTRs and 5'UTRs in the genomes of *Arabidopsis thaliana*, *Anolis carolinensis*, *Danio rerio*, *Gallus gallus*, *Mus musculus*, was studied using a bioset.org internet resource.

The amount of ACGT in the cDNA in the *Arabidopsis thaliana* genome was 237733641, of which 29% was A, 21% C, 23% G and 27% T. Nucleotides in CDS (300378035), 3'UTR (313718422) and 5'UTR (9324124706) is almost the same as in cDNA.

The cDNA of *Anolis carolinensis* was 49335708 bp, of which A28%, C23%, G23% and T26%, the total number of nucleotides in CDS was 129144116, A28%, C23%, G24% and T25%. In 3'UTR (144213099) were A29%, C22%, G23% and T26%. The nucleotides of 5'UTR are A28%, C23%, G23% and T26%.

In *Danio rerio* cDNA (426499788) nucleotide content was A29%, C21%, G23% and T27%, in CDS (129144116) - A28%, C22%, G23% and T27%. In 3'UTR (144213099) were A29%, C22%, G23% and T27%. The amount of nucleotides of 5'UTR (523554609) is A29%, C22%, G23% and T27%.

In *Gallus gallus* cDNA (565666652) nucleotide content was A28%, C22%, G24% and T26%, in CDS (592959079) - A28%, C22%, G23 % and T26%, in 3'UTR (605205374) - A28.4%, C21.8%, G23.3% and T26.5%, in 5'UTR (607496155) - A28.3%, C21.8%, G23.3% and T26.5%.

Nucleotide content of cDNA in *Mus musculus* (782781677) was A28%, C22%, G24% and T26%, in CDS (857624921) - A27.6%, C22.7%, G23.9% and T25.7%, in 3'UTR (959242634) - A27.4%, C23%, G24% and T26% and in 5'UTR (969382029) - A28.3%, C21.8%, G23.3% and T26.5%.

The analysis revealed that the total number of cDNA, CDS, 3'UTR and 5'UTR nucleotides belonging to different species were different, but the percentage of nucleotides was almost the same.

LACTIC ACID BACTERIA AND HEALTH - HOW THE MISSION IS POSSIBLE?

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Keywords: lactic acid bacteria; probiotics; anti- microbial activity; biopreservation; health.

Lactic acid bacteria (LAB) are widely accepted probiotics (Pro-for and bio-life). More and more scientific evidence for their beneficial role in gut homeostasis and progression delay of different infectious and non-communicable diseases are presented. Through the nutritional and intestinal health, they also improve oral, skin, vaginal microbiome, and overall well-being of humans. Living with recurrent Covid-19 pandemic episodes the robust defensive mechanisms of LAB are searched as a part of new therapeutic schemes or health prophylaxis. With understanding that such beneficial properties are usually strain-specific we are looking for isolation of lactobacilli from different habitats. For more than 20 years the laboratory of LAB & Probiotics (Institute of microbiology, BAS, Bulgaria) characterized LAB strains of human, dairy, and plant origin. In the present work, we summarize results from in vitro assessment of Bulgarian lactobacilli, according to the EFSA's requirements. The aim is to select candidate-probiotics LAB with high antimicrobial potential and disease-mitigating properties, promoters of gut balance and overall health.

A laboratory collection of lactobacilli, isolated from home-made dairy products (yogurt, white-brined cheeses, katak, yellow cheese), from fermented legumes and of human origin was created. With a specifically adapted protocol, their transit tolerance in conditions simulated in different parts of the gastrointestinal tract (GIT) was assessed. *In vitro* and in situ, a panel of different methods was applied to prove the antimicrobial properties and immunomodulation capacity of living cultures and/or their active post metabolites, as a key factor of robust defensive mechanism against specific pathogens [Danova, 2015].

A group of *Lactiplantibacillus plantarum* dairy isolates showed a broad spectrum of activity against Gram (+) and Gram (-) bacteria and food spoilage mycotoxins producing fungi. The impact of *L. plantarum's* and other LABs' postmetabolites with anti - Herpes simplex virus 1 (HSV1) and HSV2 activity were discussed as a factor in the prevention of these infections, or for further characterization as immunomodulators. Moreover, the high viability in stomach acidity or under bile exposure in combination with adhesion capability (on HT-29 and Caco-2 cell lines) will guarantee *in vivo* their probiotic potential. During the stable colonisation pre-selected *Limosilactobacillus fermentum*, L. *plantarum and Lacticaseibacillus rhamnosus strains* showed a protective biofilm formation with capacity of positive immunomodulation and absence of cytotoxicity.

Pre-selected LAB of human or dairy origin is candidates-probiotic strains producing a high variety of active postmetabolites. They complete EFSA's criteria for functionality, safety and technological relevance, and can act as antimicrobials and health promoters.

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BIOTECHNOLOGICAL POTENTIAL OF EDIBLE SPECIES OF XYLOTROPHIC MACROMYCETES SPREAD IN AZERBAIJAN

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Keywords: xylotrophic macromycetes; vegetative mycelium; edible fungi.

The purpose of this work is a comprehensive study of edible species of basidiomycetes belonging to the xylotrophs, widespread in Azerbaijan, depending on their species composition, frequency of occurrence, as well as the amount of fruit body (FB) in natural conditions, and is devoted to a comprehensive study of biotechnological parameters of vegetative mycelium(VM).

As a result of the research, the species composition of xylomycobit in the forests of Azerbaijan and belonging to the category of edible fungi included in the physiological-biochemical and potential both FB and VM in pure culture was determined as the biotechnology of the source of biologically active substances was evaluated from the point of view of oji.

It was found that 72 species of xylotrophic macromycetes are spread in the studied territories, 10 of which belong to the category of edible fungi. They also differ in the frequency of occurrence in natural conditions, ecological-trophic relations, distribution in different substrates, and in the case of vegetative mycelium - in the amount of biomass formed and the quantitative indicator of the biological activity of their metabolites.

The dominant *Laetiporus sulphureus* and *Pleurotus ostreatus, Armillaria mellea* and *Polyporus squamosus* were found to be the most common, while (*Fistulina hepatica, Flammulina velutipes Ganoderma lucidum Kuehnerómyces mutábilis Panus tigrinus* and *P.umbellátus*) the rest are random and rare, with only *A. mellea* being biotrophic and the rest being polytropic.

For the first time in the study, a mathematical approach was used to calculate the number of fruit bodies formed by 10 edible fungi in Azerbaijan in natural conditions, and it was determined that 217 tons of fruit bodies can be formed in Azerbaijan per year.

It has been established that both the FB, formed by fungi in natural conditions, and the biomass formed in the phase of vegetative growth, can be used as a source for obtaining biologically active substances. Nevertheless, the use of VM is beneficial both from an economic and a technological point of view.

It has been established that the use of fungi *G.lucidum* B-09, *L.sulfureus* B-18 and *P.ostreatus* B-25 as producers of biologically active substances and their carbon source for this purpose is glucose (0.97-1.0%). It is more expedient to grow such products for 5-7 days under conditions of liquid-phase fermentation (deep cultivation) at 28°C in an environment with a nitrogen source NH4NO3 (0.036-0.038% nitrogen) and peptone (0.28-0.30%).

WASTE TO ENERGY PRODUCTION BY ANAEROBIC MICROBIAL CONSORTIUM IDENTIFIED WITH METAGENOMICS

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Keywords: waste to energy; anaerobic digestion, metagenomics.

Today's civilization faces growing energy and environmental problems related to depletion of fossil energy sources [Hööka et al., 2013]. The energy requirements increase because of the rapid economic development and utilization of renewable resources for the production of valuable products and energy becomes of utmost importance. Anaerobic digestion includes sequential biological steps aiming at treatment of organic waste for green energy production [Dahlgren et al., 2020]. In the study wheat straw with no preliminary pretreatment was involved as a renewable resource using a laboratory-scale digester for biogas (biomethane) production. The process parameters - pH, t°C, total and volatile solids [APHA: Washington, DC, USA, 2005], volatile fatty acids concentration (by gas chromatography) and amount of cellulose [Updegraff, 1969] were followed. Biogas volume was measured. Metagenome library construction and sequencing were performed by Macrogen Inc. (South Korea), [Pausan et al., 2019]. Type of substrate used as well as temperature conditions appeared to be important factors with impact on anaerobic digestion process realization. The organic loading influence was estimated, showing the increased temperature during the process permitted loading with 45 g/L substrate. After completion of the anaerobic digestion process (12 days), the cumulative biogas yields were 8.22 L for 45 g/L of substrate. The degree of biodegradation reached 74%. The process for biogas production from native wheat straw appeared to be effective - high daily biogas production was registered from the second to fifth day, reaching 60% concentration of biomethane. Anaerobic digestion technology uses microorganisms to utilize waste and produce methane. The action of various microorganisms in a synergetic mode is absolutely necessary to accomplish recycling of the complex lignocellulosic materials. The anaerobic digestion process comprises four sequential biochemical steps - hydrolysis by hydrolytic bacteria, acidogenesis by acidogenic bacteria, acetogenesis by acetogenic bacteria, and methanogenesis by methanogenic archaea. The bacterial diversity in the bioreactor was analyzed using molecular

methods. Metagenomics revealed prevalence of the bacterial class *Clostridia* – about 33%, then appeared *Bacteroidia* -21.5%, followed by *Betaproteobacteria* –about 11%. Representatives of *Gammaproteobacteria* represent about 6% and that of *Alphaproteobacteria* -5%. Significant genera were *Proteiniphilum, Proteiniborus* and *Pseudomonas*. The share of *Archaea* in the bioreactor, operating at 55°C, was about 1.4% of the microflora. Important representatives were from the genera *Methanocorpusculum, Methanobacterium, Methanomassiliicoccus, Methanosarcina* and *Methanoculleus*. The identified microbiome that resided the anaerobic digester could find application for effective processes realization as waste to energy can be considered as a potential alternative source of energy, being simultaneously economically viable and environmentally sustainable.

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ANTIMICROBIAL PROFILE OF ETHYL-4-METHYL-6-PHENYL-2-OXO CYCLOHEX-3-EN-1-CARBOXYLATE; A PROBABLE NOVEL ANTI-KLEBSIELLA PNEUMONIAE COMPOUND

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Keywords: Klebsiella pneumoniae; nosocomial resistance; agar well diffusion; time kill curve; MIC.

Klebsiella pneumoniae is an opportunistic pathogen that causes nosocomial infections and high morbidity and mortality in immuno-compromised patients. Development of the high level of resistance to multiple antibiotics and lack of new drugs accentuate the need of new antimicrobial substances against this opportunistic pathogen. Ethyl-4-methyl-6-phenyl-2-oxo cyclohex-3-en-1-carboxylate was initially screened against four Gram-positive bacteria and four Gram-negative bacteria by agar well diffusion method. Minimum inhibitory concentration (MIC) was determined against all test pathogens using resazurin microplate assay. Gram-negative bacteria were found to be more susceptible as compared to Gram-positive bacteria. Klebsiella pneumoniae BDU-44 was the most susceptible test culture against tested derivatives. Zone of inhibition by agar well diffusion method was measured to be 25.7 mm

(0.3% concentration of test compound), 17.7 mm (0.1% concentration of test compound) and 15 mm (0.05%% concentration of test compound). Least minimum inhibitory concentration value of $31.25~\mu g/mL$ was recorded against *Klebsiella pneumoniae BDU-44*. Effect of test compound on growth curve of *Klebsiella pneumoniae BDU-44* was evaluated by turbidimetric method. Time kill assay was performed to assess bacteriostatic or bactericidal nature and relationship between the concentration of compound and the net growth rate of *Klebsiella pneumoniae BDU-44*. The growth curves of *Klebsiella pneumoniae BDU-44* demonstrated that the test compound could inhibit the growth and reproduction of bacteria at concentration equal to and greater than minimum inhibitory concentration value. Time kill assay showed that the test compound is bactericidal at $2\times$ MIC and bacteriostatic at MIC. Therefore, these findings specify that this compound has huge potential to be a novel anti- *Klebsiella pneumoniae* compound in future.

SYNTHESIS OF VITAMINS BY FUNGUS *PENICILLIUM*Davitashvili Magda, Zuroshvili Lamara, Margalitashvili Darejan

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Keywords: molds; tiamin; riboflavin; pyridoxine; biotin; nicotinic acid; stains; liquid culture.

Molds in the process of their development produce substances that are of great importance for the development of living organisms. Most fungi secrete biologically active substances: vitamins, enzymes, antibiotics, hormones, etc. [Kozlovskii et al., 2013]. In recent years, the number of studies devoted to the identification of stimulant microorganisms and their testing to increase plant yield has especially increased. Studies have shown that the main active factor of stimulating microorganisms in most cases are the biologically active substances contained in their metabolites. In addition, researchers suggest that the action of fungi on agricultural crops is determined by those biologically active substances that are accumulated in cells or are released into the environment during their life activity [Muratova, 2003; Malaviya, 2008; Tarkka et al., 2008; Wang et al., 2021]. In this regard, the purpose of our study was to identify the ability of fungi to biosynthesis B vitamins (B₁, B₂, B₃, B₆, H, PP). The object of the study was fungi of the genus *Penicil*lium, isolated from the soil of the vineyard of the Rkatsiteli variety, located on brown forest soil. Study of vitamin-forming aptitude of 12 species of *Penicillium* has revealed that the fungi examined are largely producents of vitamins of group "B". The content of vitamins in biomass of fungi, on an average, 3-5 times or occasionally even 10 times exceeds the amount of vitamins in culture liquid. Some fungi can synthesize and accumulate these substances in their cells and do not exude them in the environment, whereas others exude in the environment the whole quantity of synthesized vitamins. The amount of vitamins in culture liquid varies with the aging of culture. Thus, the results of the study allow us to conclude that the fungi of the genus *Penicillium*, isolated from the rhizosphere of the grapevine, are active producers of B vitamins and, undoubtedly, enrich their habitat with these substances not only after cell death but also during their lifetime.

EVALUATION OF WINES PRODUCED BY GIVING DIFFERENT FORMS TO KHINDOGNY GRAPE VARIETY

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Keywords: tin; fan; cordon; wine.

The Khindogny grape variety, which is unique to the Karabakh Economic Region, is one of Azerbaijan's oldest and most indigenous technical grape types. The study's goal is to identify the elements that influence the productivity and quality features of wines produced using various cultural operations in the growth of Khindogny grapes in order to produce competitive national brands. In the research work, fan and cordon forms are given to the vines of Khindogny grape cultivated in the soil-climatic conditions of Absheron, Azerbaijan. Productivity and quality indicators were evaluated according to the Bubal method. The average productivity of fans in the form of a fan was 115 hect / sec, and in the cordon - 85 hectare / sec. Taking these factors into account, it is determined that giving fans a fan form is more practical. Simultaneously, the qualitative attributes of wines created from grape products obtained from fan-shaped and cordon-shaped vines were compared using both traditional and modern procedures and technology [Panahov et al., 2013; Huseynov et al., 2019].

As a result of research, the red table wine made from grape product obtained by fanning the grapes of Khindogny grape variety has a sugar residue of 0.24%, ethyl alcohol content of 13.5%, titrated acidity 5.4 g / dm³, volatile acidity 0.61 g / dm³, extractability was 19.4 g / dm³, general SO_2 (sulfite anhydride) was 3.2 g / dm³, and total SO_2 was determined 23.5 g/dm³.

In red table wine made from grape products obtained by giving a cordon form to the vines of the Khindogny grape variety, the sugar residue is 0.22%, the amount of ethyl alcohol is 12.4%, the titrated acidity is 5.6 g / dm³, volatile acidity 0.75 g / dm³, extractability 19.6 g / dm³, free SO₂ (sulfite anhydride) 3.4 g / dm³, total SO₂ 27.5 g / dm³.

The organoleptic features of wine created from the products of fan-shaped vines of the Khindogny grape variety were granted a higher price, according to the findings of wine tasting. Its organoleptic characteristics are as follows: color - light purple; taste - full, fresh, harmonious; transparency - very transparent, bright; bouquet - a complex harmony of delicate fragrances, unique. In the circumstances of Absheron with the highly windy and sandy soils of Azerbaijan, research has revealed that a fan form is preferable.

Thus, in Absheron's circumstances, the yield of fan-shaped Khindogny grapes is higher, the resulting wines are somewhat extractive, have the appropriate amount of alcohol, volatile acidity, and reduced free and total SO_2 content, and are mildly extractive. The organoleptic indicators were higher.

COMPARATIVE ANALYSIS OF THE HAMASHARA AND MADRASA GRAPE VARIETIES AND THE WINES MADE FROM THEM

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Keywords: grape; anthocyanins; phenols; wine.

Hamashara and Madrasa grape varieties are of the oldest, precious and local technical grape varieties cultivated in Azerbaijan. The Hamashara grape variety belongs to the Black Sea basin group (*Convar Pontica* Negr.), and the Madrasa grape variety belongs to the technical grape varieties subgroup of Eastern group (*Convar Orientalis Subconvar Caspica* Negr.). The leaves of both grape varieties are medium-sized

(14-19 cm wide, 15-20 cm long) and five lobed. Both varieties distinguish from each other in terms of ripening process, fleshiness of berries, particular flavor and aroma, the number of seeds, the thickness of the berry skins [Huseynov *et al.*, 2019].

Through the application of traditional and modern research methods, numerous key indicators have been identified in grapes and wines made from them, and the results have been double-checked by mathematical-statistical methods [Salimov *et al.*, 2015].

According to the research results, the anthocyanins content in Hamashara and Madrasa grape varieties has been 518.0-689.3 mg/kg, while it has been 4.01-5.49 mg/g in the fruit skin. The phenolic compounds have been measured 899.0-1164.0 mg/kg in one kilogram of grape skin, 0.578-1.117 mg/b in the seeds of one berry, and 6.103-9.029 mg/g in one gram of seeds.

Physical and chemical properties of wine made from the Hamashara grape variety have been as follows: alcohol by volume - 13.1%, residual sugar - 0.03 g/dm³, titratable acidity - 5.5 g/dm³, volatile acidity - 0.24 g/dm³, extractability content - 18.5 g/dm³.

Physical and chemical properties of wine made from the Madrasa grape variety have been as follows: alcohol by volume – 12.5%, residual sugar – 0.09 g/dm³, titratable acidity - 5.7 g/dm³, volatile acidity - 0.32 g/dm³, extractability content – 19.5 g/dm³.

It's been determined that the color of wines made from the Hamashara and Madrasa grape varieties has ranged from light pomegranate to dark pomegranate, taste has been full-bodied, pleasant, velvety and harmonious, their transparency being bright and clear with a bouquet of mainly fruity tones.

The results allow us to conclude that the technological reserves of essential properties of the grape varieties Hamashara and Madrasa and in the content of each wine made from these varieties are formed at a satisfactory level.

OHRR IS A TRANSCRIPTION REGULATOR INVOLVED IN THE VIRULENCE OF ERWINIA AMYLOVORA

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Keywords: Erwinia amylovora; bacterial virulence factors; OhrR.

Erwinia amylovora is the causal agent of fire blight, necrotic disease affecting apple, pear and other plants of the Rosaceae family. The pathogen is known to rely on a range of virulence factors, including exopolysaccharides amylovoran and levan, the type III secretion system effectors, cell motility, and biofilm formation, which collectively contribute to the establishment of infections [Kharadi et al., 2021]. The MarR family of transcriptional regulators of bacteria are involved in the regulation of many biological processes, including environmental sensing of aromatic compounds (salicylate (HpaR and HpcR in Escherichia *coli*)), resistance to structurally unrelated antibiotics (fluoroguinolones, β-lactams, tetracycline, chloramphenicol), antimicrobial agents, detergents, oxidative stress agents and, in some pathogens, virulence (SlvA in Salmonella typhimurium, PecS in Dickeva dadantii, Hor in Pectobacterium carotovorum) [Ellison et al., 2006; Hao et al., 2013; Vila et al., 2012]. To study the role of OhrR (organic hydroperoxide reductase regulator) in *E. amylovora* biology, we constructed an *ohrR* deletion mutant as well as complemented strain. Interestingly, compared to the wildtype parent, the ohrR mutant was significantly attenuated in its virulence on pear shoots, but not on immature pear fruits. Inactivation of ohrR significantly decreased catalase activity and resistance to exogenous hydrogen peroxide. Phenotype analysis showed that OhrR was also involved in the regulation of other virulence traits, including the production of exopolysaccharides amylovoran, levan and cellulose and cell motility. Our findings identify a new regulator of the virulence of *E.* amylovora and add new insights into the complex regulatory network that modulates the physiology and virulence of *E. amylovora*.

MORPHO-CULTURAL CHARACTERISTICS OF PROTEOLYTIC BACTERIA LIVING IN THE RHIZOSPHERE OF SORREL, RASPBERRY, MINT

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Keywords: proteolytic enzymes; strain; morpho-cultural features.

Medicinal plants are widespread in the territory of the Nakhchivan Autonomous Republic and the research on the enzymatic activity of their living bacteria in their rhizosphere is of theoretical and practical significance.

The essential object of the research was to isolate bacteria with proteolytic activity from the rhizosphere of some medicinal plants and to study their morpho-cultural characteristics. For this aim, the rhizosphere soil of sorrel, raspberry and mint plants was used as an object of the experiment [Alakbarov *et al.*, 2013].

A total of 32 strains with proteolytic activity were isolated during the research, and the morpho-cultural characteristics of some of them were extensively studied.

Extensive information on the morpho-cultural characteristics of strains $St_{8.2}$, $St_{7.3}$, $St_{7.1}$ is given below:

1.St_{8.2} strain

Morphological features - the shape of the cells is basil, the size is 0.5×1.7 microns. They are active.

Cultural features - the colonies are white-grey, the surface is smooth, it is bright, and round in shape, the edges are indented-protruding, easily removed with a bacteriological ring, and the diameter of the colony in a solid nutrient medium is 0.71 mm. In a milky solid nutrient medium, it forms a transparent zone around the colony.

2. St_{7.3} strain

Morphological features - the shape of the cells is basil, the size is 0.5×2.0 microns, sometimes arranged one after the other to form long chains. They are active.

Cultural features - the colonies are white-gray, round in shape, the edges are indented- protruding, the surface is wrinkled, easily removed with a bacteriological ring, and the diameter of the colony is 0.51 mm. Milk agar forms a transparent zone in the nutrient medium.

3. St 7.1 strain

Morphological features - the shape of the cells is basil , the size is 0.7×2.5 microns, sometimes arranged one after the other to form long chains. They are active.

Cultural features - the colonies are white-gray, it is bright, smooth, and round in shape, the edges are indented-protruding, the colony is easily removed with a bacteriological ring, and the diameter of the colony in a solid nutrient medium is 0.56 mm. Milk agar forms a transparent zone around the colony.

The research also examined the relationship of bacteria to the pH of the medium and found that a slight change in the properties of the medium to a weak alkali had an effect on the size and colour of the colonies.

Thus, it was determined that proteolytic bacteria are found in the rhizosphere of all three medicinal plants used as the object of research, and they differ from each other in morpho-cultural characteristics. The proteolytic activity of all three strains is observed at various levels depending on the diameter of the transparent zone formed in milk agar.

GENETIC BIODIVERSITY OF NODULE BACTERIA ENTERING INTO SYMBIOSIS WITH SOYBEAN PLANTS IN THE SOILS OF CENTRAL ASIA

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Keywords: nodule bacteria; Sinorhizobium fredii; Bradyrhizobium japonicum; genes Nod; Fix.

Nodule bacteria of the species *Sinorhizobium fredii* and *Bradyrhizobium japonicum* are the most studied, but pronounced fibers in terms of genetic and morphophysiological characteristics. Comparison of modern publications on the return of a group of symbiotically significant genes (nod genes involved in the synthesis and formation of the signal molecule of the *Nod* factor, which causes the initiation of club formation in a plant-microbial environment; the groups of nif, fix and eff genes responsible for the process of nitrogen fixation and for symbiotic efficiency) shows that these studies for both fast-growing and slowgrowing rhizobia species are still fragmented, and the results obtained are fragmentary [Roumiantseva, 2019; Reis *et al.*, 2016].

The genetic characterization of 30 bacterial isolated from root nodules of cultural growth growing on soils of the Institute of Rice and Legumes of the Tashkent region (Uzbekistan) reveals that we have isolated 2 different types of bacteria that enter into symbiosis with soybean plants, Bradyrhizobium japonicum and Sinorhizobium fredii. The microbiological characteristics of the isolated strains showed that they are divided into fast-growing and slow-growing strains. Taxonomic analysis of 16S rDNA showed that the isolated strains were divided according to genetic characteristics and described into 2 different species. B.japonicum and S.fredii. Molecular genetic characterization with rep and ERIC primers showed a wide variety of intraspecific diversity in spirit rhizobia species and the relationship between rep-PCR fingerprinting and phenotype. These methods complement each other in the study of diversity and allow the identification of relationships between closely related bacterial isolates. Nod and Fix genes were amplified in two species of rhizobia strains [B.Umarov et al., 2021]. The nucleotide sequence of the amplified genes according to the PubMed NCBI Nucleotide-nucleotide BLAST database (blastn) showed that they are Bradyrhizobium sp. ISLU256 and involved partial nodC gene for Nacetylglucosaminyltransferase, strain ISLU256.

The PubMed NCBI database (https://www.ncbi.nlm.nih.gov/pubmed/) contains more than six dozen publications that include information about the genes of bacteria of the genera *Bradyrhizobium* and *Sinorhizobium*, which are involved in the manifestation of symbiotic efficiency and can be classified as *fix* and *eff*, but the number of rhizobia genes of each genus directly studied in this respect does not exceed two dozen. Until now, there has been no systematization of data on these genes, apparently due to the fact that their action is mediated and/or the products encoded by them are involved in various cellular processes [Roumiantseva, 2019].

EVALUATION OF PADDY CULTUVATION IN TERMS OF ASRENIC POLLUTION AND ARSENATE METABOLIZING AND METHANOGENIC BACTERIA

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Keywords: paddy; rice; arsenic; arsenate; methanogenic bacteria.

Rice is one of the most widely grown and consumed foodstuffs worldwide. The fact that it requires the use of more water during rice production increases the importance of water quality. However, due to the decrease in surface waters, which is one of the negative effects of global warming, and as a result, the need for deeper underground waters, arsenic accumulates at different rates in different parts of the plant as a result of the plant irrigation process carried out with waters with high arsenic content. Especially in rice, the rate of arsenic accumulation in grains consumed as food is higher than in other regions.

One of the factors of global warming is the increase in greenhouse gasses and methane (CH₄) gas is one of them. When we evaluated in terms of all these factors; the general objectives of sustainable agriculture in terms of rice will be fulfilled by providing data to help determine the production conditions for both the determination and prevention of arsenic accumulation in rice and the reduction of the amount of CH₄ emission. In this context, public health will be protected by providing access to quality and healthy end products, and since steps will be taken to reduce the amount of CH₄ emissions, the ecological balance and all life forms, including microorganisms, will be prevented from being adversely affected.

In this context, in this study; it was aimed to determine the arsenic content and arsenic cycle dynamics at the functional gene level of the areas where rice cultivation is carried out and the products consumed as food. In this way, it was hypothesized that it would contribute to the creation of the necessary production dynamics by determining the stages of increase in quantity. At the same time, the hypothesis is that it can contribute to the reduction of the effect of the earth's greenhouse gas by reducing the output of CH_4 gas, which is one of the greenhouse gases created in such agricultural areas.

For this purpose, in this study, total arsenic content was determined by taking soil and water samples from the paddy field and taking

root, shoot and rice grain samples at different stages of paddy development. At the same time, Real Time Quantitative PCR studies were completed for the arsenate reductase gene *ars*C and the methyl coenzyme M reductase gene *mcr*A in the total bacterial genomes obtained from the samples, in order to determine the dynamics of bacterial arsenate and CH₄ cycle at the functional gene level. The data obtained revealed that the type of soil and the water source used directly affect the amount of arsenic accumulated in different regions of the rice paddy. It has been determined that there are significant differences in the amount of methanogenic bacteria in the paddy fields cultivated under different conditions. It is thought that the data obtained as a result of the study will contribute to safe food consumption, sustainable environment and sustainable agriculture.

BIODIVERSITY OF BACTERIOPHAGES ISOLATED USING THE INDICATOR BACTERIAL CULTURE *ERWINIA*AMYLOVORA 1/79SM

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Keywords: Erwinia amylovora; bacteriophages; complete genome; fire blight. To create a collection of bacteriophages active against the causative agent of fire blight *Erwinia amylovora*, we isolated bacteriophages from the natural sources in Belarus in 2017–2018. The *E. amylovora* 1/79Sm strain [Bellemann *et al.*, 1994] was an indicator bacterial culture in the enrichment technique. The twelve studied bacteriophages demonstrated genetic diversity and various features of the course of phage infection According to the plaque morphology, bacteriophages were divided into four groups: Hena1; Hena2, Roscha1, Pixel, Dichka, and VarbaS; Loshitsa1; Loshitsa2, Micant, Stepyanka, Fleur, and VerbaL. Using TEM, it was found that bacteriophages can be assigned to morphological type A1 (Hena1-2, Roscha1, Pixel, Dichka, VarbaS) or C1

(other phages) according to Bradley [Bradley, 1967]. All investigated bacteriophages remained viable after cryopreservation in the presence of a protector of 10% glycerol: the titer dropped within one order of magnitude for 5 bacteriophages, and no statistically significant difference in titer was found for the others. All bacteriophages were resistant to the preservative agent chloroform.

For 11 bacteriophages with the highest sensitivity index of *E. am*vlovora strains, we studied the frequency of occurrence of phageresistant mutants upon infection of E. amylovora 1/79Sm. We established a high proportion of phage-resistant variants in the *E. amylovora* 1/79Sm bacterial culture: from 10-3% (infection with Hena2, Roscha1, Pixel, Dichka, VarbaS) [Besarab et al., 2021] to more than 20% (infection with the others). We observed differences between these bacteriophage groups when studying the growth parameters of a bacterial culture upon infection with bacteriophages. Infection with C1 morphology bacteriophages showed no dose-dependent effect on the value of the bacterial culture biomass accumulation (optical density in the experiment) after overnight incubation. In contrast, when infected with bacteriophages of A1 morphology, a higher titer of the introduced bacteriophage corresponded to a lower value of biomass accumulation [Besarab et al., 2021]. Bacteriophages (except Hena1) also exhibited a lytic activity against individual strains of *Pantoea agalomerans*. Division of bacteriophages into groups according to specificity correlated with their division according to particle morphology and features of phage-host interaction.

Complete genome sequences were obtained for seven bacterio-(NC 048828.1), Hena2 Hena1 (OM522317.1), (ON706965), Loshitsa2 (OM513680.1), Micant (OM513679.1), VyarbaL (OM486945.1), and Stepyanka (ON715521). The genome sequences of bacteriophages Hena1 [Besarab et al., 2020], Loshitsa2, and Micant did not have a high identity value with those available in GenBank. Bacteriophages Hena2, VyarbaL, Roscha1, and Stepyanka shared a high degree of nucleotide identity with bacteriophages of various taxonomic groups: Myoviridae, Ounavirinae (for Hena2 and Roscha1); Autographiviridae, Molineuxvirinae (for VerbaL) and Studiervirinae (for Stepyanka). Primers specific to the major capsid protein genes in the Hena1, Hena2, Roscha1, VyarbaL, Stepyanka genomes, and tail tubular protein B genes in Micant and Loshitsa2 genomes were developed. The PCR was positive for Pixel, Dichka, and VyarbaS DNA (Hena2 specific primers), for

the Loshitsa1 DNA (Loshitsa2 specific primers), and for the Fleur DNA (Stepyanka specific primers).

The presented collection of phylogenetically and phenotypically different *E. amylovora* bacteriophages is important in characterizing the biology of the interaction and the mechanisms of phage resistance of *E. amylovora*.

ESTIMATION OF THE NAPHTHALENE BIODEGRADATION EFFICIENCY BY RHODOCOCCUS PYRIDINIVORANS STRAIN 5AP

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Keywords: Rhodococcus; biodegradation; naphthalene; mutagenesis.

Bioremediation technology is the most effective and environmentally friendly method of cleaning the environment from hazardous pollutants, such as polycyclic aromatic hydrocarbons. Many biopreparations for this purpose include bacteria of the genus *Rhodococcus*, since they have a high degree of productivity and a wide range of hydrocarbon-oxidizing activity.

In our research we estimated the efficiency of naphthalene biodegradation by *Rhodococcus pyridinivorans* strain 5Ap of wild type and two mutant variants (*R. pyridinivorans* 5Ap *narAa*::pK18mob and 5Ap *narB*::pK18mob) derived from it by insertional mutagenesis of genes *narAa* and *narB*, respectively. Interest in the chosen determinants for mutagenesis is caused by the fact, that *narAa* encodes the large subunit of naphthalene dioxygenase and *narB* – cis-naphthalene dihydrodiol dehydrogenase.

To estimate the efficiency of naphthalene biodegradation and its quantitative determination directly in the bacterial culture liquid, we adapted the method for determining oil products in water (Federal environmental regulations, 2004). We cultivated bacteria in mineral medium K [Atlas, 2004] with 500 mg/L naphthalene and carried out the extraction of naphthalene by adding tetrachloroethylene (half the volume of culture liquid). The fraction containing tetrachloroethylene with dissolved naphthalene was purified from polar impurities using alumina column chromatography. The pure extract was diluted 2-4 times and its optical density was measured at the wavelength of 312 nm. The con-

centration of naphthalene was calculated in accordance with the calibration curve.

The efficiency of naphthalene utilization by mutant bacteria *R. pyridinivorans* 5Ap *narAa*::pK18mob and 5Ap *narB*::pK18mob can be characterized as very low, so naphthalene dioxygenase (in particular, its large subunit) and cis-naphthalene dihydrodiol dehydrogenase are the key enzymes of naphthalene biodegradation, which have no analogues in the genome of *R. pyridinivorans* 5Ap.

Naphthalene was not detected in the medium with wild type *R. pyridinivorans* 5Ap after three days of cultivation. Thus, naphthalene at the concentration of 500 mg/L was utilized. This concentration is 5000 times higher than naphthalene maximum allowable concentration for drinking water, and 125000 times higher than for water in fishery ponds (natural water) [GOST, 2019]. Based on this, it can be proved that bacteria *R. pyridinivorans* 5Ap are highly efficient naphthalene decomposers, which can be used for effective purification of naphthalene polluted aquatic ecosystems.

MOLECULAR MECHANISM ANALYSIS OF MULTIDRUG RESISTANCE (MDR) IN ESCHERICHIA COLI ISOLATES

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Keywords: Escherichia coli; multidrug resistance; resistance genes; real-time PCR Excessive use of antibiotics has made Escherichia coli resistant to a large number of antibiotics. The aim of this study was to identify the molecular mechanism of multidrug resistance (MDR) in *E. coli* isolated from Iranian eggs.

The studied *E. coli* were collected from 800 egg samples of different Iranian brands in which the resistance to tetracycline, nitrofuranto-in and sulfonamide antibiotics had been previously studied. From the collected samples, 12 samples of multidrug-resistant *E. coli* (MDR) were selected, and the presence of resistance genes in the above strains was confirmed by using specific primers and PCR.

The results showed that not all strains had the resistance genes studied and the presence of tet(B) gene in 50% of strains, tet(D) in 25% of strains, tet(E) in 35% of strains and tet(A) gene, which was identified

in 45% of strains. *sul1* gene was also observed in 25% of strains, whereas *sul2* gene in 50% of strains and *nfsA* in 30% of strains.

The results showed that not all identified genes were expressed under the influence of antibiotics, and only 60% of them were expressed, so only the identification of the gene in PCR and its expression in real-time PCR indicate the sources and mechanism of resistance. The lack of expression of some genes and the lack of identification of some of the studied genes indicate the use of multidrug-resistant bacteria from other mechanisms in the development of multidrug resistance.

MECHANISMS OF PECTOBACTERIUM VERSATILE RECOGNITION BY SOLANACEAE PLANTS

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Keywords: Pectobacterium versatile; Solanaceae plants; gormonal regulation of plant immunity.

Most of the *Pectobacterium versatile* strains we work with were isolated from *Solanum tuberosum* plants; therefore, cultivated potatoes can be considered as a natural host for *Pectobacterium* species. However, *S. tuberosum* is inconvenient for genetic research due to its resistance to the TRV virus of these plants, the use of the virus-induced silencing procedure for rapid gene inactivation is seriously complicated.

In the present work, a comparative analysis of reactions to contact with *P. versatile* of plants *N. benthamiana, S. tuberosum*, and *S. bulbocastanum* (wild tuberous diploid potato species suitable for virus-induced silencing) was carried out. The expression of key immune response genes was measured by qPCR.

Measurement of the expression levels of immune response genes in *S. tuberosum* plants showed that the detection of *P. versatile* by tuber tissue cells causes a decrease in the expression of the abscisic acid biosynthesis genes AAO3 and NCED3 more than tenfold, as well as induction of expression of the ABA hydroxylase gene, which converts this hormone into an inactive form. The expression of salicylate signaling marker gene *PR1*, which encodes a protein with antibacterial activity, decreases by 30 times. The gene of the negative regulator of jasmonate-dependent JAZ3 genes was induced by 6 times, and the expression of

the gene for the subunit of ubiquitin ligase COI1 was reduced, which indicates suppression of the jasmonate signaling pathway.

S. bulbocastanum leaves infected by *P. versatile* show reduction of abscisic acid biosynthesis genes expression and increase of its hydroxylase gene expression. The expression of jasmonate-dependent genes remains unchanged. The main differences are observed for the *PR1* gene: its expression increases, TGA transcription factor gene expression also increases. Therefore, we conclude that the salicylate signaling pathway is induced.

A number of salicylate-dependent genes are induced in the leaves of *N. benthamiana* plants in response to *P. versatile* invasion: *TGA*, *SABP2*, whose product binds salicylic acid, and *PR1*. It is worth noting that the use of a *dspE* mutant for infection reduces the expression of these genes to the level of a wound response. In the absence of the DspE effector, the listed effects are removed. Jasmonate and ABA-dependent signaling are only slightly affected.

Thus, we can note fundamental differences in the response of three related plant species of the same family to contact with *P. versatile*: multidirectional changes in the expression of the salicylate signaling pathway, differences in the intensity of ABA- and jasmonate signaling alteration. Some of these differences may be related to the use of different plant organs for the study (we plan to perform similar studies in the leaves of *S. tuberosum*), however, in general, rather fine regulation of the interaction of *P. versatile* with plants is obvious. Differences in the DspE-dependent response of different potato cultivars may indicate the presence in *P. versatile* of at least one more effector protein in addition to the only DspE effector known to date

INVESTIGATION OF MICROORGANISMS IN HOME-MADE SOUR MILK PRODUCTS FROM SOME VILLAGES OF GORANBOY REGION

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Keywords: mushrooms; bacteria; sour milk products.

"Bioprotection" of nutrients involves the utilization of the natural or added microbiota itself or the antibacterial products they synthesize to grow the safety and shelf life of the food. Lactic acid bacteria are widespread among the microorganisms present in food. Yogurt has a particular place among sour milk products. Yogurt is digested faster than other dairy products [Alvarez-Martin *et al.*, 2012]. It can be easily used by people with antimicrobial properties and lactose intolerance. It has a significant place due to its qualities such as usability [Sun-Waterhouse *et al.*, 2013].

Spontaneous yogurt samples brought from Garadaghli, Bildirchinli, Alirzali and Khangarvand villages were used as the object of research. Samples delivered to the laboratory were diluted with sterile water within 6 hours. After dilution, from the 3rd and 4th dilutions, 0.5 ml of suspension was added to Petri dishes containing malt-agar and fleshy peptone-agar. Petri dishes were incubated in a thermostat at 30° C for 3 days. After the incubation period, the colonies were identified in Petri dishes and the amount of them was counted. The number of microorganisms in the Petri dishes was determined according to the number of colonies.

The amount of lactic acid bacteria isolated from Garadaghli village yogurt was 33000, and 27000 in Bildirchinli village yogurt, 127000 in Alirzali village yogurt, and 11000 in Khangarvand village yogurt. The maximum lactic acid bacterial cell was found in Alirzali village yogurt, and less in Khangarvand village yogurt. The amount of lactic acid bacteria in Alirzali village yogurt was 11.5 times more than Khangarvand village yogurt, 4.7 times more than Bildirchinli village yogurt, and 3.8 times more than Garadaghli village yogurt.

Among the spontaneous yogurt samples researched, the number of yeast cells in Garadaghli village yogurt was 17000, in Bilirchinli village yogurt 25000, in Alirzali village yogurt 416000, and in Khangarvand village yogurt 4000.

The product was first prepared from the obtained cultures and researched under a light microscope. Pure cultures of microorganisms were obtained, morpho-cultural features were studied, and species of yeast strains and lactic acid bacteria were identified. Accurate identification of lactic acid bacterial strains was performed using gram staining and catalase tests. Two lactic acid bacterial strains *Streptococcus* sp. BSU - QI9, *Lactobacillus* sp. BSU - QI10 and one yeast strain *Saccharomyces* sp. BSU - QI11 were isolated from Garadaghli village yogurt. 1 lactic acid bacterial strain of *Lactobacilus* sp. BSU - BI12 and one yeast strain *Candida* sp. BSU - BI13 were isolated from Bildirchinli village yogurt, 1 lactic acid bacterial strain *Streptococcus* sp. BSU - AI 14 and a yeast strain of *Saccharomyces* sp. AI15 from Alirzali village yogurt, and 1 lactic acid bacterial strain *Lactobacilus* sp. BSU - XD16 and 1 yeast strain *Candida* sp. BSU - XD17 were isolated from Khangarvand village yogurt.

CHARACTERISTIC OF THE DETERMINANTS OF PHENOL DEGRADATION 5AP GENOME IN RHODOCOCCUS PYRIDINIVORANS STRAIN

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Keywords: Rhodococcus; biodegradation; phenol; environmental biotechnologies.

Aromatic hydrocarbons are widely distributed in nature, but their concentration has increased significantly in recent years. Getting into the environment with waste from the chemical, oil refining, pulp and paper industry, they have a negative impact on ecosystems and human health in general. Bacteria of the genus Rhodococcus are able to inhabit polluted ecosystems and utilize a wide range of compounds that may be inaccessible or even toxic to other microorganisms.

Rhodococcus pyridinivorans strain 5Ap is able to utilize a wide range of hydrocarbons, including aromatic ones (such as benzene, xylenes, toluene, ethyl benzene, phenol), as a source of carbon and energy source. A lot of catabolic genes for aromatic compounds are located on the plasmid pNAPH (GeneBank Acc. No. CP063451).

The aim of this research was to estimate the efficiency of phenol degradation by R. pyridinivorans strain 5Ap and to characterize the main genes of phenol utilization in its genome. Bacteria were cultivated in medium K supplemented by phenol (200 mg/L) [Atlas, 2004]. Concentration of phenol in cultural liquid was measured spectrophotometrically at a wavelength of 270 nm. To analyze the contribution of plasmid pNAPH to the ability of bacteria to utilize phenol, growth of R. pyridinivorans strain 5Ap of wild type and its plasmid-free mutant R. pyridinivorans 5Ap-6 was compared. For wild-type bacteria, a lag phase was about 14-16 hours, and the stationary growth phase was reached after 22 hours. A similar growth dynamic can be observed for the plasmid-free variant *R. pyridinivorans* 5Ap-6. The content of phenol in wild-type as well as in plasmid-free strain culture start to decrease after 16 h, and phenol was not detected after 24 h. Due to these facts we can conclude the pNAPH plasmid does not affect the utilization of phenol. Analysis of the genome of *R. pyridinivorans* strain 5Ap showed that all the key determinants encoding phenol degradation enzymes for ring ortho-cleavage pathway are localized on the chromosome. Five homologous determinants were found for the first reaction of phenol oxygenation, and each of the next reactions of the pathway was determined by a unique gene. These genes are similar in nucleotide composition to those of *Rhodococcus* sp. and *R. rhodochrous*, and the proteins form clusters on the phylogenetic tree with the corresponding proteins in rhodococcal group B.

Thus, *R. pyridinivorans* strain 5Ap is the effective phenol degrader, which is able to decrease the phenol content from 200 mg/L to undetectable (lower than 2 mg/L) in 24 hours. All catabolic genes for phenol degradation are located on the chromosome. This makes it possible to use this strain of bacteria as a promising agent of environmental biotechnologies for the removal of phenol from contaminated media.

CONTACTS OF ALVEOLAR MACROPHAGES WITH EPITHELIUM AND HEMOCAPILLARIES: ELECTRON MICROSCOPIC STUDY

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Keywords: intercellular contact; macrophage; alveoli; ultrastructure.

The intercellular contacts between pulmonary alveolar macrophages with components of the alveoli and blood capillaries studied superficially on electron microscope. This makes it difficult to objectively assess the functional purpose, activity, migratory and elimination properties of alveolar macrophages [Kopf et al., 2015]. Purpose of the study was to investigate and systematize the intercellular contacts formed by alveolar macrophages under electron microscopic investigation. The study performed on 16 outbreeding male rats weighing 200-250 grams. Specimens taken from different parts of the right and left lungs of decapitated rats prepared into araldite-epon blocks with general methods of electron microscopy. Obtained ultrathin sections with 50-70 nm thickness examined on TEM under 80.0 kV (Japan). Alveolar macrophages accounted for 44,2 ± 4,2% of pulmonary macrophages. In semithin and ultrathin sections, three localizations of the studied cells were revealed: in the lumen of alveoli (41,6 ± 2,8% of the corresponding population), on the bottom surface along the alveolar epithelium (37,0 \pm 2,0%) and in extraluminal spaces between the basement membrane of the alveoli and the hemo capillary wall (21,4 ± 1,4%). Identification of alveolar macrophages taken into account the following ultrastructural features: the characteristic shape and composition of the nucleus, osmiophilic and crystalloid deposits in the pale cytoplasmic matrix, phagolysosomes and residual bodies, few tubules and cisterns, rarely scattered cytoskeletal elements. In addition, the cytoplasm of some macrophages in the alveolar space contains lipid/lipoid droplets, pigment deposits, and cells that in contact with the capillary wall revealed pinocytotic vesicles [Hao et al., 2021]. Designated contacts are grouped as follows: 1) simple contacts; 2) interdigital contacts ("key-lock") and 3) hemidesmosomes. Simple contacts often observed between macrophages and apical surfaces of type I and II pneumocytes, as well as in the extraluminal zones of the hemocapillary. The width of the corresponding contact gap was 15.8 ± 0.9 nm. Interdigital type contacts are predominantly revealed between macrophages and type II pneumocytes, the contact gap is variable (min. 11,6; max. 22,8 nm; 18.5 ± 1.9 nm). It should be noted that in macrophages with this type of contact ultrastructural manifestations of phagocytosis and endocytosis of surfactant fragments are more intensely. Hemidesmosomes have been found, but they are few and located only between the basement membranes of alveoli .hemocapillary and specific ultrastructural macrophages. The contacts of pulmonary alveolar macrophages with the alveolar epithelium and hemocapillary wall are directly related to the functional activity of these cells and the specific phase of the displacement process. However, the smallness and simplicity of the contacts can be considered as evidence that they do not interfere with the movement of macrophages. The obtained results show the importance of continuing research in this direction in the norm and in the experiment.

STORAGE OF MICROBIAL CULTURES COLLECTION AT BAKU STATE UNIVERSITY

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Keywords: culture collection; microbial cultures; cryoprotectant.

Microorganisms isolated from nature in the form of pure culture are kept in collections in all countries over the world. During the storage of microorganisms in the collection, they can loss of their valuable properties or sudden death. Therefore, in order to keep viable cultures stable for a long time, it is recommended to keep microorganisms in different ways at the same time. Each species of microorganism has its own method of storage and requires an individual approach to each. Therefore, there is a need to develop methods for long-term storage of

certain microorganisms without losing their viability and useful properties [Rosemary *et al.*, 2015].

One of the methods of long-term storage of microorganisms is to keep them frozen at low temperatures. The creation of special environments with *cryoprotectant*s for conservation allows reducing the amount of damage and ensuring the preservation of the largest number of living and functional cells. The choice of *cryoprotectant* depends on the taxonomic group of microorganisms. For freezing new strains, it is important to first check the effect of the *cryoprotectant* on them [Kriger *et al.*, 2018].

Given the above, the mechanism of cryoprotective action of these substances is almost not fully explained. The protective effects of cryoprotectants on different microbial cultures can be very different. Therefore, the selection and use of cryoprotectants requires testing for each taxonomic group of microorganisms and determining the storage conditions for them in the culture collection.

16 strains of 5 species of *Candida* yeast and 19 strains of bacterial cultures of 6 genera and 10 species were used as the object of research. The following cryoprotectants were used for the studied microorganisms: 1) 25% glycerol (aqueous solution); 2)20% glycerin and nutrient medium; 3) sodium carboxymethylcellulose (NaKMS-1%), glycerin (5%) and dimethyl sulfoxide (DMSO-5%); 4) pectin (1%), glycerin (5%) and dimethylsulfoxide (DMSO-5%). The study of the viability of microorganisms was carried out by inoculation in a Petri dish with solid medium. Here, the principle that each colony is a descendant of a cell is taken as a basis. This test allows us to estimate the amount of live microbial cells based on the number of colonies grown after the microbial suspension under study has been transplanted into a solid nutrient medium [Lusta *et al.*, 1990].

Thus, 19 strains of bacterial cultures of the genera *Bacillus, Gordonia, Micrococcus, Staphylococcus, Pseudomonas* and *Escherichia* were studied in the collection, and the glycerin and nutrient medium complex was selected as the optimal storage method for 12 months at minus 25°C. A new method has been developed for the long-term storage of yeast cultures. In this method, the cultures are introduced into a medium containing a mixture of cryoprotectants (1% NaKMS, 5% glycerin and 5% DMSO) and stored at minus 25°C for up to 24 months. This cryoprotective composition was developed as a new method for long-term storage of yeast cultures and was patented for this invention.

ANTIBACTERIAL ACTIVITY OF LACTIC ACID BACTERIA STREPTOCOCCUS SP. BDU-SV7 AND LACTOBACILLUS SP. BDU-SV8 STRAINS

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Keywords: lactic acid bacteria; antimicrobial activity; opportunistic bacterial pathogen.

The protective properties of lactic acid bacteria are related to the antagonistic and antimicrobial compounds they synthesize in the metabolism. The antimicrobial compounds produced by these bacteria confers them a competitive advantage over other microorganisms [Jafarov *et al.*, 2015; Alvarez *et al.*, 2019]. The antimicrobial compounds of lactic acid bacteria include lactic and acetic acids, carbon dioxide, diacetyl, enzymes, hydrogen peroxide and bacteriocins. As a result of the production of these compounds, lactic acid bacteria display an antibacterial activity against the pathogens of *Clostridium*, *Listeria*, *Bacillus* and *Staphylococcus* species [Dalia *et al.*, 2013; Eiteman *et al.*, 2015].

The antimicrobial properties of the lactic acid bacteria strains isolated from yogurt obtained through the spontaneous fermentation used in Goranboy district against the opportunistic bacterial pathogens have been determined in this regard.

The antimicrobial properties of *Streptococcus sp.* BDU-SV7 and *Lactobacillus sp.* BDU-SV8 strains of lactic acid bacteria isolated from spontaneous fermented yogurt used in Sarov village of Goranboy district against the opportunistic bacterial pathogens have been determined.

In order to evaluate the antibacterial properties, the opportunistic pathogens bacterial strains - Gram-positive *Bacillus subtilis* TU-1, *Staphylococcus aureus* TU-4 and Gram-negative *Escherichia coli* TU-2 were taken from the culture collection of the Department of Molecular Biology and Biotechnologies used as test organisms.

Lactic acid bacteria have been cultured in one side of the Petri plate with meat peptone nutrient media through the streaking method, but the test bacteria used have been cultured by streaking in a perpendicular direction to the lactic acid bacteria. The Petri plate have been incubated for 3 days at 35°C in a thermostat. After the incubation period, the presence and effect of antibacterial activity have been identified in accordance with the clear lysis zone. The lysis zone has been meas-

ured with a ruler and the dimensions expressed in millimeters. The effect of the isolated lactic acid bacterial strains has varied against the opportunistic pathogenic test cultures.

The lysis zone of *Streptococcus sp.* BDU-SV7 lactic acid bacteria strain has been 12-14 mm against *Bacillus subtilis* TU-1 and 15-17 mm against *Escherichia coli* TU-2. *Lactobacillus* sp. BDU-SV8 lactic acid bacteria generated the lysis area of 17-20 mm against *Bacillus subtilis* TU-1 strain and 21-23 mm against *Escherichia coli* TU-2 strain. The weakest lysis zone has been observed against *Staphylococcus aureus* TU-4 strain of opportunistic pathogenic bacterial cultures (5-7 mm).

Thus, *Lactobacillus sp.* BDU-SV8 has been determined as the lactic acid bacteria strain with the highest antibacterial activity. It has created a lysis zone of 21-23 mm against the *Escherichia coli* TU-2 test culture.

POLYSACCHARIDE-BASED CAPSULES FOR POTENTIAL TREATMENT OF CORONAVIRUS INFECTION

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Keywords: chitosan; remdesivir; nanocapsule; Human coronavirus-OC-43; antiviral activity.

The pandemic situation with COVID-19 has shown the importance of the prevention, treatment and control of viral diseases in human society. The search for new approaches to control the pathogenesis of this viral infection, with extremely diverse symptoms, led us to build a model of nanocapsules containing the active substance Remdesivir in coronavirus infection.

The core of the composite structures was oil-core capsules produced according to the procedure originally described by Calvo [Calvo *et al.*, 1997]. A cytopathic effect inhibition test was used for assessment of antiviral activity of the compounds. The virucidal activity of the test

samples was reported by the end-point dilution method [Reed *et al.*, 1938] and the alteration in viral titer was determined as Δ lgs compared to untreated controls.

Chitosans with low (50-190 kDa), CS-L, and medium (190-310 kDa), CS-M, molecular weight and degree of deacetylation (DDA) 75-85% were used as a basis for nanocapsule construction. The produced structures contained oil-core capsules and were positively charged because of the deposition of a thick chitosan layer on their surface. The negatively charged complex of betadex sulfobutyl ether sodium - Remdesivir (SBE-REM) (Veklury) was impregnated into the chitosan layer. The final concentration of REM in dispersion was 5×10^{-5} M.

The cytotoxicity to the MRC-5 cells line and the antiviral activity to the Human coronavirus virus (HCoV strain 229E) of all nanocapsule components as well as the capsules themselves were determined. Capsules containing PEM (and constructed with CS-M) were found experimentally to show more anti-coronavirus activity (SI = 244.44) compared to pure PEM (SI = 200.0).

The introduction of Remdesivir inside nanocapsules contributes to its better bioavailability in infected cells, which leads to an increase in the effectiveness of anti-coronavirus therapy.

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NANOPRIMING WITH GREEN SYNTHESIZED CUO NANOPARTICLES ON *SOLANUM LYCOPERSICUM* L. AND THEIR EFFECTS ON GERMINATION

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Keywords: copper oxide nanoparticle; Solanum lycopersicum L.; green synthesis; nanopriming.

Nanopriming is a method based on using nanoparticles smaller than 100 nm to increase the germination percentage and viability of plant seeds [Sivritepe, 2012]. Nanopriming mechanism depends on increasing the nutrient and water uptake efficiency of seed by facilitating the penetration of nanoparticles through the seed coat [Pereira *et al.*, 2021]. Copper oxide nanoparticles (CuO NP) are used in many applications fields like biomedical, water filtration or bioactive coatings due to their antioxidant and antimicrobial effects [Costa *et al.*, 2016]. In this study CuO NP was synthesized by using laurel (*Laurus nobilis* L.) leaf extract and characterized by using UV/VIS spectrophotometry, Fourier transform infrared spectroscopy (FT-IR), Scanning electron microscopy (SEM) and Zeta potential [Vaidehi *et al.*, 2018]. UV/VIS results confirmed the formation of CuO NPs due to peaks between 210 and 340 nm. FT-IR study proved chemical composition of nanoparticles via the Cu-O specific bands at 619 cm⁻¹. SEM images showed that CuO NPs were 83 nm in diameter size with spherical shape. Zeta potential results showed -22 mV charges on CuO NPs.

Tomato (*Solanum Lycopersicum* L.) seeds were nanoprimed for 72 hours by using green synthesized CuO NPs with different concentrations (6.25-100 mg L⁻¹). Seed vigor tests were performed according to International Seed Test Association standards. Growth and development of tomato seedlings were observed for 14 days. Results showed that the germination rate of primed tomato seeds were enhanced 17% at 25 mg L⁻¹ concentration when compared to the control seeds. Similarly seed vigor of tomato seeds were enhanced 26% by nanopriming application with CuO NPs at 25 mg L⁻¹. However, CuO priming at 100 mg L⁻¹ concentration inhibited the seed vigor for 27% compared to the control group. Plant root and shoot lengths measurements showed that 6.25, 12.5 and 100 mg L⁻¹ concentrations of CuO NPs treatments decreased the growth of tomato seedlings. 25 and 50 mg L⁻¹ concentrations of CuO NPs did not change the tomato seedlings growth based on root and shoot length measurements.

As a conclusion, CuO NP nanopriming has a stimulating effect on seed vigor and seed germination at 25 mg L^{-1} without any toxic effects. On the contrary, high concentrations of CuO NPs (100 mg L^{-1}) may cause toxicity on tomato seedlings growth.

REMOVAL OF HYDROCARBONS FROM INDUSTRIAL WASTEWATER BY INDIGENOUS MICROBIAL BIOFILM IN BIOREACTORS AT PILOT-PLANT SCALE

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Keywords: hydrocarbons; bioremediation; industrial wastewater; pilot scale; biofilm. Pollution of waters with hydrocarbons is an environmental problem that causes ecological damage with negative effects in different areas. Companies in the fuel industry produce large volumes of hydrocarbon-polluted wastewater. Therefore, these companies need the development of innovative and cost-efficient new technologies for the treatment of their industrial wastewater to make the most effective use of their facilities. Bioremediation has been reported as a useful strategy for remediation of hydrocarbon polluted sites. This study, funded by Logistics Company of Hydrocarbons (CLH, Spain), aimed to develop an innovative treatment system for remediation of hydrocarbon polluted industrial wastewater based on sorption-biodegradation processes. Different tests on lab scale were performed to test different sorption material, the capacity of the adhesion of the biofilm and the operational conditions. The final pilot plant prototype consisted of four stainless steel bioreactors (ATEX Standard, h: 1.65, d: 0.5 m, v: 192.4 L). Each bioreactor contained a holder with the sorbent material to promote the formation of biofilm of autochthonous microorganisms. The selected sorbent material was Pad Sentec® polypropylene [Rodríguez-Calvo et al., 2018; Silva-Castro et al., 2021].

Wastewater with different loads of total petroleum hydrocarbons (TPH) (high: <60,000 mg L-1, low: <500 mg L-), different flows (Q1: 180 L h-1, Q2: 780 L h-1); additional aeration and recirculation times were tested [Rodríguez-Calvo et al., 2018; Silva-Castro et al. 2021]. The results showed an optimization in the removal of hydrocarbons under the following operational variables: high flow, no additional aeration and four cycles of recirculation. A post-treatment for 7 days inside the bioreactor without recirculation was performed to favor the microbial biodegradation. The microbial communities of the biofilm were analyzed by scanning electron microscopy and Illumina sequencing. The setup and optimization of the reactor represents a step forward in the imple-

mentation of bioremediation processes at industrial scale in order to encourage the preservation of marine sustainability.

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CHANGES IN THE MICROBIOTA AFFECT THE RECEPTION OF SODIUM LACTATE IN THE INTESTINE

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Keywords: lactic acid bacteria; probiotic; Bifidobacterium longum.

The gut microflora and its probiotic health benefits are being studied [Bernet *et al.*, 1994; Hooper *et al.*, 1999; Leahy *et al.*, 2005]. It is able to modulate metabolic, physiological and immunological processes in the human body [O'Hara, Shanahan, 2007]. The association of changes in the composition of the microbiota of the gastrointestinal tract with some gastrointestinal diseases is described [Ott *et al.*, 2004; De La Cochetiere *et al.*, 2004]. Members of the genus *Bifidobacterium* are among the first microbes to colonize the human gastrointestinal tract included as living components in various so-called functional foods [Ventura et al., 2004].

The objective of this study was to determine how effects of the sodium lactate influence the afferent activity of the vagus nerve (n. vagus) after the balance of the intestinal microbiota was changed.

All studies (n=13) were performed under acute experimental conditions on white Wistar rats (m=200-320 g), anesthetized with so-dium thiopental (70 mg/kg, intraperitoneally). All animals were divided into 2 groups: 1 - control group (n=6), who were on a standard diet, received intragastric sodium phosphate buffer solution (pH 7.4), 2 - group (n=7) for a month received probiotic *Bifidobacterium longum* (10°, 1 ml), diluted in a sodium-phosphate buffer solution (pH 7.4). Pulse activity of afferent fibers of the ventral esophageal trunk of the n.vagus nerve was recorded using bipolar electrodes.

It was found that introduction of sodium lactate into the colon (0.5 ml 1M) led to an increase in the frequency of vagus nerve pulsation in the ventral subdiaphragmatic trunk from 64%. The introduction of sodium lactate (intraluminal) leads to an increase in the electrical and

motor activity of the colon. Another series of experiments, long-term (within 1 month) intragastric administration of *Bifidobacterium longum* to rats (10^9) was carried out. Under these conditions, the introduction of sodium lactate (0.5 ml, 1M) into the colon was not accompanied by significant changes in the afferent activity of n.vagus et in the electrical and motor activity of the colon.

Thus, long-term use of the probiotic *Bifidobacterium longum* leads to a change in the reception of sodium lactate in the colon. The established absence of lactic acid effects on the afferent activity of the n.vagus may be associated with desensitization.

PECULIARITIES OF IMMUNOHISTOCHEMICAL POLYMORPHISM OF LUNG MACROPHAGES

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Keywords: lung macrophages; immunohistochemical study; morphometric analysis; stereometric mode.

Systematic studies of possible immunohistochemical polymorphisms of various histotopographic subpopulations of lung macrophages have not been explored. This makes it very difficult to objectively assess the pathogenesis and pathomorphosis of various pathological processes [Lee et al., 2019; Fan et al., 2021]. Aim of the study was to analyze the main immunohistochemical parameters of lung macrophages on various histotopographic subpopulations and to systematize possible relationships between these parameters and macrophage histotopography. Sixteen outbreeding white rats weighing 200-250 g decapitated after ketamine anesthesia. The tissue specimens were taken in the right lung 2 pieces in volume 0,3-0,5 cm³ from each 4 lobes, and from the left lung 1 piece in volume 1,0 sm³ around the hilum and the peripheral area, then after fixation with 4,0% buffered formalin the specimens processed in general histological methods. For selective detection of macrophages, the sections taken from paraffin blocks in 4 µm thickness stained with 0,1% trypan blue, 0,05% buffered thionin and used immunohistochemical reactions with Iba-1 (AIF-1), CD68, CD163, CD207 (langerin), CD1α, S100 protein, vimentin, Granzyme B antibodies. Serial sections dyed with epithelial membrane antigen (EMA) monoclonal antibodies [Magaki S. et al., 2019]. The slides analyzed in the stereometric mode under an Axio Scope A14 microscope (Carl Zeiss) with video camera "Axiocam ERc5s". In morphometric-stereometric analysis, macrophages constitute 8,9±1,0% of the total cellular composition of the organ (min - 3,2%; max - 13,4%). In both lungs, the frequency of macrophages is higher in the peripheral zones. Three subpopulations of pulmonary macrophages were identified histotopographically: alveolar (44.2 \pm 4.2%), interstitial (41.0 \pm 4.2%) and bronchial (14,8 ± 1,3%). Intravascular macrophages as a separate population not studied in the present study. On histological staining, cells belonging to all 3 subpopulations have acidophilic cytoplasm and lobulated nucleus; stained to varying intensity with trypan and thionine dyes. Although interstitial macrophages are located singly, they form different types of contacts with the cells of the stroma and vascular wall. On histological sections, alveolar and bronchial macrophages are also situated alone on the surface and inside of the epithelial laver. Immunohistochemically, EMA is negative (-) in all 3 subpopulations and vimentin is positive (+). In parallel with vimentin, overall positivity (100%) was noted for CD68 and Iba-1 (AMF-1). However, different results were obtained for other markers. According to the correlation analysis, the localization (histotopography) of the macrophage selectively has a statistically significant relationship with some immunohistochemical markers. Pulmonary macrophages of rats represent heteromorphic and heterogeneous populations due to their immunohistochemical properties. Individual immunohistochemical polymorphism on the histotopographic location of the 3 different subpopulations of these cells in the same genesis may be because of functional purpose and activity of a particular macrophage; however, more detailed studies are needed to clarify this provision.

BULGARIAN ROSE OIL AGAINST THE MULTIPLICATION OF SENSITIVE AND RESISTANT TO ACYCLOVIR HERPES SIMPLEX VIRUS

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Keywords: Herpes simplex virus type 1 (HSV-1); acyclovir-resistant (R-100) strain; acyclovir; Rosa damascena Mill. and Rosa alba L. oil; combined effect.

Herpes simplex virus type 1 (HSV) is a coated DNA virus of the Herpesviridae family. It causes painful infections of the mouth, throat, face, eyes, central nervous system, as well as infections of the analgenital area [Chayavichitsilp *et al.*, 2009] The specific chemotherapeutics against herpes simplex virus type 1 (HSV) are nucleoside analogs as acyclovir (ACV), but the big problem is the formation of resistant mutants [Saddi *et al.*, 2007]. The search for new therapeutic alternatives directs us to the purpose to investigate the effects of *Rosa damascena* Mill. and *Rosa alba* L. essential oils on the viral reproduction of susceptible (Victoria) and acyclovir-resistant (R-100) strains of HSV-1 replication *in vitro*, individually, and in combination with acyclovir.

After chromatographic analysis (7890A/5975 GC/MS) of the essential oils the cytopathic effect inhibition test was used for assessment of antiviral activity of the oils. The three-dimensional model of Prichard and Shipman was applied to evaluate the combined effect of oils with ACV on HSV-1 replication [Prichardi *et al.*, 1990].

Both oils do not affect the replication of viral strains, they are able to influence only the viral adsorption, extracellular virions and to protect healthy cells from subsequent infection. When the rose oils were added after the virus entered the cell, co-administered with ACV at a concentration four times lower than the IC50, they contributed to a significant reduction in viral yield by more than 20% of the expected inhibition of viral replication in the Victoria strain and more than 10% of the previously presumptive inhibition in the R-100 strain.

In combination with lower doses of acyclovir, both oils demonstrate a significant synergistic effect on the replication of HSV-1, which is more contagious than the Victoria strain.

that the nonspecific mechanism of reduction of viral reproduction caused by rose oils and the synergistic effect of their co-administration with the lower doses of specific inhibitor ACV make them suitable therapeutics and can serve as a reliable adjuvant for overcoming viral resistance of HSV-1 infections.

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DOMINANT REPRESENTATIVES OF EPIPHYTIC MICROBIOTAS OF SOME FRUITS

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Keywords: Bacillus; spore; epiphytic microbiota.

The study of the interaction between plants and microorganisms is one of the rapidly growing areas of biotechnology and modern plant biology. Among the other factors that provide immunity in plants, the epiphytic microbiota appears to be a prior protection for plants against environmental saprophytic, opportunistic and pathogenic microorganisms. Therefore, the studies in this field can be considered relevant.

During the research, the epiphytic microbiota isolated from the surface of fruits (apple, pear, pomegranate, quince, feijoa, persimmon) and berries (grape, strawberry, gooseberry) grown in various regions of Azerbaijan have been studied. The epiphytic microbiota harbors great diversity. Almost all types of microorganisms - bacteria, fungi, actinomycetes, yeasts - have been found among them.

It's been identified that the ratio of bacteria of total microorganisms varies in different fruits. For example, the number of bacteria in apples is 91 % of the total number of microorganisms, while in persimmon it is just 48 %.

In the course of study, unfavorable conditions have been created for microorganisms and thus, bacterial spores have been isolated. Cultivation has been carried out at the dilution of 1:1000 [Tepper *et al.*, 2004].

The quantity of bacterial spores has prevailed among the bacterial microbiota of several fruits. Thus, 55 % of total bacteria on the surface of apple, 55 % of quince, 55 % of feijoa, 58 % of persimmon, 67 % of

gooseberry have been bacterial spores. The corresponding figures are 44 % for pear, 36 % for pomegranate, 43 % for grape, and 46 % for strawberry.

The genus and species of the formed bacterial spores have been identified. Among them, bacteria of the genus *Bacillus* are common and the bacteria of the genus anaerobic *Clostridium* and *Desulfotomaculum* are rare. The identification has shown that *B.subtilis*, *B.cereus*, *B.mesentericus*, *B.megaterium* are the dominant forms of species.

Out of seven nutrient media with different components, it has been observed that the most productive growth of both epiphytic microbiota and non-epiphytic forms is in meat peptone agar and potato agar nutrient media mixed at a ratio of 1:1. According to the results, strawberries and grapes hold the richest epiphytic microbiota and are rich in bacterial spores.

INVESTIGATION OF THE EFFECTS OF PROTOCATECHUIC ACID ON C6 CELL PROLIFERATION USING ANTI-PCNA PRIMARY ANTIBODIES

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Kevwords: cancer; C6; PCA; PCNA.

Cancer is the abnormal growth of cells. Cancer cells multiply rapidly despite space constraints, nutrients shared by other cells, or signals from the body to stop reproduction [Baykara, 2016]. These cells are often shaped differently from healthy cells, do not work properly, and can spread to many parts of the body. Tumors are abnormal tissue growth, clumps of cells that can grow and divide uncontrollably [Gullu and Akalın, 2005].

The most common types of cancer are lung and breast cancer. As with other types of cancer, there is no clear information about the causes of brain tumors. Unlike other common cancer types, cell proliferation is observed very little in brain tumors. The average life expectancy of patients with brain tumors is less than 1 year. Even though many clinical applications are tried to be treated, this is insufficient and new drugs are needed for the treatment of brain tumors [Das *et al.*, 2008]. The fact that anthocyanins and procyanidins are easily taken from fruits and

vegetables through food as the main metabolite and that their biological activities are so wide have increased the interest in PCA in recent years.

In this study, IC_{50} values for protocatechuic acid (PCA) concentrations were determined as a result of cytotoxicity testing and subsequently with the Xcelligence real-time cell analysis system. After the IC_{50} values were determined, the anti-proliferative effects of PCA on C6 rat glioma cells were investigated in two different ways. For this, PCNA immunofluorescence method was used.

PCNA (proliferating cell nuclear antigen) is a protein with a molecular weight of 36 kDa (kilodalton) that functions as a cofactor of DNA polymerase delta. Information about PCNA was first given by Miyachi in 1978. The presence of antibodies that react with proliferating cell antigens in the serum of patients with systemic lupus erythematosus has been reported. After this, Bravo and Celis observed in their research in 1980 that a protein they called "cyclin" showed different effects in the cell cycle. Mathews et al. revealed that PCNA and cyclin are actually the same protein [Matsumoto *et al.*, 1987; Baserga, 1991; Celis and Madsen, 1986].

The effects of protocatechuic acid on C6 cell proliferation were examined using anti-PCNA primary antibody on at least 30 photos from each group. The values of the fluorescent intensity ratios of PCNA-labeled cells between the experimental groups were statistically compared with the control group. Compared to the control group, it was observed that cell proliferation decreased significantly at increasing concentrations both in the groups in which PCA was applied to C6 cells alone and in the groups in the inflammation culture model created with THP-1 human monocyte cells.

ANTIOXIDANT ACTIVITY OF METHANOLIC EXTRACT OF CYANOBACTERIA

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Keywords: cyanobacteria; antioxidant activity; extraction.

Cyanobacteria are single-celled prokaryotic organisms without a membrane-enclosed nucleus and organelles [Fogg *et al.,* 1973]. They are found in both fresh and marine waters [Bryant, 1994]. Cyanobacte-

ria have recently attracted the attention of biotechnology companies due to the high levels of protein, vitamins, minerals, fatty acids and pigments they contain and have become one of the most studied organism groups [Hirschberg and Chamovitz, 1994].

In the last two decades, besides the antibiotic, antiviral, anticancer, antifungal, antibacterial and anti-inflammatory effects of bioactive molecules obtained from cyanobacteria, hypocholesterolemia, enzyme inhibition and some other pharmacological effects have also been revealed. In the world, mass production of cyanobacteria in photobioreactors is also carried out to obtain various antibiotic and pharmaceutical active compounds [El-Sheekh et al., 2006].

One of the important research areas of recent years is on antioxidants, which play a role in scavenging free radicals that cause many diseases and aging [Atoui et al., 2005]. Antioxidants are molecules that prevent damage to the cell by preventing the formation of free radicals or scavenging existing radicals and generally carrying a phenolic function in their structure [Nagai *et al.*, 2005].

In the present study, the antioxidant activity of methanol extracts of ten different cyanobacterial species was tested by the α,α -diphenyl- β picryl hydrazyl (DPPH) method. Cyanobacteria isolates were incubated in BG11 medium for 4-8 weeks in a light environment. At the end of the incubation, it was extracted in 100% methanol at 4 °C for 12-24 hours. The sample and synthetic antioxidants, whose concentration was prepared as 10 mg/ml, were prepared in different concentrations, 250 $\mu g/ml$ of these samples were taken into test tubes and 750 $\mu g/ml$ of 0.06mM DPPH solution was added to them. After mixing the tubes roughly, they were kept in the dark for half an hour at room temperature, and the absorbance values were measured at 520 nm against the methanol blank.

IC50 values were calculated by taking into account the inhibition effects of DPPH radicals produced by all concentrations of cyanobacteria extracts used in the study. This value is defined as the amount of antioxidant required to scavenge half of the DPPH present at a certain DPPH concentration and is calculated by placing y=50 in the curve equation obtained from the graphs where the antioxidant amount versus the % inhibition values are drawn [Brand-Williams *et al.*, 1995].

When the data obtained from the study were examined, the DPPH capture activities of the cyanobacteria isolate were highest in isolate number 6 (0.3 mg/ml) when compared to ascorbic acid (0.5 mg/ml). It was determined that isolate 11 (16.55 mg/ml) showed the lowest activ-

ity. Other isolates 1 (1.12 mg/ml) > 4 (1.79 mg/ml) > 2 (2.53 mg/ml) > 3 (3.02 mg/ml) > 5 (4.94 mg/ml) > 10 (4.03 mg/ml) > 8 (5.24 mg/ml) > 9 (7.34 mg/ml) showed different scavenging activity. As a result, cyanobacterial extracts showed antioxidant activity in the study.

REVIEW ON THE PRODUCTION OF MICROBIAL PIGMENTS AS NATURAL COLOR SOURCES

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Keywords: food; biotechnology; pigment; microorganism; fermentation.

Color is considered one of the features that attract consumers' attention and increase the attractiveness of food. The use of synthetic dyes is declining day by day following changes in consumer requirements and the country's legislation. Pigments are chemical compounds that absorb light at visible wavelengths and can be identified as natural, synthetic, and inorganic based on their source. The most used foodgrade pigments are chemical compounds containing nitrite and nitrate salts [Tuli et al., 2015]. Thus, the carcinogenic and teratogenic effects of synthetic compounds have been reported, which has been one of the most necessary reasons for the growing interest in the pigment's production of biological origins, such as plants and microorganisms [Mehri, 2020]. Natural pigments are produced by living organisms such as plants, animals, fungi, and microorganisms. These pigments, such as coloring compounds are essential, which possess antioxidant, antimicrobial, and antimutagenic activity in natural products. This view is that pigments utilization of microbial origin in processed foods is a promising area with great economic potential. There are many microorganisms that produce pigment in nature and produce pigments of different colors [Stich et al., 2002]. The reason for the diversity of pigments obtained by biotechnological methods is due to their different chemical composition and the presence of specific chromophores. Microbial production in pigment production; Regardless of the seasonal changes, the use of cheap raw materials has many similar advantages, such as obtaining different color tones according to the conditions of biological cultivation, faster and more efficiently than chemical synthesis. Therefore, it is necessary to study the various natural sources of food dyes and their potential for use [Soares et al., 2016].

Presently, microbiological pigments usage as new types of food dyes is becoming a promising area with great economic potential. This study is based on the application of bacteria, fungi, and molds in food products, used in various fields (milk and dairy products, fruit juices, confectionery, etc.) as a natural dye. The diversity of extraction protocols used to remove pigment from various microorganisms can also affect the quality and efficiency of purification mechanisms suitable for food concentrates.

BIOSYNTHESIS OF SILVER NANOPARTICLES BY YEASTS Ganbarov Khudaverdi, Aliveva Nasiba

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Keywords: silver nanoparticles; yeasts; Saccharomyces cerevisiae.

Nanoparticles have unique properties that allow the application in various fields of science, technology, medicine and industry. As a result of reducing the size of particles to nano levels, their properties increase. Currently, there is great interest in inorganic nanoparticles, especially metal particles. The reason for this is that the metals made from them have a multifaceted function. Metal, including silver nanoparticles, due to their advantages over existing chemical drugs, are used as a potential tool in medicine, as well as in the treatment of diseases.

Nanoparticles can be obtained by physico-chemical and biological methods. It is a mixture of chemical reagents used in nanoparticles obtained by physico-chemical methods. And on the other hand, these chemical reagents pollute the environment. Therefore, special attention is paid to obtaining metal nanoparticles from biological systems, including microorganisms [Abbasov, 2010].

Silver nanoparticles attract the attention of researchers more, due to their unique properties and wide range of applications, including their use in medicine. In this regard, silver nanoparticle formation properties of various types of fungi and bacteria have been studied. In modern times, obtaining silver nanoparticles through microorganisms is considered one of the most important problems of industrial microbiology. The formation of silver nanoparticles by mold fungi, yeasts and bacteria has been studied by the employees of Baku State University in Azerbaijan. It is known that the properties of metal nanoparticles significantly depend on their size and shape. Metal nanoparticles formed by

different types of microorganisms differ greatly , and these different properties significantly affect the antimicrobial properties of nanoparticles [Ganbarov, 2012].

The aim of our work was to study the antibacterial properties of silver nanoparticles obtained by the yeast Saccharomyces cerevisiae which is used in households. It has been established that the cells of the yeasts are ellipsoid and in the nutritious environment of the malt juice is multiplied by active budding. The biomass of this fungi culture was collected (10 grams) and incubated at a temperature of 30C° a day with a solution of silver nitrate salt. The color of the culture reaction mixture was darkened compared to the control variant. Darkening of the color of the reaction mixture is considered as the first sign of the formation of silver nanoparticles. Studies on the isolation of silver nanoparticles and their properties are continued.

ESSENTIAL OILS FROM BULGARIAN ROSA ALBA L. AND ROSA DAMASCENA MILL. AS ANTIFUNGAL AGENTS

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Keywords: rose oil; Aspergillus fumigates; Aspergillus niger; Aspergillus flavus; antifungal activity.

Rosa alba L., also known as white Bulgarian Rose, is grown for industrial production only in the Valley of Roses in Bulgaria. Recently it is processed and distilled for rose oil separately from Rosa damascena Mill. In addition to a delicate aroma, both oils exhibit valuable biological properties (Kovacheva et al., 2010). The purpose of this work is to investigate the antifungal activity of both essential oils individually and in combination with nystatin against the human and plant pathogens Aspergillus fumigatus, Aspergillus niger, and Aspergillus flavus.

According to GC-MS analysis, the major biologically active components are as follows: *R. alba* L.-geraniol (18,28%), citronellol (18%),

nerol (7,74%), eugenol (0,38%), methyleugenol (0,1%), and caryophyllene (4,08%); *R. damascena* Mill. - geraniol (14,13%), β – citronellol (13,56%), nerol (8,34%), eugenol (0,64%), methyleugenol (2,05%) and β – caryophyllene (4,08%)[Mileva *et al.*, 2014]. Fungal cultures were grown in beer agar medium. Agar dilution method was used to analyze the antifungal activity. Mycelial growth inhibitions were determined by disc diffusion technique.

Antifungal effects of both oils (in concentrations of 10, 25 and 50 mg/L and in combination with 50 mg/L nystatin as well) were determined by measuring the inhibition zones diameter 48 and 120 hours post inoculation and were presented as antifungal index (AI). There was a decrease in the radial growth of *Aspergillus flavus* depending on the oil concentration. The most sensitive inhibition was observed with both oils at a concentration of 50 mg/l, which was more pronounced at 48 hours. The combination of *R. alba* oil with nystatin exhibited an over additive antifungal effect that was more efficient than the respective combination of *R. damascena* with nystatin against *A. niger*. The over additive effect for both combinations was the most pronounced at 50 mg/l oil and 48 h post inoculation. The combinations of Bulgarian *Rosa damascena* and *Rosa alba* oils with nystatin are promising effective antifungal formulations against *Aspergillus flavus* and *Aspergillus niger*, which pharmacological treatment is challenging [Shohayeb *et al.*, 2014].

This data indicates that rose oil could be utilized as a topical disinfectant in clinical practices. The rose oils could also be used as well as to preserve fruits and vegetables from these pathogens.

Further studies of Bulgarian rose oils *in vivo* efficacy and in animal models are needed to confirm the obtained results.

EFFECT OF DIFFERENT SUCROSE CONCENTRATIONS ON SEED GERMINATION OF PROMISING ALFALFA VARIETIES

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Keywords: osmotic stress; alfalfa varieties; drought resistant plants

Plant breeding for obtaining drought-resistant forms and varieties has recently become significantly important due to global warming. A stable increase in air temperature by only 0.8–1.2°C [Udovenko, 1988]

resulted in an increase in the frequency of droughts and an extension of dry periods. Hence, the need to obtain drought-resistant plants and especially crops has emerged. Alfalfa is a valuable and one of the indispensable fodder crops used in animal husbandry. There are a fairly large number of promising varieties that give stable yields, but once in drought conditions and subjected to osmotic stress, such varieties mostly demonstrate different levels of adaptability. Therefore, each vear it becomes increasingly difficult to get high yields. Azerbaijan is characterized by its rather complex soil and climatic conditions, and its diversity allows the use of available promising varieties specifically for each separate region. Ranking of varieties according to the degree of tolerance of their seeds to osmotic stress will make it possible to recommend these varieties for use in rainfed or irrigated conditions, as well as to include them in the breeding program for drought resistance. Therefore, the purpose of this work was to rank alfalfa varieties according to drought tolerance caused by different concentrations of sucrose [Udovenko, 1988].

Seeds of 7 promising alfalfa varieties of different origin were taken as the material of the study, including Aran, Agstafa-1, Agstafa-2, Absheron, Goyazan, Yaz Chichai and Leader. According to the guidelines, the seeds of each of these varieties were washed, sterilized, and grown in sterile Petri dishes immersed in aqueous solutions of sucrose, the concentration of which varied from 7% to 20%. Low concentrations of sucrose, which create an osmotic pressure of 7-9 atmospheres in the germination medium, did not reveal significant differences between varieties. Significant differences between varieties in the number of germinating seeds were noted at an osmotic pressure of 14 atm. With an osmotic pressure of 20 atm normally germinated seeds were not found for any variety. Therefore, for the ranking we used the solution with an osmotic pressure of approximately 14 atm in the germination medium. In this case, the varieties were arranged in the following order: Goyazan -16.7%; Yaz Chichai -8.3%; Absheron 6.7%; Agstafa-2 - 6.7%; Agstafa-1 - 6%, Aran - 2% and Leader - 0%. Differences in biometric parameters depending on the concentration of sucrose and osmotic pressure are being discussed.

THE EFFECT OF PHYTOHORMONES ON THE GERMINATION OF STE-VIA REBAUDIANA BERTONI SEEDS IN IN VITRO CULTURE

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Keywords: seed germination; in-vitro conditions; action of phytohormones; morphophysiological programs.

Stevia rebaudiana Bertoni refers to tropical plants that reproduce perfectly in nature by vegetative means and seeds. Tropical conditions are characterized by constant heat and moisture, so after the end of formation, the seeds, once in moist soil, immediately germinate. Such seeds are characterized by a short rest period, they are not resistant to drying, and, as a result, they quickly lose germination. For this reason, they are classified as recalcitrant. The physiology of recalcitrance has been poorly studied to date. It is known that the main factors of regulation of plant growth and development are phytohormones, which are the main factors of switching morphophysiological programs [Nefedieva et al., 2013]. Therefore, the purpose of this work was to study the effect of phytohormones and their combinations on the germination of seeds of various varieties of Stevia rebaudiana Bertoni under in vitro conditions [Polevoy, 2001].

The seeds of the Russian Varieties Dream, Honey grass, Detsko Selskaya, Delight, Sweetmeat, Sweet Tooth and Turkish varieties – Miracle, Sheker otu -1, Sheker otu-2, Stevia chichegi were used as the object of research.

The seeds were grown on several variants of the Murashige - Skoog nutrient medium. Option 1: nutrient medium M-S without phytohormones; option 2: M-S + 0.4 mg/l 6-benzylaminopurine (BAP); option 3: M-S + 3 mg/l 3-indolyl acetic acid (IAC); option 4: M-S+ 0.4 mg/l BAP+ 3 mg/l IUK.

The seeds were grown on several variants of the Murashige Skuga nutrient medium. Option 1: nutrient medium M-S without phytohormones; option 2: M-S + 0.2- 0.4 mg/l 6-benzylaminopurine (BAP); option 3: M-S + 0.4-3 mg/l 3-indolylacetic acid (IAC); option 4: M-S+ 0.4- 0.2 mg/l BAP+ 0.4-3 mg/l IUK.

In the first variant of the medium, normal shoots were noted only for the Dream variety. Seeds of all other varieties in this variant did not give germination experience. In the second experimental variant, seedlings with a well-developed stem part and leaves were obtained, but without roots, or with poorly developed roots. Subsequently, such seedlings were transplanted to media containing different concentrations of IUC. Using the third option did not give any results.

In the fourth version of the experiment, small seedlings with an underdeveloped root system were obtained. The stimulating effect of phytohormone combinations on the germination of *Stevia rebaudiana Bertoni* seeds with different storage periods is discussed.

BIOAUGMENTATION AND BIOSTIMULATION AS A TREATMENT FOR SOILS CONTAMINATED WITH HIGH CONCENTRATION OF HYDROCARBONS

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Keywords: bioaugmentation; biostimulation; oil products; biodegradation efficiency. Oil hydrocarbons, used as a source of energy, and as lubricants, are still the most dangerous environmental pollutants. Self-restoration of polluted sites is ineffective due to deficiency of nutrients, absence of constant aeration of the soil, and some other factors. Bioremediation is the safest way to clean the environment from oil products. However, application of this technique has some difficulties, and increasing the effectiveness of bioremediation is currently actual aim.

The purpose of this work is to compare bioaugmentation and biostimulation as a technique for treatment of soils contaminated with high concentration of hydrocarbons.

Soil model systems were contaminated with oil products with initial concentration 172,900 mg/kg, which is almost 350 times higher than the maximum allowable concentration for industrial zones. Model systems were treated at the start of experiment (0 day) and in 14 days at 20°C: for biostimulation by modified Munz medium [Pirog *et al.*, 2011] with 2% molasses; for bioaugmentation by mixed culture of bacteria of the genera Rhodococcus and Bacillus. Samples were analyzed by gravimetric analysis [Drugov *et al.*, 2009] and serial dilutions.

The most effective degradation in samples was observed during the first 14 days of experiment: the effectiveness of oil destruction after biostimulation was (42.6±17.3) %, and after bioaugmentation $(20.8\pm14.7)\%$. After 80 days of incubation, concentration of oil products in bio stimulated samples stayed the same (the final biodegradation efficiency was (42.8 ± 2.5) %. In the case of bioaugmentation, final efficiency after 80 days was $(35.1\pm6.6)\%$.

If saying about the number of cultivated bacteria in soil samples, 10 times increase in the total content of heterotrophic bacteria (from $(1.6\pm0.8)\times10^5$ to $(6.9\pm2.2)\times10^6$ CFU/g) was observed during first 14 days in biostimulated samples, and after 80 days their number decreased $(5.4\pm3.9)\times10^5$ CFU/g. At the same time, the number of bacteria was near stable (from $(1.2\pm4.6)\times10^6$ to $(7.2\pm0.6)\times10^6$ CFU/g) in the samples after bioaugmentation.

Thus, it can be concluded that the soil has a self-potential for degradation of high concentration of oil products due to presence of hydrocarbon-degrading bacteria. But this process needs exogenous nutrients. The most effective degradation of oil products is observed during the first 14 days after biostimulation and bioaugmentation. Less effectiveness of bioaugmentation can be connected with competition of exogenous oil-degrading bacteria with indigenous microbiota.

MOLECULAR IDENTIFICATION OF BACTERIAL MICROFLORA OF FRESH MILK AND ITS INFLUENCE ON SPOILAGE OF MILK

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Keywords: fresh milk, bacteria, spoilage, sequencing, identification.

The specific composition of the milk microbiota directly affects the subsequent development of dairy products. Microorganisms can cause fermentation of milk through the formation of lactate and have many different effects on the organoleptic, textural, taste and organoleptic properties of the resulting products [Wouters *et al.*, 2002]. Microorganisms can also negatively affect the quality of milk and its shelf life; for example, psychrotolerant bacteria can multiply during cooling and, due to the production of extracellular lipases and proteases, lead to spoilage [Desmasures *et al.*, 1997; Hantsis-Zacharov *et al.*, 2002]. The microbial composition of milk can also have health consequences, since the consumption of raw milk infected with pathogens can in some cases lead to serious diseases [Oliver *et al.*, 2009].

The purpose of our study was a molecular genetic study of the composition of the bacterial microflora of fresh milk from 5 different farms. DNA extraction from bacterial colonies a DNA extraction kit DNeasy Blood & Tissue Kit (Qiagen) was used. Based on the analysis of the nucleotide chains of the deposited 16SrRNA gene, 3 pairs of primers were obtained that allow amplification of a fragment of the ribosomal region with a length of 500, 800 and 1500 base pairs: 16SrRNA-8F, 16SrRNA-806R, 16SrRNA-530r. 7 samples were selected for genetic identification by determining the nucleotide sequence of the 16S rRNA gene fragment.

As a result of the research, 7 samples were collected using the Mega 3.1 computer program and the nucleotide sequences of the 16S rRNA gene fragments. Bacteria isolated from cow's milk were identified accordingly: Escherichia coli; Enterobacter cancerogenus; Enterobacter sp.; Shigella sp.; Klebsiella sp.; Enterobacter asburiae; Enterococcus faecalis; Lactobacillus paracasei.

The identified bacteria are both pathogenic and beneficial lactic acid bacteria involved in the fermentation of milk. Pathogenic microflora is potentially dangerous to human health, and is also involved in the rapid spoilage of milk and dairy products.

ISOLATION OF BIFIDOBACTERIA FROM SAMPLES OF BREAST MILK AND INFANT FACES

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Keywords: Bifidobacteria; Human milk; microbiota.

Bacterial colonization of the infant's intestines strongly influences the health status of the host, as members of the gut microbiota may contribute to barrier effects against pathogens or maturation of the gut immune system.

Of the facultative anaerobic group of bacteria, *Bifidobacteria*, are among the first colonizers of breastfed infants. The microbiota of formula-fed children is more diverse and contains more *Bacteroides, Clostridium* and *Enterobacteriaceae* [Zakharova, 2010].

Bifidobacteria were isolated from breast milk and from the intestines of breastfed infants and characterized by microbiological meth-

ods. The study involved about 10 women and their 5 and 8 day old infants, swabs and faces from the infants were collected in a sterile tube. Fecal samples were plated in triplicate on a Man-Rogosa-Sharpe (MRS) medium supplemented with L-cysteine (0.5 g/l) (MRS-Cys) agar plate, and incubated under anaerobic conditions at 37°C for 48 hours. Bacterial isolates were identified using an optical microscope to determine their morphology and Gram stain results.

Isolation and identification of *Bifidobacteria* from mammary milk samples and infant feces showed that all gram-positive and catalasenegative isolates with typical *Bifidobacteria* were identified to the genus level using the F6PPK test. Isolates belonging to three types of *Bifidobacteria* were isolated. From milk samples, *B. breve. B. bifidum* was isolated from the feces of infants.

In recent years, it has been shown that breast milk is a constant source of mutualistic and probiotic bacteria for the intestines of infants, including *staphylococci*, *streptococci*, and *lactic* acid bacteria [Rodríguez, 2016]. These groups of bacteria may also play an important role in reducing morbidity and severity. Human milk is a source of bacteria for the intestines of infants, in which they play the role of anti-infective, immunomodulatory and metabolic agents. Recent studies have revealed that the mammary glands have their own *microbiota*, which is formed in late pregnancy and during lactation. This bacterial community can vary depending on personal factors and the health of the breastfeeding woman. It is assumed that certain bacteria from the mother's intestines can colonize first the mammary glands and then the intestines of the child through breastfeeding. If future research confirms all these assumptions, there are great prospects for the use of bacteriotherapy and the use of probiotics for the treatment of a wide range of diseases in children.

MOLECULAR METHODS IN WHEAT (TRITICUM AESTIVUM L.) BREEDING

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Keywords: gliadin; locus; bread wheat; protein.

Wheat (*Triticum aestivum* L.) –one of the most important types of cereals cultivated in our republic and throughout the world. Identification of varieties, lines and hybrids is an integral element of breeding

and seed production, it allows you to monitor the purity of the variety according to its well-known standard [Wang, 2010]. Identification of varietal material is traditionally carried out according to morphological characteristics. Along with this, genotype identification methods based on the use of protein markers have been created. They are quite relevant and reliable. Electrophoresis of spare proteins is successfully used to develop methods. The high polymorphism of markers allows them to be used in determining the relationship between varieties. To determine the genetic diversity and identify wheat varieties, 30 varieties of bread wheat were used in the Agricultural Research Institute. It has been established that, basically, breeders are working on gilad blocks with a component controlled by the locus of chromosome 1A, GLd 1A4, GLd 1A5, GLd 1A6 and another GLd 1A2, GLd 1B 6 blocks. And according to the blocks controlled by the 1B chromosome GLd 1 in 1, GLd 1 in 3, GLd 1 in 4, GLd 1 in 8, in 1B each chromosome GLd 1D1, GLd 1D3, GLd 1D8, and for 6A, 6B, 6D, there is a large polymorphism. On chromosome 1a Gld6a 4, GLd 6A2, Gld 6a and 6 In each in the main GLd 6V 1, GLd 6V 4, GLd 6V2. Thus, the genetic diversity of wheat varieties for these proteins is indisputable. As a result, it was found out that breeders choose varieties with such blocks. It turned out that varieties with these blocks are generally more productive, and some are more resistant to drought, and some blocks are responsible for quality. For example, GL d1 A4, GL d1 A5 are responsible for the high quality of wheat.

DETERMINATION OF THE PRESENCE OF HIGH-MOLECULAR-WEIGHT GLUTENIN GENES IN SAMPLES OF KAZAKH BREEDING

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Keywords: wheat; Triticum aestivum; protein; glutenin.

Soft wheat (*Triticum aestivum* L.) is a globally important food crop, accounting for 20% of calories consumed by humans. It is an important source of protein, vitamins and minerals. The spare proteins in wheat are collectively called gluten, but in fact gluten is an aggregate formed from two main types of protein: gliadin and glutenin. Gliadins and glutenins make up approximately 30 and 50%, respectively, of the total protein in wheat grain. The Glu gene complex is responsible for the

quality of this protein complex. The combination of different gene alleles characterizes the quality of wheat gluten [Shewry *et al.*, 1992].

The aim of the study is to identify allelic combinations of genes Glu-A1 1, 2; Glu-B1 17, 7, 8; Glu-D1 5, 10, 2, 12 in samples of Kazakh breeding responsible for increasing or decreasing the quality of wheat grain on the protein composition of samples [Payne *et al.*, 1987].

Materials and methods: during the research, 14 lines of Kazakh wheat were used: 435/lutescens 2, 486/lutescens 22, 23/07, 218/10, lutescens 2222, lutescens 2205, lutescens 2262, lutescens 747, lutescens 2016, line P-1413, line 201/12, line 205/12, line P-1417, line 198/224. DNA isolation from plant material was performed by the methods of BECOMING [Doyle, J. J. et.al., 1987.]. The concentration was determined on NanoDrop2000. Marker genes were amplified in a final reaction volume of 15 μl containing: 1.5 mMSe buffer, 2 mM dNTP, 50 MMGCL2, 10 pmol of direct and reverse primer, 1U TaqDNA polymerase, DNA with a concentration of 100 ng/μl. Polymerase chain reaction was carried out with the following thermal cycling conditions: Glu-D1 x2-x5: 95 °C/5m., 58 °C/30c., 72 °C/1m; Glu-D1 y10-y12: 95 °C/5m., 60 °C/30c., 72 °C/1m; Glu-A1: 95 °C/5m., 58 °C/30c., 72 °C/1m; Glu-B1 x7/x17: 95 °C/5m., 58 °C/30c., 72 °C/1m.

According to the results of the study, samples with a high score of bakery qualities were identified, such as 486/lutescens 22, line 201/12, line 198/224 at the Glu-A1 locus. Samples 218/10, lutescens 2205, lutescens 2207, lutescens 2016, line P-1413, line 201/12, line P-1417 at the Glu-B1 locus and samples 435/lutescens 2, lutescens 2205, lutescens 2262, lutescens 747, lutescens 2016, line 201/12, line 205/12, line 198/224 at the Glu-D1. After the polymerase chain reaction, the following distribution of haplotypes of Glu-A1, Glu-B1, Glu-D1 loci was obtained in the wheat samples studied: allelic combinations of Glu-A1 genes 1, 2 in 3 samples, the most common allele of the Glu-B1 – x 7 locus, a combination of Glu-D1 – x locus genes 5-y10, responsible for high baking qualities, was found in 9 studied samples.

MOLECULAR AND BIOLOGICAL ASPECTS OF THE IMMUNOHISTOCHEMICAL MARKER PHH3 IN BREAST CANCER

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Keywords: breast cancer; immunohistochemistry; phosphorylated histone3; morphometry.

Phospho Histone H3 (Phh3), a sensitive marker for determining of the mitotic figure, is widely known in various forms of cancer [Baehner *et. al.,* 2000]. The advantage of Phh3 immunohistochemical staining in mitotic scoring is that the score is based on both the identification of positively stained figures and morphological confirmation of chromatin condensation [Brenner *et. al.,* 2003].

As a result of our researches, we have come to the following conclusions:

- 1. The average mitotic activity index for phh3 was 124±23 cells per 1mm², mitotic activity in the first group was 234±5,7 cells per 1 mm², in the second group it was higher 117±7,9 cells per 1 mm².
- 2. The total cell density in non-tumor structures was 2409 ± 405 in 1mm^2 , which is statistically significantly less than the cell density in the tumor 4179 ± 251 in 1 mm^2 .
- 3. When evaluating the index of proliferative activity, it is critically important to carry out the correct procedure for restoring antigenic activity if the immunohistochemical retriever is not performing adequately; there is a significantly high percentage of loss of positive cells.
- 4. The cells of the non-tumor epithelium of the ducts and lobules, on average, had a nuclear area of 41,93±2,39 μm^2 , the perimeter of the nuclei was 28,8±1,55 μm , and the nuclear roundness index was 0,65±0,04.

One of the important results of our work is the objectification of the morphological criteria of Phh3, cell density and nuclear parameters used every day in pathological practice. In our opinion, due to the development of technology for storing and processing digital data, digitized preparations will very soon create an opportunity for an objective and transparent analysis of morphological data and will underlie any clinical conclusion that uses morphological analysis data. Digital processing of histological material, based on a full scan of the histological preparation. We used the Leica QWin PRO computer analysis system for

microscopic imaging. In our investigation, fully prepared histological and immunohistochemical preparations were scanned using MIRAX MIDI (Zeiss) in order to obtain digital images of these preparations. Then, using the Pannoramic Viewer image viewer (3DHistech), epithelial complexes with maximum Phh3 expression were founded and preparations stained with hematoxylin and eosin were positioned. It would be expedient to describe the practical side of the work of the MIRAX MIDI program (Zeiss). For immunohistochemical staining, a PT Module water bath was designed to unmask the antigen. Rabbit monoclonal antibodies (1:5000, Epitomics clone) were used to detect phh3. The immune complex was detected using the Dako REAL EnVision imaging system.

IDENTIFICATION OF WHEAT RESISTANCE GENES LR AND SR IN RELATION TO LEAF AND STEM RUST IN WHEAT SAMPLES OF KAZAKHSTAN BREEDING

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Keywords: leaf rust; stem rust; wheat; resistance genes.

One of the biggest threats to agriculture is diseases that are caused by various kinds of pathogenic fungi. Diseases of this spectrum are common in almost all regions of cultivation in Kazakhstan [Koishibaev *et.al.*, 2005].

Leaf and stem rust of wheat is a dangerous disease of wheat, which causes crop shortages in all areas of distribution. At the moment, the causative agent of the leaf rust disease (*Puccinia triticina*) has about 200 races, which differ in their intensity of the degree of infection in relation to various plant species [Jin Y. Et.al .,2008]. Stem rust, a disease caused by an obligate pathogen (*Puccinia graminis* f.sp. tritici), occurs in many countries of the world and can cause crop losses of up to 50-70% [Singh *et al.*, 2006].

The aim of this work was to detect wheat samples that carry effective resistance genes Lr19, Lr37, and Sr2, Sr21, Sr32, Sr35 in relation to brown and stem rust of wheat and the selection of resistant lines of rust resistance donors.

The object of the study was 12 samples of wheat of Kazakh breeding. DNA isolation from plant material was carried out from 10-day-old wheat seedlings using the STAV method [Doyle *et al.,* 1987]. The efficiency of DNA extraction from plant material was evaluated using a NanoDrop 2000 spectrophotometer (Thermo fisher scientific, USA). Marker genes were amplified in a final reaction volume of 15 μ l containing: 1.5 mm TE buffer, 2 mMdNTP, 50 MMGCL2, 10 pmol F- and R-primers, 1U TaqDNA polymerases, DNA with a concentration of 100 ng/ μ l. PCR in order to identify the genes of resistance to stem and leaf rust was carried out under the following thermal cycling conditions with differences in annealing temperatures: 95 °C for 5 minutes, 95 °C for 20 seconds, Sr2-60 °C, Sr21-60 °C, Sr32-60 °C, Sr35-60 °C, Lr19-60 °C, Lr21-60 °C, Lr37-62 °C, Lr39-58 °C for 20 seconds, 72 °C for 20 seconds, and the final elongation of 5 minutes at 72 °C.

Thus, the conducted studies will allow us to select effective donors of resistance genes, both in relation to stem and leaf rust of wheat. In wheat breeding in the direction of resistance to stem and leaf rust, samples of domestic breeding can be recommended as the starting material of the selective feature: Tauelsizdik 20 and Akmola Niva, Akmola 2 and Russian breeding – Saratov 55, lines 21/11, 229/10, 69-08-3, 219-09-8, Lin. 201 can be recommended for the next stage of the breeding program / 21g., Lin. 205 / 21g., Lin. 225 / 21, Lutescens 2205, Lutescens 2207, Lutescens 2210, Lutescens 1519, Lutescens 2203, Lutescens 2222, Lutescens 2231, 218/10, Erit 42/12.

THE INFLUENCE OF ALTERNATIVE PROTEIN SPLICING ON THE AMINO-ACID SEQUENCE

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Keywords: alternative splicing; mRNA; exon.

When alternative splicing is transcribed from pre-mRNA, it includes several introns and exons. The exons, which should be stored in mRNA are determined during the splicing process. The regulation and selection of splicing sites are carried out by the trans-activated splicing activator and splicing repressor proteins, as well as by the cis-influence elements contained in the pre-mRNA itself, such as exon splicing enhancers (ESE) and exon splicing silencers (ESS).

RNA sequence elements and protein regulators determine, which exons are removed and which are included during splicing. The splicing is regulated by proteins (repressors and activators) acting on premRNA and corresponding regulatory cis-influence fields (silencer and enhancer). The cis-regulating elements are divided into four categories depending on their position and function:

The exon splicing enhancers, exon splicing silencers, intron splicing enhancers, intron splicing silencers. Splicing silencers are places where the repressor proteins are connected. They are different with their sequence, as well as the types of proteins binding to them. ISSs and ESSs are usually connected with heterogeneous nuclear RNPs with one or more RNA-binding domains and protein-protein interaction domains [Smith *et al.*, 2000]. Most of the splicing repressors are heterogeneous nuclear ribonucleoproteins (hnRNPs), such as hnRNPA1 and polypyrimidine-binding protein (PTB). Most splicing repressors are heterogeneous nuclear ribonucleoproteins (hnRNPs), such as hnRNPA1 and the protein binding the polypyrimidine tract (PTB).

The splicing enhancers are places where binding proteins-activator are connected.

This can also occur in the intron and exon. ESEs are usually associated with members of the SR (Ser-Arg) protein family [Graveley, 2000]

SR proteins are a protected family of proteins involved in RNA compounds. SR is so named because it contains protein domains with long repetitions of amino-acid residues of serine and arginine, the standard abbreviations of which are "S" and "R", respectively. The length of SR proteins consists of $\sim\!200\text{-}600$ amino-acids and two domains – the field of RNA recognition motive (RRM) and RS domain. SR proteins are more widespread in the nucleus than in the cytoplasm.

SR proteins are important for constitutional and alternative premRNA splicing, mRNA export, genome stabilization, and translation. SR proteins alternately generate several mRNA transcripts from a single pre-mRNA transcript. At this time, it combines the pre-mRNA by choosing various splicing sites in the pre-mRNA chains. After the completion of the splicing, the SR protein can remain connected to help remove the mRNA chain from the nucleus. The RNA polymerase enzyme transfers DNA to RNA. SR proteins prevent pre-mRNA binding with the coding DNA chain for increase of genome stabilization. SR proteins then adhere to the newly developed pre-mRNA.

INVESTIGATION OF ANTIMICROBIAL PROPERTIES OF BLACK SAXAUL (HALOXYLON APHYLLUM) SEED EXTRACT AND ITS PROSPECTS FOR USE IN ANTIMICROBIAL PREPARATIONS

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Keywords: black saxaul; oil extracts; water decoctions; water-alcohol infusions.

The desert plant saxaul is used as a source of medicinal plant raw materials. Scientists from Pakistan conducted a study on the presence and evaluation of antibacterial and antifungal activity of saxaul in various fractions. The study showed that fractions of *H. griffithii* showed antibacterial activity against *S. aureus*. Therefore, the relevance in the study of black saxaul grown on the territory of Kazakhstan is being raised.

Plant material: black saxaul seeds from 4 regions of the country: Shchuchinsk, Kyzylorda, Turkestan and Almaty regions. The preparation of extracts consists in grinding the plant material and adding an extractant in a ratio of 1:10. To obtain 50 ml of extracts, 5 g of plant raw materials were used. The extractants used are pre-sterilized for an hour at 120 °C. The two components are mixed, and then go through heat treatment in a water bath for 30-40 minutes, without bringing to a boil.

A disco-diffusion method was used to analyze antimicrobial and antifungal activity. A nutrient medium was used to determine the antibiotic sensitivity of microorganisms. Three test strains were taken: *Bacillus subtilis, Pseudomonas spp., Fusarium oxysporum.*

Extracts were prepared from the seeds of black saxaul using three substances: distilled water, alcohol diluted to 40% and linseed oil. Water decoctions, water-alcohol infusions and oil extracts were prepared with an estimated volume of 50 ml. The obtained extractions from the seeds of black saxaul were tested for antimicrobial activity and toxicity.

As a result of the analysis for the presence of antimicrobial activity of drugs, water-alcohol infusions and oil extracts had good indicators. Of the three microorganisms (*Bacillus subtilis, Pseudomonas spp., Fusarium oxysporum*), water-alcohol infusions were the most effective against *Pseudomonas spp*. The most effective were water-alcohol infusions prepared from seeds from the Kyzylorda region. In addition, water-alcohol infusions had short-term bacteriostatic activity against *Bacillus subtilis* and *Fusarium oxysporum*.

Oil extracts also had short-term bacteriostatic activity. A greater effect was observed against Fusarium oxysporum. Fungi Statistical activity was well expressed in preparations 1 and 2 obtained from seeds from the Almaty region and the Kyzylorda region.

Water decoctions had short-term bacteriostatic activity against Pseudomonas spp. of the four preparations, the largest diameter of the lysis zone was manifested under the influence of a preparation with seeds from the Kyzylorda region. Against *Bacillus subtilis* and *Fusarium oxysporum*, water decoctions are ineffective. On the contrary, water decoctions from the seeds of black saxaul showed a bacterial stimulating effect for *Bacillus subtilis*.

In conclusion, there are prospects for the use of water-alcohol infusions and oil extracts from the seeds of black saxaul as antimicrobial drugs. In addition, Water decoctions can be used as a component in nutrient media to detect the bacterium *Bacillus subtilis*.

ARTEMISIA PHYTONIOSOMES PROTECT LIVER CELLS FROM GLYCOXIDATION DAMAGES VIA CYTOKINES AND APOPTOSIS REGULATION

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Keywords: Artemisa phytoniosomes; apoptosis; liver; glycoxidation damage; cytokines. The implication of advanced glycation end-products (AGEs) in various age-related diseases is irrefutable. The chronicity of these "glycotoxins" imparts various damages that result in metabolic dysfunction and diseases. Due to the variety of AGEs, their mechanistic implication is relatively understood, however, inflammation and oxidative stress play a key role in AGE-induced disorders [Fernando et al., 2019; Rungratanawanich et al., 2021]. Hence, therapeutic approaches mainly focus on the use of anti-inflammatory and antioxidant molecules. The use of natural products such as plant extracts is of high interest in complementary and alternative medicine [Ma et al., 2018, Guler et al., 2014]. In the current work, we propose the formulation of phytoniosomes encapsulating three artemisia species (A. herba alba, A. dracunculus, and A. absinthium) for the mitigation of AGEs and their induced cell redox dysregulation in the liver. Plants were extracted using different solvents

and analyzed for their components using biochemical and LC-O-TOF-MS/MS techniques which identified their major phyto components. The phytoniosomes were explored for their anti-glycating effect in a bovine serum albumin model after which they were tested in vitro over THLE-2 liver cells challenged with AGES. In parallel, Swiss Target Prediction, DisGeNET, OMIM, and GenCLiP3 databases were used to identify gene and protein targets to create the pharmacology network. Cytoscape was used to generate and analyze the protein-protein interaction (PPI) and phytochemical-protein interaction networks to determine the major processes implicated in Artemisia's mechanism of action. Data demonstrated that *Artemisia* phytoniosomes had an important anti-AGE effect comparable to reference molecules and were able to restore cell dysfunction through the restoration of TNF-α, IL-6, nitric oxide, and total antioxidant capacity to normal levels. Phyto Niosomes were able to protect the cells from apoptosis by decreasing the caspase 3 activity, bioinformatic tools and Network pharmacology analysis confirmed the induction of the effect via MAPK and AGE-RAGE signaling pathways. The current report highlights the potential of *Artemisia* phytoniosomes as a plausible option in the therapy of AGEs-related diseases [Moulahoum et al., 2022].

INVESTIGATION OF POTASSIUM HUMATE AS AN INDUCER OF CALLUS FORMATION IN *IN VITRO* CULTURE OF *MEDICAGO SATIVA* AND ITS EFFECT ON THE PROTEIN COMPOSITION OF CALLUS TISSUE

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Keywords: Medicago sativa, callus tissue, potassium humate, protein composition. Medicago sativa is a field medicinal herb consisting of many trace elements necessary for the human body and a number of proteolytic enzymes [Bora et. all., 2010]. The alfalfa plant is used in folk medicine, agriculture and feed production. In folk medicine, the drug is widely used in the treatment of diabetes mellitus and thyroid diseases in the prevention of blood pressure, diabetes mellitus, stomach ulcers. The high content of chlorophyll in alfalfa supports the growth of connective tissue and is useful for people suffering from arthritis [Samac et. al.,

2004]. Lyophilized callus tissue of alfalfa can act as an excellent sieve of nutrients, while reducing the time for its cultivation.

The aim of this work was to study the effect of humic acids, including potassium humate, on the induction of callus formation and the effect on the protein composition of the Medicago sativa plant in vitro.

The following Medicago sativa varieties were used as research objects: Rayhan, Azure, Orai zhane Shortandinskaya 2. Culturing of callus tissue was carried out on Murashige-Skoog medium with the addition of 2,4-D and different concentrations of potassium humate (0,1%; 0,2%; 0,3%; 0,5%). The raw mass of callus was determined by weighing on Pioneer Ohaus electrolytic scales. The protein composition was studied by PAAG electrophoresis [Laemmli, 1970] with modifications. The results were analyzed using the BioCapt 2022 program.

In the research work, alfalfa leaf explants were used to study the process of callusogenesis. 4 different concentrations of potassium humate and 2 mg/l of 2,4-D were added to the MS nutrient medium, in the control variant only 2,4-D was added.

According to the results obtained, the callusogenesis of alfalfa explants cultivated on an experimental nutrient medium with the addition of 0.1% potassium humate showed an average of 62.1% for 4 varieties, at a concentration of 0.2% potassium humate - 65.7%, at a concentration of 0.3% - 75.61%, at a concentration of 0.5% -67.13%. In the control variant of alfalfa, callusogenesis was 38.58%.

When cultivating Medicago sativa callus tissues with the addition of potassium humate, it was observed that each passage added about 2 times its original mass: for example, in the first passage, the average mass of alfalfa varieties was 0.1025 grams, in the fourth passage, the average mass showed a result above 0.945 grams.

During the analysis of the protein composition of callus tissue with the addition of potassium, humate showed components in the range of 11-229 kDa, respectively, control callus tissues showed components in the range of 10-200 kDa.

As a result of the work it can be argued that potassium humate activates the callusogenesis of alfalfa to a high degree, the greatest result was shown by callusogenesis at a concentration of 0.3% (75.61%).

PERFORMANCE AND MICROBIAL POPULATION TREATING GROUNDWATER POLLUTED WITH NITRATE IN A GRANULAR SLUDGE BIOREACTOR

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Keywords: nitrate; granular sludge; groundwater; microbial population.

Nitrate and pesticides are one of the most concern groundwater contamination derived by agriculture practices to provide safe drinking water. Some diseases, such as methemoglobinemia, thyroid disease, or neural tube defects, have been linked to the consumption of drinking water contaminated with nitrate [Hurtado et al., 2021]. Nitrite has been described as a carcinogenic agent [Moreover, Brender et al., 2013] demonstrated that high concentrations of nitrate could be associated with congenital malformations such as cleft palate, cleft lip, and deformities of the arm. For these reasons, in this research, a sequential bed granular sludge bioreactor was adapted to treat nitrate-polluted groundwater. This granular sludge technology consists of a spherical biofilm, in which different heterotrophic denitrifying microorganisms are promoted to remove nitrate from groundwater, with low carbon addition, saving cost for its exploitation. During the experiment, the nitrate removal performance of the bioreactor showed a high nitrate removal performance under different carbon source concentrations. On the other hand, Molecular biology techniques were done using Illumina MiSeg high throughput sequencing protocols in order to characterize the hypervariable regions V1-V2-V3 of 16S rRNA gene of *Bacteria*, V3-V4-V5 of 16S rRNA gene of Archaea and ITS region of Fungi, [Gonzalez-Martinez *et al.*, 2018]. In this way, the Multivariate redundancy analysis showed the role of different fungal, bacterial and archaeal populations with the BOD and nitrogen removal performance. In conclusion, our research showed that the granular sludge amended with low concentrations of sodium acetate is an efficient, cost-friendly alternative for the treatment of nitrate-polluted groundwater.

ANTI-CORONAVIRUS EFFICIENCY AND REDOX-MODULATING CAPACITY OF POLYPHENOL-RICH EXTRACTS FROM TRADITIONAL BULGARIAN MEDICINAL PLANTS

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Keywords: natural extracts; coronavirus infection; virucidal activity; viral adsorption; antiradical and -metal-chelating capacity.

The use of various herbal therapists as part of traditional medicine in different parts of the world, including Bulgaria, is due to the knowledge accumulated over the centuries by people about their valuable biological activities [Todorov *et al.*, 2014; Schippmann *et al.*, 2006]. In this study we investigate extracts from widely used Bulgarian medicinal plants for their ability to prevent the coronavirus infection of cells by testing different mechanisms of antiviral protection, their polyphenol content, and redox-modulating capacity.

The influence on the stage of viral adsorption, the inhibition of extracellular virions, and the protective effect on uninfected cells of the plant's extracts were reported by the end-point dilution method, and virus titer (in Δ logs) was determined as compared to the untreated controls. The total content of polyphenols and flavonoids was determined as well [McDonald *et al.*, 2001]. We tested the antioxidant power of the extracts by their ability to inhibit generation of superoxide anion radicals and to scavenge DPPH radicals. We determined their iron-reducing, copper-reducing, and metal-chelating antioxidant powers.

Most of the extracts tested suppress the extracellular virions of HCov. They also inhibit the stage of viral adsorption to the host cell to varying degrees and have a protective effect on healthy cells before being subjected to viral invasion. The examined extracts contained significant amounts of polyphenols and quercetin - similar flavonoids and showed remarkable antioxidant, radical, and redox modulating effects.

All these 13 extracts from Bulgarian medicinal plants tested can act as antioxidants, antiviral, and symptomatic drugs for the management of coronavirus infection.

Acknowledgment: This work was supported by the National Science Fund at the Ministry of Education and Science, Bulgaria approved by Research Grant N^{o} K Π -06- Π K Π -06- Π K Π -08 we will be merbased functional platforms for advanced in vitro target and co-delivery of therapeutic payloads for the treatment of coronavirus infection.

SOME PHYSIOLOGICAL PROPERTIES OF THERMUS THERMOPHILUS AND FLAVOBACTERIUM THERMOPHILUM BACTERIA ISOLATED FROM THERMAL WATER OF AZERBAIJAN

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Keywords: thermal; thermophile; termotolerant; physiological.

Thermophilic microorganisms are sharply differing from mesophilics on their physiological properties. They are of great practical importance because they give a large amount of biomass with rapid development in a short time under high temperature conditions [Ahmadova *et al.*, 1989].

The main goal of the research work was to study some physiological characteristics of thermophilic bacteria species isolated from some thermal water of the Great and Lesser Caucasus of Azerbaijan Republic.

During the research, 12 pure cultures of 2 species isolated from thermal water were used as research objects. The species are strawshaped in morphological appearance.

During the experiments, using common microbiological methods and cultivation ways, the relationship of the species to temperature, environment pH, oxygen, natural and synthetic nutrient media of different composition, carbon and nitrogen sources was determined [Kuznetsova *et al.*, 1989; Loginova *et al.*, 1966].

Conducted scientific studies have shown that the optimal growth temperature of *Thermus thermophilus* is 60-65° C, and the optimal growth temperature of *Flavobacterium thermophilum* is 50-55° C. Neutral and slightly alkaline environments are more favorable for the normal development of species. Both types are aerobes due to their relationship to oxygen. They can develop normally in natural (meaty-peptone, potato agar) and synthetic nutrient media (with the addition

of 0.2% yeast extract). During cultivation, they need more moisture. They do not form spores.

In the researches, while studying the relation of the species to the carbon source, it was found that they easily absorb various sugars, alcohols, salts of organic acids (in Smith nutrient medium, at 0.3-0.5%) as a single carbon source, and they are more demanding of salts of organic acids. Both species absorb peptone (0.5%) as an organic nitrogen source more easily than inorganic nitrogen sources.

Thus, from the obtained results, it became clear that cells belonging to both species isolated from thermal water located in the territory of Azerbaijan Republic use the carbon and nitrogen compounds in the environment as a source of food and energy during their development. By participating in the microbiological changing of carbon and nitrogen compounds in the water environment, they participate in the formation of the chemical properties of water, and in the natural cycle of carbon and nitrogen elements in nature.

ANTIBACTERIAL EFFECT OF POLYCAPROLACTONE NANOFIBER LOADED WITH METFORMIN AND GENTAMICIN FOR USE IN SKIN INFECTIONS

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Keywords: electrospinning; nanofiber; polycaprolactone; metformin; Pseudomonas aeruginosa; gentamicin.

The increasing use of antibiotics is causing bacterial resistance to existing antibiotics. That in itself is a threat to health around the world. An alternative strategy to combat such a crisis is to find compounds that restore the antimicrobial activity of existing antibiotics against drug-resistant bacteria. Metformin is a common anti-diabetic drug. Its antimicrobial benefits have been proven. In this study, the antibacterial effect of electrospun nanofiber scaffolds based on polycaprolactone loaded with metformin and gentamicin for use in skin infections was investigated. Poly- ϵ -caprolactone (PCL) combined with gentamicin and metformin were electrospinning, and the resulting nanofibers (PCL / Gen, PCL / Met, PCL / Gen / Met) were used against Pseudomonas ae-

ruginosa. The morphology of the produced nanofibers was observed using scanning electron microscope images. FTIR was also used to determine the chemical configuration of the scaffolds. The antibacterial properties of scaffolds were evaluated by two methods: disk diffusion and bacterial growth curve test. Finally, images from scanning electron microscopy showed that the resulting nanofibers lacked vertebral structures. FTIR plots also showed the presence of polycaprolactone, gentamicin, and metformin in electrospinning samples. The results of the disk diffusion test showed a bacterial growth inhibition zone for all three models of nanofibers PCL / Met, PCL / Gen, and PCL / Gen / Met. Also, no growth aura was observed for PCL disks. Statistical analysis of the data obtained from the bacterial growth curve test showed that the simultaneous use of gentamicin and metformin in polycaprolactone scaffolds significantly reduced bacterial growth. Therefore, it can be concluded that metformin has an auxiliary antibacterial effect. It can also be a potential candidate as an adjunct therapy to reduce antimicrobial resistance. In addition, in the future, new drug delivery systems could be used to improve the antibacterial properties of many biomedical disciplines, such as drug delivery scaffolding and wound dressings, in treating drug-resistant skin infections, especially in people with diabetes and burn patients.

EFFECTS OF GREEN SYNTHESIZED MAGNETITE NANOPARTICLE (Fe₃O₄ NP) ON GERMINATION OF TOMATO (SOLANUM LYCOPERSICUM L.)

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 $\it Keywords:$ magnetite nanoparticle; Solanum lycopersicum $\it L$.; phytosynthesis; seed priming.

Stimulation of plant growth and development and protection of plants from stress factors are among the application areas of nanoparticles (NP) (Shankramma *et al.*, 2016). Magnetite nanoparticles are the most preferred form of iron oxide, which are used in a wide variety of fields due to their magnetic properties and high surface/volume areas [Spanos *et al.*, 2021]. In this study, physiological processes affecting growth and development were investigated in tomato plants primed

with phyto-synthesized Fe₃O₄ NP. Magnetite nanoparticles were synthesized using laurel (*Laurus nobilis* L.) leaf extract and characterized by UV/Vis spectrophotometry, Scanning electron microscopy (SEM), Zeta potential and Fourier transform infrared spectroscopy (FT-IR) [Iravani *et al.*, 2011]. The highest peak obtained between 300-400 nm from UV/Vis spectrophotometry proved the formation of magnetite NPs. FT-IR results displayed the NPs were coated with phyto content. Zeta potential results revealed that the NP charge was -20.7 mV. SEM images presented that NPs have average size 42 nm and spherical shape.

Phytosynthesized Fe₃O₄ nanoparticles were applied to tomato seeds at five different concentrations (0.1-1000 mg L^{-1}) by priming method. The effects of magnetite particles on the germination parameters of these seeds, accelerated aging and seedling growth parameters were investigated. Tomato seeds which were treated with 0.1, 100, and 1000 mg L^{-1} magnetite NP, showed increased germination rate. The germination percentage and germination rate of aged seeds increased at 100 mg L^{-1} compared to the control, the germination time decreased at the same concentration the highest rates of root-shoot length were observed starting from 100 mg L^{-1} magnetite NP application. Root length in aged seeds, 0.1 and 1 mg L^{-1} concentrations showed a significant increase compared to the control. However, there was no statistically significant difference in shoot length in aged tomato seeds.

Obtained results showed that nanopriming with magnetite NP did not have any phytotoxic effect on plant groups at all concentrations (including $1000\ mg\ L^{-1}$), on the contrary, it had a stimulating effect on germination and seedling growth.

EFFECT OF PENICILLIUM OXALICUM ON ENHANCING SEWAGE SLUDGE COMPOST. USING AN *IN SITU* BIOAUGMENTATION

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Keywords: bioaugmentation; sewage sludge; compost; emerging pollutants; toxicity. Thousands of tonnes of sewage sludge (SS) were produced and disposed in 2019 alone, as an inevitable residue from wastewater management [Eurostat, 2022]. This represents a serious environmental and public health concern. Composting has been applied on this waste to improve their agricultural value and to re-introduce it into the environment safely [Liu et al., 2022]. Nevertheless, the true efficiency of this technique over emerging pollutants and its toxicity remains questionable [Liew et al., 2022]. For this reason, we proposed bioaugmentation compost with the fungus Penicillium oxalicum XD3.1 [Aranda et al., 2017; Olicon-hernandez et al., 2019; Olicon-Hernandez et al., 2020]. To do so, three different piles made of SS were placed in the facilities of the company of waste recycling 'EIDER', Guadix, Granada, Spain. A control pile was inoculated with normal water, while the remaining piles were inoculated with spores of the fungus *P. oxalicum*. One of the 'Penicillium piles' was bioaugmented during the composting time while the other was inoculated before the process started. In overall, *P. oxalicum* application caused an increase on the quality of the final compost, improving their nutritional value. This mature compost was also less toxic for plants and other microorganisms. And finally, it also promotes the specific degradation of venlafaxine derivatives. Those results represent its promising future not only in bioremediation but in agriculture, and circular economy as well.

EVALUATION OF NANOMAGNETIC CONTAINING SILIBININ'S ANTIBACTERIAL EFFECTS ON BIOFILM FORMATION CAUSED BY ANTIBIOTIC-RESISTANT *PSEUDOMONAS AERUGINOSA* ISOLATE

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Keywords: Pseudomonas aeruginosa; biofilm; nanomagnetic **silibinin**; antibacterial.

One of the most significant bacterial infections, MultiDrug Resistant (MDR) *Pseudomonas aeruginosa*, causes infections with a higher mortality rate due to resistance to various antibiotics. This bacterium produces significant tissue damage with various levels of virulence and the formation of its biofilm results in recurrent infections that are resistant to antibiotics. According to recent studies, plant-produced compounds like silibinin can be important mechanisms for reducing the growth of biofilms. Due to its anticancer, antioxidant, antibacterial, antifungal, anti-inflammatory, cardioprotective, neuroprotective, and hepatoprotective properties, silibinin is gaining a lot of attention.

This study was conducted on 100 Infectious specimens collected from Health centers in Tehran, Iran. The pattern of antibiotic resistance was found using the disc diffusion method, and *P. aeruginosa* was identified using standard microbiological methods. To investigate how nanomagnetic silibinin affects *P.aeruginosa* biofilm formation, high and moderate biofilm producers were chosen as test isolates. Using a microtiter plate technique, biofilm detection was evaluated.

The findings of the microtiter plate assay test showed that 55 and 45 clinical isolates of *P.aeruginosa* were only moderately and highly capable of generating biofilms, respectively. The majority of antibiotics are very resistant to this bacterium. *P.aeruginosa* biofilm formation was decreased in 33 isolates when the strains were treated with nanomagnetic silibinin. The results of this investigation demonstrated that nanomagnetic silibinin inhibits *P.aeruginosa* biofilms in a promising manner. Nanomagnetic silibinin can be used as a suitable drug candidate and could be an effective treatment for pathogenic infections.

INVESTIGATION OF NICOTINAMIDE PHOSPHORIBOSYLTRANSFERASE (NAMPT), INTERLEUKIN-6 (IL-6) AND VASPIN SERUM PROTEIN LEVELS IN TYPE 2 DIABETES MELLITUS

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Keywords: NAMPT; IL-6; vaspin; type 2 diabetes.

In type 2 diabetes (T2D) and obesity, imbalances are seen in the production of adipokines released from adipose tissue. Adipose tissue synthesizes several adipokines, such as adiponectin, leptin, resistin, vaspin, and the recently discovered nicotinamide phosphoribosyltransferase (NAMPT). It has been suggested that these molecules may explain the relationship with obesity, insulin resistance, beta-cell dysfunction and cardiovascular diseases. Increased insulin secretion in eN-AMPT (extracellular NAMPT) B cells provides protection from apoptosis and induction of proliferation. The interaction between the insulinlike effects of NAMPT and its binding to the insulin receptor suggests that it may play a role in the pathogenesis of diabetes. Many studies show that changes in NAMPT levels constitute a risk factor for type 2 diabetes and there is a correlation between them [Grolla et al., 2016; Garten et al., 2015]. Interleukin-6 is a proinflammatory cytokine. It is involved in regulating the immune response, acute phase response and inflammation [Akbari et al., 2018]. IL-6 triggers insulin resistance by acting on the mTOR, STAT-3 and SOCS-3 pathways in the liver. Chronic low-grade inflammation is a risk factor for the development of insulin resistance and type 2 diabetes, which is manifested by high circulating IL-6 levels in T2D patients. High IL-6 concentrations suppress insulin secretion, and increased IL-6 may cause loss of function of pancreatic islet cells [Qu et al., 2014]. Vaspin (visceral adipose tissue-derived serpin) is an adipocytokine belonging to the serpin protease inhibitor family with insulin-sensitizing and anti-inflammatory effects. It is thought to be involved in the negative regulation of gluconeogenesis and the regulation of the lipid metabolic process. It has also been observed that induction of vaspin mRNA expression by human adipose tissue constitutes a compensatory mechanism against obesity, glucose tolerance and insulin sensitivity [Liu et al., 2017].

For this reason, it is aimed to study NAMPT, IL-6 and Vaspin protein levels, which contribute to the development of insulin resistance

and diabetic complications in T2D, on groups at different stages of the disease and to understand the effects of differences in protein levels on the disease.

The study was carried out with 3 different patient groups, aged between 18-70 years, with a known diagnosis of T2D for 10 years, with macrovascular and microvascular complications, without complications, and healthy control group, who applied to Gazi University Medical Faculty Hospital Endocrinology and Metabolism Department. 40 people were included in each group. Blood samples were taken from volunteers and serum part was separated and Enzyme-Linked Immuno-Sorbent Assay (ELISA) study was performed with serum samples.

Protein levels of study groups (Without complication, Microvascular complication, Macrovascular complication, Healthy (Control)) were determined according to Enzyme-Linked ImmunoSorbent Assay (ELISA) results (ng/ μ l). NAMPT levels in the groups: 18.693, 18.490, 16.563, 20.588; IL-6 levels: 24.844, 27.325, 30.687, 24.352; Vaspin levels were determined as 27.204, 30.737, 33.552 and 28.346.

According to the obtained data, serum levels of NAMPT were higher in the control group than in the patient groups. Among the patient groups, protein levels decreased further as complications increased. When IL-6 and Vaspin serum levels were evaluated, it was determined that protein levels, which were low in the control group, increased as complications increased. Low levels of NAMPT observed in advanced stages of diabetes suggest that NAMPT has a protective effect in diabetes, while increased levels of IL-6 and Vaspin suggest that these proteins play a role in the progression and pathogenesis of the disease.

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ANTIBACTERIAL ACTIVITY OF 9-PHENANTHRENE CARBOXALDEHYDE-BASEED THIODIHYDROPYRIMIDINE DERIVATIVE

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Keywords: antimicrobial activity; dihydropyrimidines; gram positive bacteria; pathogen bacteria.

The synthetic compound's antibacterial activity was assessed against *A. baumanii, E. coli, P. aeruginosa, K. pneumoniae,* and *S. aureus* in consideration of the biological activity of dihydropyrimidines. Initially, the agar disc diffusion experiment was used to check the compound's antibacterial activity [Israyilova *et al.,* 2022]. Results were contrasted with known antibiotics' antibacterial activity (cefotaxime and ceftriaxone). In comparison to antibiotics, the bacterial cultures showed a high susceptibility to the test substance. *S. aureus* showed the strongest antibacterial activity (34 mm). Most significantly, the molecule outperformed the conventional antibiotics. Additionally, the compound's antibacterial efficacy against *K. pneumoniae* was lower than that of cefotaxime but equivalent to that of ceftriaxone. The control containing DMSO did not affect the growth of the above-mentioned gram-positive and gram-negative bacteria.

Following a preliminary screening, the compounds' minimum inhibitory concentration (MIC) was ascertained against the test cultures (*S. aureus, E. coli, A. baumannii, P. aeruginosa,* and *K. pneumonia*) using the microdilution method and the resazurin dye. Results were contrasted with those from the control antibiotics (cefotaxime and ceftriaxone). It's interesting to note that the test chemical made the bacterial strains more sensitive than the controls. With a MIC value of 62.5 g/mL, S. aureus was the most susceptible organism, while E. coli, A. baumanii, and *P. aeruginosa* all displayed the same value of 125 g/mL. The least sensitive strain was K. pneumoniae, with a MIC value of 500 g/mL, which was greater than cefotaxime (250 g/mL) but equal to that of ceftriaxone.

On the other hand, dihydropyrimidines' potent antibacterial action can be attributed to their ability to penetrate bacterial cell walls. Additionally, it has been proposed that they bind to and block a number of enzymes (dihydrofolate reductase, bacterial DNA gyrase, aminoacyltRNA synthetases, etc) [Huseynzada *et al.*, 2021].

DISTRIBUTION PIGMENT FORMING ACTINOMYCETES IN DIFFERENT SUBSTRATES

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Keywords: Actinomyces; soil; microbiota; strain; pigment.

Actinomycetes are part of the microbiota of different substrates as a reducing agent. The study of mycelial actinobacteria is of particular interest due to their use in biotechnology as producers of biologically active substances (antibiotics and enzymes), bioremediation of hydrocarbon-contaminated soils and as biocontrol agents for phytopathogenic microorganisms [Bull *et al.*, 2005].

The aim of our study was to study the distribution of pigment-forming representatives of *Actinobacteria* filum in different substrates (soil, water and air) [Qauze *et el.*, 1983].

The distribution of actinomycetes in soil samples taken from the rhizosphere of figs, pomegranates, apples and grapes grown in Azerbaijan was studied. The results show that the number of actinomycetes was highest in the soils taken from the rhizosphere of the fig tree, and the least in the soils taken from the rhizosphere of the apple tree. Actinomycetes accounted for 25-30% of total isolating microorganisms.

The results show that microorganisms are unevenly distributed in different airspace. The minimum number of actinomycetes is observed on the street, the maximum number is indoors. Water samples were taken from the Vendam River and the Jeyranbatan Reservoir for analysis. The results show that the number of actinomycetes in different waters is unevenly distributed. The minimum amount is observed in the Djeyranbatan reservoir, and the maximum amount is observed in the Vendam river.

Thus, pigment-forming actinomycetes were found in all studied samples. Most of them were found in soil samples, and the least in the air. 36 strains of pigment forming actinomycetes were released into pure culture (17 from soil, 8 from air, 11 from water).

Among the isolated actinomycetes cultures with white (section *Albus*, series *Albus*) and gray (section *Cinereus*, series *Chromogenes*) pigment predominated. There are also a few red (section *Roseus*, series *Ruber*), orange (section *Cinereus*, series *Aureus*), pink (section *Cinereus*, series *Violaceus*) and purple (section *Roseus*, series *Roseoviolaceus*) pigment.

The study of the characteristics of some strains revealed that they belong to the species *Saccharomonospora viridis* (isolated from the soil), *Termomonospora alba* (isolated from water), *Actinomycetes nitrificans* (isolated from the soil), *Act.violaceus* (isolated from the air).

MYCOBIOTA AND FUNGICID CHARACTERISTICS OF ALHAGI MAURORUM MEDIC SPREAD IN VARIOUS ECOLOGICAL CONDITIONS

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Keywords: mycobiota; Alhagi maurorum Medic. Plants; fungicidal activity.

The purpose of the presented work is devoted to the comparative study of fungicidal properties of mycobiota and components of *Alhagi maurorum* Medic. plants distributed in ecologically different territories of Azerbaijan.

The research was conducted in 2017-2021 on the territory of various economic regions of the Republic of Azerbaijan (Absheron, Aran, Guba-Khachmaz and Lankaran-Astara economic regions).

The research included comparative studies on the chemical composition of *Alhagi maurorum* Medic. plants, the typical and quantitative composition of mycobiota, and the fungicidal activity of components spread in ecologically different territories of Azerbaijan.

It was found that depending on environmental conditions, the chemical composition of plants, the combination of types of components of fungi involved in the formation of mycobiota, the indicator of quantitative composition and fungicidal activity, as well as some other indicators of the plant (growth size, humidity, optical density of the obtained materials, etc.) is characterized by different indicators.

It was shown that 27 species of true fungi participate in the formation of mycobiota of *A. maurorum* plant, of which 85.2% belong to the *Ascomycota*, 11.1%-to *Zygomycota* and 3.7%-to *Basidiomycota*. Recorded *Botryosporium longibrachiatum* species such as and *Chaetosartorya ornata* are new to the mycobiota characteristic of the nature of Azerbaijan.

It was found that fungi involved in the formation of mycobiotics *of A.maurorum* plant are characterized by diversity both because of their Ecolo-trophic connections and because of the manifestation of Ecolotrophic specialization. Thus, 9.5 % of recorded fungi belong to saprotrophs, 9.5 % - to biotrophs, 81 % - to polytrophs, as well as 70.4% of them to toxins, 37.0% - to allergens, 25.9% - to opportunists.

It became clear that the distribution of fungi on the plant is also characterized by different quantitative indicators, so the marked fungi are characterized only by the frequency of occurrence (50.2-54.3%), characteristic of the dominance of *Ascochyta alhagi* and *Rhizopus stolnifer*. 10 of the other species are characterized by the frequency of occurrence that is common (14.3-36.5%), 9-random and rare (0.2-6.7%) species.

Although both aqueous extract and essential oil extracts (EO) from *A. maurorum* have a negative effect on the growth of toxigenic fungi used as test crops, the fungicidal properties of EO are relatively high in water fungicide's extracts.

It was found that the EO of the plant *A. maurorum* contains various components, including the main components by the amount of drimenol (19.2-23.2%) and 9-octyl heptadecane (7.2-10.2%). it is also possible to use EO, obtained from the plant *A. maurorum*, in the form of composites, and the combined use of EO, which contains the main component of the composition, is more effective. As a result, their fungicidal activity can be increased up to 15% in relation to toxigenic fungi, which increases their ability to use resources more efficiently.

ASSESSMENT OF ENZYMATIC ACTIVITY OF MICROMYCETES ISOLATED FROM BIOTOPES DIFFERENT BY ECOLO-PHYSIOLOGICAL AND BIOTECHNOLOGICAL ASPECTS

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Keywords: enzymatic activity; micromycetes; biotopes.

The aim of the present work is devoted to the creation of collection xylotrophic Basidiomycetes isolated from ecologically different forest ecosystems of Azerbaijan and assessment of the ecolophysiological and biotechnological potential of the enzyme system of natural strains with various ecological features.

As a result of the conducted research had created the collection of 100 strains, belonging to 25 species(*Bjerkandera adusta, Cerrena unicolor, Fomes fomentarius, Fomitopsis cytisina, F.pinicola, F.rozea, Ganoderma lipsiense, G.lucidum, Heterosporus bienins, İnonotus dradeus, İ.hispidus, İ.pini, Laetiporus sulphureus, Phellinus pini, Ph.pomaceus, Ph.robustus, Pleurotus ostreatus, Polyporus squamosus, Phellinus igniarus, Pseudotrametes gibbosa, Schizophyllum commune, Trametes hir-*

suta, T.pubescens, T. versicolor and *T.zonata*) of xylotrophic macromycetes, prevalent in the forests located in the ecologically different territories of Azerbaijan.

It was found that the species, causing white rot (corrosion) of wood quite a lot, and due to the structural features of forest ecosystems, the group of evrithrophic among xylotrophic macromycetes ranked higher. Strain differences of evrithrophic have also been characterized by high levels, thereby increasing the degree of intraspecific polymorphism.

It was found that xylotrophic macromycetes distributed in environmentally different ecosystems of Azerbaijan can actively synthesize the enzymes that catalyze the degradation of basic polymers which are part of the woody plants. Latitude of the spectrum of the enzyme system, synthesized fungi depends on the type of decay caused by them in nature as well as on the coefficient of variation, which is one of the manifestations of formed ecotrophic adaptation.

It was pointed out that the lack of digestible nutrients, which are a source of carbon in the environment, stimulates not only the hydrolytic enzyme system of fungi, but also the synthesis of oxidoreductases. It can be assessed as a sign of purchased xylotrophic macromycetes due to their adaptation to the environment.

ESSENTIAL OILS AS ANTIMICROBIAL AGENTS

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Keywords: essential oils; aromatic plants; antimicrobial activity.

At the present time the study of the antimicrobial properties of biologically active substances of plant origin, requires special attention. This is primarily due to the fact that the pathogenic microorganisms are able to adapt very quickly to individual antimicrobial drugs, primarily antibiotics [Garabadjiu *et al.,* 2011]. Essential oils take special place among antimicrobial substances of plant origin. Ether essential oil plants spread to all climatic zones of the world. Currently, 2500 species of plants are known to form essential oils, the majority of them are related to 3 families. Nonstingings – Labiateae (Laminaceae) 187 species of the genus, Apiaceae (Umbellifer-aceae) 177 species of the genus, and composite Compositeae (Asteraceae) family includes 177 species. [Vdo-

vidchenco et al., 2011]. Essential oil which extracted from different plants, have antibacterial, antifungals, antivirals, antiparasitary, antioxidant, immune stimulant, and anti-inflammatory, healing properties. First and foremost, this is associated with synergistic effect of substances which contains essential oil. The composition and properties of essential oils can be different, depending on the type of substances which generates them and climatic conditions in which they spread [Kumisheva et al., 2009]. To be learned of the essential oils' charasteristics which got from various plants is bazed for expansion of application scope, and it serves to increase quantity of industrial substantial essential oil plant types. More than 800 series of essential oil plants have spreaded in the territory of the Azerbaijan Republic. [Ibadullayeva et al., 2007]. The antimicrobial activity of essential oils of peppermint, common basil, wild mint, rosemary officinalis, catmint, wild coriander, widely distributed in Azerbaijan, has not been studied. In studies related to the study of the antimicrobial properties of essential oils, antimicrobial activity was evaluated by methods that allow only qualitative assessment of the results, and not quantitatively. The purpose and objectives of the study were to study the antibacterial and antifungal properties of essential oils obtained from 10 types of essential oil plants common in Azerbaijan, and for the first time to quantify their antimicrobial activity. To obtain essential oil 10 kinds of plants from 2 season was used. 8 kinds of them Labiateae (Laminaceae) family, 2 types of them belong to Apiaceae (Umbelliferae) family. The dispersion-contact method was used to determine the antimicrobial activity of the essential oil. It was studied the antimicrobial effect on following cultures: Gram-positive (Bacillus anthracoides TU-1, Bacillus subtilis and Staphylococcus aureus BDU-43 TU-4) and Gram-negative (Escherichia coli TU-2, TU-3 Pseudomonas aeruginosa) bacteria, Candida albicans and Candida tropicalis BSU-30.

As a result of our research, we made the following conclusion: we found that all the studied plants have antibacterial activity and antifungals, and their activity can vary significantly depending on the type of microorganism and the type of essential oil. It has been established that as the dispersion of ethyl alcohol in the essential oil solution decreases, its antibacterial and antifungal activity weakens. This is most evident in the essential oils of common basil, wild coriander, medicinal rosemary and catmint. Transcaucasian thyme essential oil is a strong antibiotic against gram-positive and gram-negative bacteria, bitter mint, calendula and yarrow essential oils are a strong antibiotic against gram-

negative bacteria and yeasts, anise common essential oil is specific only against gram-positive bacteria, and rosemary essential oil is a strong antibiotic. It has been established that the sensitivity of gram-positive nonspore-bearing bacteria *Staphylococcus aureus* TU-4 to the studied essential oils is 2-4 times higher than that of gram-positive spore-bearing bacteria. Essential oils of common basil, wild coriander and officinalis rosemary, which have very weak antifungal properties, have a fungistatic effect on yeast fungi. A new essential oil composition of essential oils of common sage and Transcaucasian thyme with high antimicrobial activity has been obtained, and high antibiotic activity has been shown against both gram-positive and gram-negative bacteria and yeasts *Candida*.

TRANSCRIPTIONAL REGULATOR SIYA OF PHYTOPATHOGENIC BACTERIA AS A SENSOR OF PLANT PHENOLIC COMPOUNDS

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Keywords: Pectobacterium versatile; Erwinia amylovora; SlyA; overexpression; plant phenolic compounds.

In their defense against pathogens, plants rely on different small molecules, such as phenolics. Many plant phenolic compounds have antibacterial activity, and some of them are important signaling compounds (such as salicylic acid, a mediator of systemic acquired resistance). However, phytopathogens can also use such compounds as signals that affect the production of virulence factors. Previously, using saturating transposon mutagenesis of the phytopathogenic strain *Pectobacterium versatile* 3-2, we identified several genes that are induced/repressed in the presence of plant phenolic compounds. Analysis of the regulatory sequences of these genes using our SigmoID program (github.com/nikolaichik/sigmoid) revealed the presence of a potential operator for SlyA, a transcription factor of the MarR family for three plant phenolics-inducible genes.

For some proteins of this family, allosteric regulation by phenolic compounds, in particular, by salicylate molecules, has been demonstrated. Among *Enterobacteriaceae* such regulation has been shown for SlyA of *Salmonella enterica*. The role of SlyA is best studied in the regu-

lation of the virulent properties of human and animal pathogens. Much less data are available on the role and functioning of SlyA in phytopathogenic bacteria.

In this work, an unexpected phenotypic manifestation (toxicity) of the heterologous expression of *P. versatile* 3-2 and *Erwinia amylovora* E2 *slyA* in cells of different laboratory strains of *Escherichia coli* was found. Via *in silico* analysis, we have linked varying SlyA toxicity in different *E. coli* strains to the SNPs within SlyA operators in front of the vital genes. However, experimental confirmation of this linkage is required. Discovered phenotype allowed us to identify two plant phenolic compounds capable of inactivating SlyA. By overexpressing SlyA in *P. versatile* cells, the regulatory role of SlyA in relation to several genes, one of which was previously identified as phenolics-repressed, was confirmed, and the participation of SlyA in the control of the pectolytic activity of the pathogen was shown, which indicates the important role of signaling mediated by plant phenolic compounds during the formation of plant-bacterial pathosystems.

STUDY THE MORPHOCULTURAL PROPERTIES OF ISOLATED YEASTS FROM VARIOUS SUBSTRATES

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Keywords: Candida; yeast; morpho cultural properties.

The role of yeasts in natural ecosystems is significant. They mainly act as harmless commensals on the surface of plants. Yeast fungi in nature are mainly saprotrophic, found in the phyllosphere of plants and in inanimate plant remains. From the above, it is vital to research each species separately in order to understand the ecological functions of yeasts. Yeast fungi *Saccharomyces, Candida, Cryptococcus* and other species are very common. The purpose of our research was to study the *morpho cultural* properties of yeast fungi isolated from various substrates.

There were 5 strains of yeast as the object of research. They are separated from substrates such as yogurt, different types of grapes, various types of apples, kiwi, bananas, different types of pears, and mandarins. Extracted into the pure culture and studied the *morpho cultural* properties of microorganisms. Samples taken for this object were dilut-

ed with sterile water and, after the third dilution, transplanted into Sabura nutrient media in Petri dishes. Petri dishes were placed in a thermostat at 30°C for incubation for 3 days. After the incubation process, the colonies were observed and examined under a light microscope with the preparation of a permanent preparation [Gasimova *et al.*, 2009].

Yeast has been found in two types of pears (winter and spring), black grapes, vogurt and apples (golden ahmadi). Bananas, kiwi and mandarins did not contain yeast. Images on black grapes (strain A) were found to be oval in shape and size 2.8x2.6 µm, the colony was round, whitish, wrinkled, socially convex, the edges were round, the diameter of the colony was 0.5 cm, and the consistency was oily. In the winter type of pear (strain B1) the new ones are ovate and size 3.7x1.8 microns, the column is oval, whitish, the edges are convex, socially concave, and the edges are round, the diameter of the colony is 2 cm, the consistency becomes non-stick. In the spring type of pear (strain B2) the cells were ovate and 2.7x1.5 microns in size, the colony was round, whitish, the edges were wrinkled, the surface was concave, the edges were round, 1.2 cm in diameter, non-sticky in consistency. The cells in apple (strain C) were found to be ovate and 1.8x1.5 microns in size, the colony was round, whitish, the edges were slightly wrinkled, the surface was convex, and the edges were round, 0.7 cm in diameter, oily and soft. The cells in the yogurt (strain D) were found to be ovate and 4.6x2.5 microns in size, the colony was round, whitish, the edges were slightly wrinkled, and the surface was convex, the edges were round, 0.9 cm in diameter, oily and soft. According to the consequence, the types of yeasts were determined: cultures strain A and strain D- Saccharomyces sp., Strain B1 and B2 - Candida sp., Strain C - Saccharomycodes sp [Fantes et al., 2016].

II. BIOPHYSICS, BIOCHEMISTRY, NANOBIOTECHNOLOGY

MAGNETITE BIOMINERALIZATION AND MAGNETORECEPTION Khalilov Rovshan, Mehraliyeva Malakkhanim, Hasanova Gunay

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Keywords: magnetotactic bacteria; magnetosomes; magnetic hyperthermia; biomineralization.

Biomineralization is the process by which organisms generate minerals to harden or stiffen their existing tissues; these tissues are referred to as mineralized tissues, while biominerals serve structural and defensive roles. But in living organism's magnetite has a navigation function.

Magnetite in magnetotactic bacteria serves the functions of geomagnetism, navigation, and magnetoreception. Magnetotactic bacteria are fully capable of regulating magnetite precipitation. This bacterial group's members are all microaerophilic, bidirectional, and possess magnetosomes and cryptochrome proteins. The majority of magnetotactic bacteria have approximately 20 magnetosomes. These morphologies are often cubic, rectangular, or arrow-shaped; they are devoid of crystallographic flaws and are composed of magnetite of the highest purity. Magnetite grains range in size from 35 to 120 nm, at which point they retain their magnetic properties. While swimming, the cells of these bacteria position themselves along geomagnetic field lines.

The formation of magnetite by magnetotactic bacteria happens in stages. First, Fe(III) is taken up by Fe chelators (siderophores), which assist the solubilization and transfer of Fe (III) into the cell. The Fe(III)-siderophore complex is then directed to the plasma membrane by a particular receptor and transport proteins. In some species, the siderophore remains outside of the cell and transfers the Fe (III) to a membrane-bound chelator, but in others, it transports the Fe into the cell. Following this, the Fe (III) is converted to Fe(II) and shuttled to a magnetosome. And in the magnetosome, oxygen molecules reoxidize the Fe(II) to ferric hydroxide. Magnetite is produced by the last reaction of ferric hydroxide with residual Fe(II).

As a conclusion, magnetosomes are nanoparticles that have applications in drug delivery, cell separation, food sciences, DNA/antigen analysis, image contrast, hyperthermia, enzyme immobilization, and bioremediation.In magnetic hyperthermia, magnetosomes are utilized.

By injecting them with magnetosomes and applying magnetic fields, scientists have been able to destroy harmful S.aureus bacterial cells. It is used to target and kill cancerous cells in cancer studies. These therapies may be effective because they preferentially target cells that have taken up magnetosomes while leaving unaffected the surrounding cells.

THE ROLE OF IL-33/ST2 PATHWAY IN LIVER PATHOLOGY IN EXPERIMENTAL MODEL OF HIGH-FRUCTOSE/HIGH-FAT DIET-INDUCED OBESITY

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Keywords: obesity; IL-33; adiposity; fructose; steatosis; fibrosis.

The metabolic syndrome and obesity-associated liver pathology is occurring at growing rates worldwide, raising extensive concerns on the mechanisms and therapeutic interventions for this disorder. The role of IL-33/ST2 pathway in adiposity and obesity-associated liver pathology is incompletely defined. The objective of the study was to investigate whether ST2 gene deletion affects liver steatosis, inflammation and collagen deposition in mice in response to high-fat diet and to investigate whether the combination of a high-fructose/high-fat diet affects liver pathology in resistant to diet-induced obesity BALB/c mice.

Male, 8-week old ST2 deficient (ST2-/-) and wild-type (WT) BALB/c mice were placed on high-fat diet (HFD; 60% kcal fat) or standard diet for 24 weeks. After 24 weeks of high-fat feeding, one group of animals was placed on a combination of high-fat diet with ad libitum access to a 30% fructose solution for another 4 weeks. No pure water was available to the mice given the fructose solution. Histological, immunophenotypic and gene expression analyses were performed.

There was no significant difference in weight gain, amount of visceral adipose tissue (VAT), liver inflammation, and fibrosis, between HFD-fed and CHOW-fed BALB/c mice. However, liver steatosis was significantly more pronounced in HFD-fed mice. Mice fed with HFD/fructose combination exhibited considerably higher adiposity compared to CHOW and HFD groups. Likewise, access to fructose exacerbates liver inflammation and fibrosis in WT mice. HFD-fed ST2-/- mice exhibited higher weight gain, amount of VAT and higher percentages of adipose-tissue associated CD11c+ dendritic cells, IFNγ+, IL-17+ and CXCR3+ T cells compared to diet-matched WT mice. However, in the ab-

sence of ST2 markedly reduced HFD-induced hepatic steatosis was accompanied with lower expression of CD36, LXR α and PPAR- γ . Decreased inflammatory cell infiltration, number of CD68+ macrophages and frequency of CD11c+ dendritic cells in livers were also observed. Further, lower collagen deposition in livers of HFD-fed ST2-/- mice was associated with less numerous profibrotic CD11b+Ly6C low monocytes and CD4+IL-17+ T cells and lower procollagen α 1, IL-33 and IL-13 mRNA expression in livers, and lower serum levels of IL-33 and IL-13. ST2-/- mice fed with HFD/fructose combination exhibited considerably higher adiposity and higher percentages of adipose-tissue associated CD11c+ , F4/80+Ly6C high, CD11b+Ly6C high and CD11b+CCR2+ cells. Percentage of F4/80+Arginase 1+ M2 macrophages in adipose tissue was markedly reduced in HFD-fed ST2-/- mice. Access to fructose exacerbates liver fibrosis in WT mice, but didn't have effect on ST2-/- mice.

ST2 deletion enhanced high-fat diet induced adiposity and adipose tissue inflammation, but attenuated hepatic steatosis, inflammation and fibrosis. The latter effect is due to the lower expression of lipid-related and profibrogenic molecules in the liver, which is in agreement with the proposed profibrotic role of the IL-33/ST2 axis. Also, IL-33/ST2 signaling is required for development of liver fibrosis in Th2 type mice. High-fructose/high-fat diet affects liver steatosis, inflammation, and collagen deposition in BALB/c mice strain resistant to diet-induced obesity.

EEG ALPHA RHYTHM IN SUBJECT WITH HYPERTONICITY OF MASTICATORY MUSCLES

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 $\textbf{\textit{Keywords:}}\ electroence phalography;\ alpha\ rhythm;\ musculus\ mass eter;\ hypertonicity.$

Conducted research aimed to compare total electrical brain activity in three groups of subjects: 1) those who did not complain about the dysfunction of the dentition; 2) a group of subjects who noted hypertonicity of masticatory muscles in the early period after waking up, 3) a group of people who did not observe any signs of hypertonicity after waking up, but do noted dysfunction of the temporomandibular joint, incompleteness in the dentition and other dysfunctions of the dental system.

Conducted investigations exhibited that subjects with signs of masticatory muscle hypertonicity had EEG alpha-rhythm episodes, preceding both oculographic artifacts and k-complexes. Electromyography, recorded simultaneously from m. masseter, haven't revealed any in-

crease in amplitude and frequency that accompanies the alpha sequences, except for the moment of blinking. K-complexes were also not accompanied by shifts in the electrical activity of m. masseter. The proportion of the alpha rhythm in the last second before the artifact was $39\pm2.5\%$. segment duration – 1.2 ± 0.1 s. While in some examined patients the alpha power in the EEG spectrum increased before each of the physiological recording artifacts, in others, episodes of the alpha rhythm accompanied only a small part of the oculograms.

For persons in the control group, similar phenomena were not recorded. The alpha-rhythm index for the last second before the interference here was 24.8±3.7%.

Breath-holding tests conducted by the controls did not cause a significant increase in alpha rhythm in the EEG preceding k-complexes and oculographic artifacts. In this group, by holding breath after inspiration, the impact of the alpha rhythm in the one-second sections preceding the oculograms was $24.8\pm3.7\%$. In the group of persons with signs of increased m. masseter tension, this parameter pointed at $57.7\pm3\%$, which significantly exceeded the control means. The duration of alpha episodes in this group did not differ significantly from the control $(1.4\pm0.02~\text{s})$.

After performing the test with breath holding after exhalation, in group with signs of hypertonicity of the masticatory muscles, an increase was also found in relation to the control of the power of the EEG alpha rhythm in the areas preceding the physiological EEG artifacts. In control, this parameter pointed at 23.7±3.4%, while in individuals with an increase in facial muscle tone it reached 54.4±2.6%.

SYNTHESIS CHARACTERIZATION OF METAL-BASED NANOPARTI-CLES AND SOME BIOLOGICAL APPLICATIONS

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Keywords: nanotechnology; nanoparticles; biomedical applications.

Nanotechnology has a very important place in science and engineering applications. It is a new and rapidly developing field of technology that aims to provide technologically advanced or completely new physical, chemical and biological properties to matter at the atomic and

molecular level. "Nano" comes from the Greek and is used to mean "dwarf". Nanotechnology deals with the synthesis and production of materials smaller than 1 mm and the properties of these materials. Particles ranging in size from 1-100 nm are called nanoparticles (NPs).

Nanoparticles have superior properties such as large surface area, chemical-catalytic and biological activity. It is a new and rapidly developing field of technology that aims to provide technologically advanced or completely new physical, chemical and biological properties to matter at the atomic and molecular level. Especially nano metals such as silver (Ag), gold (Au) and palladium (Pd) In medicine, science and engineering studies, drug delivery systems, biological labeling, optical devices, antimicrobial and anticancer agent, food and cosmetics industry, electronics, magnetic, optical They are used in many different fields such as the aerospace industry and bioremediation. Nanoparticles (NPs) are synthesized by two main approaches. Top down approach: In the methods included in this approach, it is based on the principle that the material is divided into small pieces that can go down to nano size as a result of energizing the volumetric material from the outside by mechanical and/or chemical processes. Bottom-up approach: The method is based on constructing organic or inorganic structures with atoms or molecules. Physical, chemical and biological methods are applied to synthesize nanoparticles.

Among these methods, the methods using biological resources are more advantageous. Synthesis steps made using biological sources do not contain toxic chemicals and do not require high energy. Biological methods are easy and simple as well as environmentally friendly. Many biological sources such as plants, bacteria, fungi and algae are used in the environmentally friendly (green) synthesis of nanoparticles. The nanoparticles obtained with these sources are particles that exhibit a biocompatible structure for medical applications. NPs synthesized from various plants are used in various biomedical applications including antimicrobial, anticancer, anti-parasitic, antioxidant, antidiabetic, antiinflammatory. Plant-based nanoparticles are used for various purposes according to characterization techniques (SEM, TEM, FITIR, XRD, UV). Nanoparticles synthesized in this way are used for various purposes. Examples of some metals used for this purpose are gold (Antimicrobial, biosensor, drug applications, cancer therapy, DNA marking), Copper (antimicrobial), Iron (Anticancer, molecular imaging, cancer therapy), Silver (Anticancer, antiviral), Zinc oxide (Cosmetic), Selenium (Anticancer, antimicrobial), Palladium (Anticancer) can be given.

ANTIMICROBIAL CHARACTERISTICS OF LACTIC ACID BACTERIA ISOLATED FROM PICKLED PRODUCTS

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Keywords: pickle; lactic acid bacteria; antimicrobial activity; bacteriocin; hydrogen peroxide.

In recent years, the microorganisms that are most commonly used in the biopreservation method to protect food and feedstuff from pathogenic and opportunistic microorganisms and extend their shelf life are lactic acid bacteria (LAB) with GRAS status, one of the main representatives of our resident microflora. The antagonistic activity of these bacteria with neighbor populations is carried out through a wide range of antimicrobial metabolites, such as lactic acid, carbon dioxide, hydrogen peroxide, short-chain fatty acids, bacteriocins, etc. Various acidic and pickled products among people's daily diet are considered the most favorable source of antimicrobial LAB.

Out study is aimed at to isolate LAB from traditionally fermented home-made pickles and study their antimicrobial characteristics.

As the source of LAB, the samples from 3 kinds of home-made pickles, namely, cabbage pickle (CP), green tomato pickle (TP) and mixed vegetable pickle (MP) have been used. The MP included purslane, cabbage and cucumber. The samples, each being 200g, have been transported to the laboratory in the sterile closed containers and stored in the refrigerator. Preliminary screening of lactic acid bacteria with antimicrobial activity has been conducted by replicating method. The diffusion method has been used to determine their activity. An indicator strain was *L. bulgaricus 340*.

As an outcome of our experiments, 6 new strains producing antimicrobial elements have been isolated from pickle samples and characterized. Two of the isolated strains (*CP7* and *MP24*) had a broader scope of antimicrobial activity and both strains inhibited the growth of pathogenic and opportunistic bacteria such as *Listeria innocua*, *Escherichia coli*, *Candida guilliermondii*, *Bacillus subtilis*, *Salmonella typhimurium*. Biochemical identification of the active elements of the *CP7* and *MP24* strains has been conducted and thus, it's been determined that the active element of the former is peptide, and the latter is hydrogen peroxide.

The strains have phenotypically been identified by means of the traditional microbiological methods and the API-50 (Biomereux, France) system. It's been concluded that these strains belong to *Lactobacillus pentosus* (CP5), *L. plantarum* (CP7), *Lactobacillus brevis* (TP8), *Lactobacillus fermentum* (TP16), *Lactobacillus collinoides* (MP1), Lactobacillus salivarius (MP24).

TOXICITY BIOMARKERS

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Keywords: biomarkers; evidence-based medicine methods; cancer.

Biomarkers are objective and characteristic indicators for the assessment of normal biological and pathological processes, pharmacological responses to therapeutic intervention, and toxicological exposures. Biomarkers are used to determine the risk, diagnosis and treatment of diseases, as well as to monitor treatment strategies and response to treatment.

Biomarkers used in different scientific fields (toxicology, pharmacology, epidemiology, biology and clinical sciences) show a wide spectrum ranging from simple blood hemoglobin determination to methods for detecting DNA-bound additive products in cancer. The advances made with biological-analytical techniques in the field of biomarkers are accelerating studies on the investigation of exposure to chemical agents, individual or population susceptibility, risk assessments, doseresponse relationship for chemicals, and the efficacy of treatments. The relationship between exposure and systemic toxicity and the identification of the markers that mediate them are very important for therapeutic approaches such as slowing down or reversing the development of various diseases. In addition, clinical and toxicological studies with the use of biomarkers contribute to the reduction of health costs, as well as the ease of performing with small populations.

Exposure to many solvents and chemicals used in industry can cause acute and chronic disease in all organ systems. The vast majority of these exposures act through inflammatory pathways. Evidence of the

biological relevance of various biomarkers to disease and toxicity, or their relevance to clinical outcomes, ensures the relevance of these biomarkers and their valid use as early detection markers. In addition to these, the evaluation of the analysis result of the exposed substance is important in determining the dose of exposure. Today, there are various biomarkers used in this context, but their importance is not fully known since they are not used routinely. The routine uses of early diagnosis biomarkers for the detection of inflammation, neurotoxicity and cardiovascular toxicity in various solvent and metal poisonings, in other words, toxicological exposures, is the most common in our age, such as cardiovascular diseases, diabetes, respiratory diseases, nervous diseases of unknown origin, autism, developmental delay will play a major role in the prevention of diseases. Our working group aims to broadly evaluate these biomarkers with evidence-based medicine methods in line with the above purposes, and carries out joint studies in terms of relevance, validity and routine use.

MECHANISM OF INTERACTION OF CUO NANOPARTICLES WITH ORGANELLES OF *ELODEA* PLANT

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Keywords: Elodea canadensis; nanoparticles; chloroplasts.

When any atom acts as a nanoparticle, it acquires new properties. For example, optical, magnetic, etc. We can say such features as. Nanoparticles are widely used in medicine and various industries. Nanoparticles are used in medicine for drug delivery, diagnostics, nanopharmacology, and in industry for the production of various dyes, cosmetology and food preservation. However, the use of nanoparticles is economically viable, but the widespread use of nanoparticles in nature can be toxic to living organisms. Numerous studies have been conducted to study the toxic effects of nanoparticles. Studies have been conducted to study the effects of nanoparticles on animals and plants. Temperature, humidity, drought, etc. Stress factors such as these can adversely affect the productivity and growth of plants. Various methods are used to prevent this. One of these methods is the application of new technologies. As a result of the widespread distribution of nanoparticles in nature, their interaction with the plasma membrane of plant cells can affect the

course of various physiological processes. The Elodea plant was taken as the object of research. The genus of the plant under study is Elodea canadensis. They call this plant algae. Rapid growth is one of its typical features. The leaves of this plant were used during the experiment. The leaves of Elodea are bright green, elongated and arranged in three folds around the trunk.

First, the leaves of the elodea plant are separated with tweezers and added to a pre-prepared solution containing nanoparticles. The solution consists of IPV (artificial lake water) and CuO nanoparticles. The composition of artificial lake water consists of 1 ml of CaCl, 1 ml of KCl, 10 ml of NaCl and 1000 ml of distilled water. The size of the nanoparticles used is 20-40 nm and the density is 0.5 μ g/ml. If the density of the nanoparticles is increased, the effect may change. Elodea leaves were stored for 1 day in specially illuminated conditions containing nanoparticles to control the process of phototaxis. During the process of phototaxis, chloroplasts accumulate in the direction of light. Elodea leaves stored in a nanoparticle solution for 1 day were examined at 200x magnification under a Carl Zeiss optical microscope. The observation method was used in the optical microscope.

When examined under an optical microscope, it was determined that the CuO nanoparticle did not adversely affect the process of phototaxis, i.e. chloroplasts, as well as other organelles of plant leaves. You should perform these observations in a dark- ened room [Murphy *et al.*, 2001].

The leaves were then kept in the dark for 1 day in a solution containing nanoparticles to observe the disintegration of chloroplasts. One day later, the leaves were examined at 200x magnification under a Carl Zeiss optical microscope. In this case, the destruction of chloroplasts was observed. We conclude that the CuO nanoparticle does not adversely affect the movement of plant organelles when it interacts with the plasma membrane of the elodea plant.

GREEN TEA-BASED NANO-ANTIOXIDANTS FORMULATION IN PHARMACEUTICAL INDUSTRY

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Keywords: green tea; nano-antioxidants pharmaceutical industry .

Chemicals are largely used for a diversity of purposes. Various toxicities caused by exposure to chemicals have become a major health concern. The incidence of poisoning with chemicals is highly reported due to risky handling practices and their usage. Their health hazards are mostly discussed according to their ability to produce free radicals or alter endogen antioxidant defense. As the source of pharmacologically active molecules, green tea is a vital contributor to the antioxidant food, which offers a nutritional basis of bioactive agents that support averting a wide-ranging of illnesses.

New investigations recognized green tea as a gift of nature for helping human health [Ahmadi *et al.,* 2007]. Most of the interest is placed on the anti-oxidative role of this plant on aging and progressive pathologies including diabetes, cancer, and cardiovascular diseases. The valuable health properties of green tea are mostly related to free radical scavenging and action and glutathione booster actions. As an outstanding polyphenols origin, green tea can be used as a non-toxic and powerful inhibitor of oxidation instead of chemical-based antioxidants.

In this concern, as a least-processed product of tea production, green tea comprises strong antioxidants including epigallocatechin-3-gallate, which is under serious consideration for its nanoplatforms based delivery potential and a countless quantity of research works carried out on this topic. Numerous studies have shown the probable role of green tea components and their nano-antioxidants as an attractive plan to protect humans from the toxicities caused by exposure to the chemicals. Nanotechnology-based applications display appreciated properties in increasing solubility of poor soluble antioxidants absorp-

tion and also reduction of beneficial dose to achieve the pharmacological properties.

Due to the progress in the development of nanomedicine and several nano-based delivery platforms, extract and catechins of green tea have been substantially developed in recent years. Lipid-based nanoparticles, polymeric nanoparticles, etc. have been adjusted according to catechin-sourced products with a distinct emphasis on the most effective biologically active agent (epigallocatechin gallate) in green tea.

However, it seems to be a momentous battle between the information from in vivo and in vitro studies, because of unpredictable epigallocatechin gallate bioavailability. This work emphasizes the role of novel nanomedical methods employing green tea in chemical-induced toxicities treatment in the pharmaceutical industry.

EFFECT OF IONIZING GAMMA RADIATION ON LACTIC ACID BACTERIA

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Keywords: living systems; microorganisms; gamma radiation; paramagnetic centers.

Lactic acid bacteria usually do not form spores and are used safely in food fermentation, which is the subject of research. At the same time, this research object differs from other living systems by its general metabolic, physiological properties and resistance to acidic environment. Of particular interest is the fact that lactic acid bacteria produce some substances, such as bacteriocin, against pathogenic microorganisms that cause disease in humans [Majamaa *et al.*, 2008].

In modern times, all living organisms are exposed to both natural and man-made activities, nuclear explosions and so on. Given the effects of radiation on living organisms, the study of the effects of gamma radiation in living systems is widely discussed in scientific research [Khalid, 2011]. Although the mechanism of gamma radiation on some plants and animals, the resulting paramagnetic centers have been studied by Electron Paramagnetic Resonance Spectroscopy (EPR) and other methods,

studies on the effects of gamma radiation on microorganisms are still limited [Khalilov *et al.*, 2015].

In view of all the above, lactic acid bacteria were used as the object of study. The main purpose of the study is to irradiate these lactic acid bacteria with gamma radiation in different doses, to determine the lethal dose for this strain, as well as to determine the characteristics of paramagnetic centers and other magnetization phenomena by EPR. For this purpose, the bacteria isolated from the cheese were first incubated in a DeMan Rogoze Sharpe (MRS) solid medium for 48 hours in a thermostat at 37°C temperature and refrigerated for further study. One strain of this bacteria was irradiated in the laboratory at doses of 300 Gy, 600 Gy and 800 Gy. The above experiment was also carried out on the Candida guilliermondii BSU-217 yeast strain, which has very valuable properties in practice due to its easy separation from nature, optimal size, high multiplication rate and resistance to many stress factors. Candida guilliermondii BSU-217 yeast strain was irradiated with different doses of ionizing gamma radiation in the laboratory after planting in the same manner [Khalilov et al., 2021].

We are currently conducting EPR studies on both samples.

MOLECULAR CHARACTERISTICS OF POLYGLUCIN AND RHEOPOLYGLUCIN

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Keywords: polyglucin; rheopolyglucin; blood.

Polyglucin is a 6% solution of 60,000 molar mass dextran in physiological solution. Since the molar mass of dextran used in the preparation of polyglucin is close to the molar mass of albumin in blood plasma. This solution is widely used as a blood plasma substitute in medicine. Polyglucin is transferred to the blood-carrying system in cases of heavy blood loss. The conducted studies show that even when 2/3 of the blood in the body is lost, the patient's life can be saved with the help of polyglucin. Dextran fulfills the energy requirement in blood regeneration. It should also be noted that polyglucin does not contain protein.

Therefore, polyglucin cannot perform the function of transporting oxygen to the body. For this reason, it cannot completely replace blood. Considering what has been discussed, it follows that the physical char-

acteristics of polyglucin should be temperature-dependent in a manner similar to those of blood plasma. In other words, certain inferences regarding the temperature dependence of the physical properties of blood plasma can be drawn from research on the temperature dependency of the physical properties of polyglucin. Rheopolyglucin is a 10% solution of dextran with a molar mass of 30,000,40,000 in physiological solution. This solution facilitates the transfer of fluids from the tissue to the circulatory system. As a result, the suspension property of the blood increases, its viscosity decreases, the blood flow in small capillaries is restored, and the transfer of enzyme elements of the blood to aggregates is reduced. Rheopolyglucin is most often used in disorders of blood circulation in arteries and veins capillaries, in the treatment of thrombus. in heart surgery with the participation of an artificial device, etc. is used. From the above, it can be concluded that the study of the temperature dependence of polyglucin and rheopolyglucin molecular characteristics (viscosity, density, electrical conductivity, etc.) can be useful in medicine.

Here, the viscosity (η) , density (ρ) , and electrical conductivity (σ) of polyglucin and rheopolyglucin at different temperatures (293.15K, 298.15K, 303.15K, 308.15K, 313.15K, 318.15K, 323.15K) at normal atmospheric pressure were determined. Gibbs energy of activation of viscous flow (ΔG_{η}), enthalpy of activation of viscous flow (ΔH_{η}), entropy of activation of viscous flow (ΔG_n), coefficient of thermal expansion based on the dependence of $\rho(T)$ of these substances based on experimental values (α_D) was calculated, and Walden's rule $(\eta \sigma = \text{const})$ was checked based on the dependences of $\eta(T)$ and $\sigma(T)$. It was determined that with increasing temperature for both polyglucin and rheopolyglucin, the ΔG_n , ΔH_n , and ΔS_n parameters decrease, while the αp parameter increases, and in the considered temperature range, ΔG_n (rheopoliglucin)> ΔG_{η} (polyglucin), ΔH_{η} (rheopoliglucin)> ΔH_{η} (polyglucin), ΔS_{η} (reopolyglucin) $\approx \Delta S_n(\text{polyglucin})$, $\alpha_p(\text{polyglucin}) > \alpha_p(\text{reopoliglucin})$. Also, calculations show that the product is for both polyglucin and rheopolyglucin does not remain constant depending on the temperature, that is, Walden's law is not satisfied in the considered temperature range, and in the considered temperature range $n\sigma(rheopolyglucin) > n\sigma(polyglu$ cin).

EVALUATION OF GREEN SYNTHESIS, CHARACTERIZATION AND SOME BIOLOGICAL ACTIVITIES OF GOLD NANOPARTICLES (AUNPS) FROM HYPERICUM TRIQUETRIFOLIUM L. PLANT EXTRACT

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Keywords: nanomaterials; gold nanoparticles; MIC method.

Currently, production of economically, non-toxic and fast preparing nanoparticles are more favored than conventional method used nanoparticles. In light of this, most of the academic works have emphasize on the natural-based nanomaterials including fungi, viruses, plants, and etc. because of high volume ratio and small size. In the synthesis of nanoparticles (metallic), synthesis with plant-derived biological methods has become the preferred methods of researchers, as opposed to physical and chemical methods. Recently, green biosynthesis method has begun to be more interested in areas such as the use of plant materials that are less toxic, environmentally friendly, easy to synthesize and important in nanodrug production. The aim of this study is to characterize gold phytonanoparticles obtained by green synthesis method from the leaves of Hypericum triquetrifolium TURRA plant, which contains many medically important compounds, and to investigate antimicrobial, antifunagal, anticholinesterase and antioxidant activities as a biomedical agent. For this purpose, environmentally friendly, simple and economical synthesis of gold nanoparticles (AuNPs) was carried out using Hypericum triquetrifolium (HT) plant aqueous extract.

HT-AuNPs; UV-visible (UV-vis.) spectrophotometer, Electron Scattered X-rays (EDX), Fourier Transform Infrared Spectroscopy (FT-IR), X-Ray Diffraction Diffracrometry (XRD), It was characterized using Transmission Electron Microscope (TEM), Atomic Force Microscope (AFM), Zeta potential and Zetasizer instrument data. Thermo gravimetric analysis (TGA) and differential thermal analysis (DTA) techniques were applied to examine the comparative thermal stability of the synthesized AuNPs.

The biochemical composition of the HT plant was illuminated using the LS-MS device. The suppressive effects of the synthesized AuNPs on the growth of pathogenic yeast and bacteria were determined by the Minimum Inhibition Concentration (MIC) method. Antioxidant activities

of synthesized nanoparticles were determined in vitro using Carotene-Linoleic acid lipid peroxidation inhibition, ABTS cation radical scavenging and DPPH free radical quenching activity, CUPRAC reducing power activity and metal chelating activity using spectrophotometric tests. Anticholinesterase activity of nanoparticles was determined spectrophotometrically by measuring inhibition activities against butyrylcholinesterase and acetylcholinesterase enzymes.

ANOMALIES THAT OCCUR IN THE SMALL-DOSE AREA OF THE "DOSE-EFFECT" CURVE DURING THE INFLUENCE OF UVB RAYS ON THE INTENSIVE REPRODUCTION OF *DUNALIELLA SALINA* CELLS

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Keywords: UVB; UVKV; Dunaliella salina.

As a result of classical radiobiological studies, the dose-dependent effect of ionizing and ultraviolet radiation on living organisms has been established. Thus, increasing the radiation dose causes a more pronounced effect. When studying the condition of organisms under the influence of small doses of ultraviolet rays, it was found that small doses in a certain range not only have a damaging effect on organisms, but also have an anomalous side effect – stimulation. A similar effect, the stimulation of cell division under the influence of chronic small doses of UVB rays, has been found in studies by other authors. The study of the mechanism of action of UVB rays on photosynthetic organisms is of particular importance for fundamental photobiology, cell biology and applied photobiology.

The main purpose of the study was to study the viability and photosynthetic activity of *Dunaliella salina* cells affected by chronic small doses of UVB rays during intensive cultivation.

The *Dunaliella salina* strain of the halophyte microenvironment was used as the object of study. The cells were propagated in a "UVKV"-type device using special photoreactors. Photocells with a volume of 250 ml are made of quartz and ordinary glass. The daily multiplication of microalgae was determined by measuring the optical density on a KFK-2 photocalorimeter. A high-pressure mercury lamp CVD - 120A was used as a source of UVB rays. For the study of photosynthetic activity, cell suspensions with a density of d= 0,8 were developed and kept in

the thermostat at a temperature of 28 °C for 20 minutes. The photosynthetic activity of 50 ml cell suspension samples was measured in a polarographic device using a platinum Clark electrode and compared with controls.

The results show that under conditions of optimum temperature 27 °C, salinity 1.5 M NaCI and light intensity 24 w/m² (favorable conditions for cultivation), the cultivation of *Dunaliella salina* cells the cultivation of *Dunaliella salina* cells in the "dose-effect" curve during chronic exposure to different doses of UV-B rays, survival forms more stimulation plates (up to 5-25 sec / hour dose). Increased chronic doses of UVB rays caused a slowing of cell division in the intensive-accumulation mode, LD_{50} was observed at a chronic dose of 45 sec /hour.

It should be noted that during the chronic effect of small doses of UVB rays (5-25 sec/hour), there is an additional accumulation of carotenoids, which is characteristic of *Dunaliella salina* cells. Additional accumulation of carotenoids by *Dunaliella salina* cells, compared to control, is a response to unfavorable conditions, including UVB irradiation. However, an increase in the amount of carotenoids ensures the resistance of *Dunaliella salina* cells is maintained at a sufficiently high level under the effects of chronic doses of UVB radiation. Thus, during 15 sec/hour of chronic exposure, the dysfunction is negligible and the photosynthetic activity is at the level of 95%.

The mechanism of action of UVB rays on the photosynthetic apparatus and intracellular defense systems is investigated.

STUDY OF BIOPHYSICAL PARAMETERS IN PELVIC GRAPE SNAILS (HELIX POMATIA) FEEDED WITH METAL NANOPARTICLES

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Keywords: grape snails; nanoparticles; radiation; bioindicator.

The major purpose of this research is to assess several biophysical parameters and observe the life actions, activities and morphological characteristics of radiation-fed pelvic grape snails (*Helix pomatia*), fed with different metal nanoparticles (Fe, Al and Cu). Grape snails are particularly resistant to stress compared to other living things. In grape snails hemocyanin serves as the method for transporting oxygen. Consequently, we de-

cided to study the grape snail as our study subject. Snails were gathered in several locations in Absheron. In particular plastic containers, snails are fed and kept in storage. Daily checks were made on their food and water. Under the impact of various conditions, the paramagnetism of the snail's body and pelvic regions has been examined (feeding with nanoparticles, radiation with different doses of gamma radiation).

For two months, researchers observed how feeding snails with different nanoparticles affected their behavior and daily activities. Snails fed on Fe nanoparticles show better levels of nutrient uptake and vital activity, according to observations. Cu nanoparticles were a source of rather low nutritional activity for snails. Snails that consumed Al nanoparticles died more frequently. These snails' pelvis and body parts were taken apart, let to dry at ambient temperature and then their spectra were captured using an electron paramagnetic resonance spectrometer two months later. Free radical signal (g = 2.0023), Mn signal (g = 2.01), and signal of Fe ions (g = 3.4) were seen in the control sample's spectra in the spectra acquired from the snail's body parts. Signals of high-amplitude Fe oxide particles have also been seen in the body sections of snails fed on Fe nanoparticles, in addition to the free radical signal. We see the production of free radical signal (g = 2.0023) Cu ion signal and Fe ion signal (g = 3.4) in the spectra of snail body sections fed on Cu nanoparticles. We observe the production of free radical signal (g = 2.0023) and signal of Fe ions (g = 3.4) when fed with Al nanoparticles.

In order to irradiate grape snails, they were collected in special containers with 10-12 individuals each, and then irradiated in doses of 200 Gy, 400 Gy, 600 Gy, 800 Gy and 1000 Gy. Radiation was performed on MRI gamma 25 devices. The power of the device was $P=178,259 \, \text{rad/sec}$.

On the CANBERRA Gamma Spectrometer, the radionuclide content of the samples and their unique activities were identified. The grape snails' bodies and pelvic pieces were separated from one another and completely dried at room temperature before being put in specialized containers. In this instance, measurements were taken of the samples' weights, heights, and container heights. For stability, packaged samples were held in this state for 30 days. Their radioactive concentration and particular actions were then determined before they were put in special Marinelli containers. It was discovered that the specific activity of the radionuclides ⁴⁰K and ²³⁴Pa is higher.

According to study results, pelvic grape snails can be employed as a bioindicator in the investigation of environmental pollution [Nasibova *et al.*, 2020].

EFFECT OF SYNTHETIC CU (II) COMPOUNDS ON THE PHOTOCHEMICAL ACTIVITY OF PHOTOSYSTEM II

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Keywords: Photosystem II; inhibitors; fluorescence; chlorophyll.

The reduction of land suitable for agriculture and the increase in the world's population as a result leads to an increase in demand for food. Protection of crops from weeds is one of the factors of increasing the efficiency of grain production. An urgent problem at present is the synthesis of new inhibitors of the growth and development of weeds. since many weeds eventually acquire resistance to herbicides. A promising approach to solving this problem would be creating or identifying a compound that effectively suppresses several metabolic processes, photochemical activity [Murakami et.al., 2014]. Copper (Cu) plays an important role in a number of metabolic processes in plants, cyanobacteria and algae. However, being an important cofactor for many key enzymes, free copper ions can cause oxidative damage to cells due to the formation of reactive oxygen species. There is evidence that Cu impairs the activity of the PSII reaction center, enhances the decomposition of chlorophyll and inhibits the activity of the water-oxidizing complex. In this study, thylakoid membranes enriched with PS II isolated from spinach leaves Spinacia oleracea L. by the method described in [Schiller and Dau, 2000] were used to study the inhibitory effect of Cu (II).

The kinetics of photoinduced changes in the fluorescence yield of PSII chlorophyll was measured for determination the effect of Cu(II) complexes on PSII activity by the using a fluorimeter with pulse amplitude modulation. The values of variable Chl fluorescence were determined according to the equation $F_V=F_M-F_0$, where F_M is maximum fluorescence and F_0 is initial fluorescence of the dark-adapted sample. The maximum photochemical yield (F_V/F_M) of PSII was calculated according to the equation $F_V/F_M = (F_M - F_0)/F_M$. And based on these dates the inhibitory effect of Cu(II) complexes was determined. In this work, three Cu (II) complexes with different structures, coordinated with bromine ions, were used to study their inhibitory effect on the photochemical activity of PSII. The chemical names of the complexes:

Bis[1,3,5-triazine[1,2-a] benzimidazole-2-amine,3,4-dihydro-4-(2-thiophene)} copper (II) bromide

 $Bis[1,3,5\text{-triazine}[1,2\text{-a}]\ benzimidazole-2\text{-amine},3,4\text{-dihydro-4-}(2\text{-imidazole})\}\ copper\ (II)\ bromide$

Bis[4H-1,3,5-triazine[2,1-b] benzothiazole-2-amine,4-(2-imidazole)} copper (II) bromide

All Cu (II) complexes affect the photochemical activity of PSII with different efficiency. The structure of the complex plays an important role in its inhibitory effect. The action of Cu (II) complexes is probably directed at the donor side of PSII or the components of the reaction center of the photosystem. Among complexes with a bidentate ligand, a benzothiazole fragment containing an S atom (complex 3) shows a significant increase in inhibitory effect compared to complexes containing a benzimidazole fragment with an N atom (complexes 1 and 2).

BIOCHEMICAL CHARACTERISTICS OF ANTIFUNGAL ACTIVITY OF *L. FERMENTUM* C11 STRAIN

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Keywords: flour; L. fermen; antifungal activity; organic acids; bacteriocin.

Currently, there are more than 400 mycotoxins known to science produced by a variety of fungal species and their number is growing steadily. Mycotoxins are dangerous to health and moreover, the mold of their producents can cause serious food and feedstuff spoilage. While the species of *Penicillium* and *Aspergillus* spoil a wide range of food and feedstuff products, the species of *Fusarium* mainly parasitize the grains and produce a number of mycotoxins on them. The study of lactobacilli with an antifungal activity isolated from flour samples has an important practical value in this regard.

Our study is mainly aimed at to identify the biochemical nature of metabolites that provide the antifungal activity of $\it L. fermentum C11$ strain isolated from rye flour. The flour samples have been obtained from the retail stores and the isolation of the active strain from them has been carried out through the dilution in a sterile physiological solution. To determine the antifungal activity of the strain, the sample at 10^3 /ml has been added to 15 ml of MRS agar medium and placed in Petri dishes. Following the drying of the nutrient medium, the surface has

been covered with 15 ml of soft MEA and the spores of 5 μ l *F. culmorum 302* strain at 10⁶ / ml have been injected into the center of the container. The Petri dishes have been incubated at 23° C. Within 12 days from the first day of incubation, the diameter of the mold's spreading area has been measured in the incubation media. The biochemical nature of the active antifungal metabolite has been characterized based on the influence of pH, temperature and various enzymes on the culture fluid of the producent strain. It was determined that the activity level of the metabolite(s) of the C11 strain has not changed in an acidic environment, but decreased by 30% in a neutral and alkaline environment.

The active metabolite of the strain has lost its activity by 7% at 60°C, 15% at 80°C, and 50% at 121°C. Having regard to the influence of enzymes, the active metabolite(s) has been resistant in relation to catalase, has lost its activity by 50% under the influence of proteinase K enzyme, by 19% under the influence of chymotrypsin, and by 9% and 6% under the influence of lipase and amylase enzymes, respectively. The outcome allows us to conclude that one of the active metabolites of the R11 strain belongs to the macromolecule bacteriocins of IV class and that half of its antifungal activity appears thanks to this substance. Class IV bacteriocins are thermolabile and contain compounds of lipids and carbohydrates, which play a certain role in the formation of the activity of bacteriocin. Taking into account the fact that the activity of R11 strain decreases as pH value increases, it can be concluded that the organic acids play an important role in the formation of antifungal activity of this strain.

STUDY OF RADIOPROTECTIVE PROPERTIES OF POTASSIUM HUMATE IN MODEL PLANTS

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 $\textbf{\textit{Keywords:}}\ potassium;\ morphological\ and\ biochemical\ parameters;\ photosynthetic\ pigments.$

In nature, humic substances are formed during the decomposition of plant and animal residues under the action of microorganisms. Peat, sapropel, brown coal, composts, etc. serve as raw materials for the production of humates. The technologies for obtaining humic preparations are quite simple and low cost. Many experiments with various crops

have shown that the use of sodium, potassium and ammonium humates, regardless of the source of raw materials for their production, in optimal doses significantly stimulates seed germination [Rode *et al.*, 1993], improves plant respiration and nutrition [Noble *et al.*, 1995], increases seedling length and biomass [Tan *et al.*, 1979] and reduces the intake of heavy metals and radionuclides into plants (Del Rio *et al.*, 1997).

We studied the effect of potassium humate on morphological and biochemical parameters in model plants obtained from irradiated seeds. In the experiments were used wheat seeds of the "Mirbashir" variety and corn of the "Zakatala 68" variety. Seeds were irradiated (wheat 250 Gy, corn 100 Gy) on the URi (K-25) unit, source - 60Co. Morphological parameters, growth, leaf width of wheat and maize seedlings were measured during the entire growing season of plants.

The amount of chlorophyll pigments, carotenoids, was measured on a Multiskan GO spectrophotometer. Chlorophyll fluorescence in leaves was measured using a MINI-PAM device (Germany). Seed germination potential of maize and wheat decreased by increasing the irradiation dose. Potassium humate was obtained under laboratory conditions by alkaline extraction from compost. In laboratory and field experiments, seeds were treated with 0.1%, 0.01% and 0.001% solutions of potassium humate before sowing. The results of experiments on the study of photosynthetic activity showed that when seeds of wheat and corn are treated with 0.01% and 0.001% solutions of potassium humate before irradiation at a dose of 250 Gy and 100 Gy, the maximum quantum yield of PSII increases. A 0.01% solution of potassium humate also normalizes the synthesis of photosynthetic pigments (chlorophyll a and b, carotenoids) in plant leaves. At all stages of development, a 0.01% solution of potassium humate favorably influenced the growth and development of plants. One of these methods, which allows obtaining direct information about the most important physicochemical parameters of humans, is the method of electron paramagnetic resonance (EPR). EPR is highly sensitive and gives a lot of information about the structure of substances containing free radicals. Therefore, we also investigated some physical parameters and the radioprotective effect of potassium humate using the EPR method.

We also studied the effect of various concentrations of potassium humate solutions on the productivity of wheat and corn. In these studies, 0.01% potassium humate solution showed a better result compared to the irradiated control.

Ni²⁺⁻ INDUCED CHANGES IN THE ELECTRICAL PARAMETERS OF THE PLASMA MEMBRANE OF CHARA GYMNOPHYLLA CELLS

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Keywords: hyperpolarization; KCER; KCIR.

The bioelectrical responses of the plasmatic membranes of *Chara aymnophylla* by adding of Ni²⁺ into the composition of the nutrient medium turned out to be potential-dependent. Thus, the bioelectrical parameters of cells, the membrane potential (\mathcal{O}_{M}) which was in the range of K+-channel activation of internal rectification (KCIR) (| $\mathcal{Q}_{_M}$ | \geq 160 mV), did not react to a stepwise increase of the Ni²⁺concentration in the external environment from 10⁻⁷ to 10⁻³ M .Changes in bioelectrical parameters in the presence of Ni²⁺ were detected in cells, in which membrane potential was in the range of activation of external rectification K+ channels (KCER)($\varphi_{\scriptscriptstyle M}$ ~-90 ÷-160 mV). The primary hyperpolarization of the plasma membrane by 10-15 mV with constant membrane resistance $R_{\scriptscriptstyle M}$ y in these cells occurred immediately after the appearance of 10-7 M NiCl₂ in the nutrient medium. By the increase of Ni²⁺content in the medium to 10⁻⁶ and 10⁻⁵ Min cells and the membrane potential being in the range of activation of the KCER, the value of plasmalemma hyperpolarization amounted to 25-50 mV. Hyperpolarization of the plasma membrane was accompanied by an increase in membrane resistance by 80-100% within 7-8 min. Against the background of increasing concentration of Ni²⁺ in the medium, in the range of 10⁻⁷–10⁻⁵ M, $arphi_{\scriptscriptstyle M}$, $R_{\scriptscriptstyle M}$ increased monotonically and reached saturation at 10⁻⁵ M NiCl₂ in the medium.

When 10^{-4} M Ni $^{2+}$ was included into the X-A medium, were not observed only a shift in the current-voltage characteristics and a change in its slope, corresponding to changes in the membrane resistance. How-

ever, when $|\varphi_{M}| > 250$ mV and $|\varphi_{M}| < 60$ mV appeared in non-linear sections of the current-voltage characteristics of the plasma membrane. In the range of activation of the KKER, the current-voltage characteristics tends to the asymptote $j = 0.476 + 7.516 \varphi_{M}$, and in the range of acti-

vation of the KIR to the asymptote $j=5,633+20,38\varphi_{_{M}}$, where j is measured in units of A/m² and $\varphi_{_{M}}$ – in V (volts). The increase in the conductivity of the plasma membrane was 6.6 times in the range of KCER, and more than 10 times in the range of activation of KCIR. The volt-ampere characteristic was inclined to the current axis [Plekhanov et al., 2017].

Thus, the carried investigations of the bioelectrical reactions of the plasma membrane of *Chara gymnophylla* cells showed that low concentrations of Ni²⁺ can be used as a blocker of K⁺ channels. The blocking effect of the cation may be accompanied by an increase in the electrogenic activity of the H⁺ pumps of the plasma membrane.

DETECTION OF REACTIVE OXYGEN AND REACTIVE NITROGEN TYPES BY FLUORESCENCE AND LUMINESCENCE PROBES

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Keywords: fluorescent probe (FP), reactive oxygen species (ROS); reactive nitrogen species (RNS); delayed light emission millisecond (msecDIE).

The fluorescent probe method is used to study the changes in many cellular processes in living organisms against the effects of harmful environmental factors. Reactive oxygen (ROS) and nitrogen (RNS) are known to cause oxidative and nitriding stress respectively. These stresses affect not only various physiological processes, but also various pathological processes, including cancer and neurodegenerative disorders. The difficulty in detecting ROS / RNS by a fluorescent probe is that their short lifespans and the competitiveness of different endogenous reactive species capable of interfering the probe in biological matrices not only prevent the integration of most probes, but also prevent their illumination. The investigations of new fluorescent probes capable of preventing these problems is of great interest in science nowadays. Sensitive and selective fluorescence and luminescence probe methods for the detection of ROS / RNS are widely used to monitor the in vivo formation of these species and to clarify their biological functions [Ji-TingHou et al., 2020]. The involvement of ROS and RNS species in physiological and pathophysiological processes is widely accepted. Specific detection of ROS and RNS is the key to understanding the role of ROS and RNS in various pathologies. In our study,

we focused on the mechanical and quantitative aspects of detecting ROS and RNS by selected fluorescent probes.

It is known that oxidative stress occurs either as a result of excessive ROS or as a result of depletion of the antioxidant system, resulting in an imbalance between antioxidants and prooxidants.

It can be told about the amount of free oxygen due to the characteristics of FP and msec-DIE of the luminescent probes in normal and damaged cells. In normal cells, probe molecules combine more with oxygen. In pathological cases, oxygen is used more in the cells in the process of metabolism, and in those cells the intensity of FP, msec-DIE are low, that is the indicator of cell damage. Thus, it can be assumed that antioxidants are involved in the regulation of redox- homeostasis of cells by activating various signaling mechanisms during the action of physical factors on the cell.

EFFECT OF NANOPARTICLES ON CHLOROPHYLL COMPOSITION AND ENZYME ACTIVITY IN THE LEAVES OF CORN AND WHEAT SEEDLINGS

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Keywords: nanoparticles; plant seedlings; chlorophyll; enzyme activity.

The use of nanotechnology in agricultural practice has great potential to increase crop yields. There is evidence that metal nanoparticles of different sizes, concentrations and surface charges affect the growth and development, enzymatic activity of various plant species [Ma et al., 2010]. The leaves of the seedlings of corn and wheat plants cultivated in field conditions were used for assessing various physiological and biochemical traits. The middle portion of the leaf was used for chlorophyll composition and enzyme activity studies. In our experiments, the effect of Fe₂O₃, ZnO and TiO₂ nanoparticles on the activity of the enzyme guaiacol peroxidase (GPx) in the leaves of corn seedlings was determined. In determining the activity of the enzyme GPx, 1 ml of distilled water was used in the test variant. However, 1 ml of H2O2 was used instead of distilled water in the control variant. The activity of the GPx enzyme was then determined by the optical density change method. It has been found that the optical density of corn leaves exposed to nanoparticles increases. Thus, the optical density of the extract under the action of iron oxide nanoparticles was $D_2 = 0.830$. This showed that the activity of the GPx enzyme increases under the influence of Fe_2O_3 nanoparticles. This result was obtained in other nanoparticles.

In other experiments we investigated the influence of nanoparticles on the chlorophyll contents of leaves of wheat. The effect of nanoparticles (size = 22.05 nm) at different concentrations (0, 0.25, 0.5, and 1.0 ppm) was investigated to improve drought tolerance in different wheat cultivars. The iron oxide nanoparticles positively affected growth, chlorophyll contents and enzymatic antioxidants. Thus, in our experiments, the amount of chlorophyll a, b and carotenoids in the leaves of wheat seedlings was determined spectrally and the effect of nanoparticles was studied comparatively. It was found that in wheat germ exposed to TiO2 nanoparticles, the values of chlorophyll a and b. as well as carotenoids at wavelengths of 440 nm, 665 nm and 645 nm, were the same for the control variant and the test variant. However, in plants exposed to iron and ZnO nanoparticles, the amounts of chlorophyll a, b and carotenoids differ sharply at the same wavelength. This means that the amount of chlorophyll a b and carotenoids is higher than in the control variant and TiO2 nanoparticles. Thus, it can be said that the activity of the enzyme guaiacol peroxidase (GPx) increases in corn seedlings affected by nanoparticles, and the amount of chlorophyll a and b, as well as carotenoids in wheat seedlings varies depending on the type of nanoparticles, mainly iron nanoparticles.

PS II ACTIVITY UNDER OXIDATIVE STRESS AND THE ROLE OF NA-ASCORBATE IN ITS PROTECTION

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Keywords: superoxide anion radicals; illumination; cucumber seeding.

The creation of stress-inducing factors on the photosynthetic apparatus, the leaves of cucumber seedlings (*Cucumis sativus* L.) grown under intense light and in the dark were exposed to the action of methyl viologen (MV), which catalyzes the formation of superoxide anion radicals [Foyer, 2018].

An analysis of the induction transitions of the kinetic curves of millisecond delayed fluorescence of chlorophyll a (ms DF Chl a) showed that MV blocks the primary recombination reaction with the formation

of a highly oxidized radical pair P680+ and TyrZ on the donor side and the electron transport reaction as a result of the accumulation of the reduced primary quinone acceptor QA on acceptor side of electron transport chain of the photosystem II (FS II) [Vass and Cser, 2009; Gasanov et al., 2012]. The dynamics of changes in these parameters showed a more aggressive action of MV in cucumber leaves under intense illumination. Under these conditions, the activity of the donor and acceptor sides of PS II decreased by 5 and 2 times, respectively, relative to the control. Under dark conditions, PS II activity also decreased, but was 1,6–1,7 times higher than under intense illumination. To determine the protective properties of Na-ask against oxidative stress caused by MV. the leaves of cucumber seedlings were subjected to simultaneous treatment with MV+Na-ask [Nishiyama et al., 2001]. Both in the light and in the dark mode, the recovery of the activity of both components of DF Chl a was observed relative to the effect of MV by more than 2 times. Sequential treatment with MV followed by Na-ask further restored PS II electron transport chain (ETC) activity on both the donor and acceptor sides under both light exposures.

The stationary level on the induction curve ms of DF Chl a changed in all variants, however, it was at the control level under the simultaneous action of MV+Na-ask. The greatest effect of Na-ask was observed in the leaves of seedlings under illumination. Na-ask, neutralizing the superoxide anion radical formed under the action of MV and detoxifying H_2O_2 as an electron donor to ascorbate peroxidase or O_2 and *OH prevents the inactivation of enzymes and thereby maintains the redox balance between photosystems. The ability of Na-ask to quench reactive oxygen species (ROS), preventing their migration into the PS II environment, restores its activity under oxidative stress.

STUDY OF THE INFLUENCE OF THE MICROWAVE FIELD ON THE PHYSICAL AND CHEMICAL PROCESSES OF TOBACCO

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Keywords: tobacco leaves; electromagnetic fields; UHF drying.

The influence on the tobacco leaves as the dielectric of the electromagnetic fields would allow the progression of the photo-and thermo chemical reactions not only on surface, but in the full volume. How-

ever, the method of the dielectric heating of the tobacco in the aim of the intensification fermentation process doesn't give the welcome effect, as the fermentation progresses only in the thick subsurface leaves. The welcome high effectiveness and accelerations of the fermentation process were achieved by the UHF field treatment of the tobacco leaves. One of the advantages of the UHF method is that the UHF field, besides local thermal influence initiates also the probability of the uniform progression of the photochemical reactions of the separate ferments, which gives the opportunity to obtain the qualitative products with the minimal ecological pollution.

As well known, the chemical composition of the tobacco leaves changes the color and becomes uniform and approaches to the one-color, the green disappears at the fermentation. The one of the main reasons for the most counts of green in the tobacco leaves is the residual chlorophyll. The high residual content of the chlorophyll leads to the significant storage of the substances, with the negative properties, which limit the action of the positive components in the tobacco. That's why it is possible to follow the process of the fermentation and tobacco quality on the changing of the dark-green color in the tobacco leaves and on the chlorophyll decomposition correspondingly.

In the given paper the influence of the high-frequency electric field on the processes of the drying and fermentation of the tobacco leaves has been studied. The changes accompanying these processes were controlled by spectrophotometric and thermo-gravimetric methods.

The humidity of the tobacco leaves is one of the main parameters, which strongly influences the fermentation process and the quality of the ready product accordingly. The tobacco fermentation is usually carried out at the optimal humidity and temperature. The humidity deflection from the optimal value leads to the undesirable circumstances. The dry tobacco loses elasticity, becomes brittle, and the excess by moist raw material goes moldy easily.

Among wide spread methods of the regulation of the tobacco humidity is the method of the standardization of the humidity by the way of the standardization in the drying board.

The UHF drying allows to obtain the dry tobacco leaves with the given humidity, moreover the needed time for this process decreases till the minimum.

As the DT- investigations show the green untorment to bacco leaves at $T\sim403K$ are characterized by the strong exo-effect, which is caused by the presence of the big amount of humidity. As a result of the UHF drying the endo peak intensity decreases and its maximum shifts to the low temperatures till T=373K. The humidity of the tobacco leaves after UHF drying can be controlled by the endo peak intensity.

So, by changing the frequency of the UHF field, power of the UHF generator and the duration we can obtain the dry tobacco leaves with the given color and the after humidity and later choose the optimal mode of the UHF drying and fermentation.

INVESTIGATION OF THE EFFECT OF CARBOHYDRATE MOLECULES ON THE SEDIMENTATION RATE OF NANOPARTICLES

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Keywords: carbohydrate; ZnO; TiO2; CuO; nanoparticle.

The interaction of nanoparticles with biological molecules is the basis of their biological reactivity. Clarification of the nature of the interaction of nanoparticles with biological molecules allows the creation of mainly controllable bionanomaterials. Carbohydrates, as basic biological molecules, can mediate the recognition process in living systems by interacting with proteins, nucleic acids, lipids and cellular interactions and other molecules [Grillon *et al.*, 2012]. When carbohydrates are adsorbed on the surface of small nanoparticles, their density changes. The degree of curvature of the nanoparticle surface determines the mechanism of contact with the carbohydrate, as the carbohydrate molecule bends according to the curvature of the nanoparticle surface and is subject to conformational variability [Kim *et al.*, 2015].

İn this work, the mechanism of adsorption of carbohydrate molecules on the surface of ZnO, TiO_2 and CuO nanoparticles is studied. The purpose of carbohydrats is to enhance biocompatibility. A disperse solution of ZnO nanoparticles was prepared in distilled water. ZnO nanoparticles mixed with distilled water were separated in an ultrasonographer for 5 minutes. A portion was added to the test tube. The remaining half was mixed with 0,5 gr starch and processed in an ultrasonographer for 10 minutes. It was added to the test tube to observe the rate of subsidence.

A dispersed solution of TiO₂ nanoparticles in distilled water was prepared and processed in an ultrasonographer for 5 minutes. A por-

tion was added to the test tube. 0,5 gr starch was added to the remaining half and processed in an ultrasonographer for 10 minutes. İt was added to the test tube to observe the rate of subsidence.

A disperse solution of CuO nanoparticles in distilled water was prepared and processed in an ultrasonographer for 5 minutes. A portion was added to the test tube. 0,5 gr starch was added to the remaining half and processed in an ultrasonographer for 10 minutes. İt was added to the test tube to observe the rate of subsidence.

The ZnO nanoparticles did not precipitate for 4 weeks. Rapid collapse of CuO nanoparticles was observed. The TiO_2 nanoparticle was found to be relatively less precipitated.

OBTAINING SILVER NANOPARTICLES IN *OPUNTIA FICUS-INDICA* L. EXTRACT BY "GREEN SYNTHESIS"

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Keywords: scanning electron microscope; "green" synthesis; nanoparticles.

One of the most threatening problems for humanity is the growing resistance of bacteria to antimicrobial drugs (antibiotics, antiseptics, etc.). At the same time, it is known that most microorganisms do not have the ability to withstand the damaging effects of metals such as Cd, Pb, Sn, Hg, Ag, etc. These heavy metals are good complexing agents and, interacting with sulfhydryl, carboxyl, hydroxyl, phosphate and amino groups of proteins, lipids and nucleotides, exhibit extreme toxicity to microorganisms. The task of modern researchers is to obtain forms of these metals that are non-toxic to humans and suppress the vital activity of pathogenic microorganisms. Silver nanoparticles (SNPs), having unique biological, physicochemical properties, are considered as an antimicrobial drug of the future. In our work, we studied the production of SNPs by "green" synthesis [Okafor et al., 2013] in an extract of the cactus Opuntia ficus-indica (L.). The ability of the extract to reduce silver ions, creating SNPs, was studied. An aqueous extract was obtained from cactus stems by homogenization followed by boiling and filtration. The SNP sol was prepared by mixing a 0.001M AgNO3 solution with a cactus extract in various concentrations, adjusted with an ammonia solution to 8.5 at 70C. The course of the SNP formation process was noted by the change in the color of the reaction medium from colorless to light yellow or dark yellow. The samples were analyzed on a Specord 250 spectrophotometer in the 320–600 nm region. The obtained results indicate that 700 C is the optimal temperature for the synthesis of SNPs in the cactus extract. Also, the conditions for the synthesis of silver nanoparticles were pH 8.8 and exposure time of 30 min. The sols of silver nanoparticles formed under such conditions had a light yellow color. It was found that the absorption spectra of these sols have a maximum in the region of 420 nm. Using a scanning electron microscope, images of silver nanoparticles were obtained, which made it possible to determine their size (24–40 nm). In our studies, "green" synthesis using extracts of the cactus *Opuntia ficus-indica* (L.) proved to be a reproducible, economical method that can significantly simplify the technological process. By varying the amount of extract, temperature, and duration of the reaction, nanoparticles of various shapes and sizes can be obtained.

ELECTROMAGNETIC SAFETY AND HUMAN HEALTH AT THE PRESENT STAGE OF SOCIETY DEVELOPMENT

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Keywords: electromagnetic safety; high-voltage electric field; fluorescence; blood serum.

The development of the energy system, tele-radio broadcasting, radar, etc. led to massive approximation of man-made electromagnetic fields (EMF) sources to the places of permanent residence of people, which take to need to ensure the electromagnetic safety workers and of whole population. The potential effects of EMF exposure on human health lead to the conclusion that, there is a high degree of biological activity of EMF in all frequency ranges and at all intensities. EMF affects the development of pathological disorders such as cancer, socially significant neurodegenerative diseases ets.

Our experiments show that a 30-minute exposure to a high-voltage electric field of 20 kV/m 50 Hz on human blood serum causes certain changes in the fluorescence intensity: the total fluorescence revealed a decrease in the fluorescence intensity of $\sim 8\%$, and the trypto-phan fluorescence by $\sim 15\%$. This means that with an acceptable residence time (30 minutes) exposure a high-voltage 20 kV/m 50 Hz electric field, human blood serum proteins undergo certain structural

changes in the blood serum proteins, which manifest themselves in the form of changes in the observed fluorescence maxima of protein fluorophores. This is due to the fact that biological organisms are organized by interconnected complex structural elements, and these elements are in a state of unstable dynamic equilibrium, rapidly changing in a certain time interval. If such systems are swayed with the help of low-frequency weak signals, the biosystems can move into another unstable dynamic equilibrium state. Depending on the strength of the impact, this transition can be reversible or irreversible. In our case, the absence at the moment of plausible biophysical mechanisms about the influence of lower-frequency electromagnetic fields cannot be considered as evidence of the impossibility of affecting the health of electric and magnetic fields of the environment.

According to the WHO, at present, against the background of the fact of the unconditional reaction of the human body to the impact of EMF, there is no complete clarity either on the possible long-term consequences, or on the generally accepted safety criteria under conditions of long-term exposure to EMF of modern sources. Nevertheless, the fact remains. According to the researches, against the background of an ever-increasing pressure of adverse environmental factors, including EM and informational "pressure", the number of people with various pathological disorders, including pathologies with unknown etiologies is increasing. Given the importance of the problem, developed countries are implementing their national programs for research on the biological action of EMF and ensuring the safety of humans and ecosystems.

EPR STUDY OF THE EFFECT OF RADIATION ON THE BRAIN CELLS

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Keywords: EPR method, ionizing gamma radiation, Cu nanoparticles.

It is known that radiotherapy is effective in treating many diseases, causing short and long-term side effects. Cognitive dysfunction is one of the long-term side effects of radiotherapy. Radiation exposure to rodents during brain development causes changes in hippocampus neurogenesis during adolescence.

In modern times, the mechanisms of changes caused by ionizing radiation in the brain are still not sufficiently clarified. Many studies have shown that radiation has a negative effect on the hyppocampal neurogenesis of the brain. Radiation formation in different parts of the brain and groups of cells may vary depending on the dose, duration and density of radiation damage [Siegel *et al.*, 2008]. Gamma radiation stimulates oxidative stress, changes the level of neurotransmitters, increases inflammatory and apoptotic reactions. Causes cognitive disorders with low doses of morphological changes [Brenner DJ *et al.*, 2007].

As a result of the effects of radiation, the paramagnetic centers in the body were examined by the Electronic paramagnetic Resonance Spectroscopy method [Khalilov *et al.*, 2021]. The paramagnetic centers in the brain tissue cells have not been studied.

The main purpose of our study is to study the EPR method of the paramagnetic centers in the brain tissues of laboratory mice exposed to ionizing gamma radiation and fed by nanoparticles.

The purpose of the study was to choose laboratory mice (*Wistar albino*). The rats were grouped, irradiated with a group of ⁶⁰Co-source RHUND-20000 devices (3 Gy), fed by the other group of Cu nanoparticles, held as the other group control sample and not subjected to any stress. Laboratory rats, 5 months after irradiation, they were anesthetized with 10% ketamine in accordance with bioethical rules and their internal organs were removed. The supply with the nanoparticles lasted 5 months and the rats were cut in the same way. Then the internal organs and brain tissue were removed and dried up in a laboratory environment for EPR examination. The spectrum of brain tissue is shown in Figure 1.

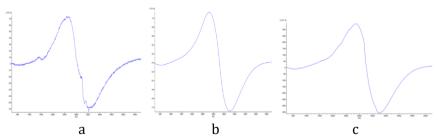


Figure 1. a) control, b) irradiated with 3 Gy gamma radiation, c) fed by Cu nanoparticles.

According to the results, larger signals were observed in rats fed by Cu nanoparticles and irradiated at a dose of 3 Gy compared to controls. At the same time, paramagnetic centers were discovered.

We continue our research on other organs.

THE IMPACT OF NANOPARTICLES OF FERTILIZATION PROCESS OF COMMON CARP (CYPRINUS CARPIO LINNAEUS, 1758)

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Keywords: Cyprinus carpio; nanoparticles; fertilization.

Today, the fact that the increase rate in food sources cannot meet the needs of the increasing population has caused Mankind to turn to fish production activities as a food source. However, it has not received enough attention in recent years. Selection of species suitable for cultivation, fast growing, resistant to diseases and environmental conditions are very important issues to be considered for a successful production [Carp breeding, 2015].

Although the source of nanoparticles is very diverse, most of them are of natural origin and can be found continuously in the environment [Wigginton *et al.*, 2007]. Colloids in water, fine-grained desert sand, oil fumes, smoke from volcanic activities or forest fires, and some atmospheric dusts represent nanoparticles produced in nature. There is not enough information in the scientific literature about the rapid development of nanotechnologies and their impact on the hydrocele, especially at the embryonic stages of development and more sensitive to environmental factors due to its application in various fields. Therefore, the main goal of this study is to study the effect of Fe₃O₄ (20-30 nm) nanoparticles on pre-fermentation germ cells (spermatozoa, eggs) of common carp (*Cyprinus carpio* Linnaeus, 1758) and embryonic developmental stages after fertilization.

The research material was carried out in June 2021 at the farm "Samukh-fish" of the Republic of Azerbaijan. During the experiment caviar was taken from the reproductive fish, smoothing its abdomen with the thumb, and placed in porcelain vessels with a smooth surface according to the number of experimental options. Experiments were carried out on different variants on given topics. The quality of sperm taken from male was initially assessed visually, and the sperm activity

in the samples was determined on a 5-point scale in accordance with the obtained methodology [Persov, 1953]. The Fe_3O_4 (20-30 nm) nanoparticles were added to the germ cells of common carp (*Cyprinus carpio* Linnaeus, 1758) before fertilization in different amounts (0.0001 g, 0.001 g, 0.005 g and 0.05 g), as well as to the fertilized egg and their embryonic. The effect on developmental stages was studied with the help of Carl Zeiss Axio Imager M2 binoculars.

Studies have shown that when Fe_3O_4 (20-30 nm) nanoparticles were added to the yeast of common carp before fertilization, during the process the fertilization rate of the eggs was higher and the yield of free embryos was higher than in other variants. Fe_3O_4 (20-30 nm) nanoparticles have a stimulating effect in the amount of 0,05 g. It can be assumed that these nanoparticles in the specified doses have a catalytic effect on the acrosome of sperm, accelerate energy activity and, consequently, increase the activity of sperm, which leads to an increase in the fertilization rate of eggs.

The results obtained in this way can be used to reduce the loss of embryonic development and increase the overall productivity in salmon aquaculture, especially rainbow trout.

EFFECT OF AL₂O₃ NANOPARTICLES ON ACTIVITY OF PEROXIDASE IN WHEAT LEAVES

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Keywords: aluminum oxide nanoparticles; antioxidant enzymes; peroxidase enzyme. From the time the seeds germinate, plants need micronutrients. Therefore, the treatment of seeds with micronutrients before sowing creates the basis for the normal development of seedlings [Yurin et al., 2015]. At present, based on the achievements of modern nanotechnology, research is being conducted to develop new, more effective, harmless drugs based on micronutrient nanoparticles. The object of research was the seedlings of hard Karabakh and bread wheat Mirbashir-128. The seeds of the experimental plants were treated with powders of AL₂O₃ nanoparticles. The seeds were then sown in Petri dishes and along with the soil in vegetable pots. The method for determining the activity of guaiacol peroxidase (APO, EC 1.11.1.11) led to the achievement of the rate of decomposition of hydrogen peroxide by guaiacol pe-

roxidase in water and guaiacol-forming material in the tested samples. The optical density was determined on a spectrophotometer (MRC, model UV-200-RS, Israel) at 440 nm. To do this, a sample of plant material (1 g) was homogenized in solution with 10 ml of 0.06 M phosphate buffer (pH 7.6).

The homogenate was centrifuged at 8000 g at 4 ° C for 10 min. The reaction mixture consisted of 50 ml of 0.1 mM EDTA, 50 ml of 0.05 mM ascorbic acid (Sigma-Ultra), 50 ml of 0.1 mM hydrogen peroxide, 2.25 ml of phosphate buffer and 300 ml of homogeneous plant extract. Different concentrations of nanoparticles affect the activity of the enzyme in different ways. The highest activity of both species is observed at a concentration of 0.001 mg / l of AL₂O₃. As the concentration of nanoparticles increases in the Karabakh variety, the activity of the enzyme decreases, while in the Mirbashir variety it remains almost the same. When determining the activity of polyphenol oxidase, it was found that at a concentration of nanoparticles of 0.001 mg / l and 0.01 mg / l, the activity of the enzyme decreases in both varieties, and at a concentration of 0.1 mg / l increases sharply. At the same time, the amount of total chlorophyll, chlorophyll a, carotenoids and anthocyanins decreased. As a result, AL₂O₃ nanoparticles caused oxidative stress in wheat after 96 hours. The activity of peroxidase and catalase increased with increasing concentration of aluminum oxide nanoparticles. Based on the data obtained, it can be concluded that each plant genotype contains mechanisms to eliminate the harmful effects of nanoparticles.

ANALYSIS OF THE ACTION OF ULTRASOUND FIELD ON ERYTHRO-CYTES – AS A MODEL OF THEIR BEHAVIOR IN THE VESSEL

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Keywords: ultrasound; erythrocytes (RBC); blood flow; deformability; haemolyse. The possibility of using ultrasonic waves in the physiotherapeutic mode for analyzing the state of cells and diagnosing damage to cell membranes has been substantiated.

Damage to biological membranes in the US field under the action of a number of biologically active drugs (polyene antibiotics, pesticides and antioxidants) is shown; studied and analyzed regularities of changes in the physicochemical properties of red blood cells under various modes of ultrasound, as well as under the action of some physical factors of the environment; priority components of ultrasound waves were identified in the mechanism of influence on blood cells and a physical model of cell behavior in the ultrasonic field was developed; the contribution of red blood cells of different ages to the hemolytic pattern of red blood (erythron) in pathologies was identified and the relationship between them was established; general regularities of the influence of physicochemical characteristics on blood cell membranes were revealed; the effect of physical factors on the functional state of red blood cell membranes in experimental leukemias was investigated and the correlation of the behavior of red blood cells in the field of action of ultrasonic waves on cellular and lipid membranes was revealed, and a model of cell behavior in physiotherapeutic ultrasound mode has also been developed [Prokop, 2007].

The general effect of mechanical factors of the cardiovascular system on erythrocytes and ultrasound field at the physiotherapeutic mode of voicing is shown [Takakuwa, 2001]. The separation of red blood cells into age fractions occurring in human and animal blood *in vivo* reveals the role of each of these groups in the hemolytic pattern of human and animal blood.

The obtained results of studying various modes of ultrasound voicing of blood cells made it possible to propose it as an analog of a model of cell behavior in the human blood flow [Slikkerveer et al., 2017].

Thus, the presented method makes it possible to assess changes in the functional state of cell membranes depending on the age composition of red blood cells, tumor location, drug concentration, chemical structure, as well as the effect of environmental factors on biological objects. This provides ample opportunities for using the kinetic method of US research as a screening method in various fields of biomedical research.

STUDY OF GROWTH AND NITROGEN STATUS IN PLANTS THAT GROWN UNDER SALINE CONDITIONS

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Keywords: chloride salinity; corn; growth and nitrogen status.

We studied the effect of NaCl (0.50, 100, 150 mM) on the parameters of the growth, of individual organs of corn plants (*Zea mays* L.), determined the length of the root and stem, leaf area, native and dry weight, content of protein non-protein, nitrogen, in the aboveground and underground parts of plants the dependence on the pH of the medium (4.3, and 6.0) and the duration of exposure (7,14,21) days.

The inhibitory effect of NaCl on the growth and development of plants as a whole was shown at the first stage of cultivation (7 days) at both pHs of the medium (4.3 and 6.0). Moreover, the inhibitory effect of NaCl at a concentration of 50 mM on plant growth was stronger in an acidic medium than in a neutral one, which is especially noticeable on the roots and leaves in the first period of the experiment (7 days). Leaves, both true and dicotyledonous, decreased in size and weight at pH 4.3 by 2 times or more, and at pH 6.0 by 3 times compared with the control.

With prolonged exposure to NaCl (100mM) (14 and 21 days) in an acidic environment, a much stronger inhibitory effect on true and cotyledon leaves is observed, which manifests itself in a decrease in their number sizes and weight. The same picture of the negative impact of NaCl (150 mM) is observed in 7 day- old plants in the accumulation of dry biomass in the shoots of experimental plants at both pH values, it decreased by 1.62-1.64 times.

With an increase in the duration of exposure, the accumulation of dry biomass by leaves still decreases (in 14-day-old plants, almost 4 times at pH 4.3 and 2.4 at pH 6.0), and in 21-day-old plants, 4 times in both variants. As for the root, in terms of the accumulation of dry biomass, it turned out to be more sensitive than the shoots, especially at pH-4.3. Here, there is a sharp decrease in the accumulation of dry matter compared to the control in terms of experience (7, 14 and 21 days) 65.7% -25.6% -18.2%, and at pH 6.0-52.6% -41.1 % -36.5%, respectively.

An excess of NaCl at a concentration of 150 mM in the growing medium caused some rearrangement of nitrogen-protein metabolism in corn plants, firstly, depending on the acidity of the medium, and secondly, on the duration of exposure. [Shirokikh *et al.*, 2022].

In the first days of the experiment, there was no effect of toxicity on the content of total, protein, and non-protein nitrogen in the shoots. With the duration of exposure to shoots in the variant with acidic pH, a decrease in all forms of nitrogen was noted compared to neutral pH.

Thus, NaCl is a strong toxicant, depending on the concentration, adversely affects growth parameters and nitrogen metabolism in an acidic environment.

THE ROLE OF VITAMIN D AND HUMAN CARTILAGE GLYCOPROTEIN IN OSTEOPOROSIS

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 $\textbf{\textit{Keywords:}}\ osteoporosis;\ osteoporotic\ fractures;\ human\ cartilage\ glycoprotein\ (HCgp39).$

Osteoporosis is a systemic skeletal disease characterized by a decrease in bone mass and a violation of the structure of bone tissue, leading to an increase in bone fragility and the risk of fractures.

According to the WHO, osteoporosis is one of the most important health problems in the world and occupies the 4th place in importance after cardiovascular pathology, oncological diseases and diabetes mellitus. The significance of osteoporosis is determined by its prevalence among the population, the severity of the course, the cause of death, disability, reduced quality of life, high economic costs for prevention and treatment.

According to the statistics, osteoporosis is more common among women, especially during menopause. In this pathology the main role belongs to metabolism of calcium and vitamin D.

Osteoporosis is manifested by low-traumatic fractures. Due to the complexity of the recovery process, the treatment of osteoporotic fractures is one of the important problems of modern traumatology. Diagnostic markers are needed to monitor the recovery period. Human cartilage glycoprotein -39, which has been studied so far in inflammatory processes in the bones, may allow the development of the correct

treatment regimen, reflecting the level of metabolic processes in the bone tissue.

The study was performed to examine the dynamics of human cartilage glycoprotein-39 (HCgp39) in the blood serum during osteoporosis and fracture healing. The material of the study is formed by the examination results of 68 people aged 38-83. Group I - control group consisted of 14 practically healthy people, group II - 14 patients with osteoporosis, group III - 15 patients with non-osteoporotic fractures, group IV - 25 patients with osteoporotic fractures. In groups, they were analyzed by enzyme-linked immunosorbent assay 3 times during the first month. As a result, in the first month of the recovery period, no significant difference was observed in the HCgp39 dynamics for groups II and IV (p> 0.05). However, there was a significant reduction in group III (p <0.05). As no osteoporotic changes were observed in this patient group, bone healing was rapid and it was possible to monitor the dynamics of HCgp39 changes within 1 month. Patients with osteoporosis and other bone fractures in the process of complete recovery need to study HCgp39 more as a diagnostic indicator [Hasanova, 2021].

STUDY OF THE QUALITY INDICATORS OF BLENDED GRAPE JUICE Musayev Teymur¹, Farzaliyeva Leyla²

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Keywords: grape juice; blending; titratable acidity; heavy metal.

The growth in the production of non-alcoholic beverages in recent years makes the increase of the varieties and improvement of their quality relevant. Therefore, the fruits are blended and the new varieties of juices are made. Demand for the grape juice in the consumer market is growing day by day. Making natural juices with the finest quality and organoleptic properties is of the utmost importance. The quality of these juices is determined through the use of modern technologies along with the classical methods [Huseynov *et al.*, 2019].

The research has aimed to make juice from the grape varieties, blend them, and study the quality of these juices. For this purpose, Bayanshira and Rkatsiteli varieties grown in the vineyards of the Scientific Research Institute of Viticulture and Winemaking in Absheron district have been selected as the research material.

The grape berries have been separated from the stems by the destemming machine, washed and squeezed by a hydraulic press under the laboratory conditions and the juice has been made. The juices have been diluted and pasteurized. The juices made from these grape varieties have been blended in 4 variants - at a ratio of 50:50; 60:40; 10:90; 30:70. The quality of each blended juice has been analyzed through modern technologies. The juice to be analyzed has been taken 10 ml at 20° C and analysis has been performed by Foss WineScan modern device.

According to the results of the analysis, the amount of dry mass has been 19.35%, whereas the titratable acidity has been 6% in the juice blended at a ratio of 50:50. The juice blended at a ratio of 60:40 has contained 19.32% dry mass and 6.1% titratable acidity. The amount of dry mass has been 19.47% with titratable acidity being 5.6% at a ratio of 10:90. In the juice blended at a ratio of 30:70, the indicators for dry mass and titratable acidity have been 19.41% and 5.8%, respectively.

The samples have been submitted to the tasting commission of the institute and the grape juice blended at a ratio of 30:70 has been highly appreciated. ICP-OES (Perkin Elmer Optima 8000) technology has been used to determine the heavy metals (Cu, Zn, Fe, Sn, PB, Cd, As) in a sample obtained from the juices of these grape varieties blended at a ratio of 30:70. 15 ml of juice have been taken for the analysis and these indicators have been identified within 3-4 minutes. In accordance with the results, the indicators have been as follows: Cu 5 mg/dm³; Zn 5 mg/dm³; Fe 15 mg/dm³; Sn 200 mg/dm³; Pb 0.05 mg/dm³; Cd 0.03 mg/dm³; As 0.2 mg/dm³.

BIOGENICITY OF STROMATOLITES AND MICROBIAL MATS Mehraliyeva Malakkhanim

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Keywords: stromatolite; extracellular polymeric substance; microbial mat; biomineralization.

Carbonate microbialites, which can indicate the formation of either a microbial mat or a stromatolite, are unique fossils that date back to the early environment of Earth. Modern stromatolites are essential to the historical record of microbial activity preserved in fossil carbonate deposits. Stromatolites are multilayered structures with a propensity to grow in shallow waters, generated by the adhesion, aggregation, and hardening of

sediment grains by microorganisms such as cyanobacteria, which is also known as blue-green algae. Forms of stromatolite include conical, branching, round, and columnar. Stromatolites are formed as a result of biomineralization, which is the creation of minerals by living organisms.

Insight into the ecosystem that existed at the time of the formation of the organo-sedimentary structures, which occurred approximately 3.5 billion years ago in the early Archean, can be gained through the complex interactions that occur between communities of microbes that form mats and the geochemical environment in which they live. The creation of stromatolite is a multistage process of biologically induced mineralization. First, the bacterial community creates a microbial mat, then the cyanobacteria generate gel-like polymeric substances on the cell's outer membrane. and a biomineralization process occurs on these polymeric substances. These extracellular polymeric substances perform a variety of activities. including acting as a physical barrier, boosting the efficiency of metabolic processes, improving attachment and stability, providing a nucleation site, inhibiting activity by binding metals, and precipitation (degradation). Over time, lake sediments attach to the microbial mat, forming microbial layers that can mix ions and sediment grains. The upshot of this process is the formation of stromatolites. Stromatolites consist of micrites as small as 4 microns, microspores between 4 and 20 microns, and spores bigger than 20 microns. Experiments have led to the conclusion that micrites may be indicative of biology.

To summarize, stromatolites can be the signature of extraterrestrial life. The biogenicity of stromatolites may be deduced from both macro- and micromorphological traits; nevertheless, the importance of size and geological context cannot be overstated.

EFFECT OF TEMPERATURE STRESS ON ASCORBATE PEROXIDASE ACTIVITY IN WHEAT

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Keywords: heat stress; ROS; APX; wheat.

Global warming is one of the main ecological problems that adversely affects agriculture. High temperature causes negative impact on plant growth in different stages of development, reduces its harvest,

causes protein and membrane damage, furthermore inhibits plant respiration and photosynthesis. Increasing the tolerance of food plants to high temperatures is considered a serious problem for food security around the world. In plants exposed to heat stress, destructive ROS are often formed, including singlet oxygen (${}^{1}O_{2}$), superoxide radical (${}^{O^{2}}$), hydrogen peroxide (H₂O₂), and hydroxyl radical (OH-), which are responsible for the occurrence of oxidative stress [Huseynova et al., 2016]. The dynamics of the activity and isoenzyme content of ascorbate peroxidase (APX, EC 1.11.1.11) in the leaves of bread wheat genotypes have been studied under conditions of short-term heat stress. Four bread wheat genotypes (Triticum aestivum L.) provided by the Gobustan RES of the Research Institute of Crop Husbandry, tolerant genotypes Zirva 85 and Murov 2, stress-sensitive genotypes Gyzyl bugda and Aran were used in the present study. Plants were grown for 12 days in an automated mini-phytotron with a controlled temperature of 19°C-23°C with a relative air humidity of about 50%, at a photoperiod of 8/16 (dark/light). 12-day-old plants were subjected to heat stress. For preadaptation, the plants were exposed to heat shock for 30 min at 38°C, the temperature gradually increased to 40°C, and the stress lasted 30 min, then the plants were subjected to severe heat shock by raising the temperature to 42°C for 2h. The leaves were wrapped in foil and immediately frozen in liquid nitrogen. The activity of ascorbate peroxidase was determined spectrophotometrically based on the decomposition of H₂O₂ by the enzyme ascorbate peroxidase at a wavelength of 290 nm for 1 minute. The study of the isoenzyme composition of antioxidant enzymes was conducted at a constant electric current (30 mA) at a temperature of 4°C for 3 hours using the PAAG electrophoresis method. Among control samples the highest activity was observed in stresssensitive genotype Aran (~10 mM/mg protein/min), however the lowest activity showed tolerant genotype Murov 2 (~4 mM/mg protein/min). Elevated temperatures lead to visible changes in enzyme activity in wheat cultivars. APX activity increased under high temperature in the Zirva 85, Aran and Murov 2 genotypes and decreased in the Gyzyl bugda genotype. Gyzyl bugda also showed sensitivity to abiotic stressors under field conditions. Further investigations, including other antioxidant enzymes and evaluation of their isoenzyme composition, are needed to add new insight to the molecular aspects of heat tolerance in wheat plants.

MOLECULAR BIOLOGY AND PROTEOMICS RESEARCH TO ENHANCE CROP PRODUCTION IN AZERBAIJAN: TOWARDS SUSTAINABLE FOOD SECURITY

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Kaywords: abiotic and biotic stresses; proteomics research; crops.

The world is facing unprecedented challenges from a growing demand for food for an increasing population, climbing starvation and malnutrition, confrontational climate change effects, overexploitation of natural resources, loss of biodiversity, and food loss and waste. These challenges to food and agriculture production systems can weaken the world's capacity to meet its food needs now and in the future. In other words, fewer people have adequate access to enough nutritious food. Therefore, the strengthening of life science institutions may help to avoid these problems. Sustainable food security will require: (a) sufficient food production and/or availability of food, (b) nutrition sufficiency and/or safety, (c) access to food, and (d) the stability and foreseeability of these conditions. There are 5 key principles of sustainability for food and agriculture: 1) Increase productivity, employment, and value addition in food systems; 2) Protect and enhance natural resources; 3) Improve livelihoods and foster inclusive economic growth; 4) Enhance the resilience of people, communities and ecosystems, and 5) Adapt governance to new challenges. Our Institute is working on the first principle – increasing the productivity of crop plants, especially bread wheat. We are investigating the effect of the abiotic and biotic stresses on plant growth, development, and yield. Drought and salt stresses are more affecting plant growth in Azerbaijan. Therefore, we have consolidated our knowledge to help solve these problems. By applying modern and highly reproducible methods of molecular biology and proteomics we can help to produce enough crops. Comparative proteomics of the photosynthetic apparatus under stress conditions and/or expression profiles of the stress-related transcription factors and proteins will be discussed. Furthermore, a genome-wide association study (GWAS) of 188 wheat genotypes by 135k SNP-Array-Chip was applied for the determination of valuable traits throughout the whole genome. In conclusion, our research indicates that by modifying current investigations much can be done in terms of improving the productivity of many food and agricultural production systems.

DIFFERENCES IN THE ROLE OF RECEPTOR-LIKE KINASES IN THE IMMUNE RESPONSE OF SOLANACEAE PLANTS TO THE PATHOGEN P. VERSATILE

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Reywords: receptor-like kinases; Solanaceae family; Pectobacterium versatile. Pectobacterium versatile is a necrotrophic pathogen of Solanaceae plants causing soft rots of plant tissues thus affecting plants productivity and also reducing the keeping quality of tubers during storage. Previously, we have partially characterized the DspE protein of P. versatile as the main effector of the type III secretion system of these bacteria [Nikolaichik et al., 2005]. However, genetic screening of potential targets of this effector was limited to N. benthamiana (tobacco) and S. lycopersicum (tomato) plants due to the greater amenability of these plants to genetic manipulation. Screening revealed several receptor-like kinases in these plants directly interacting with DspE [Nikolaichik et al., 2012; Badalyan, Nikolaichik, 2014], but the role of DspE and its receptors in the interaction of P. versatile with natural host plants (S. tuberosum) remained unclear.

Plant tissue infiltration with wild-type *P. versatile* cell suspensions caused soft rot symptoms in *S. tuberosum* tubers and hypersensitivity reactions in tobacco and *S. bulbocastanum* leaves, while infiltration with *dspE* mutant cell suspensions resulted in less severe symptoms in all three cases. However, three plants showed significant differences in the nature of changes in the expression of immune response genes.

The most intriguing changes were observed in the pattern of expression of genes for receptor-like kinases interacting with DspE. The expression of the studied genes of these RLKs was significantly inhibited by the pathogen in all three plant species. However, only in *N. benthamiana* did this reaction strictly depend on the presence of the intact *dspE* gene in the pathogen. In *S. bulbocastanum*, this inhibition of RLK expression did not depend on DspE, while in *S. tuberosum*, the reaction depended on the potato variety.

Yeast two hybrid screening detected strong interaction of DspE with RLK4 of *S. bulbocastanum* and RLK2 of *Solanum lycopersicum*, while no interaction was found with RLK4 of *S. tuberosum*. This result argues for different roles of these kinases in the studied species of *Solanaceae* plants.

COMPARATIVE ANALYSIS OF THE ACTIVITY OF COMPONENTS OF THE POTATO ANTIOXIDANT SYSTEM UNDER CONDITIONS OF PVM VIRUS INFECTION

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Keywords: potato; Potato virus M; SOD; POX; CAT.

To protect against potentially cytotoxic forms of activated oxygen, the plant cell has a powerful system of protection against oxidative stress, which includes both enzymatic and non-enzymatic antioxidant systems [Rodriguez M. et.al., 2010]. An extremely important link in the effectiveness of the enzyme antioxidant system is the balanced activity of its constituent enzymes - superoxide dismutase, catalase and peroxidase [Baxter et.al., 2014]. Suppression of the activity of one of the enzymes of the antioxidant system can lead to excessive accumulation of reactive oxygen species and cell destruction. High constitutive levels or high induced levels of antioxidants in a plant cell can provide resistance to stress factors

Potato plants of five promising varieties of Kazakh breeding ("Ulan", "Tokhtar", "Babayev", "Alliance" and "Narli") at the age of 4 weeks served as objects of research. Callus was obtained from leaves using Murashige-Skoog medium with the addition of 2,4-D (1 mg/ml) and kinetin (0.05 mg/ml). For plant regeneration, the callus was transplanted to a medium with 6-BAP (1 mg/ml) and IUK (0.5 mg/ml). Infection of plants with PVM virus was carried out by inoculation through leaf plates by micro-damage with carborundum. The activity of soluble peroxidase was determined by the method [Ermakov et.al., 1987] Determination of catalase activity [Aeby et al., 1984]. Determination of the total activity of superoxide dismutase was determined by the ability of the enzyme to inhibit the photochemical reduction of nitrosine tetrazolium (NBT) [Giannopolitis et al., 1972] with some modifications. All measurements were carried out three times. Electrophoresis was performed under native conditions [Laemmli, 1970]

The results of changes in the activity of the superoxide dismutase enzyme for the five potato varieties studied in leaf explants and in callus on the third, fifth and seventh days from the start of inoculation showed significant differences in the reaction of callus tissue and plants to viral infection. In the callus tissue in all 5 grades, there was a sharp

increase in the level of SOD on the 3rd day after infection (56-68%), which practically recovered to the original indicator on the 7th day after infection. In plants, the initial level of SOD was higher than in the callus tissue and an increase of 20-35% was observed on the 3rd day. The activity of peroxidase increased in the callus tissue up to 9 times on the 3rd day after infection, when both in plants up to 8 times more compared to an uninfected plant. The level of catalase in the studied samples also increased on the 3rd day after infection, but the level decreased only by 7 days after infection. The level in both callus and plants increased by 3-4 times compared to the control.

EFFECT OF AL₂O₃ NANOPARTICLES ON POLYPHENOL OXIDASE ACTIVITY IN SOFT WHEAT (*TRITICUM AESTIVUM* L.) VARIETIES

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Keywords: AL₂O₃ nanoparticles; polyphenol oxidase activity; soft wheat.

Polyphenol oxidase (PPO) is an enzyme found in nearly all plant species. PPO is involved in the function of the antioxidant system in plants and interacts closely with the immune system. The PPO activity in wheat grain varies across cultivars and breeding lines and is also controlled by the environment. The action of this enzyme might be one of the processes determining plant adaptation and tolerance to various stressors. PPOs are Cu-containing enzymes that catalyze the conversion of phenols to o-quinones. O-quinones are highly reactive molecules that undergo non-enzymatic secondary reactions to form melanin, a brown complex polymer [Selvarajan *et al.*, 2018]

Aluminum oxide nanoparticles (Al_2O_3 NPs) are a porous nanomaterial from the metal oxide nanomaterials family. They have a corundum-like structure with six oxygen atoms around a single aluminum atom. Al2O3 NPs have a wide range of applications in human life, particularly in biomedicine and biotechnology, where they are used in drug delivery, biosensing, disease treatment, microbe destruction, and biomolecular stabilization, due to their exceptional properties, availability of multiple synthesis routes, and strategic importance [Hassanpour *et al.*, 2018]. Al_2O_3 NPs' interaction mechanism and fate after release into

ecosystems are less well defined than other NPs', even though the mechanism of aluminum (Al³+) toxicity is generally well recognized and extensively described in several studies [Yanık *et al.*, 2015].

The study's goal was to measure PPO activity in extracts from 2-week wheat seedlings and investigate the influence of Al_2O_3 NPs on enzymatic activity. The study focused on two soft wheat (*Triticum aestivum* L.) cultivars, Ugur-17, and Shafag-2.

We have found the best conditions for evaluating polyphenol oxidase activity in soft wheat seedling extracts. We used 0.06M, pH 7.2 K-phosphate buffer (K_2HPO_4 and KH_2PO_4 mixture) to create an active enzyme preparation [Epmakob, 2005]. At 590 nm, spectrophotometry (UV-200 RS) was used to measure absorption. We employed nanoparticle concentrations of 1 mM and 5 mM. Seedlings were obtained in two ways: in soil and by hydroponics.

It was found that two-week-old wheat seedlings grown in soil showed almost 3 times higher polyphenol oxidase activity compared to seedlings grown hydroponically.

When seedlings of the Shafag-2 and Ugur-17 varieties were treated with a 1 mM concentration of Al_2O_3 NPs, PPO activity increased by 18.4% and 50.4 %, respectively, compared to the control on soil-sown seedlings. Regarding the effect of a 5 mM concentration, Ugur-17 shows a 24.7 % decrease in activity, whereas Shafag-2 shows a 433.6 % increase.

When 1 mM NPs were added to Ugur-17 and Shafag-2 of hydroponically sown seedlings, there was a 104.6 % and 148.4 % increase compared to control, respectively. With the 5 mM NPs, the enzyme activity of the Shafag-2 variety drastically rose by 522.9 %, and for the Ugur-17, this was 139.7%.

THE HEPATO-RENAL EFFECT OF AGERATUM CONYZOIDES AQUEOUS EXTRACT ON PARACETAMOL INDUCED TOXICITY IN WISTAR RATS

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Keywords: Ageratum conyzoides; antioxidants; liver damage; kidney failure; paracetamol.

Antioxidants play prominent roles in prevention of Reactive Oxygen Species (ROS) generation [Valko et al., 2006] and by extension may

offer protection against paracetamol toxicity. These antioxidants are most readily available in edible vegetables and other medicinal plants. Hence, the evaluation of medicinal plants or herbs with free radical scavenging potentials for protective roles against drug induced toxicity becomes relevant. Several plant extracts, including *Ageratum conyzoides* possess free radical scavenging potentials [Jageita, 2007]. Hepatic damage is usually associated with elevated serum ALT, AST and bilirubin concentration while renal damage is associated with elevated serum electrolyte levels. Paracetamol toxicity like many other disease conditions is widely believed to involve the generation of ROS.

This study aimed to investigate the protective potential of aqueous extract of *A. convzoides* in wistar rats following paracetamol induced toxicity. An overdose of 1000mg/kg paracetamol significantly (p<0.05) increase activity of ALT, AST and albumin from (17.33±5.33U/L), $(10.00\pm1.73\text{U/L})$, $(17.09\pm0.43\text{g/dL})$ to $(25.00\pm4.00\text{U/L})$, $(12.00\pm1.00\text{U/L})$, (18.77±0.04g/dL) respectively: levels of total protein, total bilirubin, urea. and bicarbonate from $(28.50\pm0.72g/100mL)$ creatinine $\pm 0.61 \text{mg/dL}$), (13.60 ± 0.06), (9.15 $\pm 0.48 \mu \text{mol/L}$), (34.22 $\pm 0.99 \mu \text{mmol/L}$) to (18.01±0.17). $(31.29\pm0.06g/100mL)$, $(10.23\pm0.37 \text{mg/dL})$ ±2.37µmol/L), (37.03±0.51mmol/L) respectively, whereas activity of ALP and levels of potassium and sodium were significantly (p<0.05) reduced as compared to control. Of the three experimental drug concentrations, an exposure with 600mg/kg aqueous extract of A. conyzoides yielded best results as it restored the values of ALT to 16.33±4.33U/L, AST to 10.00±1.73U/L, total bilirubin to 2.09±0.16mg/dL, urea to 9.11±0.12, creatinine to 12.47±1.92µmol/L and bicarbonate to 33.41±0.58mmol/L compared to control whereas ALP, total protein, albumin, potassium and sodium levels are not restored by administration of plant extract. It is evident that aqueous extract of *A. conyzoides* was able to restore the levels of ALT, AST, urea, creatinine and bicarbonate which indicates repair of injured hepatic tissues and previously impaired renal function caused by paracetamol.

THE IMPACT OF COVID-19 ON BIOCHEMICAL PROCESSES AND IMPORTANT BIOMARKERS (LDH, ALT, AST, CREATININE, BILIRUBIN)

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Keywords: COVID-19; oxidative stress; one-carbon metabolism; biomarkers.

Coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-COV-2) first emerged in the Wuhan City of China and began to spread rapidly among people because of its high contamination rate. After a few months, COVID-19 was reported as a global pandemic by the World Health Organization (WHO) on March 11, 2020 [Cennimo, 2021]. Although some researchers have managed to identify the biochemical mechanisms underlying COVID-19. the investigations are still ongoing to understand its impact on biochemical processes more deeply. One of the processes caused by SARS-COV-2 is the imbalance between the production of reactive oxygen species (ROS) and antioxidants that can detoxify these species [Karkhanei et al., 2021]. The mentioned process is referred to as oxidative stress. In the cases in which the metabolism is normal, reactive oxygen species play important roles in physiological functions such as proliferation, protection of the host cell, cell signaling, and several catabolic and anabolic procedures. On the contrary, if there is an imbalance between ROS antioxidants, the accumulation of ROS can lead to oxidative damage to DNA, proteins, and lipids [Małgorzata et al., 2016]. Some studies have shown that there is a significant difference between individuals with and without COVID-19: total oxidant status (TOS) level has been found lower in a group of healthy people, and patients with COVID-19 have had a higher glutathione (GSH) level [Karkhanei et al., 2021]. According to recent studies, increased levels of oxidative stress and a decrease in levels of antioxidants are the essential agents to aggravate the severity of the disease in patients with COVID-19 [Karkhanei et al., 2021]. Another biochemical process influenced by SARS-COV-2 is one-carbon metabolism. One-carbon metabolism (1C) consists of two major metabolic pathways: the methionine and folate cycles. The pathways have crucial roles in several physiological processes, such as purine and thymidine biosynthesis, generation of ATP, antioxidant defense via GSH, and providing 1C units (methyl groups) for amino acids, creatine, and phospholipids [Constance et al., 2019]. Folate and one-carbon metabolism

are taken over by SARS-CoV-2 to fulfill the need for viral replication. In accordance with several studies, homocysteine and methionine sulfoxide are elevated and glutathione levels decrease. In addition, researches have shown contradictory results in the levels of methionine and Sadenosylmethionine: upregulation, downregulation, or no change in methionine levels and increases or no changes in SAM levels in COVID-19 cases [Perła-Kaján *et al.*, 2022]. In this review, we are also going to discuss the main biomarkers that are present in COVID-19 patients' serum. The biomarkers include lactate dehydrogenase (LDH), alanine aminotransferase (ALT) and aspartate aminotransferase (AST), creatinine and bilirubin. The high levels of LDH, ALT and AST, creatinine and bilirubin have been observed in the patients with COVID-19 [Samprathi *et al.*, 2021]. Especially, two of them, LDH and ALT can have a prognostic role in determining the mortality rate of patients [Vidal-Cevallos *et al.*, 2021].

DEPENDENCE OF ANTIMICROBIAL ACTIVITY OF STRAIN P ON ENVIRONMENTAL FACTORS

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Keywords: in vitro; test-culture; Bacillus mesentericus.

The main purpose of the experiment: Selection of optimal conditions for demonstration of antimicrobial properties of the active strain isolated from cheese samples in vitro conditions and increase the efficiency of antimicrobial production, which is economically advantageous. Both of these tasks undoubtedly require optimization of antimicrobial production, which depends on many specific factors. Samples of cheese were obtained from Gabala, Ismayilli and Shamakhi regions. Isolated colonies are conventionally marked with the letter P. Phenotypic identification of an isolated strain at the sex level was performed according to standard microbiological protocols. The nutrient medium used was manufactured by Difco (Detroit, USA). The rest of the reagents are from Sigma-Aldrich firm. The antimicrobial activity of lactic acid bacteria (LAB) has been tested by agar-diffusion and stain-diffusion methods. Bacillus mesentericus strain was used as a test culture [Lyungh *et al.*, 2018].

For this purpose, firstly, the growth dynamics depending on the pH of the medium and the dependence of antimicrobial properties on environmental factors were first studied in the daily cultivation of the isolated strain. The results of these studies are shown in Figure 1. It is clear from the figure that the dynamics of changes in the optical density of the strainproducer is subject to the typical growth curve of microorganisms. The end of the logarithmic phase of growth is observed after 11 hours of cultivation. During this period, the optical density of the suspension in the liquid medium reached 1.70, and the pH decreased by 1.4 times and was 4.7. After that, the bacteria enters a stationary phase and a death phase. The curve graph shows that during the logarithmic growth phase in the third hour in the liquid medium, traces of rapidly increasing antimicrobial activity appear in parallel with the optical density, reaching 220 IU/ml at the end of this phase. The formation of an antimicrobial agent in the primary metabolites indicates that this agent is not an antibiotic in the classical sense. At the end of the experiment, the pH value of the suspension medium was 4.3. The cells of the strain studied in an acidic medium grow poorly, and as the pH of the medium increases to neutral values, the intensity of cell growth increases [Figure 1].

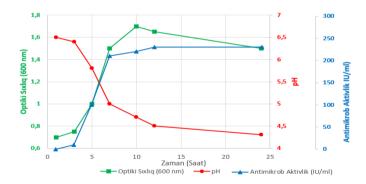


Figure 1. Growth dynamics (■) of the strain P depending on the pH(●) of the medium and the synthesis of antimicrobial agent (△) (test-culture - B.mesentericus)

Thus, according to the results of these experiments, the optimal pH value of the strain P for maximum secretion of antimicrobial agents is estimated at 6.7. However, no significant difference in optical density was observed at pH values of 6.0 and 7.0. The pH of the medium plays an important role in the formation of morphophysiological and biochemical properties of bacteria, including the intensity of synthesis and secretion of metabolites, antimicrobial agents.

ALTERATIONS IN RELATIVE WATER CONTENT AND SUPEROXIDE DISMUTASE ACTIVITY IN WHEAT GENOTYPES SUBJECTED TO DROUGHT STRESS FOLLOWED BY RECOVERY

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Kevwords: oxidative stress; ROS; SOD.

Drought is one of the most common forms of abiotic stresses having a direct impact on the viability and productivity of plants. The phenomenon of drought is based on osmotic stress, i.e. a decrease in the water potential of the environment relative to the water potential of the plant. Currently, water potential is a common parameter used to quantify the water content of the soil. Under stress, the balance between ROS generation and utilization is disturbed, which leads to the development of oxidative stress [Aliyeva et al., 2020]. Currently, several strategies are known to maintain plant viability under oxidative stress. All of them are involved in the activation or de novo synthesis of enzymatic and non-enzymatic antioxidants, i.e. substances that promote the detoxification of free radicals and hydrogen peroxide. Water deficiency provokes excessive generation of free radicals in plant cells. The superoxide radical is extremely reactive and does not spread beyond the site of its formation, while hydrogen peroxide readily diffuses through membranes. The main antioxidant enzymes with high affinity for certain ROS are various isoforms of superoxide dismutase (SOD) and catalase [Huseynova et al., 2014]. SOD forms the first line of specific antioxidant defense of the cell.

The effect of soil drought and subsequent rehydration on the activity and isoenzyme composition of superoxide dismutase in the leaves of winter wheat (*Triticum aestivum* L.) varieties such as Gobustan (tolerant) and Tale 38 (sensitive) has been studied. Significant changes in the relative water content of wheat leaves were observed during drought and rewatering. After rewatering, the Gobustan variety almost fully recovered, and in the Tale 38 variety, this process was found to be relatively weak. Under drought, the water content in the leaves of the Gobustan variety was reduced less than in the Tale 38 variety. Native gel-electrophoresis revealed 8 isoforms of the enzyme. Differences in the isoenzyme composition of SOD between genotypes under drought and rewatering were not identified. Isoform activity increased under

drought and then decreased during re-watering. Differences in the responses of the studied varieties to water stress testify, probably, to their different strategies of adaptation to drought.

The obtained data suggest that under conditions of prolonged soil drought, the coordinated system of antioxidant protection and osmotic control functioned effectively. Plants of both varieties, differing in their responses to water deficiency, maintained the ability to recover after rehydration. Thus, revealing the relationship between the accumulation of hydrogen peroxide in wheat leaves and SOD activity can solve the serious problem of developing highly efficient universal methods for the selection of plant material.

A COMPARATIVE ANALYSIS OF COVID-19 EPIDEMIC BETWEEN AZERBAIJAN AND NIGERIA USING SIR MODEL

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Keywords: COVID-19; epidemic; SIR model; susceptible; infected, removed.

In December 2019, a new kind of virus named "corona" was reported to badly affect the Chinese city of Wuhan. The said virus and its resultant outbreak hit the city of Wuhan first and later affected most of the world. It took hundreds of thousands of lives worldwide [Rahim ud Din *et al.*, 2021]. The SIR Model represents the population using a single system of three different functions: the function of the susceptible group, the infected group, and the removed group. In our application, the removed group consists of both recovered individuals as well as the deaths caused by COVID-19. While forming this model, the following assumptions were made:

- once recovered, individuals will no longer be susceptible
- deaths will only be caused by the infection
- there will be no births introduced to the population
- each individual has the same chance of susceptibility, infection, and removal.

This model will be represented by a system of ordinary differential equations (ODE) [Kaw *et al.,* 2009]. The system of ODEs that represent the changes across the population is given by

$$\begin{array}{rcl} \frac{dS(t)}{dt} & = & -\beta S(t)I(t) \\ \frac{dI(t)}{dt} & = & \beta S(t)I(t) - \gamma I(t) \\ \frac{dR(t)}{dt} & = & \gamma I(t). \end{array}$$

On 28 February 2020, Azerbaijan confirmed the first positive case of COVID-19 within its border (a day after Nigeria did). In this study, we applied the SIR model to simulate the trends of COVID-19 epidemic in Azerbaijan and Nigeria over a period of twenty-seven months. We compared data of both countries from February 2020 to May 2022. We optimized the parameters (S, I, R) using the Euler equation and created an adaptive algorithm. Our results show that the epidemic peak of Coronavirus cases in Nigeria was reached around 20 May 2020, while Azerbaijan peaked around 25 July 2020; a lower incidence of Covid-19 cases and deaths reported in Nigeria compared to Azerbaijan. The difference in peak time is most likely due to the higher temperature and lower humidity in Nigeria (warmer country) compared to Azerbaijan (colder country) while more rapid testing was deemed to have accounted for higher reported cases in the latter – given that both countries imposed strict preventive measures at the onset of the spread.

BACTERIAL SYNTHESIS OF ALUMINUM NANOPARTICLES

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Keywords: aluminum nanoparticles; lactic acid bacteria; supernatant.

Nanoparticles offer a practical technique to keep the results of a property at the atomic or molecular level. Nanoparticle synthesis and characterization have grown increasingly significant as a result of their increasing use in scientific, industrial, and medicinal applications. Aluminum nanoparticles (AlNPs) are currently attracting a lot of academic attention due to their low cost, distinctive characteristics, and interdisciplinary applications [Prabhakaran *et al.*, 2011]. The creation of aluminum nanoparticles in a mixture of DI water and visual detection and UV-visible spectrophotometric analysis of AlNPs is described in this study [Oliveira *et al*, 2008]. In this study, the characterization and synthesis of AlNPs derived from culture free supernatants of lactic acid bacteria (LAB) are the primary goals of the research.

It was possible to create the CFS by cultivating the LAB in sterile MRS broth. The infected broth was incubated micro aerobically at 37°C

for 24 hours before being strained and discarded. It was centrifuged at 5000rpm for 20 minutes after the incubation period, and the supernatant obtained was labeled with CFS and employed for the biogenesis of alpha nanoparticles (AlNPs). It was found that adding 1 ml of the CFS to 10 ml of freshly generated 10 mM Al_2O_3 in deionized water under stirring circumstances resulted in the synthesis of AlNPs. The mixture was then incubated at room temperature for 48 hours. The creation of gray color signifies the formation of AlNPs. The spectroscopic examination of the bio-reduced aluminum ion (Al+) to aluminum nanoparticles (Al0) was performed with a UV-Visible spectrophotometer with a resolution of 0.5 nm, and the results were published in the journal Nano Letters. At wavelengths ranging from 400 to 600 nm, the absorbance of the sample was measured.

To produce AlNPs, the CFS of LAB samples was employed in the production of the nanoparticles. After 48 hours of incubation, the AlNPs produced by the CFS of the LAB. The color of the reaction mixture changed from blue to gray, suggesting the creation of aluminum nanoparticles. The use of biological agents in the production of AlNPs is a cost-effective and environmentally beneficial strategy. Because of its numerous functional qualities, LABs have been used in industrial production for centuries and are being used today. The UV-visible spectrophotometer was used to characterize the biosynthesized aluminum nanoparticles. The UV-visible spectra of the biosynthesized AlNPs by LAB sample at 48 hours' incubation time are depicted. After 48 hours, a broad range of wavelengths between 400 and 600 nm was seen. The peak of surface plasmon resonance (SPR) was seen at a wavelength of 600 nm. AlNPs typically have a maximum wavelength in the visible range of 400-600 nm, with the majority of them falling in this range.

COMBINED EFFECT OF SALINITY STRESS ON THE POTENTIAL DYNAMICS OF NADPH-GENERATING ENZYMES IN CORN SEEDLINGS

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 $\textbf{\textit{Keywords:}} \ corn \ seedlings; \ combined \ stress; \ NADPH-generating \ enzymes.$

Most of the plants living in a sedentary lifestyle are subjected to negative impacts of extreme environmental conditions to a varying degree. In order to complete their ontogenesis normally and eliminate the consequences of these negative impacts, they must first generate special protective responses and activate particular adaptation mechanisms to adjust to that environment [Mosa *et al.*, 2017]. Both the initial defense and the adaptation processes are complex in nature and cover many molecular-genetic and biochemical aspects of plant cells. Implementation of both processes often requires the involvement of the NADPH molecule as a universal reduction metabolite.

NADPH is one of the most important high-energy cell metabolites specific to all living organisms. As it is involved in biosynthesis of several biomolecules, including fatty acids, carbohydrates, carotenoids, deoxyribonucleic acids, and others, it is required for growth, development. and reproduction of cells. It is also considered an important component of the eukaryotic cell's detoxification and defense system. NADPHcytochrome P450 reductase acts as a coenzyme of superoxide radicals in NADPH-oxidase enzyme and NO synthesizing NO-synthase enzyme. It also constitutes an important component of the ascorbate-glutathione cycle acting against the oxidative damage. Therefore, it is reasonably believed that the antioxidant potential of a plant cell is directly linked to the amount of reduction metabolite supply [Corpas et al., 2014]. There are several enzymes that help keep NADPH balance of plants at a certain level. Glucose-6-phosphate dehydrogenase (G6PDH, EC 1.1.1.49), (6PGDH, ES 1.1.1.44), decarboxylating malate dehydrogenase (DMDH, EC 1.1.1.40) and isocitrate dehydrogenase (ICDH, EC 1.1.1.42) are the main enzymes. Being among the most widespread enzymes in nature, they catalyze the reactions of great significance in cell metabolism.

The research is mainly aimed at to assess the role of G6PDH, DMDH and NADP-ICDH in the formation of cytoplasmic NADPH balance of root and stem system tissues of corn seedlings ($Zea\ mays\ L.$, $Zagatala\ 420\ genotypes$) under combined neutral salinity stress (NaCl + Na₂SO₄) conditions and estimate the involvement degree of these enzymes in the defense process against the stress in this regard. The activity of all three enzymes has been measured spectrophotometrically at a temperature of $24^{\circ}C$, at a wavelength range of 340 nm in accordance with the reduction rate of the NADP molecule. Measurements have been repeated for 3-4 times. Tissue extraction reagent has been taken at a ratio of 1 g:5 ml.

According to the results obtained, the increase in the concentration of Na_2SO_4 salt compared to NaCl salt in the solution has an extremely negative impact on the growth of both root and stem system of seedlings. Thus, during the early development of seedlings, as com-

pared to the control, 100 mM NaCl solution inhibited 21% of the root growth, 18% of the stem growth, analogically, 100 mM Na₂SO₄ solution inhibited 26% and 23% accordingly. 200 mM concentration of NaCl solution inhibited the growth of root system by 44%, and the stem system by 37%, while Na₂SO₄ inhibited by 55% and 47%, respectively. Increase in the rate of concentrations of both Na₂SO₄ and NaCl salts and their continuous effect have caused the plant stagnation. Under the salinity stress condition, it's been observed the induction of activity of G6PDH enzyme in the early stages of the growth of root system of seedlings. and the activity of DMDH enzyme in the relatively later stages. The activity of the NADP-ICDH enzyme has not been subjected to significant changes compared to other enzymes. The influence of Na₂SO₄ on the induction of the activity of all three enzymes has been higher than that of NaCl. Similar results have been made with respect to the tissues of the stem system, however, the effect of salts on the course of the process has been relatively low in this regard.

INFLUENCE OF BUCKWHEAT PRODUCTS ON BAKERY PROPERTIES OF FLOUR

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Keywords: gluten; bread; food product; buckwheat.

Technology for the production of gluten-free bakery products composition is significantly different from the production of a particular type of ordinary bread. Temperature, proofing time, ratio components specific to this type of dough. Gluten (gluten) is found in grains such as barley, wheat, oats and rye. Since gluten is consumed in food, the stomach suffers first, intestinal functions are disturbed, the level of assimilation decreases sugars, fats, vitamins and minerals. With constant abuse gluten leads to the accumulation of excess weight, mainly on the belly. It is gluten that makes it possible to mix cereal flour with liquid. The more gluten in wheat, the easier it is to make from it elastic dough, turning into lush and airy pastries. The low gluten content makes this nearly impossible. The end product of scientific research is gluten-free bread, a unique composition of the recipe.

Considering the high correlation between the quantity, properties of gluten in flour, rheological properties of dough and the quality of

bakery products studied the effect of various dosages powders from buckwheat processing products for crude gluten of wheat flour of the highest grade and its quality characteristics depending on the magnitude of the total deformation in units of the IDK-3M device. Buckwheat processing products were added at a dosage of 3-12% by weight of flour. The control sample was a test sample without additives. The results of the study show that with increasing dosage applied powders from 3 to 12% the amount of raw gluten is reduced compared with the control in samples with the addition of processed products buckwheat. Gluten passes from the first to the second quality group [Klimova *et al.*, 2020]. The transition of gluten from the category of "good" to "satisfactorily strong "occurs with the introduction of 9-12% powders from buckwheat processing products.

ASPAT IS AN ESSENTIAL ENZYME FOR PLANT STRESS ACCLIMATION

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Keywords: wheat; AspAT (aspartate aminotransferase); water stress; enzyme activity. Amino acids are known to play the role of protein constituents. They are involved in a plethora of cellular reactions. Therefore, they affect physiological processes such as plant growth and development, intracellular pH control, generation of metabolic energy or redox power, and tolerance to both abiotic and biotic stresses. Aspartate aminotransferase (AspAT; EC 2.6.1.1) catalyzes the reversible transamination reaction between aspartate and 2-oxoglutarate forming glutamate and oxaloacetate dependent on pyridoxal 5'-phosphate. AspAT is known to play a primary role in amino acid synthesis associated with the shuttling of carbon skeletons derived from the TCA cycle. It is involved also in the primary nitrogen assimilation, the transport of reducing equivalents, and the exchange of nitrogen (N) among subcellular compartments. Durum wheat genotypes (Barakatli 95 and Garagylchyg 2) cultivated in the experimental field of the Research Institute of Crop Husbandry located in the Absheron peninsula were used as the study materials. The plot dimensions were 1.05 m×10 m, with 15.0 cm row spacing. Light intensity and temperature at the above sampling times were 150 μ mol (photon) m_2 s_1 , 23 \pm 1°C; 1000 μ mol (photon) m_2 s_1 , 30 \pm 1°C; 2000 μ mol (photon) m_2 s_4 , 38±2°C; 600 μ mol (photon) m_2 s_4 , 31±1°C, re-

spectively. Samples for the study were taken on the 5th, 9th, 13th, 17th, and 21th days of the plant ontogenesis. To evaluate the daily dynamics of the enzyme activities, samples were taken also at the solar time in three-hour intervals on the 13th day of ontogenesis. The leaf samples were kept in liquid nitrogen, at -80°C in the refrigerator. The plant material frozen in liquid nitrogen was thawed, and 200 mg of it was subjected to quick extraction using a chilled mortar and pestle with 1 ml of medium containing 100 mM Tris-HCl (pH 7.8), 10 mM MgCl2, 1 mM EDTA, 10 mM 2-Mercaptoethanol, 2 mM phenylmethylsulfonyl fluoride (PMSF) and 2% (w/v) insoluble polyvinylpyrrolidone (PVP). The homogenate was centrifuged at 12000 g for 10 min. The supernatant was used for the enzyme activity assays. The activity of AspAT was measured in 1 ml volume at 25 mM Tris-HCl (pH 8.5). containing 2mM EDTA, 2.5 mM 2-oxoglutarate, 5 µg/ml pyridoxal 5phosphate, 10 mM DTT, 12 U/ml malate dehydrogenase, 0.1 mM NADH. Enzymatic activities of transferases were determined spectrophotometrically (Ultrospec 3300 pro, Amersham, USA). Measurements were taken at 340 nm for 1 min and the obtained results were expressed as umol mg ¹protein min¹. The significance of differences between control and experimental groups was analyzed using the unequal variance two-tailed Student's t-test. The study of biochemical changes in contrasting durum wheat genotypes, caused by adverse environmental factors, which lead to a decline in plant productivity and grain quality is of great importance. For this purpose, dynamics of the activity AspAT playing an important role in carbon and nitrogen metabolism has been studied at various stages of ontogenesis, during the light period of the day, in the flag leaves of the Barakatli 95 and Garagylchyg 2 genotypes grown under irrigated and rainfed conditions. The AsAT activity was higher in the flag leaves of the drought-tolerant Barakatli 95 genotype compared to the other variants at the beginning of the ontogenesis. Thus, at the beginning of the flag leaf ontogenesis of both genotypes, the AsAT activity was higher in the rainfed variant compared to the irrigated plants. In Barakatli 95, the enzyme activity was 2.7 times higher under rainfed conditions compared to the irrigated variant. According to the results, catabolism of amino acids is faster in the drought-sensitive Garagylchyg 2 genotype compared to the droughttolerant Barakatli 95 genotype under water stress. A significant increase in the activity of AspAT, observed in the drought-tolerant Barakatli 95 genotype, is attributed to the high glutamate demand and maintenance of the Krebs cycle to achieve the correct C: N status.

ANALYSIS OF RETROTRANSPOSON MOVEMENTS OF WHEAT (TRITICUM AESTIVUM L.) BY USING IRAP MOLECULAR MARKER METHOD

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Keywords: epigenetics; mobile genetic elements; IRAP marker; wheat.

Epigenetics is a heritable or non-heritable change in the genome without alterations in DNA, affecting gene expression. DNA methylation, histone modifications, non-coding RNAs, and mobile genetic elements are widely studied epigenetic mechanisms.

Mobile genetic elements, transposons, are DNA sequences, moving from one chromosomal site to another via a transposition mechanism. Transposons cover about 50-90% of plant genomes and even 3-45% of animal genomes. Transposons are divided into two categories in terms of their mobility: RNA transposons (retrotransposons) and DNA transposons. They move copy and paste, and cut and paste mechanisms, respectively. Therefore, retrotransposon integrations are used as markers to detect polymorphisms in both intra- and interspecies. IRAP (Inter-Retrotransposon Amplified Polymorphism), depending on the amplification of polymorphic sites between two retrotransposons, is one of the retrotransposon-based molecular markers techniques. In this method, the primers are designed according to the LTR sequence of the retrotransposon.

This study aims to investigate the movements of retrotransposons and then evaluate the polymorphism ratios among samples. At the initial stage of the research, the model collection was created, and at the next stage, the processes of clarifying the morphological characteristics and molecular methods of epigenetic changes are reflected. Important results were obtained as a result of the comparison of the callus cells obtained from the wheat germ *in vitro* using the IRAP molecular marker and their comparison with the mother plant. In this way, the movement activities of retrotransposons in the cell tissues of the mother plant and wheat callus culture subjected to various abiotic stress were monitored.

STUDY OF TISSUE CULTURE OF TOMATO (LYCOPERSICON ESCULENTUM MILL.) VARIETY SC21-21

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Keywords: Solanum lycopersicum L.; antioxidant; cancer.

Introduced to Europe in the 16th century, the tomato plant (*Solanum lycopersicum* L.) is now distributed throughout the world and has become an economically important crop. Tomato is rich in provitamins A and vitamin C and fiber, and contains important nutrients such as lycopene, beta-carotene, flavonoids and hydroxycinnamic acid derivatives. In recent years, this culture has gained immense popularity. This was due to the fact that the antioxidant and anti-cancer properties of lycopene were discovered, which is the most powerful antioxidant from the carotenoid family and protects a person from free radicals that destroy many parts of the body, and also prevents cancer. These valuable properties of the tomato have led to the fact that it is deservedly considered one of the most important trade products.

Because of its importance as a food source for humans and biological features such as a relatively small genome, diverse germplasm, and ability to transform, the tomato has become an ideal model system for improving other dicotyledonous plants. However, traditional cultivar improvement methods are laborious and time-consuming for breeding success. In addition, there is a problem with the choice of criteria corresponding to the breeding goals. Moreover, disease infestation is a wellknown factor that reduces crop yields. Successful application of plant tissue culture involves the creation of an efficient culture system consisting of a competent genotype, an explants source, as well as optimal conditions for cultivating crops. To achieve success in this case, the creation of simple and efficient regeneration systems is of decisive importance, which will be a fundamental prerequisite for the use of cell and tissue cultures for the mass propagation of virus-free plants and the genetic improvement of valuable commercial varieties. It is known that the process of tomato regeneration along the path of somatic embryogenesis is influenced by many factors, including the composition of the environment, environmental conditions, genotype, the origin of the explants, and its age.

The aim of this study is to determine the most suitable explants for a fast and reproducible protocol for the regeneration of tomato plants. The tomato (*Lycopersicon esculentum* Mill.) variety SC-2121 (Turkey) was taken as the object of the study. Segments of the hypocotyl, cotyledon, and internodes were cultured *in vitro*. It was found that in all three types of explants, the reaction to cultivation under *in vitro* conditions is different. A high frequency of callus induction and intense proliferation were observed from internode explants. However, which type of explants is the best is determined not only by the frequency of callus induction, but also by the morphogenetic competence of the cells of a given explants and by the morphogenetic potential of the genotype itself.

DETECTION OF MIXED INFECTION OF TOBAMOVIRUSES ON TOMATO PLANTS (SOLANUM LYCOPERSICUM L.) IN AZERBAIJAN

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Keywords: tobamoviruses; TMV; ToMV; ELISA; RT-PCR.

Tobamoviruses are one of the biotic stress factors that seriously affect the productivity of tomato plants in the whole world. Tobamoviruses have become a serious problem on tomato (Solanum lycopersicum L.) plants in the whole world, also in Azerbaijan. Tobamoviruses have many host species, and are commonly spread by mechanical way. Tobamoviruses could be transmitted via seeds, plant debris and on greenhouse benches etc. Tomato mosaic virus (ToMV) and Tobacco mosaic virus (TMV) infect several Solanaceous species, especially tomatoes. ToMV and TMV show symptoms such as yellowing and mosaic patterns on the leaves, stunting of the plant, premature shedding of flowers, and significantly reduce the productivity of the plant. In order to detect the mixed tobamovirus infection in Azerbaijan, phytopathological monitoring was organized in various regions where vegetables are grown. Samples of tomato plants with characteristic symptoms for ToMV and TMV viruses were collected from Salyan, Masalli and Guba-Khachmaz region, in July-August 2021. Subsequent studies were performed in the laboratory using modern serological and molecular methods. RNA extraction was carried out using the TRI-Reagent (Triozol) method. Moreover, the degree of purity and density was determined spectrophotometrically. Serological-enzyme-linked immunosorbent assay (IFA, DAS-ELISA) methods were used to analyze plant samples for TMV and ToMV. Plant samples also were analaysed by immunostris kits, which is special for each virus. Then samples were identified by RT-PCR and PCR methods. PCR analysis was carried out using specific primers such as TMV1/TMV2, ToMV6/ToMV5 and universal Tobamo-1/Tobamo-2 designed for *tobamoviruses*. Amplification products were isolated using ethidium bromide in 1% TBE agarose gel, visualized and documented using Gel Documentation (Uvitec, England).

As a result of the analysis, the expected fragments of \sim 422, \sim 320 bp and 500 bp were synthesized. It should be noted that the basis of the fight against Tobamoviruses constitute the implementation of prophylactic measures against the virus and the breeding of cultivars with resistance genes.

THE RELATIONSHIP BETWEEN ROS GENERATION AND PSII PROTEINS PHOSPHORYLATION IN RICE PLANTS EXPOSED TO INTENSE LIGHT

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Keywords: ROS; phosphorylation; PsbS, plants; PsbS-KO; light.

Under the natural environment, plants are exposed to substantial and rapid changes in light intensity which are harmful to plant growth. To adapt and respond to such changes in light quality and quantity, plants have evolved several response mechanisms. Under varying light conditions, non-photochemical quenching (NPQ) and thylakoid protein phosphorylation are two interconnected mechanisms that protect plants from photodamage. Recent studies have shown that a lack of the PsbS protein can result in increased ROS production and phosphorylation of LHCII proteins under illumination. Therefore, here we investigated how ROS production affects thylakoid protein phosphorylation and how the ROS formation depends on the presence of PsbS protein of PSII.

According to our results, there is a strong correlation between the increased light-induced phosphorylation of PSII core and Lhcb1/Lhcb2 proteins, and the enhanced generation of ROS in PsbS-less (PsbS-KO) rice mutants compared to wild-type (WT) plants. We proposed that the higher production of ROS in the PsbS-KO mutant might enhance the phosphorylation of PSII core proteins and LHCII antenna proteins in PsbS-KO plants after high light treatment. Thus, we conclude that increased light-induced phosphorylation of PSII core and Lhcb1/Lhcb2 proteins is probably due to higher ROS production in PsbS-KO mutant plants.

THE DEVELOPMENT AND TREATMENT OF ASPERGILLOSIS AND MUCORMYCOSES DURING THE COVID-19 BY NEW LIPID FORMS OF AMPHOTERICIN B

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Keywords: Aspergillosis; Mucormycosis; COVID-19; Amphotericin.

Conceptual analysis of the invasive bronchopulmonary diseases at the coronavirus infection by the help of the lipid-associated preparations of amphotericin B was presented in this abstract.

The development of coronavirus infection in 2020-2021 led to an increase in serious fungal diseases, especially bronchopulmonary aspergillosis and mucormycosis. Invasive pulmonary mycoses occur at the immunocompromised patients, protective reactions of the organisms (HIV-infection, lungs transplantation, prolonged treatment by broad-spectrum antibiotics and immunosuppressive therapy). Patients with acute respiratory syndrome, usually admitted to intensive care units, frequently receive corticosteroids, antibiotics and immunomodulatory agents. Under these circumstances, it is not surprising that the patients develop secondary complications like invasive pulmonary aspergillosis. A new term has been coined for this condition: COVID-19-associated pulmonary aspergillosis (CAPA). Hard form of COVID-19 leads to significant complications and damages in the epithelial tissues of the lungs because these tissues become more sensitive to infection of the mold fungus Aspergillus, that is to pulmonary aspergillosis. Pulmonary aspergillosis is the reason for 30% of lethal results at infection **[Arastehfar**] the coronavirus et al.. 2020.:

doi:10.3390/jof602009]. Mutation of COVID-19 led to the emergence of the new Indian strain which gave many complications such as mucormycosis to the COVID-infected patients. Mucormycosis was one of the important problems in 2021 during the pandemic of COVID-19 in India and then in the world. The Indian media called it a "black fungus" because of the change in the color of dead and dying tissues to black caused by this pathogenic strain. Mycoses of lungs is one of most important problems for life of patients [ICMR releases diagnosis and manguidelines COVID-19-associated Mucormycosis. for [Firstpost 2021]. The development of an effective formula of amphotericin B led to the creation of lipid-associated forms of preparation – lipid complex and liposomal amphotericin B. Actual formulas of lipid forms of this drug are a perspective way of the efficient treatment of mycoses of the lungs. Application of the preparation and its new lipid-associated forms is actual because it is a potential antifungal agent with good resistance and its wide spectrum of activity against many fungal infections. Lipid complex and liposomal amphotericin B are the main versions of this drug in comparison with colloid-dispersed form of preparation. They are more effective and less nephrotoxic drugs.

There is the analysis of above mentioned fungal infections during the coronavirus pandemic and suggestion of the treatment with new effective drugs based on amphotericin B, which is a key antifungal drug for mycoses in the abstract [Stone *et al.*, 2016].

We reviewed the literature regarding CAPA cases and used information from bibliographic and abstract databases of scientific publications, search systems, publishers: RSCI, Web of Science, Scopus, MED-LINE, Google Scholar, PubMed, Springer Nature, Elsevier, as well as data from modern media.

EFFECTS OF LIGHT SPECTRUM QUALITY ON GRAPEVINE (VITIS VINIFERA L.) DEVELOPMENT IN VITRO

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Keywords: light spectrum quality; grapevine; in vitro.

In addition to the effect on the physiological processes of plants, light has a morphological effect on the shape of the organs and a biological effect on the formation and flowering of flower organs. An increase

in light intensity in plants causes growth retardation, root growth and the formation of color pigments such as anthocyanins. Studying and elucidating the mechanisms of the primary processes of the effect of light on living systems is a major problem in molecular photobiology. Biotechnological approaches with micro clonal reproduction in isolated culture conditions are the most reliable and promising method for the improvement and reproduction of economically important crops. The use of existing new photo biotechnology methods will make a valuable contribution to improving the process of obtaining healthy planting material by planting isolated tissues and organs.

Literature data show that the intensity of many physiological processes, the internal structure of the plant cell and, finally, the formation of the whole plant and the product are determined by both long ultraviolet rays (300-400 nm) and short infrared radiation (780-1100 nm). The spectral composition of light and the intensity of lighting affect the growth and development processes of grape seedlings, and the morphogenesis of grape explants, which are experienced in vitro, are few today. The experiments were performed on the Shirvan Shahi grape variety, which is the most valuable, oldest local, technical grape variety of Azerbaijan. It is considered the first in the world in terms of quality. The product of the variety is a valuable source for the obtaining of highquality kagor dessert wine. The aim of the study was to examine the growth and development characteristics of Shirvan-Shahi (Vitis vinefera L.) grape plants during in vitro micro clonal propagation in photoculture using narrow-band LEDs (light emitting diodes) to optimize the production process. In photo biotechnology applications, the intensity, duration and quality of lighting should be considered as 3 main factors.

Studies have shown that the vegetation period of microclones of Shirvan-Shahi grape variety can be changed in vitro by modeling the growing conditions according to the spectral composition of light and illumination intensity. Therefore, the optimization of the production process by choosing the optimum light regime, as well as the development of technology for mass production of valuable plants, including grapes, is undoubtedly necessary and relevant.

SURVEY AND MOLECULAR DETECTION OF CUCUMBER MOSAIC VIRUS ON CUCUMBER IN THE SOUTHERN PART OF AZERBAIJAN

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Keywords: Cucumis sativus L.; virus disease; cucumber mosaic virus; serological testing; RT-PCR.

The southern part is one of the main vegetable-growing areas of Azerbaijan, with approximately 70% of commercial cucumber (Cucumis sativus L.) production areas in Jalilabad and Masalli. The estimated annual cucumber production in Azerbaijan was 746,673 tones and is forecast to change by an average of 12%. Cucumbers can be attacked by several diseases caused by bacteria, fungi, viruses and may suffer from physiological disorder due to major abiotic stresses. Among these factors virus diseases are a major cause of economic losses in commercial cucumber production around the world, and about more than 10 viruses are known to infect these crops in field conditions. Viruses also have become a problem in vegetable production in Azerbaijan in recent years. It should be noted that Cucumber mosaic virus (CMV) is the most widespread plant pathogenic virus of the family Bromoviridae, genus *Cucumovirus*. CMV is known to be transmitted by several aphid species, notably Aphis gossypii and Myzus persicae, and may quickly cause widespread epidemics. In order to detect Cucumber mosaic virus (CMV) and determine incidence, surveys were conducted in 12 fields in 6 villages in the southern part of Azerbaijan, from June to July in 2022. When examining diseased plants, virus symptoms such as stunting and wilting, leaf curling and distortions, formation of necrotic spots on the leaves, formation of brown annular spots and leaf mosaic on the leaves (replacement of light yellow and dark green parts), yellowing, excessive softening of fruits and abnormal fruit color and shape were observed. After visual diagnosis of viral diseases by occurrence symptoms, leaf samples were taken from diseased plants. A total of 44 samples with symptoms of CMV were collected. Plant samples collected for molecular analysis were placed in special bags and cooled to -80 °C. Cucumber mosaic virus (CMV) was detected in cucumber after analyzing all 44 samples by enzyme-linked immunosorbent assay (DAS-ELISA) using commercial antibodies from Bioreba (Switzerland) according to the manufacturer's instructions. CMV was detected in 42.6% of tested samples and not detected in any samples of melon and watermelon. Molecular analyses (RT-PCR and PCR) were conducted for further confirmation of the serological test. Total RNAs from the 200 mg fresh leaf tissue were extracted by the Trizol Reagent (Qiagen, Germany) according to the manufacturer's instructions, and used as template in RT-PCR. PCR was performed using CMV specific primer pair CMV-CP F/CMV-CP R which amplifies an 880-bp fragment of the entire coat protein (CP) gene. PCR products were separated using electrophoresis on 1.5 % agarose gel containing ethidium bromide (0.5g/ml). The expected sizes of the amplified fragments were estimated by comparison with 2-Log DNA Ladder (NEB), ready-to-use. The agarose gel was visualized under UV transilluminator, and the images were captured with the Gel documentation system (England, UK). This study is confirming the presence of CMV on cucumbers in the southern part of Azerbaijan using DAS-ELISA tests, and molecular detection by RT-PCR with specific primers.

ACCUMULATION DYNAMICS OF PHENOLIC COMPOUNDS IN THE VEGETATIVE ORGANS OF THE DROUGHT-EXPOSED WHEAT PLANT

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Kaywords: phenolic compounds; wheat plants; soil and atmospheric drought. One of the characteristic features of higher plants is the synthesis of large amounts of secondary compounds under stress. Phenolic compounds, unlike other compounds of secondary metabolism, are universal components of plant tissues [Harborne, 1980]. Phenolic compounds playing an important role in photosynthesis and respiration processes, growth and development, reproduction and immunity in plants, are used as important medicines and vitamin P preparations both in the food industry and medicine. Having aromatic rings and free hydroxyl groups in their structures, these highly reactive compounds can easily involve in free radical reactions and utilize reactive oxygen species and peroxide radicals under stress. At present, genotypes containing high levels of phenolic compounds - phenolic acids, flavonoids, anthocyanins, coumarins and lignans are preferred in the development of modern wheat varieties. Although progress is gained in the research of the chemical composition and biosynthesis of phenolic compounds and their intracellular localization, the role of phenolic compounds in the

protection of plants from adverse environmental factors, including drought, has not been fully studied. This problem is still relevant today, as a number of important crops, including durum wheat (Triticum durum Desf.), are exposed to soil and atmospheric drought during their development. Although there is enough information about the effect of temperature on the metabolism of lipids, proteins and carbohydrates in plant cells, little is known about their effect on phenol metabolism. The main purpose of the research was to determine the role of phenolic compounds in the protection of wheat from drought. To this end, the amount of phenolic compounds in the vegetative organs during the generative development of the plant was studied. The objects of the research were durum wheat genotypes with contrasting productivity and drought tolerance (Barakatli 95-drought tolerant, Garagylchyg 2drought sensitive) from the genefund of the Institute of Crop Husbandry of the Ministry of Agriculture of the Republic of Azerbaijan. For analysis, plant samples were taken during the generative development of the plant - flowering, milk ripeness and wax ripeness. Root and leaf samples were crushed in liquid nitrogen, and then the amount of dissolved phenolic compounds was determined based on the interaction of phenols with the Folin-Ciocalteu reagent. The amount of phenolic compounds reached the maximum at the end of the flowering phase and then decreased relatively, while this parameter remained higher than in the watered variant. The amount of phenolic compounds in the leaves of both genotypes was found to increase under drought. In this case, more phenolic compounds were synthesized in the tolerant genotype compared to the sensitive genotype. Besides, under drought conditions, wheat leaves were found to be able to synthesize more phenolic compounds than roots.

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CROSS-SPECIES ANALYSES OF DREBS IN ENSEMBL PLANTS Rustamova Samira, Aliyeva Khayala

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Keywords: DREB; AP2 domain; BLASTn; BLASTp; UniProtKB.

Dehydration-responsive element-binding proteins (DREBs) belonging to the AP2/ERF family of TFs, play a significant role in the sig-

naling network that modulates many plant processes. DREB genes share a sequence similarity at the AP2 domain and bind to the nine base pair sequence - C-repeat/DRE motif (TACCGACAT) in the promoter region of its downstream target genes. The nucleotide sequences of the DREB gene from the genome donor species of wheat were used as queries in BLAST for homology search against 10 phylogenetically close plant species genomes. The sequence of 488 nucleotides isolated from T. urartu and registered in NCBI with Accession Nr.MZ935739 was analyzed comparatively with *T. urartu* (Assembly ASM34745v1) genome in the database, and a hit corresponding to the TRIUR3 17973 gene with 97% similarity was chosen. It has the highest bit score and the lowest e value in the list of hits. This gene consists of 1367 aa and is assumed to have one splicing variant, 214 orthologues, and two paralogues. A protein corresponding to this gene - Dehydration-Responsive Element-Binding protein 2A (M7YLU1) exists in UniProtKB. As a result of a homologous search against the *T. aestivum* (Assembly IWGSC) genome. only four of the 27 hits showed significant compliance. Three of them belong to the TraesCS3A02G099200, TraesCS3B02G115400, and TraesCS3D02G099500 genes located in the A, B, and D genomes, respectively. TraesCS3A02G099200 gene has one transcript and encodes a protein of 278 aa. Dehydration responsive element binding protein W73 (UniProtKB/TrEMBL; O4U0C8) is a product of this gene. The TraesCS3B02G115400 gene belonging to the B genome has two splice variants and encodes proteins of 1008 aa and 1401 aa. The UniProtKB contains one protein corresponding to this gene (Q3LR66) and three protein sequences are available in UniParc (A0A341SESO, A0A341S9F4, A0A1D6AYT1). The TraesCS3D02G099500 gene belonging to the chromosome 3 of the D genome has two splice variants, 212 orthologues, and four paralogues. This gene encodes proteins of 1311 aa and 1225 aa and has four proteins in UniProtKB (GOYWB9; GOYWC2) and UniParc (A0A341T1H8; A0A341T611). Similar results have been observed with *T. spelta* (Assembly PGSBv2.0) but no relevant information for these genes has been found in protein databases. One hit shows a high similarity between the DNA sequence and the Ae. tauschii (Assembly Aet v4.0) genome.

Thus, the identity with significant indicators of score and e-value was 98%. This is a protein-coding gene (AET3Gv20214400), which has 30 <u>splice variants</u>, <u>214 orthologues</u>, and <u>five paralogues</u>. Four dehydration element-binding proteins (A0A2Z4JFC0; A0A2Z4JGM7; V5JE74 and M8BG30) corresponding to this gene were detected in UniProtKB. Ac-

cording to the BLASTN analysis, two of the 15 hits found in the T. dicoccoides (Assembly WEWSeq v.1.0) genome corresponding to the DREB gene sequence from *T. urartu* of the Azerbaijani origin were significantly homologous. They demonstrate compliance to TRIDC3AG011980 and TRIDC3BG016050 genes located on 3A and 3B chromosomes. Three hits in the *T. turgidum* (Assembly Svevo.v1) genome show significant homology. Among them, the similarity with the corresponding gene located on the 3A chromosome is stronger (97%), followed by the 3B and 5B chromosomes (96% and 88%, respectively). There is no information about these gene products in UniProtKB, but Pfam, Prosite profiles, SMART, Prints, CDD, Gene 3D programs predict the AP2 / ERF domain in all transcripts. One of the total 20 hits found in the *Brachypodium dis*tachyon (Assembly Brachypodium distachyon v3.0) genome is statistically significantly homologous to the BRADI 2g04000v3 gene located on the 2nd chromosome. Homology search against barley and rice genomes has gradually weakened.

III. BOTANY. FLORA CONSERVATION

PESTS OF MAIZE (ZEA MAYS L.) VARIETY SAMPLES GROWN UNDER DRY LAND CONDITIONS OF SHAKI-ZAGATALA REGION AND MEASURES TO COMBAT THEM

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Keywords: varieties; maize; helminthosporium; smut; pest.

Diseases and pests are one of the main factors affecting the yield (grain and green mass) of the maize plant [Asyka, 2007; Alexandrovna, 2009]. At present, many diseases are encountered during the growing season in the regions of the country where maize is cultivated.

At the Zagatala Regional Experimental Station of the Agricultural Research Institute of our republic, high-yielding, disease- and pest-resistant varieties and hybrids were obtained, which are cultivated in various soil and climate conditions. These varieties and samples are distinguished by their high productivity and quality, unlike other samples imported from farms.

At present, the diseases of the corn plant at the Zagatala Regional Experimental Station are blister smut, helminthspariosis and brown spot diseases. These diseases can infect most of the varieties and samples grown in the republic and cause significant damage to productivity. But, new varieties and samples are resistant to these diseases. However, favorable conditions for the disease and the extension of this period can be dangerous for plants. In this regard, blister smut disease is dangerous for the maize plant.

During the 2021 vegetation period, the registration of diseases and damage by pests was also carried out in the crops at the Zagatala Regional Experimental Station. It was determined that, in dense crops (5055 min/ha) compared to the other option (45-50 min/ha), brown spot was 1-6 points, helminthsporosis was 2-7 points, mosquito and butterfly damage was 20-40%. This is explained by poor ventilation due to plant density, poor penetration of sunlight into the crop, and excess humidity.

Diseases and pests were recorded in varieties and samples of corn in the field of experiment [Table 1]. Thus, in all varieties and samples, mainly brown spot were observed between 1-6 points, helminthsporiosis (northern) between 2-7 points, and blister smut from 0.1% to 1%. All plants were recorded to be damaged by gnat moths as early as the 8th leaf (20-40%).

Table 1. Diseases and pests were recorded in varieties and samples of cor	Table 1. Diseases and	pests were recorded	l in varieties and	l samples of corn
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N			Diseases		Pests	
No	Name of plants	Blister smut, %	Brown spot, (9 points)	Helmintho- sporiasis, (9 points)	Sovka, %	A white winged butterfly, %
1.	Zagatala-420 control	-	3	3	3	30
2.	Zagatala 68	-	2	3	3	30
3.	Gurur	0,1	4	6	2	40
4.	Emil	-	2	2	3	30
5.	Zagatala 420	0,1	5	6	4	40

Infection of maize varieties and samples cultivated in Zagatala Regional Experimental Station with blistering disease was observed in 13 samples in the range of 0.1-1%. Infection was not recorded in the remaining sample. At the same time, infection with helminthsporiasis was recorded in the samples between 2-7 points (persistent and moderately susceptible). Gnat moths were observed in the mentioned plant nursery.

These pests have weakly damaged the plant up to the 8th tier leaf.

EXPLORING AN AMAZING UNDERGROUND WORLD: ENDOPHYTIC FUNGAL BIOLOGY

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Keywords: endophytic fungus; fungal bioinoculant; salt stress.

Root colonizing endophytic fungus *Piriformospora indica* has been discovered by Varma (JNU, New Delhi) and his collaborators. It was originally found along with arbuscular mycorrhizal spores from the rhizosphere soil samples of spineless cacti and *Cenchrus* sp. (desert grass) growing in North-West Rajasthan. The fungus was named *Serendipita indica* (synonym *Piriformospora indica*) based on its characteristic pearshaped chlamydospores. According to the analysis of 18S rDNA and the ultrastructure of the septal pore, its phylogenetic relationship within the Hymenomycetes (Basidiomycota) order Sebacinales. A symbiotic fungus-*S. indica* is a potential candidate to serve as nano-biofertilizer, bioprotector, bioregulator, bioherbicide/weedicide, combats environmental stress-

es (chemical and physical), nutrient uptake, plants to survive under water, temperature and salt stress, confers (systemic) resistance to toxins, heavy metal ions and pathogenic organisms, interaction with nanomaterials, stimulates growth and seed production and an excellent source for the hardening of the tissue-culture raised crops/plants.

The fungus could be mass multiplied on a cheap and simplified medium. The several medicinal plants tested with fungus are, *Bacopa, Azadirachta, Abrus, Withania, Chlorophytum, Spilanthes, Artemisia, Stevia*, and *Coleus*. Studies have also pointed out that the fungus also helps in better survival and establishment of tissue culture raised plants (agent for biological hardening).

S. indica induces resistance in the monocotyledonous plant to fungal diseases, along with tolerance to salt stress. The beneficial effect on the defense status is detected in distal leaves demonstrating a systemic induction of resistance by a root-endophytic fungus. Recent experiments have amply demonstrated that *S. indica* provides resistance against heavy metal contamination in the soil. The soil treated with fungal bioinoculant, promoted the growth of the grass, turned greener, early flowering and seeding were set in, whereas, in the untreated soil plants failed to grow.

The fungus has great potential for application in nano-agriculture, agroforestry, flori-horticulture, arboriculture, viticulture and especially for better establishment of tissue culture raised plants- much needed for the application in plant industry. This would open up numerous opportunities for the optimization of plant productivity in both managed and natural ecosystems, while minimizing risks of environmental damage. The increasing interest in this fungus worldwide will lead to novel information that will disclose potential agronomical and biotechnological applications [Chodhary *et al.*, 2015; Potshangbam *et al.*, 2017].

WORMWOOD SEMI-DESERTS OF THE MIL PLAIN OF KURA-ARAS LOWLAND

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Keywords: semidesert; wormwood; ephemeral; vegetation.

In the Kur-Aras lowland, semidesert vegetation is as common as desert vegetation. The flora composition of this vegetation is mainly composed of annual plants, but they are mainly seasonal in nature.

Wormwood semi desert dominates the area. Wormwoods, belonging to the Compositae family are of great importance not only in the winter pastures with saltwort, but also in all semi deserts of the Kur-Aras lowland.

Basically, two formations of semi deserts have been identified in the region: 1. Wormwood-ephemeral semi deserts (Artemiseto-Ephemeretum) with the presence of annuals (ephemeris): 2. Wormwood-saltwort semi deserts (Artemisieto-Salsoletum). There are 20-30 kinds of plants that can be found within the Artemisia genus. *Artemisia lerchiana, A.annua* and *A. meyeriana* are among the more widespread types of wormwood. At the same time, species belonging to the genera Alhagi and Chenopodium are also found. There is a big difference in the vegetation of wormwood-ephemeral semi deserts between rainy and dry years [Gurbanov, 2004].

Usually, in years with little rain, the development of both wormwood and ephemerals is very weak. In the spring season with abundant rain, Artemisia species, *Poa bulbosa, Bromus japonicus* Thunb., *Dolium rigidum* Ejand, *Erodium cicutarium*, and in some areas of the plains with a sloping terrain, with wormwood and ephemerals Tulip, Matricaria creates a special scene in vegetation. In such years, the amount of biomass in wormwood-ephemeral semi deserts increases by 2-3 times compared to normal average rainy years, and abundant fodder resources are supplied in many areas. Wormwood-saltwort semi deserts are the most widespread vegetation type in the plains of Kur-Aras lowland plain. In general, in the areas used as winter pastures of the Kur-Aras lowland [Hatamov, 2000], wormwood occupies an important place, and in their botanical composition important forage species of grains participate as the main component by increasing the quality of grass cover.

EFFECT OF ISOCATION SODIUM SALTS ON THE ACTIVITY OF PEROXIDASE IN WHEAT SPROUTS AT THE EARLY STAGES OF ONTOGENESIS

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Keywords: NaCl; Na₂SO₄: ontogenesis; peroxidase; plant cells.

The negative effect of salts on plants is sharper observed in the early stage of ontogenesis. It is therefore of great theoretical and practical importance to study physiological and biochemical processes at the

early development stage of sprouts in order to clarify the mechanism of impact of salts on the plant organism, because the initial physicochemical processes, which take place in plant cells, have a significant impact on subsequent change of intracellular metabolism [Blish *et al.*, 1935; Lori *et al.*, 1995; Kruger *et al.*, 1974]. One of the key issues in increasing of the plant salt-resistance is first of all the solution of a problem of development of its early diagnosis. In this regard, 6-day "Azamatli-95" type wheat sprouts cultivated in aqueous culture was used in different sodium salt concentrations (NaCl, Na₂So₄) widely applied in agriculture.

The activity of peroxidase in plant sprouts is based on determination of the rate of oxidation reactions of benzidin to form blue oxidation solution. The concentration of the blue oxidation solution is determined in advance by photoelectrocolorimeter. The activity of peroxidase was calculated according to the reaction rate.

Studies have shown that peroxidase activity is higher in the roots of wheat sprouts than in the stem.

The activity of peroxidase in 6-day wheat sprouts grown in aqueous culture depends on the concentration of salts. As the NaCl concentration in the medium increases (25-100 mM), the increase in peroxidase activity in the root system is linear.

In the surface part of sprouts, the activity of peroxidase increases at relatively low NaCl concentration (25-50 mM) and then decreases with increasing concentration (75-100 mM) but is not linear, although is relatively higher than control.

In experiments with Na_2So_4 , the increase in the activity of peroxidase in the root system is linear with an increase in the concentration of the root system (25-100 mM). In the surface part of the sprouts, a different picture occurs in the sulfate salinity conditions. Thus, starting with a concentration of Na_2So_4 at 50 mM, the activity of peroxidase began to decrease and went below control at 75-100 mM. The ions of the salts used are arranged in the following sequence weakening the activity of peroxidase.

$$SO_4^2 > Cl$$

It should be noted that the linearity of the activity of peroxidase in extreme salinity conditions can be explained by the failure of the hydrogen peroxide used as an enzyme substance in the tissues to reach the level of saturation. Therefore, any enzymatic reactions including those involving peroxidase are described as one-component reactions until the substance is saturated. However, after saturation, the enzymatic reaction is zero-content and does not depend on the amount of substance.

CHARACTERISTICS OF ORGANOGENESIS OF THE BELLEVALIA ALBANIA INTRODUCED IN THE ABSHERON PENINSULA

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Keywords: monopodal; organogenesis; shoot; bulb; monocarp.

Planting materials (introducers) collected from different ecological conditions in the eastern part of the Great Caucasus were planted and phenological observations were made in the test area at the Central Botanical Garden of Absheron Peninsula. Biomorphological features of Bellevalia Albana which is the one of the Caucasus endemics of the eastern part of the Great Caucasus, have been studied under the conditions of introduction. Observations found that the plant's shoot is monocarpic, scaled cotyledon and assimilated leaves. Shoot grows monopod ally until it reaches a generative maturity condition. It slowly turns into acro sympodial shot. It is a perennial bulb with regeneration buds which grow simpodial [Brullo *et al.*, 1997]. The monocarpic shoots of the plant are monocyclic and branched [Shuka, 2010]. The development cycle of mono carp shoot consists of the condition of bud and extra bud processes, and the development rhythm reflects on the phase alternation of shoot forming.

While analyzing the formation characteristics of organs in the regeneration shoot of the Bellevalia albana species, it was found that the growth cone with primary embryonic embryonics formed in the first stage of organogenesis (end of June - beginning of July). The second stage is characterized by the formation of the active form formation processes in the growth cone, the development and formation of the vegetative part of the plant. In the next year of vegetation, at the end of June, at the third stage, the growth cone grows to its height. The process of growing of the flower axis takes place and in July the formation and furnishing of the flower parts begins. The parts of the flower (internal and external bubbles of the perianth, inner and outer circular parts of the stamens) are different during the growing process in the cone. In November, the process of microsporogenesis occurs in the pollen and results in the formation of mononuclear pollen. Male and female gametophytes are formed before winter. In this time, the plant will pass winter. The blooming occurs at the end of March and early April, and bloom in the third decade of April. In the next stages of vegetation, the life cycle ends in mid-May, when a regenerated bud and its growing plant produce fruit and seeds. After the fruit formation, the upper part of the generative shoot will be destroyed. The remains of the flower axis are mixed with the top of the shoot. Spring-summer vegetation lasts 55-70 days. The results obtained during the introduction of the species are as follows:

- 1. Ontogenesis of mono carp shoot of Bellavalia albana lasts 48 months, as previously stated.
- 2. Regeneration buds are formed, this process takes place 12 months (end of June to end of July). The organ formation continues in the second year (July-October). Intensive formation of generative embryo is observed before winter.

CURRENT STATE OF VEGETATION OF THE LIBERATED TERRITORIES

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Keywords: vegetation; species; dominant; association; formation.

Determining the current state of the vegetation of occupied territories for about 30 years, the number of species included in the flora of the plant, as well as the bioecological characteristics of the vegetation of the area is one of the issues of our research.

Climate change in the environment for 30 years has also affected the flora and bioecological features of the area's vegetation. In addition, the damage caused to the environment, especially vegetation, by degradation, erosion and finally fires in certain areas must be identified. In some years, Armenian fascists started artificial fires in the natural vegetation of the area. As a result of these fires, the vegetation in some areas was completely destroyed.

The rough and unplanned exploitation of gold deposits in the Zangilan region also had a devastating effect on the vegetation of the area. Excessive pollution of river water in the occupied territories has also affected plants.

After the liberation of the territories from occupation and demining, it is planned to conduct field research, as well as field experiments on the vegetation of the area. Seasonally, it is now possible to obtain basic information about the vegetation types and vegetation of

the liberated area using modern technical equipment and drones. For this purpose, the identification of the main types of vegetation in the territory of Karabakh, which has a complex fragmented relief, and the specification of the natural soil-climatic conditions of their distribution areas should be carried out first of all.

Taking into account the wide distribution of areas with mountainous terrain in the area, the current state of the mountain-forest vegetation type is important is one of the important signs and characteristics [Aliyev *et al.*, 2004].

INTRODUCTION OF NEW APPLE (MALUS MILL.) SPECIES IN ABSHERON

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Keywords: apple; introduction; Absheron; species.

The experience of world scientists shows that the introduction is very important for the enrichment of the phytocoenosis with new valuable plants, the protection of biodiversity and the world's plant gene pool [Aliyev et al. 2008; Alexandrova, 2009]. For this purpose, the introduction of new species and the study of the bioecological characteristics of introduced plants are important issues. Thus, the results of the study of bioecological characteristics of wild apple species in Absheron conditions may be important in the future by increasing the number of newly introduced varieties in landscaping, ornamental horticulture and use in various fields, cultivation of varieties resistant to environmental factors and biodiversity conservation.

A research work was dedicated to the study of features of apple (Malus Mill.) species introduced in Absheron. As a research object was taken 23 apple species: M. spectabilis, M. hupehensis, M. sargentii, M. floribunda, M. zumi, M. prunifolia, M. mandshurica, M. halliana, M. micromalus, M. niedzwetzkyana, M. prattii, M. cerasifera, M. baccata, M. hissarica, M. kirghisorum, M. sieversii, M. platycarpa, M. pumila, M. purpurea, M. orientalis, M. coronaria, M. ioensis, M. toringo. The research was carried out in the Central Botanical Garden of NAS of Azerbaijan, where we created a collection which consists of 23 species (108 samples) from us. Classical and modern methods were used in the research.

During the investigations have been studied the development and the growth features of sprouts, morphology and growth features of the root system, phenology. Investigated apple species normally pass the periods of embryonic, germinale, juvenile, virginal, reproductive. Strongly advanced root system consists of well-developed main roots and the second, third lateral roots. On the basis of the phenological observation the investigated apple species are divided into five phenological groups. It was known that the apple species has a feature of growing rapidly. To increase in mass and simultaneously to be capable of sowing in spring and autumn in Absheron the seeds must be stratificated before spring planting.

At the end of the research it is recommended to use apple species in the different areas of agriculture, planting of the parks and gardens in dry subtropical conditions of Absheron. Selected species due to clasters results and due to their decorative features, ecological factors, durability and a wide range of adaptive capabilities can be used. As a first material on the works of selection and hybridization for getting new variates.

EVALUATION OF APPLE (MALUS MILL.) PLANT GROWN IN THE TERRITORY OF GUBA REGION ACCORDING TO THEIR MYCOLOGICAL SPECIES CONTENT

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Keywords: apple; cultivars; fungi; species.

From ancient times to nowadays the fruits have taken an indispensable place among the foodstuffs used buy the human. In the course of a long evolutionary process, it is possible to see fruits among the initial food of the human. The rich chemical content of the fruit, its ability to be stored for a long time, its high productivity and its ability to be grown in different soil and climatic conditions have led to its cultivation in large areas. Apples rank first in terms of area under cultivation and total food production. The amount of substances in the fruit varies depending on the genus, species, cultivar characteristics and growing conditions of the plant. Apples contain up to 13-15% of sugar, carotene, various acids, Fe, Na, K, Ca, Mg, P, etc., 4.92-14.61% of sugars, 0.20-0.86% of acids, 0.07-0.26% tanning substances,

0.28-0.50% ash elements and various vitamins (A1, B1, B2, C, E, P and PP). The various substances contained in the fruits stimulate the appetite, prevent weight gain and slow down the aging process. They strengthen the activity of organs, increase the body's resistance to external influences (heat, cold, thirst, etc.). Due to the richness of nutrients in them, fruit plants are good in preventing many diseases. Some fruit plants contain coloring agents in their barks, covers, flowers and stem barks. [Khudayev *et al.*, 2017]

Apple plant Roside (*Rosidae*) subclass belongs to *Rosales* row, *Rosaceae* family, *Pomideae* subfamily, *Malus* Mill genus *Domestika Borhk* species. The flowers are unigenus, white, whitish, white-pink. The flower group is a simple umbrella. The leaves are simple with short stalks, alternately arranged and simple. In addition to the ovary, the fruit is a pseudo-berry in the presence of a cup and flower bed attached to the lower ovary in its formation. Pollinated by insects. [Gurbanov, 2009]

There are 50 species and about 20,000 cultivars of apples in the world. More than 325 of these cultivars are regionalized in the fruit-growing regions of the CIS. There are 2 species of apples in our country. These are: Oriental apple (*M. orientalis* Uglitiz), Forest apple (*M. sylvestris* Mill.). Apples make up 50% of the total fruit plants in the republic according to the planting area.

Due to the character of its natural growth, the apple is a tree plant. It is of medium height, has a woody body and is perennial. Its fruit is a seed fruit. According to the time of ripening, apple cultivars are divided into 3 groups: spring, autumn, winter.

Summer cultivar: it is grown in July and August; Autumn cultivar: it is grown in September and October; winter cultivar: it is grown in November – February.

Samples were taken from different cultivars of apple plants grown in the Guba region and research was conducted. Sampling of fungi and their release into pure culture was carried out in accordance with known mycological methods. Cultural-morphological indications were determined on the basis of prepared determinants, and the naming and systematization of fungi was carried out in accordance with the data posted on the official website of the International Mycological Association. As a result of the research, it was found that *Aspergillus niger, Aspergillus flavus, Rhizopus, Mucor mucedo* and other fungi species were found in the samples taken from the stem, leaves, flowers and fruits of the apple.

Thus, the study of the effects of fungal species identified in the cultivars of apple plants studied may play an important role in the prevention of serious diseases that they can cause.

THE EFFECT OF SALT STRESS ON PHOTOSYNTHESIS AND RESPIRATORY PROCESSES

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Keywords: salt stress; CO2 absorption; photosynthesis.

During salt stress, the process of photosynthesis in plants undergoes certain changes, mainly due to a decrease in its intensity. This occurs as a direct or indirect effect of salt stress [Brugnoli et al., 1992]. As salinity increases, mouth closure, thickening of the mesophyll layer and decreased CO2 absorption, breakdown of photosynthetic pigments, and weakening of photosynthetic metabolism are directly related to or oxidative stress. Recent extensive research suggests that photosynthetic genes are expressed under the influence of salt stress as well as other stressors. Expression of photosynthetic genes becomes more intense and acute during salt stress. In the first stage of the process of photosynthesis, the absorption of photons depends directly on the state of its reaction centers, and during salt stress, first, the absorption of photons decreases as a result of disruption of the structure of chloroplasts in FSI and FSII reaction centers. In the high-salt Chenopodium quinoa plant, under the influence of NaCl salt at 500 mM concentrations, plant growth was reduced by 82%, water potential in the leaves was reduced, and photosynthesis was reduced by 28%.

During salt stress, the process of glycolysis in seed respiration is inhibited, the formation of ATP in the Krebs cycle is reduced, and, accordingly, the energy supply of tissues is weakened. I. In the experiments of the day, during salinization with NaCl, activation of an alternative pathway of respiration in pea varieties, which is not accompanied by ATP synthesis, was observed. By increasing the salinity, the excess of respiration in pea leaves was determined. At this time, the cytochrome respiratory tract was weakened. Weakening of cytochrome respiration in native leaves weakens ATP formation. However, during salinity, additional energy is required for the transport of Na ions and the synthesis of osmotics. The importance of the alternative is that the electronmotion chain from ubiquinone to water does not generate membrane potentials and transmits 2 out of 3 energy ratios, phosphorylation at NADH-dehydrogenase levels is maintained, which results in a small amount of energy generation.

MICROMYCETE DIVERSITY ON THE SPECIES OF THE GENUS *QUERCUS* L. IN MYCOLOGICAL HERBARIA

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Keywords: family; fungus; morphology; oak; parasite; saprobe.

The genus Quercus L. (Fagaceae) which includes nearly 500 species in the world is one of the dominant forest tree genus in Azerbaijan. Totally 6 oak species (Q. ilex L., Q. robur L., Q. suber L., Q. castaneifolia C.A. Mey, Q. macranthera Fisch. & C.A.Mey ex Hohen, Q. petraea (Matt.) Liebl.) of oak were recorded in the country. Few of them are considered as rare and included in the second edition of the Red Book of Azerbaiian. Oak is one of the main forest forming tree species. The natural distribution area of oak is rather wide, being encountered in all physicalgeographical regions of the country. The highest number of species was observed in the Samur-Shabran region. The mycobiota of oak was studied at the beginning of 20th century in Azerbaijan [Guseinov, 1989; Guseinov et al., 1994; Axundov et al., 2000]. The aim of current study was to investigate fungal diversity associated with oak kept in the mycological herbarium of the Institute of Botany, ANAS. In total, 318 specimens were involved in the research, which were collected mainly in May and September at different years. Specimens were studied based on morphological characteristics by using a light microscope (Nikon Eclipse E100). Novel taxonomical and nomenclature changes were considered for species. As a result, 198 species belonging to 241 genera, 60 families and 19 orders were identified. Most of them are related to Erysiphaceae (60), Botryosphaeriaceae (19) and Phyllostictaceae (18). The genera Phyllosticta Pers. and Erysiphe R. Hedw. ex DC., dominate in the number of species. Fungi recorded on oak can be categorized as belonging to the following ecological groups: saprobes and parasites. Herbarium specimens were categorized based on host diversity. Fungal species were registered in all *Quercus* species. Among them Q. robur (95), Q. petraea (61), Q. castanefolia (57) and Q. macranthera (56) possess more fungal diversity.

STUDY OF THE MYCOBIOTA OF CUCUMBER PLANT GROWN ON THE ABSHERON PENINSULA

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Keywords: cucumber; fungal diseases; pathogenic fungi; Absheron peninsula.

Cucumber is a plant in the Cucurbitaceae family and currently, one of the major widespread vegetables. Its fruits contain mostly 94-97%, water and 3-6% dry mass. Despite the fact that there is a small amount of dry mass, it includes many complex and valuable compounds that contain minerals, organic acids, enzymes, essential oils and vitamins that are absolutely necessary for the human body. Ash of cucumber contains sodium, potassium, magnesium, phosphorus, chlorine, iron, sulfur salts and microelements as well. Cucumber plant needs consistent watering. It cannot grow in dry soil. Productivity can be further increased through fertilizers. The growth stops below 14°C and above 42°C. The optimal outdoor growing temperature for the growth of cucumber is between 25°C and 30°C during the day. As is the case with other vegetables, cucumbers suffer from a number of diseases. Fungal diseases caused by pathogenic fungi are also widespread. The most common fungal diseases of cucumber are white rot, gray rot, powdery mildew, false powdery mildew, anthracnose [Mammadzade, 2015].

Samples have been taken from the Dervish, Dolev and Kvamimant-F1 varieties of cucumber grown on the Absheron Peninsula and analyzed in accordance with the modern mycological methods relevant to the purpose of the work. The results have been processed statistically, and the species composition of the final pure culture has been identified. Cultural and morphological characteristics have been determined on the identification guide, and the naming and classification of fungi have been carried out in accordance with the rules set out on the official website of the International Mycological Association [Aghaeva, 2011].

The research has found out that there have been fungi species such as Colletotrichum orbiculare, Aspergillus Niger, Rhizopus Nigricans, Rhizopus Oryzae, Aspergillus Flavus, Verticillium Nigrescens, Penicillium Chrysogenum, Penicillium Variable on the roots, stems, leaves and fruits of the Dervish variety, Aspergillus Niger, Botrytis Cinerea, Cladosporium Cucumerinum, Rhizopus Stolonifer, Verticillium Albo-atrum, Penicillium Trichoderma, Rhizopus Oryzae, Aspergillus Fumigatus, Pythium Debaryanumon the samples isolated from the Dolev variety, and Alternaria Cucumerina, Aspergillus Niger, Rhizopus Stolonifer, Sphaerotheca fuliginea on the samples isolated from the Kvamimant-F1 variety. Thus, 10 species and 17 genera of fungi have been identified on the samples isolated from the varieties of cucumber plant.

MORPHO-PHYSIOLOGICAL INDICATORS OF PUMPKINS GROWN UNDER CONDITIONS OF CHLORIDE SALTINATION AND WITH PHOSPHORUS DEFICIENCY

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Keywords: impact of salinity; negative effect of phosphorus; pumpkin plant (Cucurbita pepo L.); chloride salinization.

An analysis of the results of studies conducted on different plants and under different conditions based on the literature shows that the effect of phosphorus deficiency on the development of root and aboveground organs of plants is different. Some note that the root biomass increases against the background of the total mass of the plant, some researchers note that it has not changed, while others note that it has decreased. On the other hand, given the negative impact of salinity, we see how different opinions are on this issue [Gadimov *et al.*, 2022; Adnan *et al.*, 2020]. Considering the above, we think that an objective idea of the degree of negative effect of phosphorus deficiency under conditions of chloride salinization on the accumulation of biomass by roots and shoots can give an indicator of the quantitative ratio of the mass of roots to the mass of shoots.

In connection with this, the article studied the effect of phosphorus deficiency on the morphometric parameters of a pumpkin plant (*Cucurbita pepo* L.) of the "Perekhvatka" variety under chloride salinization (100 mM NaCl). The plant was grown in aquaculture in Knopa nutrient mixture. Scheme of experience: 1. complete nutrient mixture (CNM); 2. Nutrient mixture without phosphorus (NM-P). To exclude phosphorus from the nutrient medium, KH_2PO_4 was replaced by an equivalent amount of KCl; 3. CNM +NaCl; 4. NM-P +NaCl.

Samples were taken three times every 7 days, and the materials previously killed by dry heat were dried for 10 minutes at 150°C in an oven to constant weight at 60°C. The dry weight and water content of the plants were determined by drying the materials to constant weight under the above conditions. In addition, in the studied plants, the volume and surface, as well as the length of the roots, were determined [Kokko *et al.*, 1993].

Analysis of the data suggests that the time of exposure to phosphorus deficiency sharply reduces the biomass both in individual organs and in the whole plant. The ratio in the accumulation of dry biomass compared to the control between the 7th day of the impact of phosphorus deficiency and the 21st day is more than 3 times for the shoots, and two times for the roots. The

value of the ratio of the dry weight of the roots to the dry weight of the shoots is static in the course of the deficit and tends to increase only during prolonged starvation of the plant.

It is shown that, under chloride salinization as a result of phosphorus starvation, the roots behave more stably in comparison with the shoots in terms of changes in dry and wet weight, water content and morphometric parameters (volume, surface, length). This is reflected in an increase in the ratio of quantitative indicators of roots to similar indicators of shoots. Despite the fact that 100 mM salinity in the first days of development has a negative effect on morphometric parameters, a positive effect is observed already by day 21.

DETERMINATION OF POLYPHENOLE OXIDASE ACTIVITY IN BAR-LEY AND WHEAT SEEDLINGS UNDER NaCL SALINITY

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Keywords: salt tolerance; polyphenol oxidase; water culture; biodiversity.

Soil salinity is one of the abiotic factors of the environment having a serious impact on the development and productivity of agricultural crops. According to modern estimates, 1/15 of the soil, including agricultural lands, is saline. Besides, about twenty percent of irrigated lands are more or less saline. According to the current prognosis, by 2050, about 50% of arable lands will be subjected to salinization.

It should be noted that chloride-sulfate or sulfate-chloride salinization is more widespread in Azerbaijan. In addition, carbonate salinity is not uncommon, and sodium salts are predominant.

Salinization of areas leads to a decrease in the productivity of agro- and biocenoses and biodiversity. Soil salinization is one of the most important stressors limiting global food production.

Thus, salinization of soils is one of the main problems facing the world today, and in this regard, the study of the salt tolerance of plants, the impact of salts on plant life, and, in particular, the physiological and biochemical processes at different stages of development is one of the most pressing issues. Some researchers have linked the toxic effects of salts on plants to disrupted activities of cellular enzymes.

Considering the above, we studied the activity of polyphenol oxidase, an enzyme of the alternative respiratory tract, in barley and wheat seedlings under salt stress.

Barley and wheat varieties widely used in agriculture, such as "Garabagh-22" (*Hordeum Vulgare* L.) and wheat "Azamatli 95" (*Triticum aestivum* L.) were used as research objects. Experiments were performed with 5-day-old seedlings cultivated in water culture.

The activity of polyphenol oxidase was determined spectrophotometrically and calculated according to the reaction rate. Based on the results, the activity of polyphenol oxidase in the roots was relatively high compared to that in the shoots of the wheat and barley seedlings.

In the experimental variants, the activity of polyphenol oxidase depended on the concentration of salt in the medium. At 25 mM NaCl, the activity of polyphenol oxidase in the roots and shoots of seedlings increased compared to the control. The enzyme activity decreased to control levels with the increasing salt concentration (50-75mM).

The results of the experiments with barley seedlings differed from those with wheat seedlings. The activity of polyphenol oxidase in the roots and shoots of barley seedlings was higher in experimental variants compared to the control.

At 25 mM NaCl, the activity of the enzyme increased sharply. Although the activity of the enzyme weakened slightly with increasing salt concentration (50-75 mM), it was higher than in the control in both the roots and shoots, but the change in the activity of the enzyme was not linear.

Thus, it is clear from the results that stress induced by NaCl increases the activity of polyphenol oxidase in wheat and barley seedlings at low concentrations, while at high concentrations it decreases the activity to control levels in wheat and the activity is slightly higher than in the control in barley. This can be attributed to the higher salt tolerance of barley compared to wheat.

Thus, based on our results, we can conclude that one of the mechanisms of adaptation to salt stress is a change in the activity of the antioxidant system as well as some enzymes including polyphenol oxidase. Activation of polyphenol oxidase neutralizes the effect of salt, allows maintaining a certain stable level of oxidative metabolism, and increases the adaptation mechanisms and adaptive capacity of the plant organism.

MAJOR FUNGAL DISEASES OF TREES AND SHRUBS GROWING ON THE TERRITORY OF SIYAZAN REGION

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Keywords: conidia; monitoring; assimilation; transpiration; productivity.

The most common fungal diseases adversely affect the life of trees and shrubs, reducing their productivity and longevity. The disease of trees and shrubs is accompanied by profound disorders of their functions: assimilation, transpiration, respiration, the water supply by the roots is often delayed or stopped, its movement through the vascular system is disturbed, and the outflow of assimilates from the leaves to the stem and roots is weakened. Therefore, in fungal diseases, one or another pathological process is observed. Currently, the forests of Siyazan region are also affected by fungal diseases, which may lead to a gradual reduction in forest area. Therefore, the identification and study of various kinds of fungal diseases is especially important. In this regard, the objects of research are some trees and shrubs growing in this area. These - oak (Quercus sp.), pomegranate (Punica granatum L.), hornbeam (Carpinus sp.), beech (Fagus orientalis L.), ash (Fraxinus sp.), juniper (Juniperus L.), cotoneaster (Cotoneaster sp.), wild olive (Elaeagnus angustifolia L.), willow-leaved pear (Pyrus salicifolia Pall.), maple (*Acer campestre* L.), wild rose (*Rosa* sp.), hawthorn (*Crataegus* sp.).

As a result of the monitoring, which the purpose was to identify various fungal diseases, rust was found on the plants. This type of disease is caused by rust fungi. Leaves and young shoots are affected. Numerous bright yellow, orange or brown blisters form on leaves and shoots of hardwoods, often covering the entire surface of the affected organs.

This disease is caused by fungi - *Melampsora populina*, *M. salicina*. Powdery mildew is characterized by the formation of superficial white, initially cobwebbed, later compacted powdery leaves on the affected organs. Leaves and young shoots are covered with an abundant white coating of powdery mildew fungus conidia. This disease is caused by fungi - *Microsphaera alphitoides*, *Sawadaia tulasne*, *S.bicornis*. Black spot-alternariosis manifests itself in the formation of black spots of various shapes, sizes, structures on leaves, fruits and seeds. Alternariosis is caused by fungi-*Rhytisma salicinum*, *R.acerinum*, *Polystigma ochraceum*.

As a result of observations, it was found that some trees (oak, beech, maple, ash) and shrubs (wild rose, hawthorn) growing in the middle and lower mountain belt are susceptible to fungal diseases [Ray et al., 2017; Martinelli et al., 2015].

DETERMINATION OF FUNGI ENCOUNTERED IN SOME HORTICULTURE PLANTS PLANTED IN AGHSTAFA REGION (ASHAGI GOYJALI, YUKHARI GOYJALI)

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Keywords: pathogenic fungi; Agstafa region; watermelon; melon; pumpkin.

In our country, which is confidently following the path of independent development, as in other sectors of the economy, reforms are being expanded in the agricultural sector, new forms of economy are being created, new processing and industrial sectors are being formed in accordance with market relations. From ancient times, horticulture in Azerbaijan has had a large industrial character, with a special weight among the agricultural sectors. Therefore, the protection of horticulture plants, one of the oldest and richest formations of the flora of Azerbaijan, their transmission to future generations, the efficient and sustainable use of genetic resources is of great importance, both experimentally and scientifically. [Qeribov *et al.*, 2015]

The natural climatic conditions of Agstafa region are favorable for the cultivation of many plants, including horticulture plants, as well as for the spread of some fungi.

The purpose of the presented work is based on mycological assessment of varietal samples of some horticulture plants grown in Agstafa region. The species composition of fungi inhabiting the horticulture plants the sample of which was taken during the research was characterized. [Agayev, 2007]

Bleached malt juice (NAA), starch agar (NA) and potato agar (KA) were used to bring the fungi inhabiting the leaves, flowers, stems and fruits of some varieties of horticulture plants to pure culture. The pH of the nutrient medium was 4.5-5, placed in a thermostat at $25-28 \circ C$. Observations were made 3 days after inoculation depending on the growth and development of the fungi.

During the analysis of samples of some horticulture plants taken from some villages of Agstafa region, it was determined that 23 species of fungi were inhabited in watermelons, melons and pumpkins. The taxonomic structure of fungi is presented in accordance with the system on the official website of the International Association of Mycology (IAM). [http://mikrobiyolbul.org]

The following results were obtained from the researches carried out on some varieties of horticulture plants studied in Agstafa region (Ashagi Goyjali, Yukhari Goyjali):

- 1. As a result of the experiment, *Aspergillus niger, Aspergillus flavus, Rhizopus oryzae, Rhizopus nigricans, Neurospora sitophila, Fusarium culmorum* fungal species were observed to be spread in the cultures where samples were taken from the leaves, flowers, stems and fruits of the I field watermelon sort were planted.
- 2. Aspergillus ochraceus, Rhizopus oryzae, Rhizopus stolonifer, Rhizopus nigricans, Colletotrichum lagenarium fungal species were observed to dominate in the cultures where leaf, flower, stem and fruit samples taken from the II field watermelon sort were planted.
- 3. Aspergillus flavus, Aspergillus carbonarius, Aspergillus niger, Aspergillus fumigatus, Rhizopus nigricans, Rhizopus stolonifer, Mucor mucedo fungal species were observed to be spread in the cultures where samples were taken from the leaves, flowers and stems of the 1st field sort of melon were planted.
- 4. Rhizopus stolonifer, Rhizopus oligosporus, Aspergillus ochraceus, Fusarium culmorum, Botrytis cinerea fungal species were observed to be spread in the cultures where samples were taken from the leaves, flowers and stems of the II field melon were planted.
- 5. Mucor racemosus, Aspergillus carbonarius, Aspergillus fumigatus, Aspergillus flavus, Aspergillus niger, Alternaria cucumerina, Fusarium culmorum fungi were observed to be spread in the cultures where samples were taken from the leaves, flowers and stems of the pumpkin variety were planted.
- 6. Rhizopus stolonifer, Trichothecium roseum, Aspergillus fumigatus, Fusarium oxysporum, Fusarium solani, Alternaria alternata, Penicillium chrysogenum fungal species were observed to be spread in the cultures where samples taken from the pumpkin fruit were planted.

HEMEROBIA AND ECOLOGICAL FEATURES OF SOME RARE SPECIES IN THE NORTH-EAST PART OF THE GREATER CAUCASUS

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Keywords: rare species; cenopopulation; hemerobia; ecology; altitude.

The current study is conducted to identify and protect populations of rare species and deal with the hemerobia features and anthropogenic impacts on them which were investigated in the north-eastern part of the Greater Caucasus in 2017-2021 years. Each species included in plant communities has an individual spectrum of tolerance to anthropogenic influences. An extended version of the Yala's system was used [Ishmuratova *et al.*, 2003].

As a result of the study of the species composition of plant communities with *Iris reticulata*, it became clear that in those cenoses o (oligo) hemerobia fraction is 15%, m (meso) fraction is the highest and reaches 40%, but a (ahemerobia) fraction species are more sensitive to anthropogenic influences, up to 7%. In all cases, including *I. reticulata*, the share of t (metahemerobia) fraction species was only 2%. In the cenoses with *Ophrys apifera*, the percent of oligo-hemerobia reaches 18%, and meso-hemerobia 48%. Ahemerobia species are more susceptible to anthropogenic influences, up to 3%. t (metahemerobia) fraction was only 1%.

In cenoses with *Ophrys sphegodes* subsp. *mammosa* plant, the share of oligo-hemerobia is 20%, and the share of m (meso) is 43%. a (ahemerobia) species were only 3%, and t (metahemerobia) - 1% [Figure 1].

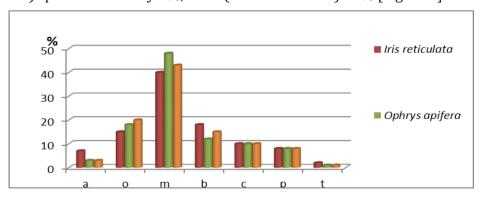


Figure 1. Hemorobia spectrum of plant communities with *Iris reticulata* M.Bieb., *Ophrys apifera* Huds., *Ophrys sphegodes* subsp. *mammosa* (Desf.) Soé ex E. Nelson taxa (absis axis - a-o-m-b-c-p-t hemerobia fraction; ordinate axis - hemerobia level)

Hemerobia assessment of the species showed that *Iris reticulata*, *Ophrys apifera* and *Ophrys sphegodes* subsp. *mammosa* taxa are mesohemerob.

Cenopopulations of *Ophrys sphegodes* subsp. *Mammosa* were found from a height of 9 m a.s.l. to 1025 m. According to the results of the regression analysis between the number of individuals and altitude was observed a decrease in the number of individuals with increasing altitude. Thus, the highest number of individuals (549) was recorded at an altitude of 9 m a. s. l. The number of individuals in the cenopopulation of *Ophrys sphegodes* subsp. *mammosa* recorded at altitude 1025 m a.s.l. decreases to 123. The results of regression analysis of *Iris reticulata* show that with the increasing altitude, there is an increase in the number of individuals. The highest number of individuals (516) was recorded at an altitude of 1342 m a.s. l. *Ophrys apifera* cenopopulations are found at various altitudes ranging from 603 m a. s. l. to 1326 m. The results of the analysis show that with the increasing altitude, an increase in the number of individuals was also observed. Maximum number of individuals (70) was recorded at an altitude of 1326 m a.s.l.

The results of a regressive analysis showed that as the altitude increased, the number of individuals increased in the cenopopulations of *O. apifera* (16-124) and *I. reticulata* (48-516), *O. sphegodes* subsp. *mammosa* (549-25).

ANTIOXIDANT PROPERTIES OF LIQUORICE EXTRACT IN PROTECT-ING PHOTOSYSTEMS UNDER OXIDATIVE STRESS

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Keywords: pigment; reactive oxygen species; antioxidant; extract.

Under conditions of oxidative stress caused by exposure to NaCl at a toxic concentration (10^{-3} M) on wheat ($Triticum\ aestivum\ L$.) seedlings, the antioxidant properties of an extract obtained from liquorice roots ($Radix\ glycyrrhizae$) were determined. An increased content of reactive oxygen species (ROS) led to a change of the fluorescent characteristics of the millisecond delayed fluorescence of chlorophyll a (ms DF Chl a). The change in the state of the antenna complex of the reaction center (RC) during the recombination reaction on the donor side of photosystem II (PS II) was determined. The activity of this phase ms DF Chl a

was 66% relative to the control. The stability of electron transfer to the quinone acceptor Q_A on the acceptor side of PS II was disturbed. Its activity was 45% of the control [Gunell *et al.*, 2020]. Analysis of the absorption spectra under these conditions showed quantitative changes in the content of chlorophyll forms –Chl a_{680} and Chl b_{645} . The content of Chl a_{680} decreased by 73%, and Chl b_{645} by 38% relative to the norm. The change in the ratio of Chl a_{680} /Chl b_{645} showed a greater resistance of Chl to this stress. The addition of liquorice extract to the seedling growing medium under stress conditions (24 h) showed a corrective effect on the content of Chl a and Chl b forms and on PS II activity. An increase in the Chl a_{680} /Chl b_{645} ratio showed that liquorice extract protects the Chl form under stress [Dadashova *et al.*, 2018].

The corrective effect of liquorice root extract depends entirely on its phytochemical composition, the main component of which is saponin-glycyrrhizin. It is concluded that liquorice root extract is able to extinguish ROS, therby stimulating redox processes in chloroplasts.

WINTER PASTURES ON THE LEFT BANK OF THE KURA RIVER IN SALYAN DISTRICT

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Keywords: Kura iver; semi-desert landforms; soil-climatic conditions.

The left bank of the Kura River is within the territory of the Kura plain of the Kura-Aras lowland. The semi-desert landforms and semi-desert vegetation are widespread in the Kura plain.

The flora of the semi-desert vegetation type includes the plant species belonging to various families. The type of soil in the area is mainly saline soils. Plants adapted to the existing soil-climatic conditions are able to survive in such soil types.

The biochemical composition of these plants is rich in particular organic and inorganic compounds thanks to the mineral content, pH value, characteristics of the parent rock, etc. of the soil surface of the area. Among these plant species, the species with high nutritional quality such as *Setaria viridis*, *Carex riparia*, *Avena clauda*, *Bromus japonicus*, *Bromus arvensis*, *Bromus squarrosus*, *Bromus scoparius*, *Bromus commu-*

tatus, Eremopyrum orientale, Aegilops cylindrica, Cynodon dactylon, Phalaris minor, etc. can be exemplified.

These fodder plants are eagerly eaten by small horn cattle. Animals eat these fodder plants from the beginning of autumn, even on frosty winter days. The vegetation of the study area is of utmost agricultural importance as is the case with winter pastures. It is used for grazing small horn cattle in winter.

The meat of animals grazed in these areas is considered high quality one. Taking into consideration the growing demand of people for animal-based meat products, specific action plans should be developed and implemented to improve the current condition of winter pastures and restore the vegetation. Simultaneously, the grazing norms and regular grazing rules should be followed. Sowing the seeds of domestic fodder plants as part of the improvement measures is considered an important step taken.

Mass increase of winter ephemerals and ephemerides with the characteristics of short-term vegetation is observed on some slopes seen in the area relief in winter depending on direction. After the rains, noticeable revival is seen in winter pastures [Aliyev *et al.*, 2007]

BIOECOLOGICAL CHARACTERISTICS OF THE AQUATIC PLANTS OF KHUDAFARIN WATER RESERVOIR

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Keywords: Karabakh; plant; leafy; stamens; status.

The Khudafarin water reservoir was built on the Araz River on the international border between Iran and Azerbaijan. It is the third reservoir in Azerbaijan in terms of capacity and volume, covering the administrative region of Jabrail and Zangilan districts. From 1993 to October 18, 2020, the reservoir, together with the Hydroelectric Power Plant of the same name, was under the control of the Republic of Armenia. With the liberation of historical Azerbaijani lands from occupation, the Khudafarin reservoir is under the control of the Azerbaijan Republic and it is advisable to conduct relevant scientific research there.

The rivers starting from Karabakh lands mainly flow into Kura and Aras rivers. The high tops of the mountains located here form a basin between the Kur and Araz river. The rivers here are fed by rain and snow waters and used for irrigation. Studies on rare and relict aquatic plants shows that *Nelumbo nucifera, Nymphaea alba, Trapa hyrcana, Nymphoides peltata, Hydrocotyle vulgaris, H.ranunculoides*, etc. formed communities before, today their area has decreased significantly due to anthropogenic factors.

Nymphaea alba L. – belong to *Nymphaeaceae* Salisb. According to the IUCN Red List, the category and status of the species belong to the category "Vulnerable to extinction" - VU D2. It is a rare species in Azerbaijan. It is a perennial aquatic plant with strong roots. The leaves are very large, solitary, long with dense stalks; Leaf blade heart-oval, sometimes rounded, 10-25 cm wide. Sepals are oblong or ovate-oblong, up to 7 cm long, less fused at the base. There are also transitional forms between petals and stamens.

Trapa hyrcana is a herbaceous annual plant (according to some sources). At the bottom of the basin with spherical, grayish roots, the lilac collected there hardens or floats freely. The leaves are rhombic, petiolate, and serrated. The flowers are regular, bisexual, located in the axils of individual leaves. The fruit is monoseeded, drupelike with 2-4 silique-like protuberance. Some authors note that it is self-pollinatedç while others point to insect pollination. Its flowers only open for a few hours in the morning. The fruit can stay in water for a long time (10-50 years). It has been known as a valuable food plant by people since ancient times. It is collected and used as food by the population of Southeast Asia and Central Africa. It is also useful as a medicinal and dye plant [Doyle et al., 1997; Lodge, 1991].

During the restoration of our 30-year-old occupied lands, it is necessary to re-examine aquatic plants and to develop protection measures. Therefore, there is a need to protect aquatic plants. There is a danger of extinction of aquatic vegetation as a result of the drying up of some large lakes (Lake Mehman).

PHYTODIVERSITY OF FOREST MASSIFS OF SHABRAN DISTRICT

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Keywords: phytodiversity; Shabran district; Caucasian endemics.

In the forest massifs of Shabran district, 85 species belonging to 35 families and 75 genera were registered. Seven species (Aristolochia iberica, Corylus colurna, Primula woronowii, Pyrus salicifolia, Rubus bushii, Salvia verbascifolia, Symphytum caucasicum) of them are Caucasian endemics (Red list of the endemic plants of Caucasus, Ali-zade V., Hajiev V., Abdiyeva R., Farzaliyev V., 2014), 5 species (Galanthus caucasicus, Ophrys oestrifera, Orchis purpurea, Pyrus salicifolia, Rhus coriaria) are rare (Red Book of the Republic of Azerbaijan, 2013) and 1 species (Ailanthus altissima) is invasive. New distribution areas for the species Hirschfeldia incana were identified.

As a result of the taxonomic analysis, it was found that the family Asteraceae is represented by more genera and species (20 genera, 23 species) in the studied areas. The second place is occupied by Rosaceae (11 genera, 15 species), the third place by Orchidaceae (9 genera, 13 species), the fourth place by Poaceae (8 genera, 9 species) and the fifth place by Fabaceae (5 genera, 9 species). Other families are represented by 1-5 species.

In addition, useful plants were recorded. Thus, out of 85 species included in the list 64 are medicinal, 23 - ornamental, and 13 - food plants.

Biodiversity α -assessment was carried out in the forest massifs of the studied district, density of species per $1m^2$ and biodiversity indices were calculated. Thus, according to the Menhinick index, the α -diversity was 1.72, the species density ranged from 3.7 to 6.5 (in shady places the average density of species per $1m^2$ reaches 3-4 species, in the open part of the forest up to 6-7). Species growth in open forest areas is mainly due to shrubs and meadow plants.

The presence of Acer campestre species as a component in the studied forests is slightly higher than in the forest masses of other districts. The associations Quercus anatolica+Crataegus pentagyna+Mespilus germanica, Carpinus caucasica+Fagus orientalis+Quercus macranthera can be mentioned among the most widespread associations in the

forest massifs of Shabran district. The vertical structure of forest associations is 7-tiered: tall trees (edificators), medium-tall tree species, undergrowth (young virginia individuals of trees) and shrubs, tall grasses, medium-sized grasses, low grasses, mosses and lichens.

The state of coenopopulations (CP) of 3 out of 5 rare species on different zones noted in the forest massifs of the district was studied and their types were determined. It was clear that in CP of the species Ophrys oestrifera, percentage of juvenile (j) individials was – 20%, immature (im) – 14%, virginile (v) – 27%, young generative (g1) – 18%, mid-generative (g2) – 14%, old generative (g3) – 7%. Subsenile (ss) and senile (s) individuals were not registered. According to the Delta (Δ) and omega (ω) indices, the studied CP was rated as "young" type. In CP of the species Pyrus salicifolia, the share of individuals was 6%, v – 11%, g1 – 10%, g2 – 21%, g3 – 38%, ss – 10%, s – 4%. According to the Delta (Δ) and omega (ω) indices, this CP is of the "transition" type. In CP of the species Rhus coriaria, the share of j individuals was 5%, im – 34%, v – 9%, g1 – 31%, g2 – 2%, g3 – 15%. Ss and s individuals were not found. According to the Delta (Δ) and omega (ω) indices, this CP is of the "young" type.

Monitoring of the state of forest massifs in the Shabran district has shown that the growing global warming, soil degradation and the development of tourism have a negative impact on vegetation [Lubini, 2013; Ndiaye, 2013].

EFFECT OF DROUGHT AND SALT STRESSES ON THE ACTIVITY OF THE ENZYME ALCOHOL DEHYDROGENASE IN MAIZE LEAVES

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Keywords: salinity; drought stress; alcohol dehydrogenase (ADH); maize.

Plant tolerance to drought and salt is one of the most studied directions in plant physiology in recent decades. It is attributed mainly to the unexpected occurrence and different characteristics of drought in most regions, and constantly increasing salinity on the Earth.Currently, drought, which is a natural stress factor on our lanet, covers more than 26% of the land used, salinity covers 20%, and only 10% of the lands not affected by certain stress factors.

Drought and salt stresses are some of the most common environmental factors affecting many metabolic processes in plants, especially respiration, photosynthesis, growth, development, etc. Enzymatic reactions are of exceptional importance in the regulation of such physiological processes. The study of enzyme kinetics is important in assessing the degree of plant tolerance. Therefore, the activity of the enzyme alcohol dehydrogenase (ADH) was measured spectrophotometrically according to the rate of NADH oxidation in 5, 10, and 15-day-old leaves of maize grown under drought and salt stresses.

It should be noted that despite a number of important biological functions of the ADH enzyme in plants, very little scientific information is available about ADH activity in a stressful environment. Unlike the control variant, ADH activity decreases over time in stress-exposed variants. Under water and NaCl stresses, this decrease was ~1.5-fold greater on the 15th day of stress compared to the 5th day, and \sim 1.8fold greater under stress caused by Na₂SO₄ Optimal activity for ADH was recorded at pH 6.8-7.2 of the reaction medium. However, in a reaction medium with the same parameters, the activator had a different effect on ADH activity. For example, ADH, which has the lowest timedependent activity in leaves under Na₂SO₄ stress, had the highest activity in the presence of an activator. It is followed by NaCl and drought stresses. Besides, according to the spectrum of inhibition, in the variants that are activated more rapidly by the action of the activator, inhibition occurs faster, i.e. there is an antagonism between the effects of the inhibitor and the activator [Kakumanu et al., 2012; Song et al., 2017].

Thus, the enzyme in leaves of the maize plant was found to be highly regulated at 1-20 mM concentrations of the activator $MgCl_2$ and at 1-10 mM concentrations of the inhibitor ATP. The results show that LDH is a more active enzyme than ADH and is involved in the energy metabolism of the cell.

PROTECTION OF PHYTOCENOSES PRODUCED BY DISTRIBUTED BEAN PLANTS IN THE DESERT AND SEMI-DESERT PLANT (VEGETATION) OF ABSHERON PENINSULA

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Keywords: desert; semidesert; phytocoenosis; legumes.

Oil fields near Absheron have been operated improperly for decades, failing to meet basic environmental protection regulations and also extraction of oil, gas, highly mineralized and radioactive pollutants to the surface caused pollution and degradation of some landscapes of the Absheron Peninsula. The Absheron Peninsula's desert and semi desert vegetation is similarly affected by this scenario.

The phytocoenosis generated by legumes in the desert and semidesert flora of the Absheron Peninsula were studied from this perspective. For this purpose, the species composition and structure of the formations formed by the edification of legumes and research facilities or stops by route for the study of ecological features mentioned in the desert and semi-desert vegetation spread in the territory of the Absheron Peninsula were selected [Field geobotany, 1959-1976].

In the classification of phytocenoses of leguminous plants scattered in desert and semi-arid vegetation of the Absheron peninsula, four formation classes, four formation groups, and six associations belonging to two plant kinds were discovered.

Artemisieta-Astracanhetum, Alhagieta-Artemisietum, Salsoleta-Alhagietum and Glycyrrhizeta-Ephemeretum formation groups, psammophytes and xerophytes are edificatory, as well as dominant and subdominant. The degradation of soil and vegetation has escalated and the economic relevance has deteriorated as a result of poor utilization of these phytocenoses from anthropogenic and man-made influences.

Legumes distributed in the territory of the Absheron Peninsula are relatively reduced in cenoses due to the influence of environmental factors that have a direct impact on plant ecosystems. In addition, they are rarely found in the vegetation formed by legumes, and are less common in the semi-desert. In the desert and semi-desert vegetation of the Absheron Peninsula, *Vicia* L., *Trigonella* L., *Medicago* L., *Melilotus* L., *Trifolium* L., *Astragalus* L., etc. are found in such species [Flora of Azer-

baijan, 1950- 1961]. These species can be found in the peninsula's investigated phytocoenosis in coastal sands and gray-brown soils.

From the monoecious, biennial and perennial grass species registered in the species composition of the studied phytocoenosis, *Vicia grandiflora, V.peregrina, V.villosa, V.narbonensis, V.dasycarpa, V.cinerea, Trigonella coerulescens, T.gladiota, T.orthoceras, T.minspelica; Medicago lupulina, M.minima, M.caucasico, M.rigidula, M.littoralis, M.tribuloided, M.denticulata, M.coerulea, Trifolium tumens, T.tomentosum, T.arvense, T.repens, T.medium, T.pratense, T.campastre, T.scabrum have special feed quality. In the desert and semi-desert vegetation of the peninsula <i>Alhagi pseudoalhagi, Glycyrrhiza glabra, Astracantha igniarius, Acaspicus*, etc. Legumes together with other plants form phytocoenosis with *Artemisia arenaria, Ascoparia, Salsola dendroides* [Gurbanov et al., 2011]. When planted with cereals, these phytocenoses have excellent nutritional and economic value, and are regarded more nutritious fodder, also, selenium, kitra, etc. from some species of the genus *Astragalus* L are used in agriculture and medicine [Larin et al., 1951].

Study of phytocoenosis formed by legumes in desert and semidesert vegetation of Absheron peninsula, the endemic, rare, endangered species found there, which are included in the "Red Book" of Azerbaijan, also provide a basis for the protection of the environment.

AQUATIC AND WETLAND PLANTS OF SHIRVAN PLAIN Bakhshiyev Vazeh

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Keywords: Shirvan plain; aquatic plants; hydrophytes; hydatophytes; hygrophytes.

The Shirvan plain has the largest area in the Kura-Araz lowland, occupying 859.7 thousand hectares. It is located on the left bank of the Kur River and stretches from the Mingachevir reservoir in the west to the foothills of the Langabiz, Great and Small Harami mountains in the east. Absolute elevations are positive (0 to 150-200 m) in most parts of the plain. In a small part near the Caspian Sea, the altitudes fall from 0 to minus 25.6-25.8 m.

Although the history of botanical research in Azerbaijan is ancient, very little is known about aquatic and wetland vegetation due to the lack of attention paid to the study of the plants of lakes and wet-

lands. The study of water and wetland areas in Azerbaijan began in 1956 and is found in the works of J.A. Aliyev, A.M. Babayeva, Sh.M. Afandiyeva, M.G. Musayev and others.

There are various reservoirs in the research area - Girdimanchay, Agsuchay, Upper Shirvan canal, Main Shirvan collector, pits and others. These reservoirs can be divided into two groups according to the richness of the nutrient environment: a) aquifers rich in nutrients and vegetation - eutrophic; b) oligotrophs, which are low in nutrients and vegetation. The reservoirs in the study area are eutrophic.

We collected 63 species of aquatic and wetland plants (family- 28, genus- 35) from the study area, 25 of which are widespread and play a significant role in the formation of vegetation.

According to the classification given by Katanskaya, aquatic and wetland plants distributed in the Shirvan plain can be divided into the following groups:

- I. Hygrophytes (28 species) plants that grow in very humid soils, in conditions of high humidity. Representatives of this group include *Juncus acutus, Carex diluta, Schoenoplectus lacustris, Eleocharis uniglumis* and others.
- II. Hydrophytes (25 species) are aquatic plants, half of their trunks are in water and the rest in air. For example: *Butomus umbellatus, Scirpus lacustris, Epilobium hirsutum, Sparganium erectum, Phragmites australis* and others.
- III. Hidatophytes (10 species) are true aquatic plants, the entire life cycle is associated with water. For example: *Potamogeton pectinatus, Potamogeton crispus, Batrachium trichophyllum, Lemma minor* and others.

In the aquatic and wetland vegetation of the area, hydatophytes form *Potamogeton pectinatus* and *Batrachium trichophyllum* and etc., hydrophytes form ordinary reeds *Phagmites australis* and *Typha angustifolia* and etc., and hygrophytes form *Carex diluta, Schoenoplectus lacustris* and other formations.

Among the aquatic and wetland plants, there are many plants that can be used as raw materials in the feed, food, medicine, fiber, cellulose and paper industries. A method of purification of domestic and wastewater by aquatic plants has been developed, as a result of which the amount of biochemical requirement of oxygen, chemical requirement of oxygen, ph, N in water has been reduced by macrophytes (*Phragmites australis, Typha angustifolia, Scirpus litoralis* and etc.).

DATABASE OF ORNAMENTAL HERBS OF GUBA AND GUSAR DISTRICTS

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Keywords: data, Delphi programming, Microsoft Access, morphology, plant. Biological diversity is one of the units of measurement of the health of biological systems and life on Earth. It is estimated that there are between 450.000 - 500.000 plant species in the world including flowering plants (Angiospermae), gymnosperms (Gymnospermae), ferns (Polypodiophyta), lycophytes (Lycopodiophyta) and mosses (Briophyta), moss of which are found in the humid tropics, and that many species are still unknown to science [Corlett, 2016, Trunbull, et al., 2016]. It is impossible to imagine natural ecosystems without plants, but few of them are used by people, and the vast majority of their uses are unknown or unexplored in medicine, industry etc., that is the reason they have received little attention. However, ornamental plants, including flowering plants do not directlv meet the vital needs of humans, although they are of great aesthetic importance [Mohamad et al., 2013, Petřík et al., 2019]. The purpose of the work is to create an electronic database on the studied and established species composition of wild ornamental grasses in the Guba and Gusar regions of Azerbaijan using classical morphological approaches. The work was conducted during 2013-2021 years. The plant database was created based on materials collected in the study area. The database software consists of three parts: interface, database and files. The interface is written in the Delphi programming language. A database is an organized set of related information (relational data tables) that is presented in a Microsoft Access database and consists of many tables of recorded data that maintain data in accordance with standards. Due to the interface, users can easily and quickly enter data and search and retrieve reports. The programme consists of 23 sections. The plants are grouped by division, class, order, family, genus and it is possible to conduct search according to each feature (life forms, flower color, biologically active compounds, ecological groups, place of collection, etc.). The database operates in Azerbaijani, English and Russian languages. The database may be expanded in the future and an online version is planned. This type of information is of great scientific value, and is also a useful link between the citizen and the science involved in plant conservation programs, which promotes cooperation and contributes to the environmental consciousness of the population.

IV. PHYSIOLOGY, ZOOLOGY AND AQUACULTURE

INFLUENCE OF PLANT ANTITOXICANT ON LIPID METABOLISM IN POISONING WITH NICKEL NITRATE ON THE BACKGROUND OF EXPERIMENTAL

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Keywords: anti-toxicant; lipid metabolism; atherosclerosis; malondialdehyde; catalase.

`The purpose of the research was to study the effect of a complex plant anti-toxicant from the flora of Azerbaijan on lipid metabolism and lipid peroxidation in chronic nickel nitrate poisoning against the background of experimental atherosclerosis. The studies were carried out on 55 white nonlinear male rats weighing 180-250g. The model of atherosclerosis was created according to I. V. Savitsky [Savitsky et al., 2016] and is based on the poly etiological theory of the development of the disease (the animals received Mercazole - 25 mg/kg of weight, methylprednisolone - 0.17 mg/kg and 15% aqueous solution of ethanol instead of water against the background of an atherogenic diet for 2 weeks). Exposure with nickel nitrate was carried out through drinking water for 60 days at a dose of 2 mg/kg. Lipid metabolism and free radical oxidation processes were monitored by the level of total cholesterol, high-density lipoproteins, low-density lipoproteins, malondialdehyde and catalase in blood serum. The studies were carried out before and after modeling of atherosclerosis and, respectively, after exposure with nickel nitrate on the background of atherosclerosis after 30 and 60 days. In the experimental group, after exposure against the background of experimental atherosclerosis, the animals received a complex antitoxicant (a mixture of licorice, rose hips, grape seeds, oat and burdock bran in the ratio 3:2:1:1:2 - Eurasian patent 201600043 dated 06/25/2018) for a month, which was added at a dose of 8 mg/kg to the drinking water of the drinkers.

The results of the study showed that in experimental atherosclerosis after exposure with nickel nitrate, disturbances in lipid metabolism and lipid peroxidation processes were aggravated, meaning that heavy metal intoxication is a factor aggravating atherosclerotic processes. There was a direct proportional relationship between the severity of the degree of disorders with the duration of intoxication with

nickel nitrate, with a maximum of disorders on the 60th day after exposure. However, in the experimental group with the use of a complex plant anti-toxicant, there was a significant improvement in the state of lipid metabolism and oxidative stress that occurred after chronic intoxication with nickel nitrate. The revealed corrective effect of the plant anti-toxicant indicates the detoxification effect of this complex herbal preparation and the possibility of its clinical approbation both for the prevention and treatment of chronic nickel nitrate poisoning in patients, especially in those with existing atherosclerotic vascular lesions.

BACK REMODELING OF BRAIN NEURONS IN EPILEPTIC PATIENTS Ibadova Rimma, Mekhtiyev Arif

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Keywords: patients; epilepsy; dihydropyrimidinase-related protein 2 (DRP2); natural autoantibodies; ßIII tubulin; nerve growth factor.

To-date sharp debates concerning the possibility of neurogenesis in pathogenesis of epilepsy in the patients, having prolonged course of disease, have still been going on.

The studies were carried out on the children of pre-puberty term having typical signs of epileptic bursting activity on EEG (n=21). Blood samples were taken from the veins of these children in the inter-seizure period into sampling tubes containing 0.5 mL of 5% EDTA as an anticoagulant. Samples were centrifuged at 600 g for 10 min and then plasma from each tube was saved and transferred into Eppendorf sampling tubes and centrifuged at 9000 g for 15 min. Pellets were saved as platelets and supernatants were saved as serum. It should be noted that the levels of sero-tonergic metabolites and other proteins in the platelets reflect their levels in the brain cortex [Elliott *et al.*, 1989; Collins *et al.*, 2013], though the levels of proteins in the serum reflect their levels in subcortical structures of the brain [Mekhtiev, unpublished]. Blood samples from healthy children of the same age were used as controls (n=15).

Protein extracts from the platelets were used as antigens at a concentration of 20 $\mu g/mL$ in 0.1 M tris-HCl buffer (pH 8.6) in the indirect ELISA-test to evaluate the levels of dihydropyrimidinase-related protein 2 (DRP2) and the levels of a marker of differentiated neurons – βIII tubulin with application of antibodies to each protein as the first antibodies. The samples of serum were used as the first antibodies diluted

75 times with a buffer for antibodies for the purpose of measuring the levels of natural anti-DRP2 autoantibodies. Besides, the levels of nerve growth factor (NGF) in the serum were measured with application of anti-NGF antibodies.

The results revealed downregulation of DRP2 in the platelets of the epileptic patients relative to the healthy persons (p<0.001). Besides, sharp downregulation (by 42%) of the levels of β III tubulin in the platelets of the epileptic patients relative to the control samples (p<0.001) was observed. The level of natural anti-DRP2 autoantibodies in the serum of the patients declined by 2.5 times in comparison to the control values (p<0.01). At the same time the levels of NGF in the serum of epileptic patients increased (p<0.01).

Taken altogether, these results indicate prominent downregulation of DRP2 and β III tubulin in the platelets, indirectly indicating similar changes in the brain cortex of epileptic patients. Besides, downregulation of natural anti-DRP2 antibodies in the serum reflects downregulation of DRP2 in the brain subcortical structures of these patients. Interestingly, downregulation of β III tubulin in the platelets and upregulation of NGF in the serum of the epileptic patients are reliable indices [Zhang *et al.*, 2019] of back remodeling (dedifferentiation) of the brain nerve cells in long-lasting epilepsy. This means that mature neurons in the brain structures of epileptic patients can undergo the process of remodeling, this way increasing the pool of neuronal precursor cells capable of differentiating into the certain mature nervous cells according to the phenotypic requirements of the surrounding brain neurons of epileptic patients.

PERIPHERAL BLOOD SATURATION AFTER THE MARTINET TEST CORRELATES WITH THE SPRINTING ABILITY OF YOUNG BASKETBALL PLAYERS

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Keywords: peripheral blood; sprinting ability; basketball players; method of pulse oximetry.

When performing physical exercises, the value of oxygen saturation of peripheral blood is usually maintained in the region of 97-99%. However, well-trained athletes often experience hypoxemia and significant desaturation (decrease in normal blood oxygen saturation) during

maximum physical exertion. It was previously believed that desaturation during or immediately after exercises was indicative of decreased exercise tolerance. However, recent evidence has emerged that desaturation is not a limiting factor for the performance of athletes [Martín-Escudero *et al.*, 2021]. Thus, the level of blood saturation in healthy young people at rest and during exercise vary within certain limits, but the physiological significance of these fluctuations is not known exactly.

The purpose of the study was to establish a relationship between the level of peripheral blood saturation and indicators of general physical fitness in young basketball players.

The study involved 20 basketball players of the Republican State School of Olympic Reserve aged 14-16, who take part in the official basketball competitions of Belarus. To assess the physical form of athletes, the Martinet test was used, and data from regular control examinations conducted at the School were also used. For the analysis, the following indicators of general physical fitness were chosen: sprint time (10 m), middle distance run (5-minute run) and the maximum number of pushups. Saturation was recorded on an automated multifunctional spirometer MAS1 (Unitekhprom BGU, Minsk) immediately before exercise and during the first minute after the Martinet test. The data were accumulated in the memory of the spirometer and then analyzed. Correlation analysis of the relationships between saturation and sports performance of athletes (determination of the Pearson coefficient r) was carried out using the Excel 2016 software.

An analysis of the relationship between indicators of physical fitness and blood saturation of female athletes at rest did not reveal significant correlations between them (coefficient r lies in the range of 0.15-0.23). However, after the Martinet test, the correlations between the studied parameters increased. So, for the number of push-ups and the level of saturation of peripheral blood, the coefficient r was -0.35, and for the distance of a five-minute run and saturation was r=-0.26. Most importantly, a significant positive correlation was found between sprint time and peripheral blood saturation of female basketball players (r=0.71) after the Martinet test. The converse statement is also true: the higher the speed developed by athletes over a short distance, the deeper they develop blood desaturation after the test.

The obtained results indicate that the higher the sprinting ability of young basketball players, the greater the amount of blood desaturation during the Martinet test. Thus, the method of pulse oximetry in combination with functional tests can be used to assess the ability of athletes.

INTERACTION BETWEEN THE AMYGDALA AND THE VISUAL SYSTEM IN ALZHEIMER'S DISEASE AND EPILEPSY

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Keywords: amygdala; Alzheimer's disease; the Morris Maze; visual system; bulbectomy.

In experimental models of Alzheimer's disease and epilepsy, we studied the nature of the effect of the Basolateral Amygdala on the generation of: 1) visually controlled spatial memory in the Morris water maze before and after surgery for bilateral total bulbectomy [Gashimova *et al.*, 2018]. This operation was carried out in order to create an experimental analogue of Alzheimer's disease; 2) In electrophysiological experiments on rabbits, we studied the mechanisms of generation of evoked potentials in response to stimulation by a single photo stimulus in the Retina (ERG), Superior Colliculi, Lateral Geniculate Body, and Primary Visual Cortex (field 17).

EXPERIMENT 1. Experiments were carried out on old male albino rats. The results obtained showed a significant increase in the influence of the Amygdala on the function of the Visual system. This was manifested in an increase in the latent period of the search for an invisible platform in white rats with an analogue of Alzheimer's disease. The model of Alzheimer's disease was created by the known method of bilateral surgical bulbectomy. Three months after the operation, the animals developed a stable analogue of this disease. The evidence was a change in visually controlled behavior in a pool (diameter 102 cm) with water whitened with milk. An invisible round platform 10 cm in diameter was located 1.5 cm below the liquid level [Morris, 1984].

EXPERIMENT 1. Experiments were carried out on old male albino rats. The results obtained show the Amygdala effect on the visual system function. This was manifested in an increase in the latent period of the search for an invisible platform in white rats with an analogue of Alzheimer's disease. The model of Alzheimer's disease was created by the known method of total bilateral surgical bulbectomy. Three months after the operation, the animals developed a stable analogue of this disease. The evidence was a change in visually controlled behavior in a

pool (diameter 102 cm) with water whitened with milk. An invisible round platform 10 cm in diameter was located 1.5 cm below the liquid level [Morris, 1984].

Long-term navigation training was accompanied by a shortening of the search time for a saving island. Well-trained rats before bulbectomy found the platform in 10-20 s, and 3 months after the operation, their search greatly increased in time. The specified search parameters approached the figures observed or even exceeded the time of islet search in naive (untrained) rats and amounted to 120-180 s. After the Curcuma administration solution for 10 days, a reduction in platform search time to 4-5 s was observed. The results suggest the rehabilitative properties of turmeric, as well as the possible expression of neurogenesis in Basolateral Amygdala [Galandarli *et al.*, 2021].

EXPERIMENT 2. On the model of amygdala epileptogenesis induced by instillation of penicillin solution into a basolateral amygdala, awake rabbits of the "gray chinchilla" breed were observed to generate epileptiform discharges in the Visual cortex, Lateral geniculate body, Superior colliculi and Retina (electroretinogram - ERG). In these structures, as well as in the Amygdala itself, ictal and interictal adhesions were recorded. A few hours later, an almost complete recovery of neuronal activity in the studied structures to the background level was observed.

It is suggested that the different influences of the Basolateral part of the Amygdala spread along the entire visual pathway and reach the neuronal apparatus of the retina [Aghayev *et al.*, 2009].

IMPLEMENTATION OF THE BLINKING REFLEX IN PEOPLE DIAGNOSED WITH BRUXISM

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Keywords: blinking reflex; bruxism; temporomandibular joints.

Bruxism is stereotypical movements of the mandibula accompanied by clenching of teeth. Bruxism has a high frequency of occurrence in the population, which determines the relevance of the topic. There is evidence in the literature indicating that bruxism may reflect events associated with hyperexcitability of the brain stem centers. In particular,

increased respiration and tonus of masticatory muscles are characteristic [Pantileev V.D., 2011]. The aim of the study was to study the components of the blinking reflex in patients with bruxism and dysfunctions of the temporomandibular joints.

The results of the study were obtained during a neurophysiological examination of 13 patients with bruxism and dysfunction of the temporomandibular joints aged 16 to 64 years.

In patients, the reflex activity of the brainstem was studied by recording and analyzing the blinking reflex (BR), which is a short-term contraction of the circular muscle of the eye (*m. Orbicularis oculi*) in response to electrical stimulation of the branch of the trigeminal nerve (*n. Supraorbitalis*) in the region of the supraorbital foramen. The BR was recorded with surface electrodes, the distance between the electrodes was kept 2.5 cm. The blinking reflex was recorded without exercise and during inspiration. For the study, a computer multifunctional installation "NeuroMVP-4" manufactured by the company "Neurosoft" (Russia) was used.

When registering the BR, a two-component response was recorded: early (R1) and late (R2) on the ipsilateral side, only late (R2) on the contralateral side. The recorded responses were evaluated for latency, which for healthy people has an average value of 11.1±1.5 ms (R1) and 35.0±1.5 ms (R2) [Gainutdinov *et al.*, 2009].

At rest, both in patients with bruxism and in patients with dysfunction of the temporomandibular joints, an early component of R1 is recorded with a latency corresponding to the normal values, 10.1 ± 0.4 ms and 10.7 ± 0.5 ms, respectively. When making a breath, the indicators did not change 10.0 ± 0.3 ms and 11.0 ± 0.6 ms. In patients with bruxism, the latent period R2 is 25.8 ± 2.0 ms, the contralateral side R2 is 26.3 ± 3.2 ms. When inhaling, there is an increase in the latent period for both indicators 33.5 ± 3.1 ms and 39.4 ± 3.9 ms, respectively. In patients with dysfunction of the temporomandibular joints, R2 latency is 34.1 ± 1.3 ms, on the contralateral side R2 is 34.3 ± 2.9 ms. And when inhaling 33.3 ± 1.6 ms 36.4 ± 4.3 ms, respectively.

The revealed features of the components of the blinking reflex in patients with bruxism suggest the presence of increased excitability of brainstem neurons.

ANTIOXIDANT SUPPLEMENTATION IN THE TREATMENT OF ECOTOXICANT-INDUCED ANXIETY IN RATS WITH DIFFERENT ACOUSTIC STRESS RESPONSES

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Keywords: stress – stable; stress – unstable; heavy metals; antioxidant; monoamines. The modern environmental situation is characterized by a supersaturation of pollutants of different nature, the most common and dangerous among which are super toxicants - heavy metals (HM). They have multifaceted negative effects on the central, peripheral and autonomic nervous systems in animals of different species, in particular, impaired memory, learning, anxiety, etc. [Revich et al., 2006].

It has been shown that HMs affect the body not in isolation, but simultaneously with such factors as stress, neurotropic drugs and so on. The antioxidant system of the body, which plays an important role in the response of the central nervous system to stress, can serve as an important substrate for the combined effect of HM and neurotropic drugs [Pshennikova, 2001]. It is known that neurotransmitter and neurohumoral mechanisms are involved in the formation of the state of anxiety, which is an emotional state of mental tension. At the same time, the primary neurotransmitter in the brain is serotonin, which is an important biochemical factor in the formation of anxiety-depressive disorders [Veyn *et al.*, 2004].

In this research, we have studied the combined effects of a heavy metal (lead acetate salt) and an antioxidant (ascorbic acid) on the level of anxiety in male Wistar rats with different sensitivity to the action of an acoustic stress stimulus and different innate activity ratio of monoaminergic (MA) brain systems. The sensitivity indicator was the intensity of the seizure manifestation in rats (90-120 dB, 2 min). The difference in response to acoustic stress allows us to divide animals into two groups: stress - unstable (SU - prone to seizures), characterized by a higher level of dopamine (DA) and serotonin (5-HT) in various structures of the brain, and stress - stable (SS - without motor excitation), characterized by a higher baseline level of norepinephrine (NA).

Two series of experiments were carried out. Each series contained 4 groups of animals. Group 1 - control (equivalent volume of distilled water); Group 2 - ascorbic acid (AA-2 ml) was administered one

hour before the experiment; Group 3 - lead acetate (Pb) was administered (10-7 solution at a dose of 2 ml) 5 hours before the experiment; Group 4 - (combined effect): Pb was administered 5 hours before the experiment + AA (2 ml) was administered 3 hours later. All injections were given parenterally.

According to the indicators of the level of anxiety in the "elevated plus maze" test, combined administration of lead acetate and ascorbic acid to SS rats, the latter prevents neurotoxic effects of the heavy metal, which leads to a decrease in the level of anxiety. However, in the SU rats, ascorbic acid does not counteract the neurotoxic effect of lead acetate. It is can be explained by the fact that the aggravation of the anxiety state in the SU rats, in contrast to SS, is due to decrease in the levels of both 5-HT and DA in the brain structures, which leads to neurotoxicosis, which is not removed by a neurotropic drug.

These studies are of practical importance for understanding individual reactivity in pathology in regard with the widespread use of medicinal metabolic agents that interfere with the exchange of neurohormones in the brain.

INVESTIGATION OF THE PROTECTIVE ROLE OF SAFFRON IN CREATING A MODEL OF ALZHEIMER'S DISEASE

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Keywords: saffron; Alzheimer's disease; the Morris pool; spatial memory and behavior; bulbectomy.

Alzheimer's disease is the initial dementia of the most insidious and widespread neurodegenerative diseases. It is obvious that in the future this will happen even more widely. The characteristic features of Alzheimer's disease are a prolonged decrease in cognitive functions, which is associated with a predominantly initial impairment of memory impairment. In the future, in patients with the formation of pathology, the death of pyramidal neurons of the large brain and the total destruction of cognitive processes occur.

The experiments were carried out on old albino rats (n=10) treated with saffron extract for 21 days prior to the start of the experiments. The animals were then trained in the Morris water maze. A pool with a diameter of 102 cm was filled with warm water at a temperature of 25

degrees, painted over with milk. The invisible platform was 1.5 sm below the water surface [Galandarli *et al.*, 2021].

As a filler liquid in the Morris water maze, water fermented with milk is used. This creates conditions for intuitive search of the platform, since rats do not see it [Morris, 1984]. This behavior is provided by spatial memory. When developing an experimental model of Alzheimer's disease, the spatial memory of rats is disrupted, this is explained by an increase in the time of the search behavior of rats.

At the first stage, naive rats initially spent up to 2 minutes searching for a platform. After training for 7-10 days, the search period for the platform was reduced to 3-10 seconds.

At the second stage, the trained animals underwent a surgical operation of bilateral bulbectomy (removal of olfactory bulbs) [Gashimova *et al.*, 2018].

10 days after the operation (the third stage), rats were tested. It was found that the spatial memory of trained animals was preserved. The search time for the platform was, as during the training, about 5-10 seconds.

The data obtained indicate a significant protective effect of saffron on the cognitive processes of the brain of experimental animals in which it was not possible to develop an analogue of Alzheimer's disease.

THE ROLE OF PRE- AND POSTNATAL FACTORS IN FORMING THE FUNCTIONS OF A DEVELOPING ORGANISM

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Keywords: prenatal ontogeny; hypoxia; electroencephalography.

The modern environment is characterized by unfavorable conditions for the normal functioning of both individual systems and the whole organism. Numerous environmental stressors, including hypoxia, cause significant changes in the functional activity of many body systems. In response to the effects of hypoxia, a complex of complex adaptive processes develops in the human and animal organisms. It is known that oxygen deficiency adversely affects the structure and function, primarily of the cerebral cortex, both in developing and adult or-

ganisms [Dubrovskaya *et al.*, 2002, Juravin 2005, Neakas *et al.*, 1996, Lipton, 1999]. The most serious and diverse are the consequences of hypoxic exposure during intrauterine development, when the organs of a growing organism are laid down. The main stages in the formation of the mammalian brain occur during embryogenesis. In this regard, the influence of external factors during certain periods of prenatal development can contribute to the disruption of the structural and functional organization of the brain, and, as a result, cause changes in adaptive-adaptive and behavioral reactions in further ontogenesis [Bokeria, 2001; Rayevskiy, 2002; Bagolepova *et al.*, 2005; Boldireva *et al.*, 2005; Mishima *et al.*, 2005].

The aim of this work was to study the effect of hypoxia, applied in certain periods of intrauterine development, on the dynamics of the formation and development of electrophysiological parameters (EEG) in animals of early age of postnatal life. Determine the level of viability of animals in the early period of postnatal life in the norm and after prenatal exposure. To study the dynamics of the formation of the bioelectrical activity of scattered mature brain structures in the early ontogenesis of animals in the norm and after prenatal hypoxia. It was revealed that the impact of the factor coinciding in time with the period of intensive proliferation and migration of the cellular material of the developing brain region (the embryonic and pre fetal periods of ontogenesis) causes the most pronounced changes in the composition and structure of the bioelectrical activity of the brain.

The study made it possible to describe changes in the representation of individual waves of the EEG spectrum as a functional diagnostic indicator of the development and formation of the functions of the nervous system under the influence of extreme environmental factors.

For the first time, the most sensitive periods of intrauterine development to hypoxia factors were determined in the studies and the boundaries of deviations from the norm of electrophysiological criteria of the brain in the subsequent stages of development of newborns were shown. A different degree of severity and heterochrony of the observed changes in the studied parts of the cerebrum, as well as their dependence on the period of hypoxia, were established. Based on the analysis of our own and literature data, it was established that prenatal hypoxia contributes to the development of destructive processes, as a result of which heterochronous development deepens and slows down the processes of consolidation of scattered mature elements of the developing brain.

THE EFFECT OF ACUTE PROTEIN DEFICIENCY IN FOOD ON MEMORY FUNCTIONS

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Keywords: protein-deficient nutrition; learning and memory; conditioned reflex of passive avoidance.

Currently, WHO experts believe that about half of the world's population lives in conditions of protein hunger, and protein-deficient nutrition has become a global problem due to the great danger to human health. Proteins entering the body with food carry out the transfer of genetic information as irreplaceable morphofunctional elements of all living cells, which ensures the synthesis and functions of neurotransmitters, hormones, enzymes that carry out metabolism [Berger et al., 2017]. Proteins also play an important role in the regulation of intracellular functions of reflex activity, immunoreactivity, being the plastic basis of neurochemical processes occurring in the central nervous system, which arouses interest in studying adaptive changes occurring in the body with protein-deficient nutrition. From these positions, the purpose of our research was to study changes in the learning and memory processes of laboratory animals as a result of a long-term protein-deficient diet.

The studies were carried out on 3-month-old white male rats, and the experimental animals were divided into 3 groups: I-rats fed in a vivarium - intact group; II - group, which was fed according to Nikonorov's recipe with a complete protein content; Group III, which was fed according to Nikonorov's recipe [Nikonorov *et al.*, 1973] with a protein deficiency of 80%. On the 40th day of feeding, the animals were trained and tested for a conditioned passive avoidance reflex (CPAR) [Yarvik *et al.*, 1967]. During testing, the following indicators were recorded: training time, latent period, vertical search function, horizontal search function and the amount of defecation.

The results of the study show that in rats that were fed a full-fledged protein food compared to the intact group, the reflex training time is reduced by 2 times. Also, in the group that was fed with a protein deficiency of 80%, there was a decrease in training time to 50.1 seconds (p<0,05). But as a result of post-training tests, it becomes clear that the reduction in the time it takes for rats to enter the dark chamber in this group is precisely an indicator of emotional tension. Since, in the

group receiving 80% protein deficiency, there was a decrease in the vertical search function by 95% (p<0,001) compared to the intact group, and the horizontal search function by 91% (p<0,05). The high threshold of their emotional tension is also evidenced by the fact that the animals are in a state of freezing during the observation period. At the same time, a decrease in the total latency period by 43.3% (p<0,05) indicates a weak memory in this group of rats.

Summarizing the results, it can be concluded that the duration of reflex memorization is high in animals that received a full protein meal for 40 days. And in the group fed with a protein deficiency, the memorization of the reflex is much weaker and, in general, the behavior of animals in this group is characterized by emotional tension and constant freezing.

CHANGE OF HEMOCOAGULATION FACTORS IN THE CONDITIONS OF PHYSICAL ENERGY

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Keywords: epiphysis; epiphysektomy; hemocoagulation.

Physical exertion causes muscle tension in the body, which in turn can affect hemocoagulation. The task is to study the time of blood clotting, plasma tolerance to heparin and thrombin time in epiphysectomy, enucleation and in animals with olfactory bulbectomy under physical conditions.

We used 3-month-old white rats with a mass of 150-180 g, in a quantity of 200.

Blood clotting time was determined by Lee and White, plasma tolerance to heparin by the Bergerhoff-Rock method and thrombin time by Sirmai [Cost, 1975].

Epiphysectomy was performed by the method of D.M. Aulova [Aulov, 1969], enucleation by the method of V.S. Galkina, deception of the olfactory bulb by the method of A.V. Pogrebkova (1959) [Cost, 1975]. Physical activity was determined by swimming in water. The experimental material was statistically processed.

In intact animals' blood clotting time was 101.0+3.2 sec., Plasma tolerance to heparin was 138.0+0.8 sec., thrombin time was 26.0+0.3 sec.

In epiphysectomized animals, the time of blood clotting is sharply reduced and is 38.0+0.4sec., Plasma tolerance to heparin is reduced to 177.0+1.5sec., thrombin time is reduced to 13.0+0sec.

In enucleated animals, the time of blood clotting is shortened and reaches 32.0+0.7sec., Plasma tolerance to heparin is subjected to some enhancement in relation to epiphysectomated (9.0+0.1sec).

Further these factors were studied in animals with the reception of the olfactory bulb. The study's results revealed that in animals with deceptions of the olfactory bulb during blood clotting was 85.0+3.09 sec., Plasma tolerance to nonparin was 11.3+0.7 sec, thrombin time 16.0+4.0.

All of the above gives us a reason to conclude that the time of blood clotting is sharply reduced in enucleated animals, plasma tolerance to heparin is enhanced, and the thrombin time is shortened by shortening.

The following studies were devoted to studying factors of hemocoagulation in short-term and long-term physical activity conditions.

Short-term physical activity (5 min) in control animals shortens the blood clotting time (60.0+0.4 sec.), plasma tolerance to heparin weakens (146.0+3.7sec.), thrombin time (36.0+2,1sec.); in epiphysectomized animals, blood clotting time (25.0+0.2sec.) and thrombin time (15.0+0.1 sec.) shortens, and plasma tolerance to heparin (90.0+2.1sec.) weakens. We observed the same pattern in enucleated animals (24.5+1.3 sec; 92.0+4.2 sec; 31.0+2.7 sec, respectively) and in animals with olfactory bulb deception (33.0+1.2sec; 32.0+1.7sec; 22.0+0.7sec respectively). With prolonged physical activity (20 min), the same changes in hemocoagulation factors are observed, but in a more pronounced form.

STUDY OF THE EFFECT OF LIGHT DESYNCHRONIZATION ON IMMUNE STATUS OF OLD AND YOUNG MICE

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Keywords: alpha tumor necrosis factor; interleukin-1; light desynchronization; immune inflammation.

Disturbance of biological rhythms is caused not only by external influences, but also by dysfunction of one or another organ.

The level of necrosis factor of alpha tumor determines the inflammatory mechanisms in the body and is considered as a marker of developing immune inflammation. It has been found that in the process of aging, i.e. in old age, there is an inadequate pathological weakening of the ability to adapt to stressful stimuli, increased immune inflammation, its long duration and decreased ability to restore neuroendocrine regulation of physiological processes due to light desynchronization.

The body's regulatory mechanisms have clearly articulated biological rhythms, and one of the factors that disrupts rhythms is light desynchronization.

Circulating distant signaling molecules, as well as locally active neuropeptides and neurotransmitters, are involved in the regulation of the neuroendocrine response, especially in antigen presentation, antibody production, lymphocyte activity, and cytokine formation [Shurlygina *et al.*, 2013]. During the activation of stress systems, the immune response of type Th2 is induced, which allows the body to protect itself from overload with inflammatory cytokines [Kruglov, 2010].

Tumor necrosis factor manifests its biological activity after binding to specific membrane receptors. It should be noted that TNF has a pathogenetic significance as an immunomodulator, has an inflammatory effect, but also has a proathrogenic effect, causes endothelial dysfunction and stimulates the expression of other inflammatory cytokines.

To assess immune status, we determined the ratios of alpha tumor necrosis factor, interleukin-1. The method of determination of interleukins is based on the solid-phase "sandwich" ELISA-test [Dolgov $et\ al.$, 2006]. The laboratory animals used for the study were young and old mice. They were divided into 2 groups: young (n = 170) and old (n = 182).

The daylight hours were taken into account within 12 hours. In order to evaluate the results of the research, we chose a period of physical rhythm with a timeframe of 23 days.

Telezola (Zoetis Inc., USA) was injected intramuscularly with 0.1 ml (0 kg body weight) and Xilantina (Huma-Farm, Russia) 0.15 minutes before the manipulations (blood draw for analysis).

The animals were exposed to combinations of natural light and at night of artificial light provided by a daylight lamp equivalent to a 60-watt incandescent lamp.

The results of the study show that the stress response in older mice is higher than in young mice, and shows that in old age in response to the effects of light desynchronization upregulation of stress-inducing factors and downregulation of stress-blocking factors are noted. It has also been shown that the rate of chronic immune inflammatory response in older

mice is higher than in young mice, which is reflected in upregulation of inflammatory factors and downregulation of anti-inflammatory factors in older mice in response to light desynchronization.

DETERMINATION OF CHANGES OF BLOOD MELATONIN IN HYPOXIA CONDITIONS

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Keywords: KEDTA; hypoxia; melatonin.

Hypoxia is a common pathological condition marked by a reduction in oxygen levels in the blood and tissues, the emergence of metabolic and functional disorders, and an adaptive response. Hypoxia is caused by a dysfunction of any of the functional systems involved in the transport of oxygen to the tissues. Due to impaired compensatory ventilation of the lungs, the quantity of carbon dioxide emitted increases. The body's energy supply is disrupted during hypoxia, when the amount of oxygen in the blood falls, as a result of decreased tissue respiration and aerobic breakdown of carbohydrates in the tissues. Hypoxia activates a number of physical, chemical and biological factors that cause cell damage and death. The main dysfunction during hypoxia is due to a lack of energy in the cells. Hypoxia accompanies all pathological processes in the body to varying degrees. Due to the inadequacy of adaptive mechanisms during hypoxia, the formation of decompensations in the body is accelerated, which leads to the development of functional, biochemical and structural disorders in organs and tissues. There are endogenous and exogenous types of hypoxia. The quantity of oxygen in arterial blood decreases during exogenous hvpoxia. This is due to a drop in the partial pressure of oxygen in the air as a result of breathing. When there is a normal quantity of oxygen in the environment, endogenous hypoxia is a disorder of the body's oxygen absorption. Hypoxia can range in severity from minor to severe. The cardiovascular system plays a critical role in the execution of compensatory mechanisms during hypoxia.

The studies were performed on 5 8-month-old male rabbits belonging to the genus Chinchilla (*Oroktoloques Cuniculus*). Hypoxia was performed by the method of Khvatov V.P and Khvatova Y.M [Khvatova, 1978] in barochambers with a total area of 0.12 m². The animals were

exposed to oxygen deficiency in light and dark conditions in baroque chambers with a gas mixture of 7% O₂ and 93% N₂. Thus, under hypoxia, the parameters of the blood change. Because hypoxia is seen as a source of stress for the body. The amount of melatonin in the peripheral blood was analyzed by enzyme-linked immunosorbent assay. KEDTA preservative was added to plasma samples to maintain the molecular integrity of the hormone. The statistical variation method was used to generate the research findings [Rokitski, 1964].

Studies have shown that the amount of melatonin in control animals reached 12.24 u / ml, 9.2 u / ml 1 day after hypoxia and dark mode and increased to 12.28 u / ml 10 days later. Melatonin levels were 6.4 u/ml on the first day of hypoxia and continual light and 8.4 u/ml on the tenth day. Melatonin has an antioxidant effect and has a regulatory and protective effect, such as protecting against oxidative stress, regulating energy metabolism and the immune system, delaying the aging process. As a result, while the amount of melatonin drops on the first day of hypoxia, it increases on the tenth day, protecting the body from the negative consequences of hypoxia.

ROLE FOR ADULT NEUROGENESIS IN FORMATION OF MEMORY TRACES

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Keywords: adult neurogenesis; memory traces; periglomerular neurons; back remodeling.

Although numerous multidisciplinary studies including behavioral, biochemical, molecular biological and immunohistochemical approaches have been undertaken for the purpose of unraveling the mechanisms underlying memory formation, these mechanisms still remain unclear.

To-date standpoint, widely accepted by most scientists, concerning the mechanism of memory formation is the one saying that underlying mechanism concludes in formation of new synaptic contacts between the neurons, engaged in the process of remembering of acquired information. This standpoint is supported by the results of ultrastructural studies, carried out on transmission electron microscope, which

revealed the increased number of dendrite spines in the brain cortex of the learned animals or the animals, kept in an informational enriched milieu [Leuner *et al.*, 2004].

Along with it, recent years different researchers showed that during elaboration of conditioned behavior on different kinds of models. new neurons are formed in the certain brain structures of the adult animals, so-called process of neurogenesis [Sherstnev et al., 2015; Yau et al., 2015]. These researchers could manage to demonstrate in their experimental studies of the engagement of such newly formed neurons in the processes of memory trace formation. The process of adult neurogenesis, originating from neural progenitor cells, has been consistently observed in two regions of the adult brain of the animals: the subventricular zone (SVZ) of the lateral ventricle and the subgranular zone (SGZ) of the dentate gyrus in the hippocampus. Neurons born in the SVZ migrate through the rostral migratory stream and become granule neurons and periglomerular neurons of the olfactory bulb. Neurons born in the SGZ differentiate and integrate into the local neural network as granule cells of the dentate gyrus [Deng et al., 2010]. The newly formed neurons are capable of migration to different brain structures and integrate in the previously formed neural circuits.

Besides, the process of adult neurogenesis, giving rise to novel brain neurons in adult organisms, there is another recently discovered pathway of formation of neural precursor cells in the adult brain – it is the process of back remodeling (dedifferentiation) of mature neurons [Mekhtiev, *unpublished*]. Such a process brings to elevation the pool of precursor cells of the brain neurons during different physiological and pathological processes, occurring in the brain structures.

INFLUENCE OF THE TOXICAL FACTOR ON THE HEMATOLOGICAL CONDITION OF FISHES

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Keywords: Cyprinus carpio; concentration; hematocrit; erythrocyte; average volume of erythrocyte.

Hematological research takes one of the leading places among several biological methods of indication and is one of the highsensitivity methods of reflecting the level of anthropogenic loading. Hematological indicators possess high lability and dynamically react to any change of conditions of dwelling [Al-Attar, 2005]. Therefore, the estimation of changes in indicators of blood under the influence of adverse conditions of the environment plays a large role in the definition of a functional condition of an organism of fishes. The value of indicators of blood is specific to each kind of fish and it allows us to use them as indicators of the pathological processes occurring on an organismic level. Studying the hematological parameters of fish is used to establish the level of toxicity in the environment. In this connection, we have decided to investigate the influence of such phosphoric fertilizer as Ammophos on hematological indicators of fishes on an example of Cyprinus carpio at the age of 6 months, weight 25 – 30 grams. It is necessary to notice that these preparations were not investigated on fish earlier. For research on Cyprinus carpio we went to the Khilly fish-breeding factory of the Neftchala city. Keeping all conditions of transportation, further placed them in the aquarium ANAS Institute of Physiology, Before starting the research, we have defined lethal, sublethal, and chronic concentrations for Cyprinus carpio [Finney, 2005] which have made 97,21 mg/l, 72,91 mg/l, 9,721 mg/l. In the experiments, we have defined the number of erythrocytes, size of hematocrit, and the average volume of erythrocytes [Ivanov, 1983] which in norm have made 1,70±0,15×10₁₂/l, 26,00±2,67 %, 180,00±35,90 fl accordingly. As a result of the research, we have revealed that in comparison with the norm at lethal concentration 96 - an hour exposition in all defined factors level has been raised. The sublethal concentration level of erythrocytes has been considerably raised for 6 days of experiments, hematocrit size has been raised for 6 and 8 days of research, and the average volume of erythrocytes throughout all days of research has been considerably lowered. At chronic concentration for 10, 20, and 30 days of research we observed a considerable fall in indicators of average volume of erythrocytes and quantity indicators of erythrocyte and hematocrit increase.

The system of the blood of fishes is presented by body hemostasis and peripheral blood. Unlike the higher vertebrates' fishes do not have a red brain, and process hemopoiesis occurs in the gills, heart, spleen, kidneys, and thymus of fishes. The orientation and rate of process hemopoiesis fishes are dependent on the influence of various factors in the environment. So, those or other changes of inhabitants can lead to a decrease of quantity, increase in erythrocyte, and hematocrit sizes in the blood of Cyprinus carpio. Simultaneously, change of indicators of

the blood of Cyprinus carpio in circulating blood occurs also at the expense of their emission from the depot of blood which at fishes contains in liver and spleen capillaries.

THE EFFECT OF HYPOXIA ON THE SPATIAL MEMORY IN MODEL OF ALZHEIMER'S DISEASE

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Keywords: hypoxia; Alzheimer's disease; the Morris pool; spatial memory; behavior.

Alzheimer's disease is the most widespread neurodegenerative disease, which has recently been observed not only in older people, but also in younger patients aged 33-45 years. In this regard, there is a need to model analogues of this disease on various animals. The classical method of J. Morris allows neuroimaging of the occurrence and course of Alzheimer's disease in rats [Gashimova *et al.*, 2018]. Currently, theories are being considered about the possible effect of hypoxia on neurodegenerative diseases, in particular, on Alzheimer's disease.

Initially, the experiments were carried out on albino rats grown in laboratory conditions. 4 albino rats participated in the experiment. For the purpose of comparison and calculation with respect to each object, each of the rats was marked in a certain area of the body with picrin dye (not soluble in water) as follows: base of the tail; dorsal side of the body; base of the head; base of the head and tail.

The experiment was carried out in a water maze (pool) Morris, which was filled with water, painted over with milk. The maximum water temperature was from 20 to 25 degrees (in order to avoid catalepsy). The invisible platform was located 1.5-2 cm below the water surface level [Morris, 1984].

At the first stage, naive (untrained) rats, when they were immersed in the Morris pool, were able to find a platform and climb on it for a period of time from 38 seconds (minimum) to 1 minute 8 seconds (maximum). After conducting the same experiment for 7 days, the latency period of the search was significantly reduced and ranged from 9s to 27s. The rats were then hypoxic for 20 minutes. in a pressure chamber, which received a mixture of gasses consisting of nitrogen (97%) and oxygen (3%).

After a certain period of time, an experiment was conducted to study the behavior and spatial memory of previously trained animals. It was important to determine the modulations of the behavior of experimental rats after exposure to hypoxia and to identify the effects of its use. The search for a platform in the Morris water maze revealed some features of the spatial memory of animals. Initially, it was assumed that there would be a deterioration in cognitive functions, but during the swim, the rats spent from 7 seconds (minimum) to search for a platform up to 26 seconds (maximum). This means that the time (latent period) of platform search in rats exposed to one-time hypoxia significantly decreased when compared with previously well-trained rats, which indicates an improvement in their cognitive functions.

According to the results of our experiments, the following was established: in trained albino rats, an improvement in spatial memory was observed after exposure to hypoxia. This was explained by the fact that under the influence of the second, more powerful stress factor (hypoxia), the instinct of self-preservation increased in rats, which can explain the significantly accelerated detection of an invisible platform.

INFLUENCE OF PRENATAL HYPOKINESIA ON THE BEHAVIOR, LEARNING AND MEMORY OF THE PROGENY DIFFERING BY EMOTIONAL ANXIETY LEVEL IN EARLY PERIODS OF POSTNATAL ONTOGENESIS

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Keywords: emotional anxiety; rat-pups; behavior; learning; memory.

The present study examines the ways of grouping of control and hypokinetic progenies differing by emotional anxiety (EA) level according to the parameters of horizontal (crossing) and vertical (rearing) activity (by means of generalization of the data) in 3 behavioral tests (open field test with white arena, the elevated plus-maze and mink chamber) in lactate and early prepubertal periods. While the number of the crossed squares (crossing) and stantes (rearing) was higher in the rat-pups with low emotional anxiety (LEA-aktiv), rat-pups with high emotional anxiety (HEA-passive) level had increased the latency of leaving the center and the number of grooming acts. Together with readings the increasing in the number of grooming, rotation and at-

tempts of looking out of the closed arm revealed under comparison of the results of LEA subgroup hypokinetic progeny in the behavior tests with the correspondent control animals in lactate and early prepubertal periods points to the increase of emotionality of these specimen as well.

In addition the influence of mother's hypokinesia during the fetal period of prenatal development on learning and memory processes of the progeny has been studied. Individuals of this progeny in the prepubertal period of development originally differ by emotional anxiety level. According to the results of the conducted retest sessions in passive avoidance conditioning (PAC) model in 24 hour after the learning sessions no reliable changes were noticed in the latency of animals' first entering into the dark chamber of the experimental box. In spite of that it has been stated that a great deal of the rat-pups with high level of emotional anxiety both in the experimental and control group remembered the negative effect of the electric shock which they were exposed in the dark chamber of the experimental box.

Thus, in the offspring subjected to hypokinesia during the fetal period of the mother's pregnancy, changes were observed towards an increase in the activity of some indicators compared to the inborn behavioral reactions of the rat pups of the control group.

EFFECT OF HYPOXIA FACTOR ON SPACE-NAVIGATION MEMORY IN WHITE ALBINOS RATS

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Keywords: hypoxi; space-navigation memory; the Morris Pool.

Development of hypoxia functional disorders, disruption of metabolic processes and against the background of the reaction of the adaptive mechanisms of the organism is a certain pathological process that develops under the influence of oxygen starvation of organs and tissues and low levels of oxygen in the blood.

Hypoxia is a state of oxygen starvation of the whole organism and individual organs and tissues caused by various external and internal factors. Oxygen shortage (also known as hypoxia) may affect anybody from baby to an older person and can affect people of different ages. The intensity of the procedure is the sole difference between manifestations. The initial stage of oxygen deficiency triggers a compensatory-

adaptive mechanism, mainly carried out by the cardiovascular and respiratory systems and biochemical intracellular reactions. After the functions of the adaptive mechanism are exhausted, the stage of decompensation begins. Hypoxia can manifest itself in acute and chronic clinical manifestations.

Twenty white male rats weighing 250-300 g were used in our research. The animals were housed in a normal vivarium. With 12 hours of day and night lighting, the Morris Pool was utilized to explore navigation mechanisms. The animals were taught in the hands of the researcher for 4-5 days before the experiment. Control and experimental groups of animals were employed. Inside the Morris pool, spatial navigation memory occurs in both groups of animals. Morris pool is a pool with a height and diameter of 1 meter. A platform is placed in the center of the pool. Four directions have been identified in the pool (north, south, east and west). The pool is filled with milky water. The animals are immersed in milk-filled water to search for an invisible platform. In the next stage of the experiment, the rats were subjected to acute hypoxia.

In a specifically built baroque chamber with a total space of $0.12 \, m_2$, hypoxia conditions were generated [Khvatova, 1978]. The animals were breathed for 20 minutes in a closed chamber with a combination of gasses comprising 95 percent nitrogen and 5% oxygen.

The body's reaction to irritants in the external and internal environment is known as reflexes. Genetically transmitted congenital reflexes and conditioned reflexes developed as a result of life processes are the two forms of reflexes. The running reflex was developed to help people escape the harmful effects of their surroundings. The running reflex switches between being passive and vigorous. An active running reflex is used in our experiment. Morris's pool is said to have a detrimental effect here, while the platform concealed beneath the water is thought to be a haven of redemption.

In the first stage of the experiment, the rats found the hidden platform for 1.5-2 minutes. After repeating this experiment 4-5 times, in the second stage of the experiment it takes 38-40 seconds. After hypoxia, he finds the hidden platform in 2-3 seconds.

From this we can conclude that hypoxia activates the function of the vision analyzer. As a result, internal resources are mobilized and the latent period of the search-navigation process of the invisible platform is sharply shortened. This phenomenon is observed in all research animals. It can be concluded that hypoxia has a stimulating effect on the formation and memory of spatial memory.

COMPARATIVE ANALYSIS OF EXCITING INDICATORS OF 19- AND 20-YEARS-OLD SANGUINE TYPES

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Keywords: personal anxiety; emotional stress; situational anxiety; sanguine types of the central nervous system.

Under the influence of emotional tension syndrome, several psychophysiological changes are noted, which can hinder the full development of the individual as a person. Exam stress is one of the many causes of complex psychophysiological stress in students. One of the modern problems of electrophysiology is studying the mechanism of action of high anxiety levels in students during and after the exam. An indicator of changes in the functional state of the CNS during emotional stress is noted. However, some aspects of the mechanism by which sanguine-type students' personal and situational arousal indicators change relative to the effects of high levels of emotional stress on students during a normal school day and exam process remain unexplored.

3rd and 4th-year sanguine students are required to identify age characteristics of changes in various psycho-emotional arousal indicators that arise during the examination process [Eysenck,1993].

The study involved 15 sanguine-type male students aged 19 and 20 (3rd and 4th-year students) studying at Ganja State University. The studies were conducted on normal days (AG) 2 months before the exam, 30 minutes before the exam (EA) and 30 minutes after the exam (IS).

The results of our study show some differences in situational and personal anxiety indicators of sanguine-type students aged 19 and 20 (III and IV courses). Thus, in 19-year-olds, the level of situational anxiety from high emotional stress before the exam (CA) and after the exam (IS) increases during the exam. Personal arousal levels increased compared to sanguine and choleric [Spielberg, 1983].

In 20-year-old sanguine-type students, there is a difference in situational anxiety indicators in AI and IS compared to a typical day. Personal anxiety indicators AG, AE, and IS rose sharply [Khanin, 1978]. Thus, situational and personal arousal indicators vary in different directions due to the excitement experienced by 19- and 20-year-old sanguine residents with AI and IS. Comparing the excitement indicators of the III course with the IV course, it can be concluded that in the final courses the personal excitement is strong in the exam situation.

THE USE OF FIRE-BELLIED TOADS, BOMBINA BOMBINA, AS AN ECOTOXICOLOGICAL TEST ORGANISM

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Keywords: ecotoxicological risk assessment; ecotoxicological test; new toxicity test procedure; fire-bellied toads; B. Bombina.

Amphibians are being increasingly used for toxicity screening purposes due to their high sensitivity to physico-chemical stress. In particular, amphibian embryos are useful indicators of environmental pollution and they are employed in toxicity studies of single substances, complex mixtures and environmental samples. They are sensitive to environmental contaminants because they inhabit aquatic and terrestrial realms, and their thin, highly permeable skin can rapidly absorb toxic substances. Amphibians are key components of many ecosystems and the impacts of pollution upon this class of animals are important to an understanding of ecosystem health. One of the most known standardized developmental toxicity tests is called FETAX (Frog Embryo Teratogenesis Assay: Xenopus). However, this test has a number of deficiencies which make its use for ecotoxicological risk assessment less suited in Europe and Turkey. Because of representing a very special limited ecosystem in Africa, X. laevis has a disadvantage in the evaluation of the xenobiotics' effect on amphibians in Europe. Therefore there is a requirement to introduce a new test with amphibians from Europe for ecotoxicological risk assessment. B. bombina is chosen for this purpose due to the considerable geographical distribution and being a single representative species of Bombina in Turkey by considering that test organisms to be used for ecotoxicological risk assessment have to satisfy both ecological and economic criteria. The main objective of this oral presentation is to introduce a new toxicity test procedure with B. bombina which inhabits eastern, western and middle Europe and northwestern Turkey, and to compare advantages and/or disadvantages of this test with that of FETAX. Newly described test procedure is a set of customized toxicity tests for acute, short term chronic, chronic and early life stages of amphibian embryos which allow selecting the most appropriate exposure period and end points according to the toxicity of the sample and the purpose of the study.

FORMATION AND ULTRASOUND DIAGNOSTICS OF REPRODUCTIVE SCHOOLS OF STERLET (ACIPENSER RUTHENUS LINNAEUS, 1758) IN AZERBAIJAN

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Keywords: Acipenser ruthenus; reproductive brood fish; ultrasound diagnosis.

One of the main directions in the development of artificial breeding of sturgeons in modern ecological conditions is their large-scale commercial breeding. In recent years, fish rearing stations and fish farms in Azerbaijan have been using non-traditional fish species for commercial production, one of which is sterlet (*Acipenser ruthenus* Linnaeus, 1758).

Despite the fact that sterlet sturgeon is included in the ichthyofauna of Azerbaijan in the Caspian region, due to the lack of natural resources in the Kura River and the impossibility of supply of its producers, their artificial breeding in sturgeon farms has not been carried out in the republic. The main purpose of the research is to determine the morpho-biological characteristics, growth rate and sex and maturity of the formed reproductive schools of different age groups of sterlet sturgeon bred in aquaculture in Azerbaijani fish farms by the method of ultrasonic diagnostics.

The research was carried out in 2021-2022 at the Samukh fish farm. In order to form reproductive schools of sterlet sturgeon, 3-yearold and 4-year-old sterlet sturgeons bred on the farm, as well as 5-6vear-old female individuals bred for re-spawning were used. In the research process, the dynamics of development of individuals of different age groups, morpho-biological indicators (length, weight, coefficient of fullness, daily growth rate, gonado-somatic index and other indicators to the rules adopted in ichthyology [Weinberg, 1956; Pravdin, 1966; Milstein, 1982; Detlaf et al., 1982; Mamedov et al., 2021] were determined accordingly. In order to determine the sex and maturity of gonads of reproductive schools of sterlet sturgeon formed in aquaculture conditions, the farm used an ultrasound scanner MEDISON SA 600 and the relevant methodology [Chebanov et al., 2004; Chebanov, Galich, 2010]. The production of sexual products from sterlet sturgeons was carried out by the method of "cutting the ovary" without killing the brood fish [Podushka, 1999; Mamedov et al., 2009]. The presented material analyzed the morpho-biological and reproductive characteristics of 20 sterlet sturgeons for the second time in comparison with the reproductive indicators of the same broad fish for the first time in 2019.

In February 2021, the total number of reproductive sterlet sturgeons re-analyzed by ultrasound was 87. 39 of them were male (σ) and 48 were spawned (φ). Thirty-five males and 40 females of the sterlet sturgeon (*Acipenser ruthenus* Linnaeus, 1758) re-analyzed by ultrasound diagnostics method were in the fourth stage of maturity. In February 2021, 18 out of 20 sterlet sturgeons injected into the pituitary gland produced a second sexually mature hardroe.

In 2019, the gonado-somatic index of reproductive individuals who received hardroe for the first time was small and fluctuated between 15.4-18.5%. Due to the small size of the hardroe grains, the number per gram varies between 128-132 [Mamedov *et al.*, 2021]. Fertilization of the obtained hardroe fluctuated between 44-53% in the stage of small jaundice plug (stage 17). The yield of free embryos averaged 55%. In 2021, the gonado-somatic range of reproductive individuals who received hardware for the second time changed in a wide range (8.0-16.5%), but the average number of grains per gram of hardroe was 83. Fertilization of spawns fluctuated between 70-80% during the stage of small jaundice plug. The release of free embryos averaged 70%.

The results of the study can be used to ensure the optimal development of sterlet sturgeons, as well as other species of sturgeons bred in fish farms and sturgeon farms, at different stages of development, to develop biotechnical standards for their artificial breeding and for formation of reproductive schools. The obtained results can be used in the economic calculation of the strategy of rearing sturgeon fry in the fish-rearing station and in commercial fisheries.

DIVERSITY OF FISHES IN THE TRIBUTARIES OF THE SYRDARYA RIVER WITHIN THE REPUBLIC OF KAZAKHSTAN

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Keywords: biodiversity conservation; fish; tributaries; Syrdarya river; aboriginal; commercial; alien species.

Human activity on fresh water bodies leads to the loss of species diversity and transformation or disappearance of biotopes in inland

waters [Closs et al, 2016]. The Aral Sea (lake) basin is one of the largest oases in Asia. Only the Amudarya and Syrdarya rivers delivered water to this lake. Irrational use of water led to an ecological crisis in this region in the second half of the last century. The Syrdarya river is a major transboundary river, the last section of which is located in the Republic of Kazakhstan. Here the river passes through the territory of two regions. The Syrdarya basin within the boundaries of South Kazakhstan province is characterized by high population density and significant water consumption for agriculture. In the Kyzyl-Orda region, a significant part of the population and cultivated land are concentrated near the Syrdarva River. Water resources of most tributaries are fully used by the population and do not reach the Syrdarya River. In this regard, the assessment of the current state of the diversity of organisms and elucidation of existing and possible directions of subsequent changes is relevant [Mamilov, 2021]. The aim of the research was to study the diversity of ichthyofauna of small water bodies flowing through the southwestern Karatau macro-slope. The material was collected from the rivers Arystandy, Shayan, Bogen and Karashik. To catch fish, we used a small-cell dragnet, a standard set of gill nets with a cell size from 16 to 100 mm in length of 25 each, fishing nets of various designs with 3-5 mm cells and a hook-and-line tackle. Large fish were analyzed in situ, small fish were fixed in formalin and further processing was performed in the laboratory according to the schemes generally accepted in ichthyology [Pravdin, 1966]. The fish population of tributaries of the Syrdarya River is concentrated mainly in the foothill semi-arid areas. Common species for the Syrdarya River and its tributaries are the native roach Rutilus rutilus, carp Cyprinus carpio, asp Aspius aspius, silver carp Carassius gibelio, and the alien fishes stone moroko Pseudorasbora parva and bitterling Rhodeus sp.. Increased water content in the rivers in 2013 and the first half of 2014 resulted in the appearance of juvenile commercial species - carp, roach and asp - in the rivers Arystandy, Bogen and Shayan. The most widespread species were the Tashkent riffle bleak Alburnoides oblongus, the Turkestan gudgeon Gobio gobio, and the snowtrout Schizothorax intermedius. Results showed that the studied tributaries of the Syrdarya river play an important role in the conservation of the diversity of native ichthyofauna. However, their long-term survival depends on climatic factors and water use by the local population.

TOXIC BASED WATER QUALITY IN THE LOWER GEDIZ RIVER BASIN. ANATOLIA. TÜRKIYE

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Keywords: Amphitox; teratogenesis; amphibian embryos; environmental pollution; Gediz River, Anatolia Türkiye

The Gediz River is one of the most important rivers in the West Anatolian Region of Türkiye. Within its basin of 17.500 km² there are about 1.7 million inhabitants, intensive agricultural activities with over 190.000 ha irrigated with water from the river and more than 340 industries located in the area. Using the AMPHITOX early life stage toxicity test with Bombina bombina from acute to chronic exposures, we evaluated the water quality at six sampling stations of the river valley and expressed the results as acute and chronic toxicity units. In 50% of the sampling stations the toxicity was higher than the allowable level for whole industrial effluents toxicity recommended by US EPA. For acute toxicity in two sample stations, the Muradiye bridge and the Emiralen dam, the water was about 7 times more toxic than the Criteria Maximum Concentration (CMC) recommended by US EPA for industrial effluents. It is noteworthy that for most cases, prior to dead, the embryos exhibit delayed development and after neurula stage also retarded growth, tail flexures and in some cases asymmetries and edema. SEM studies in sublethal exposure conditions show dramatic alterations in ectodermal tissue including a large number of apoptotic cells. The three sample stations with high toxicity had, in one case, very low DO, in other very high DO while in the third very high conductivity reflecting in all cases very intensive anthropogenic activities. In all places where the water quality was better than CMC some of the following macroorganisms were observed: insects, fishes, amphibians, turtles and water snakes. Our study point out that the AMPHITOX early life stage toxicity test, conducted with a native amphibians could be appropriate for ecotoxicological monitoring of water quality, essential for the preservation of the environment and human health in the region.

ROLE OF THE SKIN OF LACERTA STRIGATA (EICHWALD, 1831) IN MICROEVOLUTION

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Keywords: lizard; skin; epidermis; microevolution; adaptation; chromatophores. The skin of the *Lacerta strigata* is the most exposed organ to external influences and protects the body from water loss. The outer shape of the skin and the oberhoutchen layer are adapted for the rapid removal of harmful substances. The epidermis is covered with a stratum corneum from the outside. The stratum germinativum cells of the epidermis are located on the surface of the basal membrane and form a whole layer [Alibardi, 2014]. One of the evolutionary adaptations is the absence of blood vessels and nerves in the epidermis. If lizards had blood and nerves in the epidermis, this would lead to rapid damage and death from mechanical impact. The basal membrane of the lizard is formed by both epithelial cells and the activity of fibroblasts. In the case of the absence of the basal membrane, dividing epithelial cells would penetrate the connective tissue. One of the adaptations achieved in evolution is that the α , meso, and β layers of the epidermis are composed of dead cells. In case cells were alive, they would be reflected in the weight and size of the animal, prevent the extraction of heat from the body, and the body would heat up faster from the outside. The oberhautchen layer of the skin has more keratin matter and is joined to each other by tighter bonds. Blood and lymph vessels, nerves, large amounts of fiber, and pigment cells are found in the dermal layer inside the skin [Duarte et al., 2017]. This layer is full of collagen fibers and also bony osteoderms can be found. Rising above sea level, we have witnessed that the innermost part of the dermis (stratum compactum) consists of relatively dense and compactly arranged elements of connective tissue. It has been observed that the upper layer of the dermis (stratum spongiosum) is thicker as we descend from the heights. The chromatophores provide camouflage and protection from harmful sun rays. Caspian green lizards have 3 types of chromatophores. Melanophore cells accumulate dark pigment depending on the amount of pigment around the nucleus or in the pseudopodia, the upper part of the reptile's skin becomes light or dark. Lipophores turn yellowish because they collect lipochrome droplets. Guanophores cells do not accumulate pigment, since guanophores

have platelets, they reflect light. The hypodermis is located under the dermis and contains fibroblasts, adipose, and macrophages. Fat cells transform into two forms: brown-colored and yellowish adipose cells. At the end of autumn, the number of brown adipose cells in the lizard increases. It is assumed that the accumulated lipids are used during the brumation period. The nuclei inside yellowish adipose cells are compressed towards the membrane and large lipid droplets are observed. The hypodermis is an elastic layer that connects to the organs in the bottom layer of the skin. The elasticity of this layer allows the skin to slide over the body and return to its previous position easily.

AQUACULTURE OF THE SOUTH CASPIAN ASP (ASPIUS ASPIUS TAENIATUS EICHWALD, 1831) IN AZERBAIJAN

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Keywords: South Caspian asp; reproductive school; aquaculture.

The resources of the South Caspian basin in the water basins of Azerbaijan have significantly decreased compared to previous years, and in the current environmental conditions, the restoration of their resources can be carried out artificially only in aquaculture conditions. No research has been conducted on the artificial breeding of asp in Azerbaijan and in the Caspian region, and no biotechnology for its artificial reproduction has been developed. In this regard, one of the urgent issues is to determine the biological and technological aspects of artificial breeding of aquaculture in the South Caspian Sea in Azerbaijan.

The first research on the cultivation of the South Caspian asp in Azerbaijan in aquaculture conditions has been carried out since 2015 at the farm "Samukh-fish" (Barda region). For this purpose, initially, the asp caught from the Mingachevir reservoir was used. Male and spawned asp were hormonally injected into the carp pituitary gland in 2015 according to the instructions and sexual products were obtained from them [Kozlov *et al.*, 1980]. The hardroe were fertilized by the "dry" method and the fertilized hardroes were incubated in the Weiss apparatus. The larvae and fries were bred up at the Samukh-fish farm by the pool method.

In 2016, 40,000 asp fries with an average weight of 25 grams were relocated to the Sari-Su and Ag-Gol water basins for fish farming, and 100 were reared in aquaculture on the farm to establish a breeding

pool. Their initial breeding was carried out together with sturgeons, and sprat minced meat and mixed feeds were used to feed them.

In 2019, 6 asp fries with an average weight of 0.7 kg were transferred to cages with an area of $40~\text{m}^2$ placed in the Mingachevir reservoir, where they were fed mainly by live fish entering through the glasses of the cages. By 2020, asp fries were bred up in cages with sturgeons and research was carried out on them in accordance with the accepted ichthyological methods. Their length (L), weight (W), coefficients of fullness (F), sex and other morpho-physiological parameters were determined.

On March 12, 2021, in the process of research, it was determined that the average length of breed asp was 53.5 cm, and the average weight was 2.5 kg. Over the past year, their weight gain was 1.8 kg. As a result of visual examination, 4 of the breeders were found to be spawning (99) and 2 were male. On that date, as the breeders reached sexual maturity, they were brought back to the Samukh-fish farm and kept in partitioned concrete pools for adaptation. The water temperature in the pool was gradually increased from 10° C to 14° C. After being kept in such conditions for 4 days, on March 16, carp pituitary was injected into the breeder spawned asps at a rate of 4 mg per kilogram of body weight (total dose), and male at a rate of 2 mg [Ganizade et al., 2021;]. After 1 day, sex products were taken from the breeders. In total, 235 thousand hardroe was taken from 2 spawning asp. The average diameter of the hardroes was 1.9 mm and the weight was 2.3 mg. It was not possible to get sex products from the other two spawning asp.

The hardroes were fertilized by "dry" method and incubated in the Weiss apparatus. During the incubation period (7 days), the loss of fertilized hardroe during the incubation period was 30%. *Artemia salina* nauplius was used as the first live feed for larvae and fries, and later mixed feeds produced by *Aller Aqua*.

By the end of the year, the length of one-year-old fries was 7-10 cm. At present, the number of one-year-old asp fries bred up in the aquaculture conditions at the "Samukh-fish" farm is 100,000. It is planned to release most of the fries into natural water bodies, and to form the rest as a breeding pool.

The process of reproduction of the South Caspian asp in aquaculture conditions and breeding is currently at its starting stage in Azerbaijan. In this regard, the formation of their reproductive schools in aquaculture conditions and the development of technologies for their artificial reproduction allow increasing the amount of South Caspian asps in the inland waters of the republic.

ECOLOGICAL FUNDAMENTALS OF BEHAVIORAL MANAGEMENT OF ANIMALS

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Keywords: behavior; rhythm; ecology.

Parameters of endogenous rhythms of laboratory-controlled animals (white rats of the genus *Vistar*) do not allow studying the effects of many environmental factors. Animals kept in the laboratory are deprived of the influence of such a natural factor. These are the factors that determine their activity under natural conditions. The rhythms and factors of the same behavior and the effects that determine their recurrence are not clearly known. Each biocenosis consists of a complex biological system. Living things in these systems are directly or indirectly affected by space, geological, weather and other factors. Therefore, the use of repetition of natural cycles in biological systems has become relevant for each period.

Environmental management of animals should not be considered as a biological phenomenon. At the same time, this problem should be considered as a biological problem of anthropogenic origin, which constantly affects animals in the environment. Natural cycles can be created in the laboratory by creating factors that model the internal and external environment of animals in the aviary, laboratory and indoor conditions. In our research, we studied the rhythmic active and passive (sleep) phases of animals in natural conditions, applied them in the laboratory, and managed to change their behavior in closed conditions and the corresponding physiological processes. Invention-Patent. N I2007.0031. Musayev AM, Yolchuyev Y., Musayev MA, Aliyev AH, Invention-Patent. N I2012.0109. A.M.Musayev, N.A.Sadigova, Ch.Y.Mammadova, A.H.Aliyev.

Thus, it is one of the ways to study the biological nature of daily and seasonal rhythmic behavior in natural, aviary and laboratory conditions, to determine the sequence of environmental signals that regulate animal behavior, to determine the specific form of behavior, when it occurs, to optimize human-animal interactions.

The direction and purpose of the research:

• to identify signals that theoretically regulate diurnal and seasonal rhythmic behavior in natural, aviary and laboratory conditions, acting

first as a warning signal and then acting as a power signal in later stages.

- to determine the sequence of signals that synchronize the biological rhythms of animals with geophysical diurnal and seasonal rhythms, and to ensure the repetition of these signals in the aviary, laboratory conditions.
- To study the effects of the two day and two-night phases of the astronomical day on animals kept indoors in different aspects.
 - Influence of social factors:
- Social synchronization of animal behavior is important in herd animals or in large artificial populations. Managing the behavior of herd animals by influencing the leader of the herd, the dominant individual.
- Sexual activity of some animals is activated under the influence of social factors. For example, in white rats, the smell of a male rat stimulates the hormones of female rats. To study research in this direction in large and small horned animals.

The main purpose of the practical part of the work is to develop an optical-acoustic program that regulates the daily and seasonal rhythmic behavior of animals at different stages of ontogeny in the aviary, indoors and in the laboratory, depending on the ecological and physiological characteristics and conditions.

IMPACT OF URBANIZATION ON THE ABSHERON PENINSULA ON THE BIODIVERSITY OF HERPETOFAUNA

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Keywords: reptile, urbanization, Absheron Peninsula, Testudo graeca, herpetofauna.

The process of urbanization observed on the Absheron Peninsula of Azerbaijan in recent years is affecting all components of the ecosystem. As a result of population growth, reptiles on the peninsula face both anthropogenic and technogenic factors. Urbanization is accompanied by the construction of new settlements and cities, and the expansion of existing ones. In connection with population growth, strong infrastructure changes took place in the peninsula, factories and plants were built to provide people with jobs, and also rest areas and high-

ways were built. Along with all this, almond and grape orchards have been planted, and numerous greenhouses have been established to develop floriculture and vegetable growing, which is typical for the peninsula. Thus, resulting in the capture of soil-related reptile biotopes, shrinking their range, and depletion of food supplies.

The research was conducted from 2015 to 2019 and aimed to study the impact of urbanization on the peninsula on the bioecological characteristics, adaptations, and changes in population dynamics of selected background reptile species. For this, the peninsula was analyzed by the level of urbanization and the stationery was identified by dividing it into one control and five research zones. These include I-single-storey residential area, II-mixed-storey residential area, III-multi-storey residential area, IV-industrial facilities, V-forest area, and VI-non-urbanized control area. Species of reptiles have been identified according to Ananyeva et al., 2011, Bannikov et al. (1977), Berejnoy, and Barbashova (1981) [Ananyeva et al., 2011, Bannikov et al., 1977, Berejnoy et al., 1981]. To determine the degree of anthropogenic adaptation and population density, the observed area was based on the number of individuals of the species found in each km².

The object of research was taken from the Mediterranean tortoise – *Testudo graeca* L, 1758, the Caspian thin-toed gecko – *Gymnodactylus caspius* E, 1831, and the water snake – *Natrix tessellata* Laurenti, 1768 widespread on the peninsula. During the research, the methods [Levykh *et al*, 2011] were used to monitor the urban ecosystem, and zoological research methods [Romanov *et al.*, 2005] were used to study herpetofauna.

In recent years, a new form of negative anthropogenic impact on Mediterranean turtles has been observed. The garden areas on the peninsula, along the highways between villages and settlements, are cleaned with special mowers. In this case, due to the careless approach of the workers, the turtles are injured, and if the cutting part of the mower is metallic, then it is destroyed on the spot. Such incidents are common during the April-May-June months on the Baku-Novkhani-Fatmai-Mardakan-Mashtaga-Bilgah and other highways. In particular, newborns, as well as one-year-old and two-year-olds, are more likely to die from damage to the plastron, because they are softer than adults. At first glance, this seems inevitable, but if Mediterranean tortoises are killed by cars in early spring, eaten by raptors, and destroyed during cleaning works, then their progeny are more likely to die out on the peninsula. As a way out of the situation, it is important to conduct seasonal explanatory work with the involved people.

CURRENT STATE OF THE MEDITERRANEAN TORTOISE (TESTUDO GRAECA L., 1758) IN THE HERPETOFAUNA OF ABSHERON

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Keywords: Mediterranean tortoise, Absheron, herpetofauna, urbanization.

Despite the fact that the Mediterranean tortoise is widespread in many countries across the world, its dynamic growth has been falling sharply in recent years [Alekperov, 1978; Najafov *et al.*, 1992; Najafov *et al.*, 2015; Novruzov, 2016]. The decrease in their number is extensive in the areas where the urbanization process is observed. Having regard to the political and social situation in Azerbaijan in the last 30 years, a large part of the population has inhabited the peninsula, therefore, this area is considered a significantly urbanized. While participating in the food chains, the Mediterranean tortoises also play an important role in the spread of some parasitic diseases. On the other hand, they are of exotic importance being kept in zoos and even on private farms. However, sometimes they look like pest animals by eating freshly sprouted garden plants and vegetables.

It is not a coincidence that the Mediterranean tortoise as a conservation-reliant endangered species has been included by the countries in the International Red Books (VU A1cd), in Appendix I of CITES, in Appendix II of Bern Convention, in the Red Book of the Republic of Azerbaijan, the Red Data Book of the RF, Krasnodar Territory and the Republic of Dagestan, etc. Moreover, with the support of IFAW, a special farm has been established to study and protect the Mediterranean tortoises in the Krasnodar territory of Russia within the project "Attention: Turtles".

According to their phylogenesis, tortoises have acquired specific adaptation characteristics by returning from an arid climate to an aquatic environment and vice versa. Mediterranean tortoise, better adapted to arid climates, is drought-resistant, feeds on grasses and animal source foods, and is a cold-blooded animal that hibernates in winter and estivates in summer at high temperatures. One of the species (*Testudo graeca* L., 1758) of the genus *Testudo* is widespread in Azerbaijan. They have survived to the present day without undergoing significant morphological changes.

The research carried out in the Absheron Peninsula shows that the dynamic growth of the Mediterranean tortoise has been declining in recent years. The construction and expansion of cities and settlements caused the biotopes inhabited by these animals to be captured by humans. Except for the Shah Dili territory, in other parts of the peninsula, their biotopes are seen in small fragments. It is high time to take the appropriate measures to preserve the biodiversity of these animals on the peninsula, otherwise, they would become endangered in the near future. Actually, these species are included in the second edition of the Red Book (2013) of the Republic of Azerbaijan and are expected to be included in the third edition. In our opinion, the establishment of a herpetology lab would be one of the important steps for their reproduction and release into nature.

ABOUT THE NEW PROTECTION STATUS OF TURTLE DOVE (STREPTOPELIA TURTUR LINNAEUS, 1758) IN AZERBAIJAN

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Keywords: European Turtle-Dove; vulnerable status of Streptopelia turtur; red book of Azerbaijan.

Turtle dove *Streptopelia turtur* [Linnaeus, 1758], belongs to the family *Columbidae* now has a vulnerable status of İUCN in Europe. In our country turtle doves always have a large population during the breeding season.

The European turtle dove has a very large breeding range, stretching from the western coast of Europe and Africa eastwards as far as north-west China. In Europe, the population is estimated to be decreasing by 30-49% in 15.9 years (three generations) (BirdLife International 2015). The species was uplisted in 2015 from the IUCN Least Concern to Vulnerable category. It has been identified as having an Unfavorable Conservation Status within the EU because populations are decreasing in many Member States. Breeding numbers show an overall decline (from the 1970s), especially in western Europe where the decrease seems to be strongly linked with the intensification of agriculture [Species Status Report European Turtle Dove, 2016].

The number of *Streptopelia turtur* is a rapidly decreasing species within its range. This trend is also reflected in the number of nesting populations in the Republic of Azerbaijan. By 2000 years, the local population was estimated at 100,000 pairs. However, by 2016, the decline

in the total area in Europe reached 35%. The density is higher around Baku and in the northwestern part, while the density decreases in the plain area and towards the south. A more accurate count is needed now.

The main threats and limiting factors are reduction of habitats – capture of natural biotopes by farms, also a hunting factor on the migration period is actual. Measures adopted for its protection: it is included in the Red List of the International Union for Conservation of Nature, it is a species belonging to the Bonn Convention/CMS, Bern Convention, a fine is imposed for its hunting in our country.

Recommended measures for protection are - protection and increasing of green areas, correct orientation of farming and reclamation activities, organization of educational training. As a new vulnerable species already in Azerbaijan too the Turtle dove added to the list of birds of III edition of Red Book of Azerbaijan.

FOOD SPECTRUM OF SOME REPTILE SPECIES ON ARID TERRITORY OF AZERBAIJAN

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Keywords: food range; lizards; snakes.

When analyzing the food spectrum of species living in the same habitat, it becomes clear that these species are active at different times, take food from different places, etc. which allows each species to use slightly different resources, which reduces the intensity of competition.

Snakes leading a secretive and burrowing lifestyle (*Eirenis, Rhynchocalamus*) can feed on invertebrates leading a secretive lifestyle without coming to the surface of the earth. The comparison of the food composition of 3 species of *Eyrenis* revealed that their trophic positions are somewhat different, which gives reason to associate the dominance of spiders in the food of *E.collaris* species with the secret lifestyle of the species, living and feeding under stones. Other eyrenis species (*E.modestus, E.punctatolineatus*) are relatively more abundant on the surface of the earth, and this is accompanied by the predominance of flat-winged birds in their diet by feeding more actively [Tuniyev *et al.*, 2009; Jafarova, 1984] shows the dominance of spiders and caterpillars in the diet of the spotted erysipelas, and of the calf in the food of the peaceful erysipelas.

Platyseps najadum, Coronella austriaca, Malpolon monspessulanus species are mainly zoophagous, although snakes and rodents are found in their food. I.S.Darevskiy (1967) shows the Coronella austriaca as the main predator of rock lizards and notes that if the area overlaps with the rock lizard, it completely switches to feeding on representatives of this group. The author associates the large number of Coronella austriaca in the mountain steppes and subalpine zone of the Great Caucasus Range and the South Caucasus with the widespread distribution of rock lizards. Since the birth of Coronella austriaca babies coincides with the hatching of rock lizards, brown snakes are saurophagis from birth. This is evidenced by the fact that the *Coronella austriaca* lives sympatrically with the Azerbaijani lizard in Nakhchivan [Jafarova, 1984] and Zuvand [Asgarova, 2010], among the areas we studied. Unlike the Smooth snake (C. austriaca), the Dahl's whip snake (P.najadum) lives in the same ecosystem and feeds not only with rock lizards, but also with other lizard species. For example, in Gobustan, it lives sympatrically with the species of the Caucasian gecko, the Caspian gecko, the swift lizard, and the Montpellier snake (M.monspessulanus) The main saurophagis throughout its range is the arrow snake [Bogdanov, 1965], [Ananyeva et al., 1997].

The South Caucasian lizard and Strauch's lizard are fast-moving and feed on larger and more active invertebrates. Sunwatcher toadhead agama (*Phrynocephalus helioscopus*) prefers ants that are easy to get to because they are slow. Pleske's racerunner (Eremias pleskei and Eremias strauchi) differ in seasonal and diurnal activity, as well as in the microstation they occupy. While the Strauch's lizard can live in different biotopes, the biotope of the South Caucasian lizard is the hard sandy archillean semi-deserts (Sherbak, p. 237). Since this species is thermophilic, it starts its daily activity later than other species of lizards living with it - 9-10 o'clock. While other lizards hide in their shelters to protect themselves from the hot midday sun, high thermophilicity allows the South Caucasian lizard to remain active. The biotope of the delicate snakehead is hard stony and clay soils. Thus, while the South Caucasian lizard belongs to the same food guild as the Strauch's lizard and the elegant snakehead, it belongs to a different clay according to microstation, diurnal and seasonal activity. After all, they belong to a different food guild with wormwood [Jafarova, 1999; Askerova et al., 2012].

THE SETTLEMENT OF BIRDS IN BIOTOPES ARRIVING FOR BREEDING IN THE GIZILAGAI NATIONAL PARK

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Keywords: biotope; nesting; feeding; roosting; resting.

The settlement of breeding birds in biotopes in the Gizilaghaj National Park - the comprehensive use (cu), nesting (n), feeding (f), roosting (r), resting (re) is studied for the first time at the population level. In the modern age, the preservation of the genetic fund at the level of biological diversity is important for the protection of the environment and the implementation of the effective use of natural biocenosis on a scientific basis. The study of the use of different biotopes by birds is important for solving the problem of the conservation of the genetic fund and natural biological diversity.

The wide lanes of the separate biotopes of the southwestern coast of the Caspian Sea, the multifacetedness of the area and the location at the junction of the migration roads are of significant importance. The settlement of some bird species on biotopes in the area that came to Gizilagaj National Park from south-eastern Asian countries and North Africa to breed and their use of biotopes for various purposes has not been studied so far. Global climate change, exploitation and degradation of natural resources and natural habitats cause birds to be deprived of breeding or to change breeding places. This makes it difficult to ensure and develop sustainable development of the environment.

During the reproductive period, 28 species of birds (27 species for feeding, 1 species for comprehensive use) use the meadow swamp, 23 species (12 species for feeding, 11 species for comprehensive use) the blackberry jungle, 23 species (17 species for feeding, 6 species for comprehensive use) the coastal lakes, ponds and channels, 22 species (15 species for comprehensive use, 7 species for feeding) the reedy swamp, 19 species (6 species for comprehensive use, 6 species for resting, 7 species for feeding) the dry tamarisk jungle, 19 species (7 species for feeding, 6 species for resting, 6 species for comprehensive use) the dry reed jungle, 18 species (11 species for feeding, 7 species for comprehensive use, 7 species for feeding, 1 species (8 species for comprehensive use, 7 species for feeding, 1 species for resting) the tamarisk swamp, 16 species (11 species for feeding, 4 species for comprehensive use, 1 species for resting) the spiny rush swamps, 11 spe-

cies (6 species for feeding, 5 species for comprehensive use) the semideserts and ravines, 11 species (1 species for comprehensive use, 2 species for resting, 8 species for feeding) the water area of the Lesser Gizilagaj Bay, 6 species (5 species for feeding, 1 species for resting) the water area of the Great Gizilagaj Bay, 28 species (10 species for feeding, 18 species for comprehensive use) the orchards, 14 species (12 species for feeding, 2 species for comprehensive use) the grape plantations, 10 species (10 species for feeding) the fields and vegetable gardens, 4 species (1 species for resting, 1 species for feeding, 2 species use comprehensive use) the old platforms in the Gizilagaj National Park [Babayev, 2007; Mustafayev, 2011; Mustafayev, 2008; Taghiyev, 2011].

MODERN ICHTHYOFAUNA OF GUDYALCHAY

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Keywords: Gudyalchaych ichthyofauna; bioecology; Tufan Mountain; Guba-Khachmaz region.

Gudyalchay is one of the abundant rivers formed within the borders of our Republic. It begins at an altitude of 3000 m above sea level from the northern slopes of Tufan Mountain in the Greater Caucasus range. It crosses the territories of Guba-Khachmaz regions and flows into the Caspian Sea near the village of Niyazabad. The length of the river is 108 km. The catchment area of its basin is 799 km2, and it is the largest river among the rivers located in Azerbaijan in terms of annual water flow. 51% of the annual flow occurs in May-July. The water of the river is mainly used to irrigate the land allocated for the purpose of growing agricultural products.

Bioecology of Gudyalchay, quantitative and qualitative indicators of living organisms living here, including information about fish species are described in the materials of research conducted in different years [Abdurakhmanov, 1965; Agamaliyev *et al.*, 2010; Kuliyev *et al.*, 2011; Bahaddinov, 2021]. It should also be noted that the materials known in the literature mainly represent the results of research conducted in the second half of the 20th century and the beginning of the 21st century. The main goal of the scientific research works is to study the modern ichthyofauna of Gudyalchay under changed ecological conditions and to investigate the state of its biological resources.

Research works related to the study of the modern ichthyofauna of Gudyalchay were carried out in 2021-2022 in various locations of the lower and middle reaches of the river. Information about ichthyofauna was determined based on the results of fishing conducted using different fishing tools (drift nets, set nets, conical venters and ichthyoplankton nets). A trawl net with a mesh size of 6x6 mm and a length of 20 m was used for catching baby fish. In areas where it is not possible to use a trawl net, a domcha with a diameter of 35 cm and a depth of 50 cm was used to catch larvae and babies. Fries were fixed in 4% formalin solution and was determined using appropriate methodological tools [Pravdin, 1966; Koshelev, 1984]

Passive fishing tools - cone-shaped ichthyoplankton nets (small and large) were used to catch fries in the part of Gudyalchay that connects with the sea. The diameter of the entrance of the small-sized conical ichthyoplankton net was 0,2 $\,\mathrm{m}^2$ (cone bag is No. 13 capron mesh material), and the diameter of the entrance of the large-sized ichthyoplankton net was 1,0 $\,\mathrm{m}^2$ (cone bag is mesh material of size 6 mm). The collection of samples with cone-shaped ichthyoplankton nets was carried out according to the standard methodology, the amount of migrating fries was calculated according to the following formula:

$$C_{1000} = N * 1000/Q$$

 $Q = S * V * t$
Here,

 C_{1000} – the number of fries in 1000 m3 water volume, units; N – the number of fries in the sample, number; Q – the volume of water passing through the conical ichthyoplankton net, m³; S – the area of the entrance of the conical ichthyoplankton net, m²; V – water flow rate at the entrance of the conical ichthyoplankton net; t – time of fishing with conical ichthyoplankton net, seconds.

The analysis of the materials collected as a result of the conducted researches showed that Gudyalchay, although not of great importance in fisheries, is one of the rich rivers in terms of species diversity. The ichthyofauna of Gudyalchay includes 32 species and subspecies. Fish species common in the river can be attributed to 3 ecological groups fresh water, transient and semi-transient groups. According to the distribution in the basin, 10 species are distributed in the mouth of the river, 13 species are distributed in the lower, 6 species in the lower and middle, 1 species is distributed only in the upper reaches, and 3 species are distributed along the entire river.

CHANGES IN THE FAUNA OF BUMBLEBEES IN BELARUS DURING THE LAST CENTURY

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Keywords: bumblebees; cuckoo bumblebees; the fauna of Belarus.

The purpose of the work is to study the dynamics of the fauna of bumblebees and cuckoos in the Republic of Belarus based on the analysis of literature data and our own research.

The work of O.V.Prishepchik indicates 32 species of bumblebees already registered for the Republic of Belarus - on seed crops of earlyripening and late-ripening red clover in the Minsk region [Prishepchik, 2000]. Based upon the field studies conducted in 2017-2021 years on the territory of Vitebsk, Minsk, Gomel, Brest, and Mogilev regions of Belarus, 23 species of bumblebees and 8 species of cuckoo bumblebees have been registered. The analysis of changes in the structure of the fauna of bumblebees and cuckoos in the central part of the Republic of Belarus, carried out by us, showed a significant depletion of the fauna of the genus Bombus in the study area. The B. muscorum species is currently listed in the Red Book of the Republic of Belarus. Based on the results of our collections, the dominant species on the territory of Belarus are the species of bumblebees B. pascuorum, B. lucorum, B. lapidaries. from cuckoo bumblebees - P. bohemicus, P. campestris, P. barbutellus. B. sylvarum, B. muscorum, B. hypnorum, B. jonellus, B. ruderarius (5 species) are classified as subdominant species. Other species were found much less frequently or in single specimens. Based on the obtained data, two species of bumblebees (*B. muscorum* and *B. lapidarius*) were classified by us as predominantly open space species, B.pascuorum as a forest species, B. lucorum, and B. soroeensis as eurytopic species.

A great attachment of females and drones of bumblebees to leguminous plants, primarily on red flowers, as well as the preference of males of both genera of the flowers of plants of the Asteraceae family, but with highly located inflorescences were noted [Khvir, 2019].

SCANNING ELECTRON MICROSCOPIC STUDY OF TESTATE AMOEBAE (AMOEBOZOA, TESTACEA) FROM LANKARAN FRESHWATER BASINS

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Keywords: protozoans; SEM; ultrastructure; shell.

During the 2013-2021 years testate amoebae fauna of different freshwater basins in the Lankaran natural area has been studied.

Testaceans are ameboid protozoans that inhabit a shell. They are found worldwide in soils, wetlands and freshwater. These microorganisms are of ancient origin. About 2000 species have been described, a number that can be easily doubled with comprehensive studies [Smith *et al.*, 2007].

The research was conducted in more than 30 water bodies of the Lankaran natural area, and the morphological and ecological characteristics of testate amoebae were investigated. More than 2200 water samples were collected and processed throughout the study.

Testate amoebae shells exhibit a broad range of micro-scale morphology. The ultrastructure of all species was studied using a scanning electron microscope JEOL JCM-6000 (Japan) and micro photos were taken. The method we used for this purpose allowed us to protect the studied shell surface to be examined with as little change in a spatial arrangement as possible. Before the scanning process, the specimen has been dehydrated and dried. After the drying processes, the specimens were coated with a layer of gold to ensure adequate production of secondary electrons and avoid charging [Brunk *et al.*, 1980]. In this way, internal structures are directly related to surface morphology. The coating is achieved by ion sputtering in the SMART COATER device.

Overall, 126 species and subspecies of testate amoebae belonging to 11 families were recorded [Tahirova et al., 2020]. They are as follows: 17 species of Arcellidae, 18 species of Centropyxidae, 2 species of Plagiopyxidae, 6 species of Trigonopyxidae, 70 species of Difflugiidae, 2 species of Lesquereusidae, 1 species of Heleoperidae, 3 species of Pseudodifflugiidae, 3 species of Euglyphiidae, 3 species of Cyphoderiidae, 1 species of Cryptodifflugiidae. 8 species and subspecies were recorded for the first time. Representatives of the families Arcellidae (13%), Centropyxidae (14%), and Difflugiidae (55%) dominated in all studied wa-

ter bodies. The maximum abundance of testate amoebae was recorded in summer (7.4 thousand ind/dm²) and the minimum total number in winter (0.1 thousand ind/dm²) [Tahirova, 2014, 2020].

SPECIES COMPOSITION OF MICRO- AND MACROZOOBENTHOS OF GUMBASHI AND BOLADI RIVERS OF LANKARAN NATURAL REGION

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Keywords: species; river; fauna.

The rivers of the Lankaran Natural Region start from the Talish Mountains and they have own great economic potential. Among these rivers, Gumbashi and Boladi rivers join Lesser Kyzylagach bay. They play an important role in the reproduction of fish species in the bay. In this regard, it is important to study the micro- and macrofauna of the rivers. It is obvious that micro- and macrofauna actively participate in the generation of biological productivity of water basins, and serve as biofiltrators in the natural purification of water.

Most of the species play a major role in the food chain of the ecosystem, one serves as a consument for another one. Some species are the first and secondary interim owners of parasites. Therefore, hydrobiological samples were collected from the mentioned rivers in 2021 for the seasons and analyzed in the laboratory. 52 species of organisms belonging to 7 systematic groups (Mollusca, Amphipoda, Odonata, Ehemeroptera, Coleoptera, Diptera, Chironomidae) were found in Gumbashi river. Among the species found, Costatella integra, Pontogammarus sarsi, Enallagma cyathigerum, Limnochironomus nervosus, Laccophilus hyalinus, Hydrometra stagnorum and others are dominant. The maximum development of the species was recorded in spring and summer, and the minimum in winter [Aliyev, 2021]. During the study of the river, 35 species of macrobenthic organisms were recorded. P.elephantilus, P.conicus, Didinium nasutum, Loxophyllum helus, Chaenea vorax, Tetrahymena pyriformis, Paramecium caudatum, *Uronema marinum, Euplotes eurystomus*, etc. species differ in the intensity of occurrence.

64 species of macrobenthic organisms (Aelosoma tenebrarum, Hirudo medicinalis, Plumatella emarginata, Valvata pulchella, C.purpurea, C.pubera, Gammarus lacustris, Diplodocus despiciens, Lestes sponsa, No-

tonecta lutea, etc.) belonging to 10 systematic groups (Mollusca, Hirudinea, Ephemeroptera, Hemiptera, Amphipoda, Odonata, Hydracarina, Coleoptera, Diptera, Chironomidae) were found from Boladi river. Also, 46 species of microbenthic organisms were recorded for the river. We tried to provide information on the distribution of main microbenthic groups for the seasons based on the ciliates species. Because ciliates are one of the leading groups in microbenthos.

The number of species increases from winter to spring, having its highest species complex in spring (40 species), and decreases to 20 species in summer and begins to increase again in autumn. More precisely, there are two minimums (winter and summer) and two maximums (spring and autumn) in the development of ciliates. While the formation of winter minimums is associated with low temperatures, the summer minimum can be achieved due to high temperatures and the associated increase in the amount of hydrogen sulfide gas in the basins. The basis of the winter complex are species such as *Coleps hirtus, L.helus, P.caudatum, P.elephantilus, F.elliptica, Stylonychia mytilus*; the basis of the spring-autumn complex are 30-35 species (*P.conicus, D.nasutum, L.helus, Ch.vorax, T.pyriformis, F.elliptica,* etc.), and the basis of the summer complex are *D.nasutum, T.pyriformis, S.teres, S.minus, Metopus contortus, M.es.* The number of species encountered during the whole year varies between 15 and 35 species.

FLIGHT PHENOLOGY OF WASPS BELONGING TO THE FAMILIES VESPIDAE AND SPHECIDAE IN LANKARAN TERRITORY

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Keywords: wasp; month; decade; summer.

Fold-winged and digger wasps as entomophagous have a certain significance in reducing the number of agricultural crops. These wasps play an especially important role in the pollination of fodder and medicinal plants. Flight activity is one of the important factors in the biology and ecology of insects, including vespids and digger wasps.

In contrast to vespid wasps, in which wintering occurs at the adult stage in a fertilized female, in digger wasps, in most cases, the prepupa hibernates, and sometimes at the adult stage [Kazenas, 2016].

The main method is the non-selective capture of species in various habitats. Analysis of the studied objects on the territory of Lankaran showed that

the maximum seasonal activity of adults of certain species occurs in different summer months. Vespids and sphecids appear in the surveyed area mainly in the third decade of April.

Vespa crabro, Vespa orientalis, related to Vespids, S.maxillosus from digger wasps of the genus, A.heudeni from the genus Ammophila were found by us in the second decade of April. Wasps species of the genus Paravespula - P.vulgaris, Paravespula germanica, P.chinensis, P.gallicus, species of the genus Polistes - Sulcopolistes sulcifer, digger wasps species of the genus Sceliphron – A. sabulosa, A. terminata, S. destillatorium, species of the genus Cerceris - C.arenaria, C. quadrimaculatus were observed in the third decade and the beginning of the second decade of May. All these species continue their flight activity in May and June. Dolichovespula sylvestris was found in the forest in the first decade of May.

In June, due to the arrival of warm weather and the abundance of flowering plants, a large number of vespids and digger wasps have been recorded. These include *Polistes nimpha, Sulcopolistes atrimandibularis, Sulcopolistes semenovi* and from digger wasps *A.campestris, A.dives*.

Vespa crabro, Vespa orientalis, Paravespula germanica, S.destillatorium, A.sabulosa are represented by the highest number. According to our observations, vespids and digger wasps reach their maximum abundance and flight activity in the second half of July.

In August, the number of wasps decreases, and no species are found. In September, the flight activity of most species decreases and a representative of the genus *Ammophila* occupies a dominant position among **species**. Thus, vespids and digger wasps are most diverse in May-August, with a maximum abundance in June-July.

SPECIES COMPOSITION OF MACROZOOBENTHOS OF LESSER KYZYLAGAJ BAY

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Keywords: macrozoobenthos; hydrobiology; Kyzylagaj bay; biomass.

Almost more than a half-century has passed since the first hydrobiological studies were conducted in Lesser Kyzylagaj bay, and 40 years passed since the studies focused on macrozoobenthos.

The objectives of this study are to determine the changes in the bay and the composition of its fauna, to reveal the factors causing those changes, and to provide their scientific justifications.

The study of macrozoobenthos of Lesser Kyzylagaj bay, as mentioned above, was conducted during the years 2020-2022, for the seasons. The collection and processing of materials in the laboratory were carried out by the generally recognized methods in hydrobiology [Jadin, 1956].

As a result of quality (165) and quantity (up to 70) analysis of materials collected from various parts and ranging biotopes of the bay (from the silt and sand biotopes and among the plants) 80 species and forms of invertebrate fauna were recorded in the macrozoobenthos of Kvzvlagaj bav. 5 of the recorded species ((H.orientalis, S.vulgatum, E.vulaata, H.staanorum, O.caucasica caucasica) are new for the fauna of the bay. According to the number of species in macrozoobenthos, chironomid larvae (26 species) dominate. They are followed by dragonfly larvae with 9 species, annelid worms with 7 species, and mollusks (4 species). Due to intensity of encounter (IE) in macrozoobenthos, those species are distinguished: from annelid worms - T.tubifex (I.E. 70 %), O.serpentina (I.E. 65%), from leeches - H.orientalis (I.E. 40%), from mollusks - P.planorbis (I.E. 45 %), from dragonfly larvae - C.scitulum (I.E. 75%), S.metallica (I.E. 75%), from Mayfly larvae - O.macrura (I.E. 70%), from true bugs - C.dentipes (I.E. 70%), C.affines (I.E. 65%), from chironomid larvae - C.conjugens (I.E. 65%), Ch.plumosus (I.E. 75%), *P.ferrugineus* (I.E. 70%), *Ch.thummi* (I.E. 45%), and *Culicoides* sp.

Over the study years, the total number of species found in macrozoobenthos was close to each other, in particular, 39 species in 2020, and 40 species in 2021. The number of macrozoobenthos species varies depending on the season as follows. The maximum number of species (44 species) appears in spring, and the minimum (30 species) in winter. The reason why the number of species in winter is 14 units less than in spring is most likely due to the small amount of material collected in this season. In summer and autumn periods, 41 and 39 species were recorded, respectively.

The following species are encountered almost in all seasons of the year in lesser Kyzylagaj bay, including such species as *D.dorsalis. O.serpentina, T.tubifex, H.orientalis R.auricularia, P.planorbis, C.scitulum, C.pulchellum, A.grandis, S.metallica, L.depressa, E.vulgata, O.macrura, C.dentipes, C.affinis, N.lutea, H.fuscipes, P.lauterborni, C.conjugens, Ch.plumosus, Ch.thummi, P. nubeculosus, Procladius ferrugineus, and Culicoides* sp.

Whereas, among the species that are encountered for the entire year, species like *T.tubifex, H.m.orientalis P.planorbis, C.affinis, N.lutea,*

C.conjugens, Ch plumosus, Ch.thummi, P. nubeculosus, Pr. ferrugineus are found in all the parts of the bay and in abundant quantities. Those species may also be referred to as the representative species of macrozoobenthos in the bay.

IMPORTANT RESULTS OF THE STUDY OF HELMINTH FAUNA OF SHEEP IN THE ABSHERON REGION

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Keywords: helminth; Absheron peninsula; Khizi; sheep.

To study the distribution of the main causative agents of sheep helminthiasis in different landscape-ecological zones of the Absheron region, the location and grazing areas of private farms engaged in sheep breeding in different villages and settlements, the number of sheep, etc. were determined in 2015-2020. The permission of entrepreneurs was received to conduct research in farms. Coprological examination and complete helminthological dissection were performed with samples collected from these farms, helminths were collected and preserved [Mammadov, 1986].

The major helminth fauna in sheep in the private and farmer farms of the Absheron region was found to consist of 18 helminth species (4 of them are geohelminths and 14 are biohelminths), with 4 species belonging to trematodes, 6 species to cestodes, and 8 species to nematodes. Trematodes: Fasciola hepatica, F.gigantica, Dicrocoelium lanceatum, Paramphistomum cervi; Cestodes: Moniezia expansa, M.benedeni, Taenia hydatigena, T.ovis, Multiceps multiceps, Echinococcus granulosus; Nematodes: Protostrongylus hobmaieri, P.kochi, P.railleti, Muellerius capillaris, geohelminths Trichocephalus ovis, Chabertia ovina, Haemoinchus contortus, Dictyocaulus filaria.

Higher invasion levels were identified for *Tr.ovis* (43.2%, 1-53 samples), *E.granulosus* (39.2%, 1-18 samples), *H.contortus* (35.0%, 2-56 samples), and they were considered the dominant helminth species of the region.

The extensiveness and intensity of the invasion were found to be higher in the Khizi region than in the Absheron peninsula. According to coprological examinations, IE was 19.4% in the Absheron peninsula, 31.4% in the Khizi region. Based on the complete helminthological dis-

section, in the Absheron peninsula, IE was 17.7% and II was 1-64 samples, and in the Khizi region, IE was 29.0% and II was 1-83 samples [Agayeva, 2020].

High extensiveness and intensity for all main helminths in the region were recorded in the low mountainous belt. The average infection rate for main helminths was 15.1% (1-51 samples) in the plains, 19.2% (1-64 samples) in the foothills, and 37.1% (1-83 samples) in low mountainous areas. The main helminths in domestic and wild animals were investigated, and it was found that 10 species of domestic animals and 16 species of wild mammals were involved in the development cycle and distribution of helminths to various degrees.

It was found that a 6.0% solution of sodium hydroxide had a higher desi invasion effect against the eggs of dictyocaulus and haemonchosis pathogens and was highly effective in destroying 91.4% of helminth eggs (*H.contortus* and *D.filaria*). The application of this solution in the farm resulted in the economic efficiency of 13 manats 60 kopecks per one sheep, which makes it expedient to use 6.0% NaCl. This substance has a high deinvation effect and is practically convenient and profitable [Agayeva, 2021].

NUTRITION AND TEMPERATURE EFFECTS ON THE GROWTH OF TETRANYCHUS CINNABARINUS (ACARIFORMES, TETRANYCHIDAE)

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Keywords: Absheron district; tetranychid mite; spider mite; vegetable crops; herbaceous plants.

During our research of the effects of temperature on vegetable crops and herbaceous plants on some ecological features of *T.cinnabarinus* in the climate of the Absheron district, it was found that the fertility and lifespan of this pest are closely related to the state of plants and the temperature of the environment. The highest egg growth occurs in cucumber and bean plants for vegetables and in plantain for wild plants, which plays an important role in the natural reservation of pests.

The growth and reproduction rate of tetranychid mites mostly depends on the ecological conditions, primarily, on the condition and quality of edible plants and the climatic features [Shek, 1936; Kurbanov,

1955] of the habitat. The fertility of spider mites on cotton plants has received relatively adequate research. According to Tibilova [Tibilova, 1935], fertility of female mites in the climate of Central Asia can reach up to 610 eggs, with an average of 140 eggs, and 80-100 eggs in Georgia [Siyazov, 1930]. According to Rekach, and Stregulina (1932), this number can reach up to 130 eggs per female. According to G.G.Kurbanov [Kurbanov, 1955; Muradova *et al.*, 2019], in Azerbaijan, one female mite on a cotton plant can lay from 42 to 215 eggs.

The literature provides no information on the fertility of these mites on vegetable crops. In this regard, we studied the fertility of *T.cinnabarinus* on vegetable crops and herbaceous plants in the climate of the Absheron district both in the insectarium and in nature. Experiments and data analysis have been carried out in accordance with Weinstein, Livshits' technique [Livšits, 1971]. The fertility of the mites has been studied on the following vegetable crops - cucumber, eggplant, beans, and on the herbaceous plants - marshmallow, bindweed, plantain, and sow thistle.

Our findings revealed that the fertility of *T.cinnabarinus* on vegetable crops and herbaceous plants varies significantly depending on the edible plants. Thus, having regarded the vegetable crops, the cucumber plant was found to be the most suitable for their reproduction, on which the bite has the highest average daily temperature of 3-4°C higher than in northeastern Azerbaijan.

A BRIEF HISTORY OF THE STUDY OF THE TREMATODE FAUNA OF FRESHWATER MOLLUSCS

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Keywords: trematodes; helminths; Varvara reservoir; cercariae.

Trematodes of helminths, distinguished for being seriously pathogenic to humans and animals in many parts of the world, as well as in the territory of Azerbaijan, have been one of the noteworthy research targets of scientists and specialists for almost 200 years. The study of larval stages, particularly the cercariae, developed in molluscs, which are the first intermediate hosts of trematodes, is of great scientific and practical interest as it enables an effective assessment of the actual parasitological situation in the study area in a short time and carrying out

parasitological monitoring. Thus, while the sexually mature forms of trematodes with a very complex life cycle parasitize on organisms from all systematic groups, the development of cercariae with more reliable species properties only in specific mollusc species increases the interest in such type of research.

Therefore, the complex zoo-parasitological study of parthenites and cercariae of trematodes using the *Melanopsis praemorsa* mollusc, widespread in the Varvara reservoir, as the first intermediate host is relevant both from a zoological and parasitological point of view.

In the second half of the 19th century, many prominent scientists dedicated their works to the study of trematode life cycles. The studies have concluded that there have been relations between the larval and adult stages of trematodes, and it has been established that the cercariae, which were studied, described, and presented as free-living organisms, have been the larval stage of trematodes. The collected materials have set up a base for M.F.Lüe to establish a very practical classification system based on the free-living cercariae stage parallel to the adult stages of trematodes.

Until the 1970s, the trematode fauna of freshwater molluscs in the Caucasus had been unexplored. Information about the trematode fauna of molluscs spread in this area consisted of partial information on the cercariae of molluscs of several water basins of Eastern and Western Georgia [Djavelidze, 1973; Olenev, 1972; 1979].

The systematic study of trematode fauna of freshwater molluscs of Azerbaijan has been started in the middle of the 1970s on the recommendation and under the guidance of prof. T.K.Mikayilov in the laboratory established by him at the Institute of Zoology. The only study on this relevant direction so far in Azerbaijan had been a dissertation on trematode larvae of freshwater molluscs of the Lankaran region conducted by F.B. Garayev [Garayev, 1968].

A comprehensive zoo-parasitological study of the trematode fauna of freshwater molluscs of the *Melanopsis* genus, widespread in Azerbaijan, has first carried out by A.A.Manafov [Manafov, 1990, 2010, 2012]. As an outcome of the systematic studies since 1982, the specific trematode fauna of the *Melanopsis praemorsa* molluscs has been analyzed in detail and based on the study of the micromorphological structure of different developmental stages of these parasites (cercariae, metacercariae, adolecer caria, sporocyst, rediae) more than 30 species of trematodes new to science have been described. The information has been

provided on natural and mixed foci of more than 10 trematodes of significant pathological importance for humans and carnivores.

DEVELOPMENT OF A NEW WAY TO INCREASE THE VIABILITY OF SILKWORM IN AZERBAIJAN

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Keywords: silkworm; a new trial, antherin; physiological effects; viability.

Despite the high biotechnological indicators of silkworm cocoons obtained in Azerbaijan in recent years, their intolerance to the effects of various diseases and unfavorable conditions in the process of processing, feeding period of caterpillars, egg-laying, especially during hibernation period remains the main limiting factor. Even if optimal hydrothermal conditions are maintained on farms, the viability of eggs and caterpillars is low. This is due to the influence of pathogenic microorganisms since various microflora (with a predominance of bacterial nature) accumulate on the eggs at the initial stage of development of mulberry silkworm. It is known that the protection of mulberry silkworm eggs from pathogens is carried out by various physical and chemical methods, unfortunately, it is often not effective since the physiological response and biochemical reactivity of various species are different.

Since the end of the XX century, the combination called antherin and considered a medicinal extract has been tested on oak silkworms in Ukraine and Belarus [Denisova, 2007; Guliyeva *et al*, 2019]. These researches have been conducted in Azerbaijan on mulberry silkworm since 2021 at the Department of Zoology and Physiology of Baku State University and are currently ongoing. The aim is to determine the physiological effect of other developmental phases after treatment of the bioextract of antherin (extract obtained from pupae) on the caterpillars of the V age of the mulberry silkworm. The method of preparing an extract from silkworm pupae is carried out according to V.A.Radkevich and S.I.Denisova [Radkevich, 1983; Denisova, 2007].

At the initial stage of the research, the influence of antherin on the development of eggs and ovulation was studied. It has been established that the hatching of caterpillars from eggs (March 27, 2022, at 21° C and 64% relative humidity) treated with pupae extract (5%, 10%, and 20% water solutions) occurs in all series. However, compared with the con-

trol variant (mortality 57.1 %), this indicator varies depending on the dose and duration of action, i.e. dose reduction from 20 % to 10 % increases the survival effect. It was revealed that the treatment with water solution pupae extract of eggs in experimental variants reduces mortality to 12.7 %. The effect of the compound on caterpillars is currently being investigated.

RESEARCH ON THE ZOOPLANKTON OF THE LESSER KYZYLAGAJ BAY IN MODERN CONDITIONS

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Keywords: bay; zooplankton; Rotatoria; Copepoda; Cladocera.

Lesser Kyzylagaj bay is located on the south-western coast of the Caspian Sea, in a part of the Lankaran economic region. It's been long times since there have been operating fisheries. Recently, the environmental conditions of the bay have changed, and its connection with local rivers has become weaker. The decrease in water balance has paved the way to the shallowing and the increase in the process of siltation in the bay. For this purpose, we have collected and analyzed the samples by seasons on the species composition of zooplankton in the bay in 2020-2022 years. The samples were collected from different parts of Lesser Kyzylagaj bay – from the open spaces, among the bushes, from canal and fishing line areas. The samples have been collected using plankton net. The species of zooplankton were identified by referring to different reference books. As a result, 38 species of zooplankton belonging to 3 systematic communities have been found in the zooplankton of the bay. 16 species belong to rotifers, 8 species to Copepoda, and 14 species to Cladocera. Thus, rotifers comprise 42% of zooplankton, Copepoda 21 %, and Cladocera 37 %. The research was carried out based on the method of V.I.Jadin [Jadin, 1956].

In 2021, there has been an increase in the development of zoo-plankton communities. For the most part, it has been observed in summer and autumn, and the least in winter. Rotifers have seemed to predominate in these seasons. *Synchaeta pectinata, Asplanchna priodonta, Brachionus calyciflorus* species from rotifers, and *Daphnia pulex* from cladoceran have been seen in all seasons.

The study of species composition, quantity, and development dynamics of zooplankton is of utmost importance in determining the productivity of plankton phagous fishes. Currently, favorable conditions have been created for feeding baby fishes in Lesser Kyzylagaj bay. Moreover, it is necessary to reinforce the fight against aquatic plants to improve the feeding of baby fishes.

MICRODISTRIBUTION OF FREE-LIVING CILIATES IN THE AGZIBIR LAKE

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Keywords: Agzibir; ciliates; biotope; species diversity.

Free-living ciliates are a very important link in the food chain in water and soil biocenosis. As primary consumers, ciliates play an important role in the transformation of organic matter in nature. According to its importance, special studies on the biodiversity of free-living ciliates in different biotopes in the Agzibir lake have been carried out.

Samples were collected in various biotopes of Agzibir lake. A total of 380 samples were taken and processed from 8 stationary points.

To quantify the number of free-living ciliates, we used a universal method of direct counting of non-concentrated samples. The essence of this method is simple, the ciliates are counted in vivo in 3 or 5 ml of water by the Bogorov chamber. This process is repeated 3-10 times, the average value is found for each species, and the total number in the water basin is calculated in 1 dm² of soil for benthic species and 1 liter of water for plankton species [Alekperov *et al.*, 1996].

During the study period, 169 species of free-living ciliates were recorded. Among these, 34 species were registered for the first time in the fauna of the Caspian Sea. The lowest species diversity (46 species) was observed in plankton. In the benthos, ciliate communities have been studied in different biotopes. In order, 58 species were recorded in the sandy biotope, 80 species in the silty-sandy biotope, and 72 species of ciliates were found in a gray silty biotope. The maximum species diversity was observed (with 84 species) in a biotope rich in plant remains. 66 species of free-living ciliates were found in black mud with sapropelic areas. Also, 71 species of free-living ciliates were observed in

the periphyton and 79 species in the phytociliocenoses [Alekperov *et al*, 2020].

To compare the coastal zone of Lake Agzibir, we selected two areas: the first is an area without coastal vegetation cover and the second is an area heavily overgrown with algae. The results obtained showed that free-living ciliates are fairly evenly distributed in areas without vegetation. And the difference in the total number of individual samples at a distance of 30 cm from each other usually does not exceed 25-40 samples/l. This situation is explained by the shallowness, which leads to a relatively uniform distribution of free-living ciliates both vertically and horizontally.

A similar comparative analysis of the total number and species composition of free-living ciliates in the coastal zone heavily overgrown with algae (phytociliocenosis) showed that the distribution in such a biotope both vertically and horizontally is characterized by extremely sharp jumps in both the total abundance and species composition.

V. SYSTEMS' ECOLOGY

THE REGULATORY FUNCTION OF SOIL ORGANIC CARBON IN GLOBAL CLIMATE CHANGE

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Keywords: climate change, soil organic carbon; soil ecology; digital map; GIS. The study of soil components has always been in the focus of researchers. As is known, soil organic matter is one of the decisive factors in terms of soil fertility, productivity and food production. It is no coincidence that soil carbon is one of the main topics of discussion at all international conferences on climate change held under the auspices of the UN (FAO. 2020). In order to know the distribution of organic carbon in soils in different continents and countries, it was necessary to prepare a Global Soil Organic Matter Map (GSOCmap) (Minasny et al., 2013). For this purpose, in 2016, FAO began to implement the GSOCmap project within the framework of the UN Global Soil Partnership program. Azerbaijani soil scientists actively participated in this project, in which 150 soil scientists representing 110 countries took part, and in 2017 they prepared the first member carbon map of soils of Azerbaijan by FAO requirements (FAO, 2017). By FAO recommendations, Digital Soil Mapping (DSM) was used to allow for a more comprehensive geospatial analysis of soil properties. The development of soil property maps using DSM is spatially flexible. For different soil properties (e.g., soil nutrient concentration and stocks, carbon, heavy metals, pH, cation exchange capacity, soil physical properties such as particle size and bulk density, etc.), different depth classes and spatial resolution can be modeled. depending on project and mapping objectives and available input data (FAO, 2018). The soil organic carbon map developed using GIS technologies used humus and bulk density as soil indicators. The map legend is divided into appropriate gradations, and the areas corresponding to each gradation have separate layers of information on the map. This map is part of the first global map of soil organic carbon published by FAO in 2017. The map presented provides reliable information about the carbon stocks in the top 0-30 centimeters of soil. The final map shows that the 0-30-cm soil layer on Earth contains approximately 680 billion tons of organic carbon, twice as

much as the atmosphere. The FAO calculates that global vegetation is 560 billion tons, 120 billion tons less than the carbon stock in the soil. The degradation of one-third of the world's land is now a major concern not only for food security, but also for global climate change. Restoring degraded land could sequester up to 63 billion tons of carbon beyond the atmosphere. As part of the global ecosystem, measures based on scientific principles must be continued to prevent the degradation and desertification of Azerbaijani lands [Ismayilov *et al.*, 2020]. Occupying twenty percent of Azerbaijani lands for 30 years is not only a material loss. Not working these lands for 10 years, plundering, cutting down the forests, and destroying vegetation intensified degradation processes and led to a sharp decrease in organic carbon stocks in the soil and additional emission of carbon dioxide into the atmosphere. This has not only affected the ecological condition of our republic, but has also caused an ecological imbalance on a global scale.

In conclusion, it should be noted that the protection and increase of soil organic carbon stocks against the background of modern global climate change is one of the most pressing environmental issues and needs to be studied in more detail.

THE IMPORTANCE OF SYSTEMIC ENVIRONMENTAL RESEARCH FOR THE SUSTAINABLE ECONOMIC AND SOCIAL DEVELOPMENT OF AZERBAIJAN

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Keywords: biomonitoring; bioindication; biotesting; sustainable development.

The successful economic policy pursued during the independence allowed Azerbaijan to achieve high economic growth rates. At the same time, the development of the economy began to be carried out without serious consideration of ecology and, the possibilities of the environment, the permissible industrial and economic loads on this environment. These contradictions have led to an aggravation of environmental problems in the country: deforestation, depletion of natural resources, lack of fresh water, pollution of the atmosphere and soil, extinction of animal and plant species, degradation and erosion of soil, etc. There-

fore, a special place in the system of the country's most critical problems belongs to problems in the field of ecology.

Today Azerbaijan needs a well-developed, scientifically based environmental legislation that should contribute to protecting the natural environment. This makes it necessary to conduct comprehensive environmental studies on the territory of the Republic. Along with other areas of environmental research in the country in recent decades, much scientific work has been carried out in biomonitoring, bioindication and biotesting of natural, and technogenic landscapes. [Ismaylov et al., 2002; Mammadova, 2008; Hajiyeva et al., 2018; Samedov, 2018]. However, it should be noted that most of these studies are fragmented and do not cover all landscape components. Therefore, carrying out complex systematic studies in the field of biomonitoring, bioindication and biotesting of landscapes as a single biosystem in a particular soilclimatic zone is of scientific and practical importance. Such systematic studies will allow obtaining an objective assessment of the ecological state of the entire landscape biosystem and, on this basis, building an effective modern system for managing them, considering the requirements of sustainable development. The effective management of ecological and economic systems and the successful implementation of environmental policy are possible only if there is reliable, most complete, and timely information about the availability and condition of natural resources, the quality of the environment and its pollution, about the causes and consequences of emerging adverse environmental situations. Moreover, the means for obtaining and processing information, which serves as the basis for forecasting the development of the ecological situation and developing environmentally safe and cost-effective decisions, is a set of systematic studies in the field of biomonitoring, bioindication, and biotesting. The critical element in this system is assessing the impact of the economic system on the environment when preparing and making decisions on the socio-economic development of society and the development of programs and proposals for optimizing the environment, taking into account the environmental requirements of national legislation.

THE PROBLEM OF THE NEGATIVE IMPACT OF ANIMAL WASTE ON THE ENVIRONMENT

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Key words: ecology; biogas; microorganism; methane.

Currently, there is an acute issue of disposal of production and consumption waste generated at livestock enterprises, preparation, processing of huge volumes of manure and manure produced at the complexes, which are potential sources of anthropogenic impact on the environment. At the end of the 20th century, the increase in the large number of livestock in livestock farms in connection with the transfer of animal husbandry to an industrial basis was of a global nature and was noted in many countries of the world. One of the directions of the economic development of society is the development of resource-saving technologies. Such technologies ensure the production of products with the lowest possible consumption of fuel and other energy sources, as well as raw materials, materials, air, water and other resources for technological purposes. They include the use of secondary resources, waste disposal, as well as energy recovery, and a closed water supply system. Allow to save natural resources and avoid environmental pollution. Proper use of agricultural waste is a global and important problem in our world. On the one hand, it is associated with the possibility of utilizing biomass energy and obtaining liquid and gaseous fuel (biogas) from it, on the other hand, it helps to prevent pollution of water bodies, contamination of the soil cover with pathogenic microorganisms and helminths that are in the manure runoff of livestock farms. Many scientists argue that significant damage to nature comes from animal husbandry. Every year, tons of manure and dung are accumulated on farms. Many industries do not have wastewater treatment plants - all this has a detrimental effect on the environment. In order to prevent nitrate and microbial contamination of soils, air, surrounding vegetation, surface and ground waters, it is necessary to follow the technologies for processing and storing animal waste [Alivev et al., 2012].

Manure contains many pathogenic bacteria. When waste is accumulated without processing, it can be a source of negative impact on humans and animals and lead to various diseases. Great damage to the environment is possible from large livestock production. In order to fol-

low modern trends, production data must be modernized. Most of these enterprises install biogas plants based on the production of biogas and biofertilizers by anaerobic digestion of animal waste under the influence of microorganisms [Hajiyeva *et al.*, 2018]. Biogas production helps prevent methane from being released into the atmosphere, the best way to prevent global warming is to capture methane. Consumption of such gas reduces the impact of methane. The main activity of livestock farms and poultry farms, along with the production of meat, milk, eggs and their products, should be aimed at greening production and transferring enterprises to waste-free technologies.

In general, the fermentation of organic waste can satisfy a large part of the energy needs of the population and contribute to resource conservation. Bioenergy installations save resources and remove part of the energy deficit in agricultural areas, in the field of small-scale industrial activity, in everyday life, and can become an essential element in the system of a regional energy and environmental strategy. The problem of disposal of waste from livestock complexes is particularly relevant and unresolved in Azerbaijan. At present, a large amount of manure and dung masses accumulate around many livestock and poultry enterprises, which, if the problem of their disposal is properly solved, can provide additional profit and, at the same time, turn farms into practically waste-free production. In the meantime, the functioning of large livestock, poultry complexes and farms endangers the ecological well-being of the environment due to the lack of organized work on the disposal of organic waste.

HAKARICHAY BASIN LANDS AND USE CONDITION

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Keywords: land; Hakarichay; forest; agriculture.

The Hakarichay basin, located in the southeastern part of the Small Caucasus, is represented by the Mikhtoken Range in the north, the Garabagh volcanic plateau in the north-east, the Bargushad and Susandag rivers in the south, and the Silgaran-Suyrgan in the south. In the south-east, it joins the Araz River gorge. The relief of the basin was

mainly techno-denudation, and the canyon was severely divided by erosion-tectonic river valleys.

The Hakarichay basin is located at an altitude of 300-3600 m above sea level. The average altitude reaches 1650 m. Such heights created conditions for the formation of vertical zones and complex mountainous slopes. The forest lands, which are the main research areas, cover 800-2,200 m and sometimes 2,300 m above sea level. The riverbed and its aquifers played an important role in the fragmentation of the relief. The main air masses affecting the climate of the Hakarichay basin are hot air and local circulation over the Iran, Iraq and Arabian peninsula. Due to the complex orogeomorphological structure, the air temperature in the basin is unevenly distributed.

In the 1970s, forests, which created a special mountain-forest landscape in the basin, covered 30% of the total land area. Such forests are mainly composed of oak, hornbeam, maple, ash, linden and other trees. 58% of the forests are composed of oaks, most of which are Eastern and Iberian oaks. Iberian oak grows better on skeletal soils on the slopes at an altitude of 1400-1800 m.

The process of soil formation in the Hakarichay basin includes three main bioclimatic zones-mountain-meadow, mountain-forest and steppe. Bioclimatic conditions have a major impact on the soil cover and ensure the formation of a specific soil cover for each zone. The economic activity of people in the Hakarichay basin also had a strong impact on the process of land formation. Thus, it is almost impossible to find a natural area in the region that is not affected by human economic activity.

M.E.Salayev distinguished the following types of soils in the Hakarichay basin: mountain-meadow, mountain-meadow steppe, brown mountain-forest, mountain-forest grassy carbonate, mountain black, brown mountain-forest, gray-brown, alluvial-meadow. These soil types have also developed in the Lachin region.

In the Garabagh Range, on the north-western and eastern slopes of the Mikhtoken Range and Zangazur Range, mountain-meadow soils occupy a large area, the main part of which is used as summer pastures.

A large part of the lands of the Hakarichay basin falls on the territory of Lachin region. If we look at the use of common land resources in Lachin region, in the pre-occupation period, arable lands such as arable lands, perennial crops, hayfields, yards, pastures and meadows were also used. The territory of Lachin region was 183500 ha, of which 17.7% in the pre-occupation period was sown, 0.3% perennial crops, 5.5% hayfields, 1,5

yards, 36.8% More than 46% of the land used for agriculture was pastures and meadows. According to 1992 data, about 19% of the land fund in the region is given as forest, and about 35% as other areas.

If we look at the distribution of agricultural areas in the region by quality group, we can see that about 85% of the area belongs to the I quality group, ie to the category of high quality lands (81-100), 8.5% to the II good quality lands (61-80), 4.5% belonged to III medium quality soils (41-60), 1.2% to IV low quality soils (21-40). It should be noted that all figures are for the pre-occupation period. The inefficient and spontaneous use of the research facility during the 28-year occupation has had a devastating effect on soil fertility and legal use. Based on the information received from the sources, it was found out that the lands of the Hakarichay basin have undergone a large-scale military degradation process. However, for the restoration, efficient use and protection of fertility of these lands, extensive measures have been launched and conditions are being created for the start of scientific research.

ASSESSMENT OF THE GENUS *QUERCUS* L. SPECIES AS BIOINDICATORS OF ENVIRONMENTAL QUALITY IN AZERBAIJAN

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Keywords: bioindication; fluctuating asymmetry; fluorescence; Quercus.

The increasing scale of environmental pollution is an urgent problem in the modern world. The intensive increase of environmental pollution is associated with anthropogenic pressure on the natural environment as a consequence of acceleration from year to year of the pace of urbanization and industrialization. In these conditions, it becomes necessary to monitor the quality of the environment constantly. For an objective assessment of the ecological state of the environment, bioindication is considered an effective method, which makes it possible to assess the degree of environmental pollution comprehensively [Melekhova et al, 2007].

The morphogenetic method is one of the convenient ways to bio indicate the quality of the environment by indicators of organisms' individual developmental stability disruption. In particular, the most

widely used method to study the changes in individual developmental stability is the assessment of variability in the degree of fluctuating asymmetry indicators of leaves' bilaterally symmetrical traits [Mammadova, 2008]. Fluctuating asymmetry analysis characterizes minor disruptions in developmental stability, which are the organism's responses to the state of the environment. Therefore, this method makes it possible to assess both the state of an organism and the ecological condition of the environment.

In plants as phototrophic organisms, one of the most sensitive processes to environmental influences is photosynthesis. An assessment of the state of the photosynthetic apparatus is possible using the method of studying the parameters of chlorophyll fluorescence. The fluorescent methods have also been used in express diagnostics of the state of the environment [Rubin, 2000].

The research aimed to assess comparatively the bioindicative properties of five species of the genus Quercus L.: Quercus. castaneifolia C. A. Mey., Quercus pubescens Willd, Quercus iberica Stev., Quercus macranthera Fish. et C. A. ex Hohen., Quercus longipes Stev., distributed in various environmental conditions in the territories of the Azerbaijan Republic. For this, the fluctuating asymmetry indicators of leaf morphometric traits and the chlorophyll fluorescence parameters of the leaves were studied. Territories differing in the degree of environmental pollution were selected for each species based on the appropriate laboratories' soil and air samples analysis. To determine the degree of individual developmental stability at the ontogenesis of the species 5 bilateral morphometric traits were measured for each leaf. The measurement results were processed by a specially created computer program "STATISTIKA 6" prepared in Java script (ECMAscript 6) programming language [Salvatore, 2002], based on known mathematical formulas [Lakin, 1990]. In addition, to determine the physiological state of plants, the phases of the induction curves of millisecond delayed chlorophyll fluorescence of intact leaves were studied [Abdullayev, 2014].

The obtained results revealed that the species of the genus *Quercus* L. react differently to changes in environmental conditions. Therefore, a comparative analysis of morpho-biophysical studies showed that *Q. pubescens* is the most stable and adapts better to stressful environmental conditions. *Q. iberica* shows the most sensitivity to environmental conditions. This opens up new possibilities for using *Q. iberica* as a bioindicator in the initial assessment and forecasting of the ecological state of forest ecosystems.

MOLECULAR PROBLEMS OF CHEMICALS AND NATURAL NANO-ANTIOXIDANTS AS A POSSIBLE SOLUTION

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Keywords: nano-antioxidants; ROS; pollution.

Chemicals are broadly used for a multiplicity of purposes. Various environmental problems and toxicities caused by exposure to chemicals have become major health concerns [Alharbi *et al.*, 2018]. The incidence of poisoning with chemicals is highly reported due to risky handling practices and their usage. Their health hazards are mostly discussed according to their ability to produce Reactive Oxygen Species (ROS) or alter endogen antioxidant defense [Eftekhari *et al.*, 2018].

Environmental pollution, climatic changes, and unhealthy lifestyles have increased the prevalence of serious and chronic diseases and age-related disorders. In vitro/In vivo toxicological studies showed a robust and straight association between exposure to toxic contaminants and oxidative stress which is lead to an increase in the chance of excess pathologies. Numerous studies have shown the probable role of natural components and their nano-antioxidants as an attractive strategy to defend humans against chemical induce pathologies [Ahmadian *et al.*, 2020]. The antioxidants are manmade or natural, and play a very important role against free radicals, pathogens, and diseases by providing a physiological shield against oxidative stress. Nanoantioxidants comprise nanoparticles functionalized with antioxidants or antioxidant enzymes to function as an antioxidant delivery system and mineral nanoparticles with fundamental antioxidant features.

Numerous pharmacological efforts have been started to improve their beneficial effects. In this concern, the use of nanomedicine has been confirmed to be the superlative line to increase clinical effectiveness and compliance by revolving around the difficulties related to natural-derived pharmaceutical agents. Nanotechnology-based practices show valuable effects in increasing the absorption of poor water-soluble antioxidants and also decreasing the therapeutic dose required to reach pharmacological effects [Green *et al.*, 2019]. Abundant teams

have newly produced, natural metal nanoparticles using numerous Biological resources including fungus plants, bacteria, etc. The application of nano platform-based carriers revealed high permanency and solubility of transported plant-based bioactive agents, decreased early enzymatic deprivation, and upsurge gastric absorption [Eftekhari *et al.*, 2017]. Manufacture of nano-based carriers can be suggesting improved loading volume of drugs, slow-release, therapeutic effectiveness, and low toxicity of the preparations. Even though the outward perspective of natural-based antioxidants delivery systems, numerous significant questions still stay unsolved. This study highlights the role of novel nanotechnological techniques using natural components in the treatment of chemical-induced problems.

THE TREND OF SOIL DEHUMIDIFICATION IN NORTHERN KAZAKHSTAN

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Keywords: soil; humus; dehumidification; degradation; anthropogenic factor.

At the stage of development of virgin and fallow lands, the territories of Northern Kazakhstan turned out to be almost completely plowed, which was largely facilitated by the flat nature of the relief and fertile soils. Along with chernozems, various salt complexes were involved in agricultural turnover. Deforestation of forests in large areas, dump plowing with a plow with a reservoir turnover and harrowing led to the development of deflation, and, consequently, to the processes of dehumidification. Dust storms have been taking place on the territory of Northern Kazakhstan for many years. This phenomenon was especially catastrophic in 1968, as a result of which the arable horizon of soils in significant territories was blown out. These and other factors significantly affect the humus content in soils [Kozyibaeva, 2014.].

In order to study the factors influencing the process of dehumidification of the soils of Northern Kazakhstan and to assess the degree of its depletion, 80 soil samples from 10 sections near Lake Zholdybai were studied.

The objects of the study were the soils of the near-lake semihydromorphic and automorphic landscapes of the moderately moist steppe of Northern Kazakhstan. Our research is based on a comparative geographical method, in which the soils formed on the terraces of the lake were compared. Zholdybai and the adjacent watershed territory. The cuts were laid on the catena, which crosses the eastern shore

According to the conducted studies, it was revealed that the rates of dehumidification are not the same for different genetic types of soils. More significant losses of humus are observed on irrigated soils compared to non-irrigated ones. Humus losses in irrigated soils occur as a result of flow regulation in river deltas and desertification of surrounding areas, as well as irrigation erosion. The dehumidification of pasture soils arose as a result of overgrazing and degradation of vegetation in general, the balance of humus on arable land is negative. Of the total area of non-irrigated arable land, equal to 33.2 million. ha, desolated due to dehumidification to a weak degree - 4.5, moderate - 5.2 and to a strong degree 1.5 million hectares. Of 1.8 million ha of irrigated lands, 0.7 million hectares account for the share of dehumidified lands .The humus content reaches 5.59%, due to its partluvation from horizon A. The enclosing thickness of the horizon ABc - 2.51% humus. According to the content of humus, ordinary chernozems belong to medium humus.

Currently, there is no reliable data on the dehumidification of pasture soils, because long-term observations on the dynamics of humus were carried out only on arable land. It is difficult to determine the loss of humus on sandy forage lands even approximately due to the extreme unevenness of grazing and degradation of pastures, the development of dust storms in different years, the redeposition of part of the blown material into negative relief elements and other reasons.

STUDY OF RADIOPROTECTOR PROPERTIES OF ZINC INOSINATE COMPLEX

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Keywords: inosine; seeds of wheat; Zn inosinate; radioprotective properties .

At present, the acquisition and research of microelement complexes with organic ligands has become one of the most important scientific directions. Numerous studies show that inosine and some of its derivatives prevent the negative effects of gamma radiation on living organisms. Inosine has been shown to have a positive effect on the survival of mice irradiated at critical doses of γ -radiation [Veyalkina *et al.*,

2019]. For this reason, we conducted experiments to obtain and study the radioprotective properties of inosine complexes with a number of biogenic metals (Cu, Zn) [Shamilov *et al.*, 2022]. The purpose of our study was to study the radioprotective properties of the Zn inosinate complex in the model experiments.

The Zn inosinate complex was synthesized according to a known methodology. The composition and structure of the obtained complex were studied by physical and chemical analysis methods [Shamilov et al., 2022]. The objects of research were the seeds of "Tartar" and "Gunashli" wheat varieties. Wheat seeds were irradiated on the K-25 unit in doses of 100 Grav and 200 Grav. The seeds were treated with 0.1%. 0.01% and 0.001% solutions of the Zn inosinate complex before irradiation. The amount of malondialdehyde, chlorophyll pigments, and carotenoids was measured on a Multiskan GO spectrophotometer. Photosynthetic activity was determined on a MINI-PAM device (Germany). As a result of the research, it was determined that 0.01% and 0.001% solutions of Zn inosinate complex had a positive effect on the growth and development of plants under radiation stress. The complex also had a positive effect on the amount of photosynthetic pigments and carotenoids and photosynthetic activity in seedlings grown from wheat seeds exposed to different doses of radiation. We also investigated the maximum quantum yield - Fv/Fm (photosynthesis efficiency). It was found that the treatment of wheat seeds with a 0.001% solution of the Zn inosinate complex before irradiation leads to the normalization of the biosynthesis of photosynthetic pigments and carotenoids, as well as photosynthetic activity. The process of peroxide oxidation of lipids is one of the important indicators of the effect of radiation on living organisms. The 0.001% solution of the complex significantly reduces the amount of malondialdehyde compared to the irradiated control variant. Productivity parameters (spike length, weight and number of grains) were also higher in the variants treated with 0.01% and 0.001% solutions than in the irradiated control. The radiation-protective properties of the Zn inosinate complex have also been tested on laboratory mice irradiated at a critical dose (8 Gy). These studies also showed a positive effect of the complex on the viability and normalization of certain blood parameters in mice exposed to critical doses of radiation [Veyalkina et al., 2020].

STUDY OF THE EFFECT OF SOIL DROUGHT ON THE DEVELOPMENTAL STABILITY OF *PHASEOLUS VULGARIS* L.

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Keywords: drought resistance; fluctuating asymmetry; Phaseolus vulgaris L. In the modern world, the problem of global climate change is becoming more and more acute. One of the severe consequences of climate change is warming, which induces such a threat as drought, which poses a danger to all living organisms and the environment. Drought causes drying and salinization of the soil due to increased moisture evaporation from the soil surface. Plants can adapt to drought within limits determined by their genotype. Water deficiency leads to physiological, biochemical, anatomical, and morphological changes in plants' organisms while significantly impacting their growth, development, and productivity. [Rocio, 2012; Semenov, 2009]. Therefore, the study of these changes to identify the most drought-resistant plant species and, in the future, the development of methods to increase the resistance of agricultural plants to the action of water stress is a very urgent task.

In our country, the devastating effect of drought on agricultural plants has always been the focus of attention of the government and the public since the country's main agricultural areas are located in a zone of insufficient moisture. So, the purpose of our research was laboratory diagnostics of the drought resistance of the "Sevinc" bean sort cultivated in Azerbaijan by studying their morphological parameters and development stability in soils differ in the degree of moisture. The sort belongs to the genus Bean (*Phaseolus*), a species of Common bean (*Phaseolus vulgaris* L.) from the Legume family (*Fabaceae*). The plant, like all legumes, has a high nutritional value.

It is known that externally manifested intra-individual variability in the phenotype of bilaterally symmetrical morphological traits of an organism is due to changes in the biochemical and physiological processes occurring in the organism [Sakai, 1965; Mammadova *et al.*, 2020]. Therefore, the study of the fluctuating asymmetry of phenotypic changes in morphological traits, which manifests itself under stress factors, as a reaction of the organism at the macroscopic level, makes it possible to predict the processes occurring inside the organism at the

microscopic level [Mammadova, 2008]. Under drought conditions, violations of the processes in the plant organism occur, which can externally manifest themselves in the fluctuating asymmetry. Thus, we investigated the possibility of assessing the drought resistance of a plant using the method of fluctuating asymmetry.

It was found that under different soil moisture conditions, the leaves' number and surface area, the stem height, and the indicators of leaf fluctuating asymmetry vary. Biometric measurements of the morphological parameters were carried out in thirty, forty-five, and sixty-day samples. At all stages of the study, under conditions of sufficient soil moisture, the plant stem's average height and the leaf surface area were more significant than under drought conditions. In conditions of water deficit, despite the decrease in the size of the leaves, the value of the fluctuating asymmetry indicators increases. It shows that the moisture supply conditions impact the dynamics of bean biomass accumulation. Moreover, the leaves' fluctuating asymmetry indicators can be used as a test to determine the degree of drought resistance of the plant.

BIOREMEDIATION OF OIL-CONTAMINATED SOILS OF THE BALAKHANI DISTRICT

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Keywords: oil-contaminated soils; bioreclamation measures; Balakhani; winter wheat. The Absheron Peninsula is one of the regions of the country where the soil cover is most susceptible to anthropogenic impact. In general, 33,300 hectares of the peninsula are technologically disturbed, of which 8,124 hectares are completely polluted soils and 25,176 hectares are partially polluted soils. Our research is devoted to the bioremediation of oil-contaminated soils in the Balakhani district, which is very important in terms of restoration and reuse of land resources in oil-contaminated areas, as well as improving the environmental situation of the Absheron Peninsula. 1158 hectares of oil-contaminated soils of the Balakhani region were taken as the object of study, morphogenetic features, mechanical, physical, physico-chemical, agrochemical composition of oil-contaminated graybrown soils of the territory were comparatively studied. It has been established that these indicators vary depending on the degree of oil contamination of the soil. The amount of heavy metals on the oil-contaminated soils

of the Balakhani region was determined and a comparative analysis was carried out in relation to the control variant.

It was found that the amount of titanium in the oil-contaminated soils of the study area exceeds the norm by 6 times - 600 mg / kg, chromium - 2 times more - 420 mg / kg, manganese 2 times more - 1200 mg / kg, lead - 7 ,5 times more - 3.2 mg/kg than in uncontaminated soils. The influence of the amount of oil products that cause pollution in the Balakhani region on the dynamics of changes in humus, total nitrogen, phosphorus and potassium in the soil was studied. It has been established that the content of humus in uncontaminated soils is 1.66%, total nitrogen 0.14%, phosphorus 0.12%, potassium 1.6%. In heavily polluted soils of the territory (oil content 20.5%), the content of humus is 0.60%, nitrogen 0.06%, phosphorus 0.06%, potassium 1.0%, in moderately polluted soils (oil content 7.5%) the content humus is 1.04%, nitrogen 0.08%, phosphorus 0.09%, potassium 1.0%.

In order to determine the results of reclamation on oil-contaminated soils, experiments were carried out in the Laboratory of Reclamation of Ekol Engineering Service CJSC with winter wheat varieties on oil-contaminated and unpolluted gray-brown soils, taken in various proportions, and positive results were obtained. It was determined that in the variant of 3 kg of pure soil mixed with 7 kg of oil-contaminated soil, the height of wheat seedlings 30 days after sowing was 9.6 cm. In the variant of 6 kg of oil-contaminated and 4 kg of pure soil mixture, it was 13 cm, in contrast to these two options, the germination of wheat seeds was more intense in containers mixed with 3 kg of oil-contaminated soil and 7 kg of clean soil, and after 30 days it was 26 cm. As a result of research in order to restore the fertility of oil-contaminated soils of the Balakhani district, measures have been developed for the bioreclamation of heavily, medium and slightly oil-contaminated soils of the territory.

ABOUT CONTENT OF HEAVY METALS IN PLANTS IN TERRITORIES POLLUTED WITH OIL WASTE

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Keywords: plants; oil waste; heavy metals; conversion factor.

Oil industry wastes create technogenic pollution zones in the area of their emissions, while playing the role of a permanent source of pollution. These zones are characterized by an increased content of oil products and heavy metals, which subsequently lead to their pollution of other environmental objects, in particular, plants. In this regard, it is of interest to study the concentration of a number of metals in some plants growing in areas where oil production wastes are stored.

The determination of metals was carried out by atomic absorption spectrophotometry, which has a special sensitivity and selectivity in the presence of numerous elements.

The research results showed that heavy metals contained in oil waste are capable of translocation from soil to plants. Regardless of the place of sampling, the concentrations of metals in soils correspond to their content in plants. This rule is subject to the content of manganese, chromium, zinc, copper, cadmium. That is, high levels of, for example, manganese and chromium in soils correspond to the same values of the content of these metals in plants: the minimum (compared to other metals) concentration of cadmium in soils is also accompanied by its minimum accumulation in plants.

The averaged data on the content of pollutants in wild grasses indicate that the dependence of the intake of metals into the soil on the distance of sludge dumps is also preserved for plants growing in the areas of waste storage. In other words, the highest levels of heavy metals in soils at different distances from the pollutant correspond to their highest levels in plants. Thus, the concentration of cadmium in herbs collected near the sludge dump 1.5 years ago and at a distance of 5 m from it is 0.01 ± 0 and 0.63 ± 0.07 mg per 1 kg of dry matter, respectively (t = 8.85; P<0.001). These values correspond to the concentration of cadmium in the soils of the same plots (1.63 \pm 0.08 and 2.63 \pm 0.15 mg/kg; t=5.85; P<0.01). The dependence of the accumulation of pollutants in plants on the distance of the emission source is especially pronounced for cobalt, copper, and zinc.

The studies established the coefficients of transition of the exchange forms of metals into plants. An analysis of the data obtained shows the unequal nature of the transition of metals into plants. For example, different levels of certain metals are determined both in soils and in plants - in plants collected near a 20-year-old sludge dump; the concentration of cadmium, lead and vanadium are respectively 0.014±0.001; 0.09±0.014 and 0.80±0.15 mg/kg. As well as the content in the soil, the concentrations of these metals in plants differ from each other by an order of magnitude. However, the coefficients of their transition to plants were in the range of 0.006-0.009.

The conducted studies have shown that among the studied oil sludge both in terms of chemical composition, i.e., in terms of the content of more harmful ingredients, a 20-year-old sludge dump occupies a priority place. The high levels of heavy metals in this release make it a more dangerous soil pollutant.

PHYTOMASS AS ECOLOGICAL EDIFICATORS IN RIVER FLOODPLAINS

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Keywords: phytomass; meadow; floodplain; edificatory.

The amount and stock of humus in various types of soils common in the river basins of the Azerbaijan Republic corresponds to the amount of phytomass of grass-meadow plants. Compared to the phytomass of plants in the zonal soils, the phytomass of meadow-grass and meadow-swamp plants distributed in alluvial-hydromorphic soils of river plains is 1.5-2 times higher. In the republic, meadow plants growing in favorable conditions of surface floods and low-mineralized groundwater (1.0-1.5 m) in floodplains also have sufficient surface phytomass (24-34 s) and root mass (123.9-140.2 with).

Table 1. Amount of phytomass in alluvial-hydromorphic soils in 2019-2021 (abs.dry.s/ha)

Soils and Plants	Layers depths, sm	Root mass	Surface phyto mass	
Qanikh-Ayrichay valley				
Meadow plants in washed alluvial- meadow soils	AY'iaz 0-20 AY''ai 20-50	285.9	51.6	

	Bi 0-50		
	Kur river floodplai	in	
Meadow grasses in Carbonate alluvial-meadow soils	AY'iaz 0-20		
	AY''ai 20-50	132.9	30.1
	Bi 0-50		

The maximum amount of root mass (240.8-279.3 c/ha) is observed on alluvial-bog and alluvial-meadow-bog soils in muddy-bog vegetation groups. There are differences in the phytomass of vegetation, depending on various climatic features of the Oanikh-Avrichav and the Kur river plain, also various relief conditions and the degree of development of the soil profile. Fraction and group composition of humus and its supply were identified according to the suborders of alluvial hydromorph soils. The ratio of Cha to Cha alluvial soils in Lankaran plain and Oanikh-Ayrichay valley varies between 0.88-0.94 and 1.06-1.14. This ratio reaches to a value of 1.36-1.68 in the alluvial-hydromorph soils of Kura river plain where arid bioclimatic conditions prevail. The content of humic and fulvic acids contain preliminary fractions (65-70%). Due to preliminary long-term dynamic and seasonal measurements on active ferrous oxides (Fe₂O₃-FeO), water soluble humus, oxidationreduction potential (ORP), soil temperature, soil moisture and groundwater levels, the typical feature of clay formation in humid and arid regions of alluvial-hydromorph soils was investigated. The maximum content of active ferrous oxides (Fe₂O₃=745-937 mg, FeO=169-354 mg) and water soluble humus (0.074-0.165%) being principal indicator for clay formation process was found in the alluvial rot bog soils of humid subtropical Lankaran plain. The maximum content of oxidation-reduction potential (ORP=479-611 mv) and considerable high content of ferrous oxides (Fe₂O₃=549-646 mg, FeO=77-11 mg) of alluvial-hydromorph drift soils was found in Oanikh-Avrichav valley. The content of active ferrous oxides is considerably low (Fe₂O₃=240-350mg, FeO=25-50 mg) in the calcaric-alluvial hydromorph soils of arid subtropical Kur river floodplains as well as ORP varies between 378-449 mv. The following stone content rates of conditionally useless alluvial-hydromorph soils occurred on alluvial cones of mountain rivers in Oanikh-Ayrichay valley according to 0-25cm, 25-50cm depth were determined: less stony, medium stony, much stony and extreme stony. Recommendations on the agricultural use plan of less and medium stony soils were prepared.

PHYSIOLOGICAL ASSESSMENT OF SUSTAINABILITY OF BEANS (PHASEOLUS VULGARIS L.), PEAS (CICER ARIETINUM L.) SYMPTOMS TO ABIOTIC STRESS FACTORS

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Keywords: abiotic stress factors; proteins; genetic donor.

At present time the environment is hot and salty. The increase in abiotic stress factors has led to the depletion of plant genetic resources, the destruction of many valuable plants, on the other hand, the formation of harmful gene combinations, mutant forms. One of the most pressing issues in the agricultural sector is the conservation and efficient use of agricultural plant genetic resources, including biodiversity of legumes. Abiotic stress factors such as drought and salinity are among the main environmental factors that reduce plant productivity. especially in arid climates [Mikayilova et al., 2021]. From this point of view, it is very important to create new varieties and forms of legumes that can meet the requirements of intensive farming and are resistant to changing environmental conditions. The A characteristic feature of the proteins of these plants is that they are easily soluble in water, in a neutral salt solution. The amount of protein in the seeds of legumes is 2-3 times higher than in grains. Beans (Phaseolus vulgaris L.) and peas (Cicer arietinum L.), which are important representatives of legumes, are important as a source of protein for the human body.

11 bean and 18 pea plant samples from the gene pool collection of the Institute of Genetic Resources of ANAS were used in the research. The degree of drought and salinity resistance of the leaves of those samples planted in the field and taken during the flowering phase was assessed on the basis of physiological indicators. Changes in the amount of chlorophyll a, chlorophyll b, chlorophyll a + b, one of the main indicators of photosynthesis due to drought and salt stresses in the laboratory, were determined on the basis of approved guidelines, drought and salinity resistant samples were selected [under the direction of G.U. Udovenko, 1988].

Three of the studied bean samples were selected for their high resistance to both stresses. These are AGHPA-18; Aze PHA-t / 15; Aze PHA-t / 10. The increase in chlorophyll in the AGHPA-18 sample was 9% in drought and 22% in salinity; In the Aze PHA-t / 15 samples; the increase in chlorophyll from both stresses was 3%. In the Aze PHA-t /

10 sample, the increase in chlorophyll did not change during the drought, and the salinity increased by 2%. Four of the studied samples (Aze PHA-t / 3; K-15274, Aze PHA-6; Aze PHA-33) were moderately resistant to both stresses. Sample K-13044 is drought tolerant and highly salt resistant. F.13-20C, Jamila variety, F.13-364C, F.13-278C, F.13-358C, Flip of 18 pea plants studied. 13-154C, White grain, F.13-227C - samples for drought, F. 13-320C, F.13-358C, White grain, F.13-278C, F.93-93 C and F.11-01 - samples was rated as highly resistant to salt stress. The samples evaluated and selected can be recommended for use as a genetic donor in future selection work for sustainability.

DANGEROUS CATEGORIES OF PYRUS L. SPECIES OF THE NORTH-EAST PART OF THE GREATER CAUCASUS

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Keywords: Pyrus L.; relict; rare; endemic.

Currently, the following categories have been adopted in version 3.1 to identify dangerous categories of rare plants around the world, and these categories are used (IUCN Red List Categories and Criteria: Version 3.1, 2001). Danger categories of rare pear species distributed in the north-eastern part of the Greater Caucasus studied in the study 3.1. version (2001) [Table 1].

Table 1. Phyto-geographical region of the studied plants, life form, IUEP categories, relict, endemic and rarity analysis

No	Species	Phytog- raphic region	Life form	EX EW CR EN VU	NT LC DD NE	Relict Rare	Endemic
1	P.caucasica	Iran-	Mesapha-	VU		+	
		Turan	nerophyte	D2			
2	P. georgica	Iran- Turan	Mesapha- nerophyte		NT	+	
3	P. vsevo- lodii	Iran- Turan	Mesapha- nerophyte		NT		Caucasian endemic
4	P. salicifo-	Iran-	Mesapha-	VUB:	L	+	
	lia	Turan	nerophyte	b			
				(i, iv)			

Analysis of the taxonomy of taxa showed that 2 of the 4 species were classified as VU (susceptible species) and 2 species were classified as NT (endangered species). It can be concluded that the rare pear species in the study area need protection. If no action is taken today to protect these plants, it is clear that in the near future, the gene pool of most of these plants will be endangered. When analyzing the distribution of pear species studied according to the categories of version 3.1 of the IUEP by dangerous categories, it was found that no other taxa has been included in the other risk group. The results of the analysis show that if the impact of biotic and abiotic factors on the studied plants continues, there will be uncertainty in the distribution of the studied pear species over a certain period of time. In this regard, after some time, the division of these plants into danger categories should be reconsidered. Our analysis of the life forms of research plants showed that all the species studied according to this feature belong to the group of mesophanerophytes. The distribution of the studied plants according to phytogeographic regions was also found to be similar. As a result of the analysis, it became clear that all the plants studied belong to the Iran-Turan phytogeographic region [Table 1].

THE ROLE AND PLACE OF HIGHER PLANTS IN THE OPTIMIZATION OF THE ECOLOGICAL CARCASS IN THE ABSHERON PENINSULA

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Keywords: ecological carcass; biodiversity; irrigation; vegetation.

The socio-economic development of the Absheron Peninsula depends on the ecological balance and the stable functioning of all components of nature. The ecological carcass of the area-EEC acts as a stabilizing element.

The property of forest plantations is even more crucial for cleaning the atmosphere from distinct pollutants. The existing protected area in the Absheron Peninsula is just a collection of objects, which must be complemented by a network of phytocoenosis systems that will serve as a multifunctional ecological carcass. Lack or poor development of vegetation, low biodiversity is one of the extreme features of the natural environment, including the Baku-Sumgayit area around industrial en-

terprises and the area where mud volcanoes are located, mainly due to the unfavorable ratio of heat and humidity.

Plant associations and microorganisms are able to destroy pollutants independently of each other, but plant-microbial interactions are of great importance for the biodegradation of stable compounds in the rhizosphere [Anderson *et al.*, 2004; Barton *et al.*, 2013].

As part of the proposed solutions, fundamental work should be done in the first stage:

- On the maps of industrial enterprises and mud volcanoes in Baku-Sumgait, it is necessary to determine the location and plans of green areas and their area, taking into account the territory of industrial enterprises and the manifestations of volcanism.
- Given the low fertility of soils around industrial plants, highways and mud volcanoes, increasing soil fertility for planting trees is a key task at this stage. For this purpose, innovative biotechnologies can be used to increase the fertility of soils exposed to man-made impacts using microbial preparations.
- The main types for planting trees and shrubs should be identified;
- Water sources for irrigation of green areas should be defined, modern irrigation technologies and schemes of irrigation systems drip irrigation, etc. can be used.

The proposed solutions are aimed at the sustainable development of Azerbaijan in the XXI century.

THE INFLUENCE OF SLOPE EXPOSITIONON ECOLOGIC CHARACTERISTICS AND DIAGNOSTIC PROPERTIES OF KASTANOZEMS IN THE LESSER CAUCASUS

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Keywords: relief, exsposition of slopes, soil profile, morphogenetic diagnostic, humus.

The role of relief in soil forming and soil cover structure in the mountainous lands was particularly emphasized in the study examples from European and Russian soil scientists at the beginning of last century. The relief was considered as the "mirror" of soil. The studies showed that not only elevation, but also slope exposition plays an im-

portant role in formation of diagnostic properties and soil cover structure in different climate-landscape zones of the mountainous lands in Azerbaijan.

The study site is at elevations of 650-700 m above sea level and significantly fragmented with slopes and valley-shaped microdepressions. Parent materials contain silty calcareous diluvial sediments. The vegetation is characterized by the well-developed grass and shrubs. The climate is aridic with annual precipitation and average temperature of 380-400 mm and 11.8-12.5 C, respectively.

A site-specific study area was selected in the area of the Kastanozems in the north-east part of the Lesser Caucasus. Soil surveys were conducted based on a geographical-comparative approach. The soil pits with 1.5 m depth were bored and georeferenced using GPS in shady north-west faced and sunny south-east faced slopes and the soil samples were collected from genetic horizons. The morphological properties of genetic horizons were described and the soil samples were tested for chemical analysis as accepted methods. At the same time plant biomass of surface and subsurface was determined on the noted slope expositions.

The comparative assessments showed that the significant differences exist between the soils of shady and sunny slopes despite the same elevations. In particular, the depth of humus accumulated horizon (AUv), leachingthe carbonates, formation of illuvial carbonated horizon (Bca) and its depth and solidity, structural aggregates and texture of genetic horizons, soil moisture, and degree of soil erosion are different [Doran *et al.*, 1996; Gee *et al.*, 2002].

The soils of north-west faced shady slopes are characterized with optimal moisture regime consequently well-drained grasses vegetation and accumulative topsoil (AUv=45-50 cm), high humus (4.3-5.4%) and nitrogen content (0.34-0.38%), a high absorption capacity (50-53 meq.) and slightly alkaline soil environment (pH of 7.0-8.1). The leaching of carbonates from topsoil (AU=45-50 cm) and its accumulation (Ca-CO₃=11.6-20.8%) in the middle part of the soil profile is typical soil forming process.The density of soil is 0.12-0.15 and 1.35-1.38 g/cm³ in topsoil (0-25 cm) and subsoil (50-80 cm) horizons, respectively.Biomass of surface grass is 11.3 t/ha while its root biomass is 30.3 t/ha.

The soils on sunny south-east facing slopes are characterized by fragility to erosion, consequently, decrease in humus (2.6-3.9%), nitrogen content (0.25-0.29%), absorption capacity (30.1-42.8 meq.), surface

biomass of grass(8.9 t/ha) and its root mass(19.7 t/ha), finer texture (<0.01mm=51.8-54.2%; <0.001mm=20.4-25.0%) and existence of carbonates ($CaCO_3=4.6-5.4\%$) in the topsoil.

The complex assessments we undertook in the north-east part of the Lesser Caucasus showed that the sunny slopes are capable of generating specific local climate features compared to shady slopes which ultimately influences soil temperature regime, soil formation, soil erosion, plant biomass and diagnostic parameters.

EFFECTS OF DROUGHT ON THE PRODUCTIVITY OF BEAN PLANT

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Keywords: bean; productivity; drought; stress.

Recently, the rapid acceleration of climate change requires a more serious approach to the work carried out in increasing the food supply and creating the productive and high-quality new varieties. Selection of drought-tolerant plant varieties and forms having regarded the lack of water is a priority matter. Azerbaijan is also affected by global warming as is the case all over the world. Water scarcity is a global issue. In this regard, our research is aimed at the selection of drought-tolerant, productive forms in the samples of edible beans.

The research has been carried out in Absheron Scientific Research Experiment Area of the ANAS Institute of Genetic Resources. 56 varieties of common bean collected and introduced from the country's different regions have been used for the experiment. The samples have been sown by making use of the inter-row method [Asadova *et al.*, 2016]. "Descriptors for bean" defined by the Biodiversity International (IBPGR) have been used during the research [Methodology for the definition of a key set of characterization and evaluation descriptors for bean, 2011]. With the help of these descriptors, the analyzes have been performed and certain results have been obtained.

The experiments have identified the correlation between the morphological and agronomic traits, the quantitative and qualitative characteristics of plants. According to the outcome of the experiment, during these years, 20 out of 56 samples have completed the vegetative phase to some extent, while the other plants have died. As a result of the experiment, K-13044, AzePHA-6, Local Pedestrian, Aze-PHA-36/2 sam-

ples of Phaseolus vulgaris L. plant have yielded certain productivity in drought conditions. Moreover, it should be noted that they are tolerant to drought stress thanks to a number of genotype-dependent traits [Chaves et al., 2002]. In this regard, a number of criteria have been put forward for the selection of genotypes under stress or non-stress conditions [Naghavi et al., 2013]. According to our research, the highest average productivity of bean genotypes has been in the T/H-1 genotype (MP=156). The high limit of MP is assessed as a tolerance to stress. The highest tolerance among genotypes has been recorded in the AzePHA-6 genotype (TOL=-68). The low indicator of this index is considered as a high tolerance. The use of STI, OHM, and MP indicators to assess the drought tolerance and to select the highly productive genotypes have been identified by Fernandez [Fernandez, 1992]. The correlation between TOL and STI has been like 0.448** and like r=0.975** between OHM and STI. The stress tolerance index (STI) defined by Fernandez in 1992 allows identifying the high yield and tolerant genotypes. The highest tolerance to the tolerance index has been recorded in the AGHPA-18 genotype (STI=2.09).

It is intended to use the results obtained in our research in the selection process to create new drought-tolerant forms.

DISTRIBUTION OF MALVA SPECIES IN PASTURES AND HAYFIELDS AND ECOBIOLOGICAL FEATURES (GANJA-GAZAKH ECONOMIK- GEOGRAPHICAL REGION)

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 $\textbf{\textit{Keywords}}: \textit{Ganja-Gazakh region; Malva species; meadow vegetation; pastures; hay fields.}$

The article is about the distribution of Malva species in the pastures and hayfields of the soils in the Ganja-Gazakh economic-geographical region. The species composition of meadows includes groups of perennial, annual, and duality grasses dominated by mesophytic plants. The meadow vegetation has been divided into five subtypes, fourteen formation classes, forty-three formations, and fifty-two associations. At this time Malva species participated as a component. *Elitrigia caespitosa, Cynodon dactylon* and etc, Malva *nicaeensis* species with them are found in the plain, low, and middle mountain meadows,

but Myricaria bracteata, Juncus effusus, J. compressus, Carex acutiformis, Xanthium spinosum and other species of mallow are found in the lower tier. Urtica dioica, Filipendula ulmaria, Achillea millefolium, Persicaria hydropiper, Ranunculus repens, Rumex acetosa, Plantago Lanceolata, Prunella vulgaris, Malva pusilla, and other species included in phytocoenosis of the flood and hole meadows. The flood meadows of the Ganja-Gazakh economic-geographical region developed well, and more than thirty plant species concerning various ecological groups have been noted. As a result of the cluster analysis of the species composition in the meadows thirty species of plants are combined in two main groups and seven subgroups according to plant density, and two main and seven subgroups according to their height. Grain-various grassy, grainlegume-various grassy, and different grassy moisture meadows were noted for the subforest, post-forest, and bushy meadows zone in the Ganja-Gazakh economic-geographical Grain-chilly-various region. grassy mesophilic sub-forest meadows occupy a small area in the Ganja-Gazakh economic-geographical region, though the mallow species are more in the pastures of this region. The pasture reaches a maximum height in the second half of summer, from late July and early August, and gives a high yield. After it, the mallows enter the fruiting phase before the meadows have not withered yet. In August, and at the beginning of September long-stemmed perennials still continue to grow and bloom. In the mesophilic sub forest meadows of grain-chilly-various grass, the cluster analysis was carried out according to the density and height of plants by species, in terms of density, plants are grouped in 2 main and 7 subgroups, and in terms of height, plants are grouped in 2 main and 5 subgroups. Trisetum flavescens, Vicia elegans, Helichrysum plicatum, Xeranthemum squarrose, Chardinia Orientalis, Cephalaria kotschyi, Scorzenera latifolia, Centaurea squarrosa, Thalictrum minus, and others species are characteristic fost-forest dry meadows, though we got information about mallow species in these meadows, before, at present, they are not found.

ANALYSIS OF MANAGEMENT STRATEGIES AND PROSPECTS OF THE CLASSIFIED FOREST OF FAYA IN MALI

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Keywords: forest management; Faya; strategies; prospects.

Mali is a continental state located in West Africa which covers an area of 1,241,238 km2. State of the Sahel, the vast majority of the population lives in the southern part of the country, home to most of the forest formations estimated at 37,741,231 ha. The country has thousands of forests with different statuses, including 113 classified forests, including the Faya classified forest.

The classified forest of Faya in Mali which covers an area of 79947 ha and located 40 km from Bamako does not escape destruction despite its classification before independence in the colonial era and today. This article aims to analyze the various strategies which were carried out by the various authorities of various times for the safeguarding and the protection of this vast ecosystem called "Green Lung" of Bamako thus to release and analyze the prospects for a durable management of this vast forest massif. The methodology was based on the collection and analysis of documents, cartographic analysis, interview surveys with resource persons in charge of this forest and the processing and analysis of data.

The study revealed to us that there have been several programs for the preservation of this forest by different authorities but all of them turned out to be failures due to the bad design of the programs, the non-monitoring of the achievements, the bad interpretation of management and especially by many other anthropogenic factors including agricultural clearing, increased consumption of wood and charcoal, the removal of wood and service wood, sawn timber, pharmacopeia, the needs socio-cultural, bush fires (early and late) that devastate more than 100,000 ha per year and harvesting for traditional medicine (National Forest Policy 2017). It is however urgent to save this vast ecosystem like all the other forests in a spirit of sustainable development, the fight against poverty in particular of the local populations and to face the challenges of climate change.

ECOLOGICAL ANALYSIS OF FLORA BIODIVERSITY OF TALISH

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Keywords: phytocenosis; flora; ecomorph; mesophyte; hidrofit.

For the ecological investigation of the biodiversity of the flora of the mountainous part of Lankaran, it was divided according to different soil-climatic conditions where plants are spread in natural phytocenoses, especially according to humidity [Gurbanov *et al.*, 1998] and water [Khrjanovski, 1986, Shennikov, 1964] demand.

The distribution of 1071 species included in 102 families and 437 genera was found in the flora of the mountainous part of Lankara.

Anthophyta represents 97.7% of the phytodiversity of the mountainous flora of the region; of which 840 species (78.4%) belong to Dicotyledoneae and 207 species (19.3%) to Monocotyledoneae, including, 19 species (1.8%) of Embryophytes - (Pterodophyta) , 1 species (0.1%) of Sphenophyta and 4 species (0.4%) of Pinophyta are identified in the systematic structure of the flora.

Systematic taxa in the flora biodiversity of the Highlands, compared with the flora of Azerbaijan [Aliyev C.A. and other., 2008, Asgarov A.M., 2005, Hatamov V.V., 2000], revealed that 102 families, which include plants distributed here, are equal to 81.6% of the families in the flora of the Republic, 46.9% to 437 genera, and 1071 species to 23.8%.

Here, the classification and composition of ecomorphic species systematized by groups, xerophytes, mesoxerophytes, mesophytes and hydrophytes are defined. In particular, the percentage of the total number of species corresponding to the groups or the ecological spectrum [Salimov *et al.,,* 2008] is reflected in table 1.

Table 1. Classification and composition of floral biodiversity of Talish on the ecological groups

No	Ecological groups		Sorts
		Number	% for common number
1	Xerophyte	548	51,2
2	Mesoxerophyte	288	26,9
3	Mesophyte	197	18,4
4	Hydrophyte	38	3,5
	Total:	1071	100

As can be seen from the table, as a result of the analysis of local flora according to ecological groups, 4 groups were found. On the ecological spectrum, xerophytes are present with 548 species or 51.2% of the species composition. The remaining places are occupied by mesoxerophytes with 288 species (26.9%), mesophytes with 197 species (18.4%) and hydrophytes with 38 species or 3.5% of the species composition [Gurbanov *et al.*, 2012].

STUDY OF THE EFFECT OF IONIZING GAMMA RADIATION ON THE OSMOTIC SUSTAINABILITY OF ERYTHROCYTES IN ANIMALS

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Keywords: laboratory mice; gamma radiation; osmotic pressure; erythrocytes.

Rats are rodents that make up 40% of mammals. The rat is a laboratory animal commonly used in research due to its relatively short life, short fetal period, rapid adaptation to the environment, well-studied physiology and genetics. In many biomedical studies, laboratory mice are used as a live system to study the effectiveness of drugs and treatments. Human disease is one of the first model systems to develop new drugs and to examine reactions to environmental changes. Albino rats were first used in physiological research in 1828 [Kaliste *et al.*, 2007].

When the body is exposed to gamma radiation, the red blood cells cause changes in 3 different functional components of the membrane - the double lipid layer, protein compounds, and the cell frame on the membrane surface. Deterioration of membrane lipids results in hemolysis [Parasassi *et al.*, 2007].

The experiments used 13-month-old lab rats. In the rats, we applied ionizing gamma radiation (6 Gy) to analyze the effects of stress on the osmotic pressure tolerance of erythrocytes. The rats were exposed to radiation from a source of 60 Co at the RHUND-20000 facility. After irradiation, the rats were kept in the laboratory for 5 months and then cut with 10% ketamine according to bioethical rules.

Blood samples were taken into test tubes containing a special citrate solution that prevents blood clotting. Blood samples were then washed with 0,5 mM 9% of NaCl saltwater. Samples were measured on

a CF-46 spectrophotometer with a wavelength of 414 nm. The results are shown in Table 1.

Table 1. Percentage indicators of resistance to osmotic pressure of erythrocytes in blood samples of control and 6 Gy irradiated rats

	0,45%	0,9%	Degree of hemolysis
	solution	solution	
Control	82,5 %	4,67	100 %
	%		
6 Gy	96 %	11,8 %	100 %

According to the results of spectrophotometric blood analysis, the osmotic pressure resistance of erythrocytes in the blood of rats was reduced by 3 times in a 6 Gy irradiated sample compared with the control.

SPECIES OF THE FAMILY CRASSULACEAE DC. OF LESSER CAUCASUS Akbarova Chichek

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Keywords: sedum; sempervivum; Lesser Caucasus.

The flora of Azerbaijan is characterized by rich vegetation. Among these plants, species of the Crassulaceae family have their own place. Species of this family are widely distributed throughout the world, mainly in dry, hot and temperate regions. The family includes 1500 species in 33 genera all over the world and 36 species in 4 genera in Azerbaijan, 18 of which are distributed in the Lesser Caucasus, the area of our studies. The main objective of our studies is to determine the taxonomy of species distributed in the territory of Aghjakand, Goranboy region and Khoshbulag village of Dashkesan region in the northern Lesser Caucasus, to determine their exact ranges and to study morphological and bioecological characteristics of the revealed species. For this purpose, the flora of Azerbaijan, Caucasus and the former USSR, as well as determinants, many literary sources, comparative-morphological, areological and systematic methods were used [Grossheim, 1946, 1953]. Herbal specimens were studied by comparative-morphological methods [Askerov, 2006, 2013]. For this purpose, herbarium materials stored in the herbarium fonds of the Institute of Botany, Baku State University, and collected by us were used. The collected herbarium specimens were identified by us and confirmed as 3 species.

Sedum album L. - white stonecrop. It is a creeping perennial plant with many-branched rhizomes. The leaves are arranged alternately, with flower stalks longer or shorter than the flowers. The disheveled flowers are gathered in an ascending group of flowers. The flowers are white or pink. It blooms in June and August and bears fruit in July and September. In Yuhari Aghjakand, in an area of up to 10 squares, it is found in numbers of up to 10. Dispersed over an elevation of 1450 m in the mid-mountain belt at coordinates N40.41771' E046.47174'.

Sedum spurium M.Bieb. - false stonecrop, the Caucasian stonecrop or two-row stonecrop. A perennial short-stemmed plant with a thin creeping rhizome. Suprotic ovate or oval leaves, compressed at the base, ciliate on the front side. Its densely arranged flowers on short or long stems are arranged in an umbrella-shaped cluster, blooming in June-July, bearing fruit in August-September, and commonly found on stony and rubbly soils. Scattered over an altitude of 1350 m in the midmountain belt at coordinates N40.41228' E046.45176'.

Sedum oppositifolium Sims. – opposite - leaved stonecrop. It is a perennial plant with a long creeping rhizome, the leaves are opposite-ovate and oblong-ovate. White, yellowish-green or purple flowers are sessile or on short stems, gathered in a shield-shaped group of umbrel-la-shaped flowers. Grows on rocks, rock outcrops or rocky slopes; blooms in July and August; bears fruit in August and September. Scattered over an elevation of 1450 m. at coordinates N40.41771' E046.47174'.

A comprehensive study of species of the Crassulaceae family and the study of their taxonomic composition are among the most important tasks before us. We believe that the study of species included in the taxonomic composition of the family will continue, and new species and new ranges will be discovered.

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