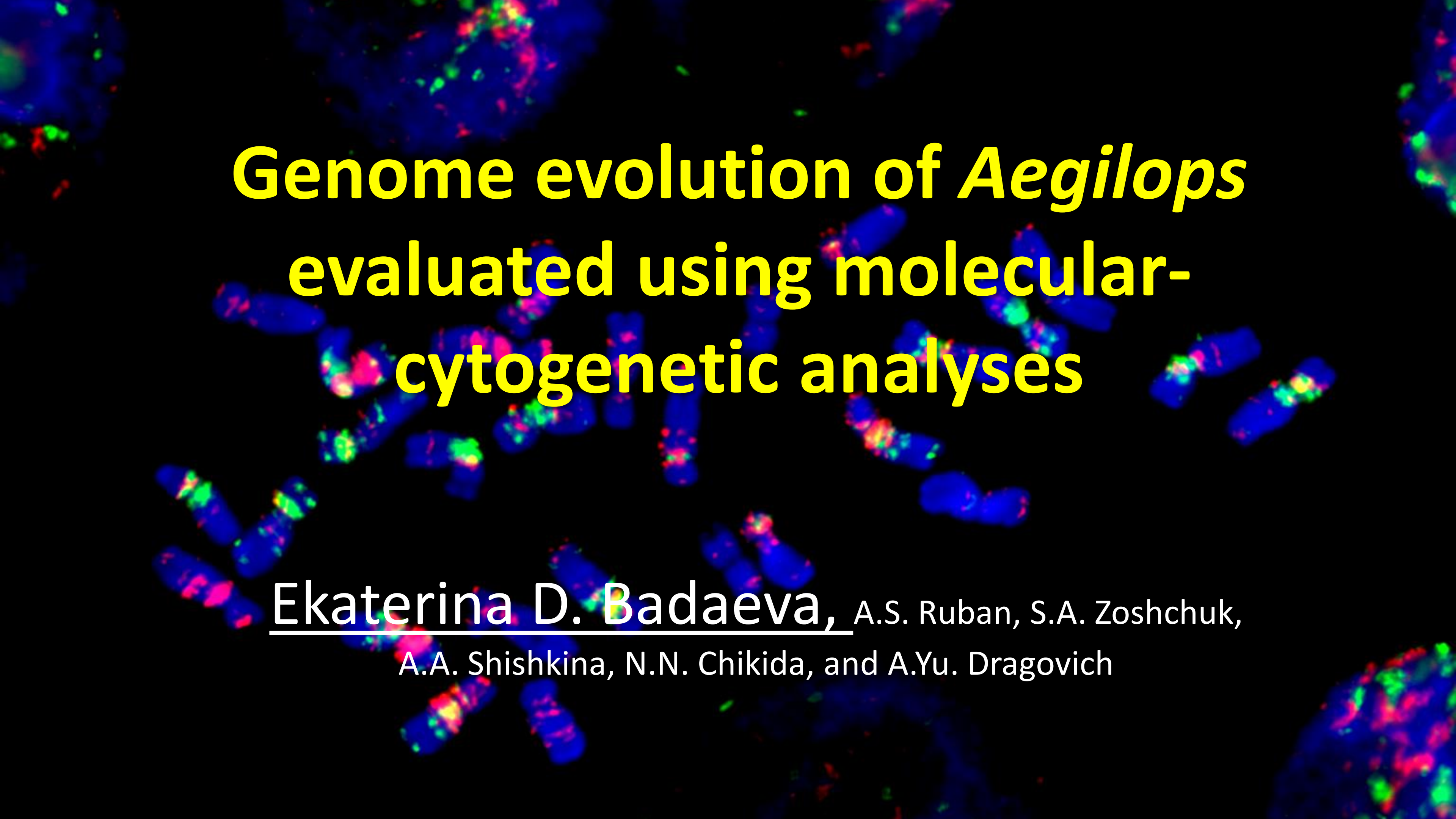


Genome evolution of *Aegilops* evaluated using molecular-cytogenetic analyses

Ekaterina D. Badaeva, A.S. Ruban, S.A. Zoshchuk, A.A. Shishkina, N.N. Chikida, and A.Yu. Dragovich

Diploid species:

Aegilops speltoides (S)
Aegilops longissima
Aegilops sharonensis
Aegilops searsii
Aegilops bicornis

Aegilops mutica (T)

Aegilops tauschii (D)

Aegilops comosa (M)
Aegilops heldreichii (M)
Aegilops uniaristata (N)

Aegilops umbellulata (U)
Aegilops caudata (C)

Polyploid species:

D-genome cluster

Aegilops cylindrica (DC)

Aegilops crassa (4x, DS^c)

Aegilops ventricosa (DN)

Aegilops crassa (6x, DS^cX)

Aegilops juvenalis (6x, DS^cU)

Aegilops vavilovii (6x, DS^cS)

U-genome cluster

Aegilops triuncialis (UC, CU)

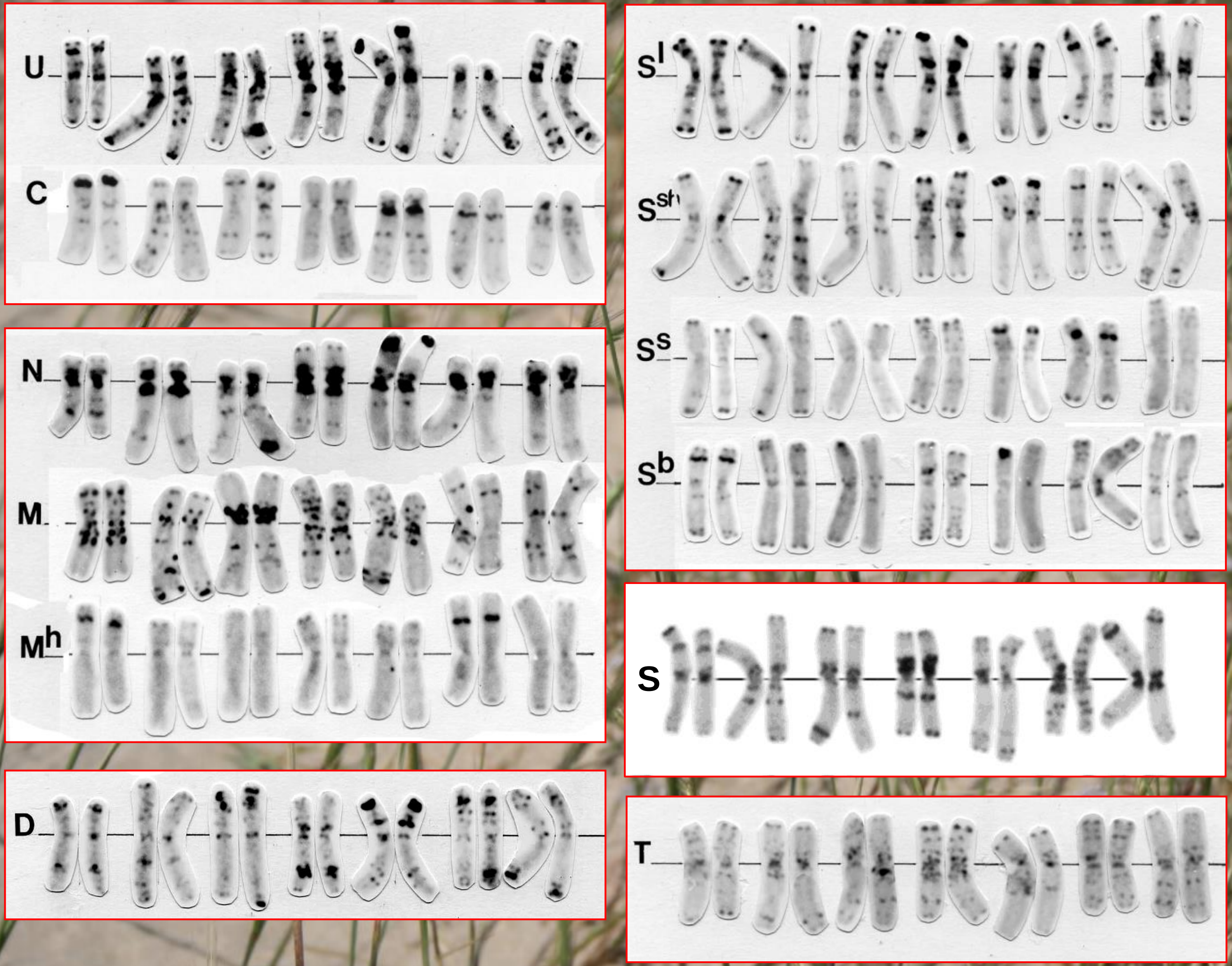
Aegilops variabilis (US)
Aegilops kotschyi

Aegilops geniculata (UM)
Aegilops biuncialis

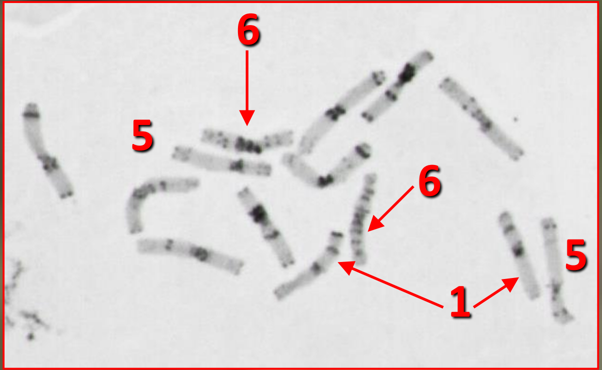
Aegilops columnaris (UX)
Aegilops triaristata

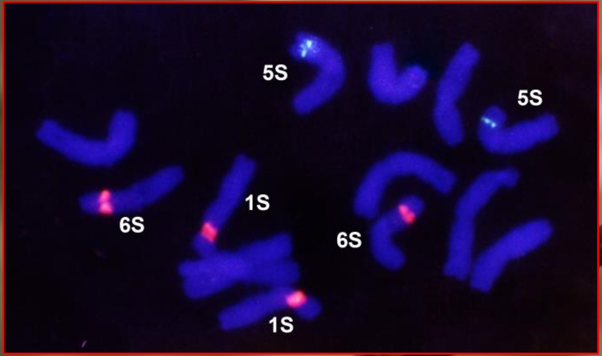
Aegilops recta (6x, UXN)

Diversity of karyotype structure and C-banding patterns in diploid *Aegilops* species

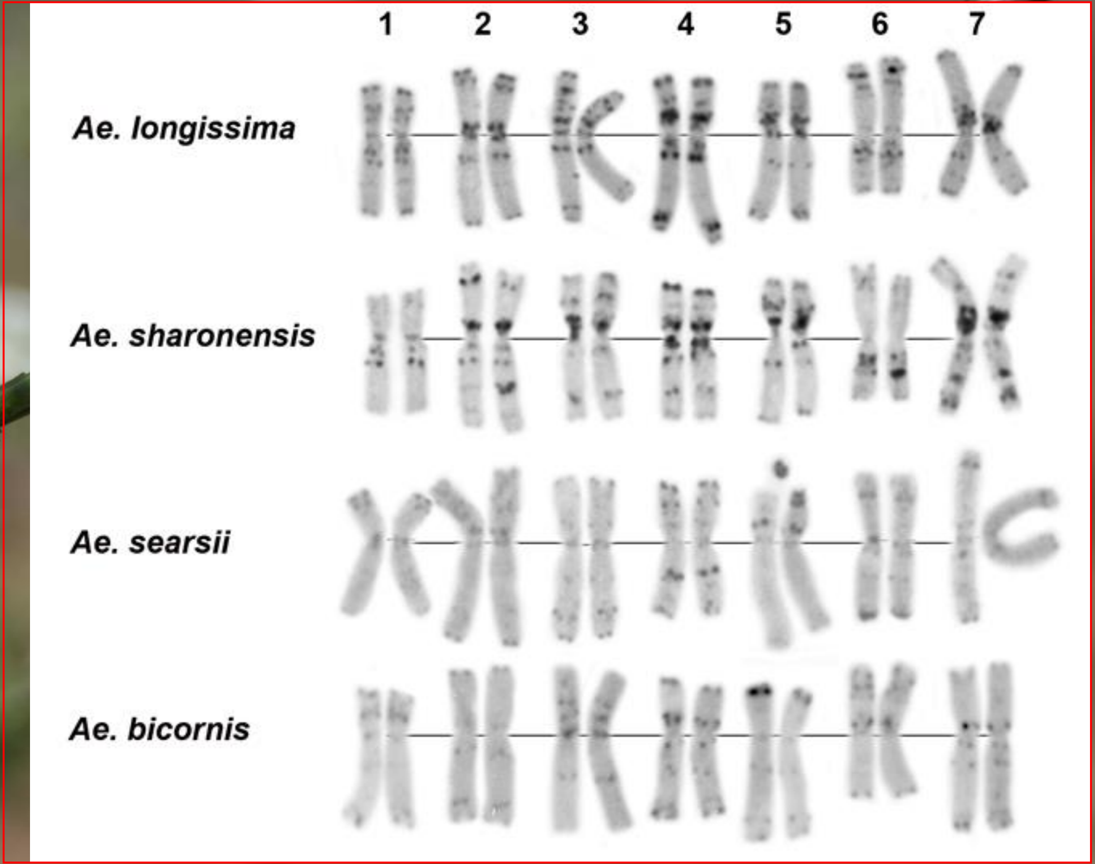


Karyotype differences between five *Aegilops* species carrying the S-genome.

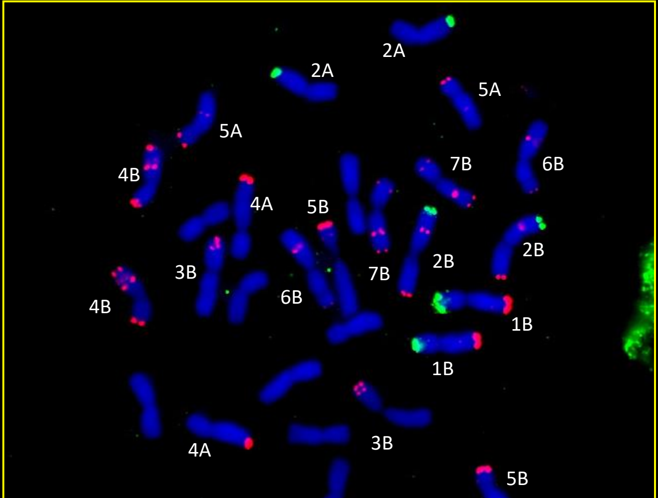




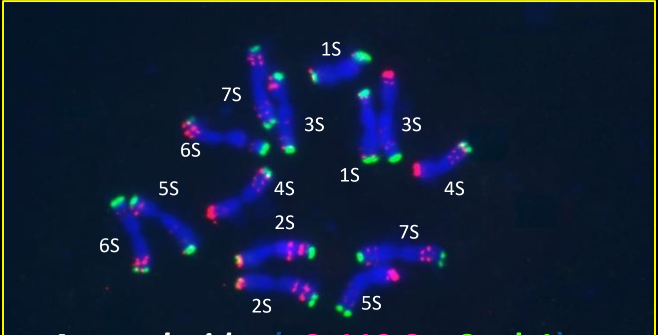
Ae. speltoides is the only species of the section Sitopsis, in which the satellites are located on group 1 and 6 chromosomes (in the other four species they are found on group 5 and 6 chromosomes). The satellites on the wheat B genome are located on chromosomes 1B and 6B, therefore, *Ae. speltoides* is more closely related to the B- genome than four other Sitopsis species.



Ae. speltoides is most closely related to the B-genome donor

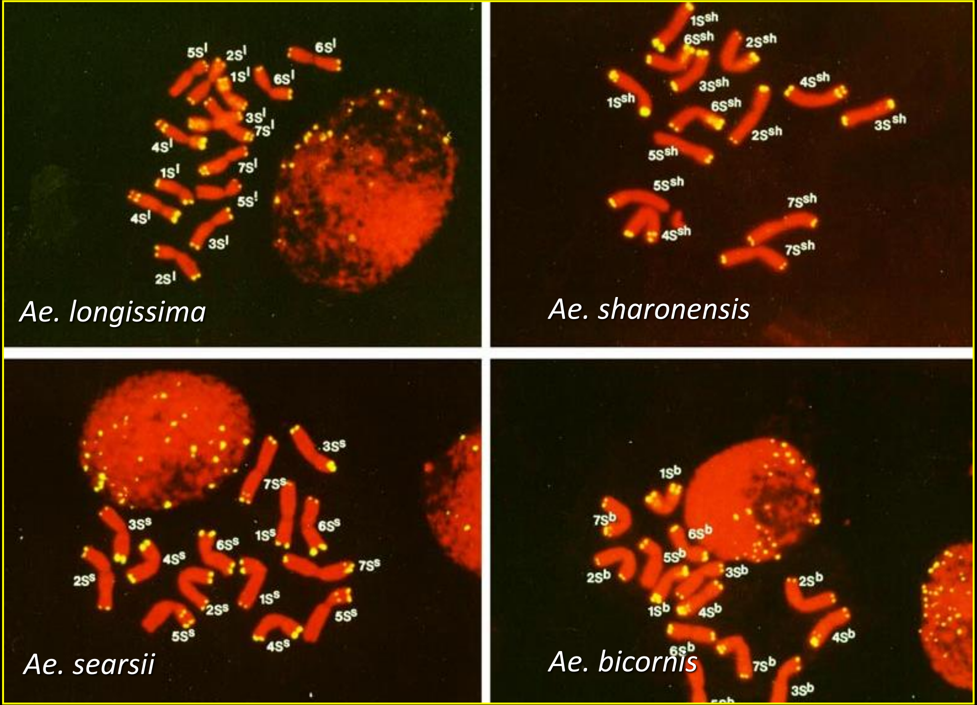


T. dicoccum **(pSc119.2 + Spelt1)**



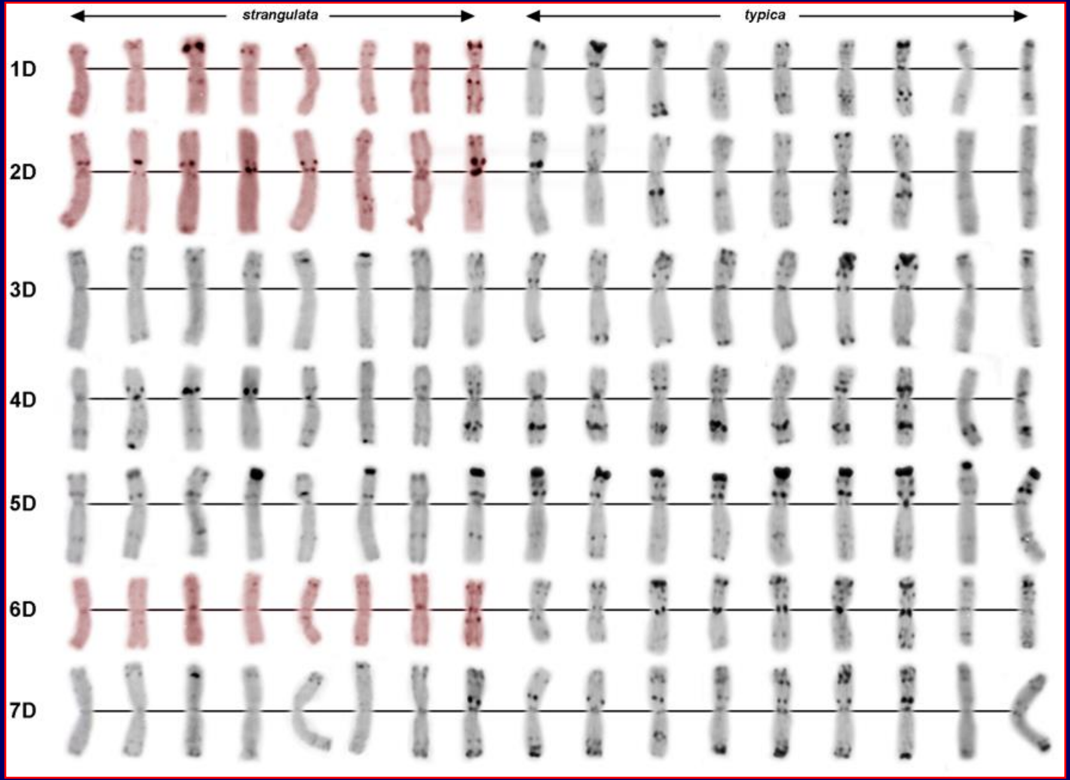
Ae. speltoides **(pSc119.2 + Spelt1)**

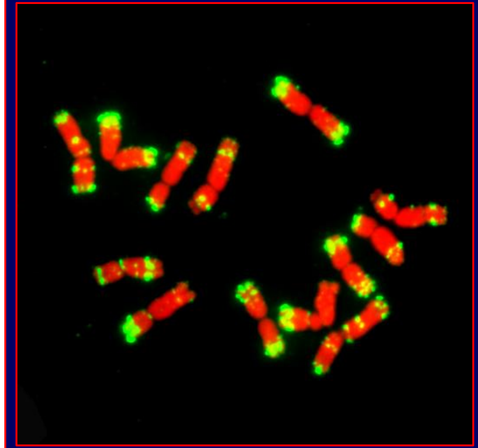
The B-genome chromosomes of polyploid wheat and the S-genome chromosomes of *Ae. speltoides* show similar hybridization patterns of the *pSc119.2* probe. Four other species of the Sitopsis section – *Ae. longissima, Ae. sharonensis, Ae. searsii, Ae. bicornis* are similar with each other in the distribution of this probe, which is different from that on the B- or S-genome chromosomes.



Distribution of pSc119.2 probe on chromosomes of *Aegilops* species; the chromosomes of these species do not hybridized with Spelt-1 probe

N. Pathak (1940) was the first who suggested *Aegilops tauschii* as the D-genome donor. His assumption was further confirmed by many authors (McFadden & Sears, 1944; Kihara, 1944). Biochemical and molecular analyses revealed that the wheat D-genome was contributed by *Ae. tauschii* ssp. *strangulata.*

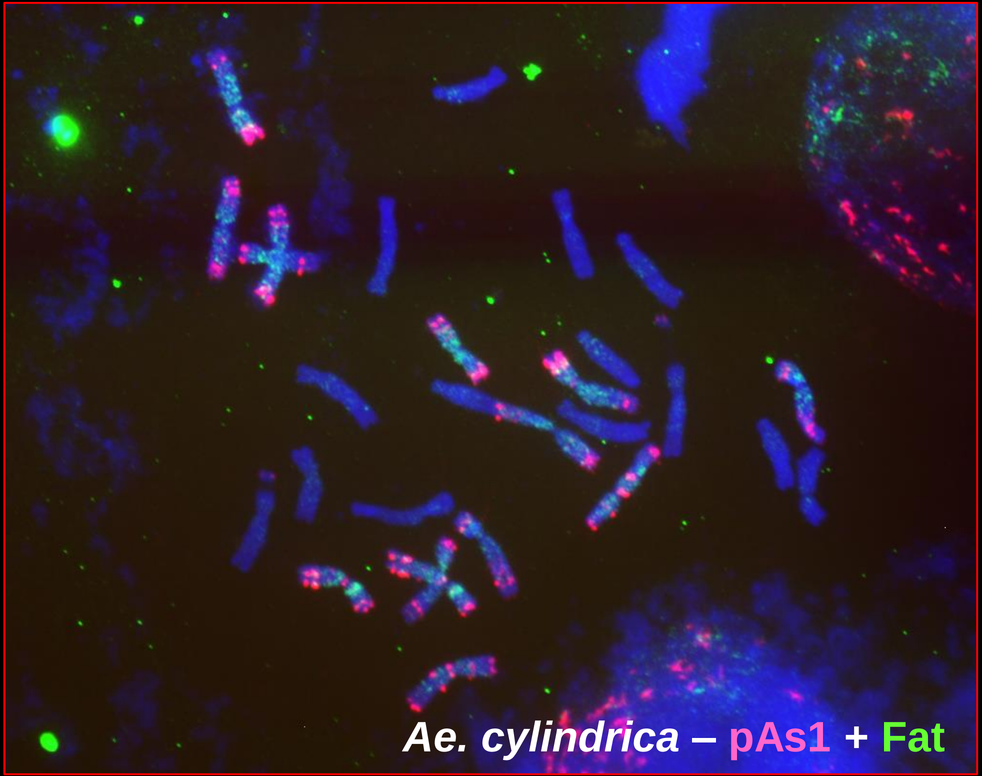




Ae. tauschii

- the D-genome donor to polyploid wheat and *Aegilops* species

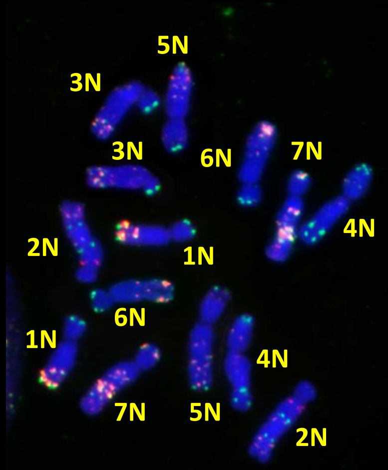
Polyploid *Aegilops*: D-genome cluster



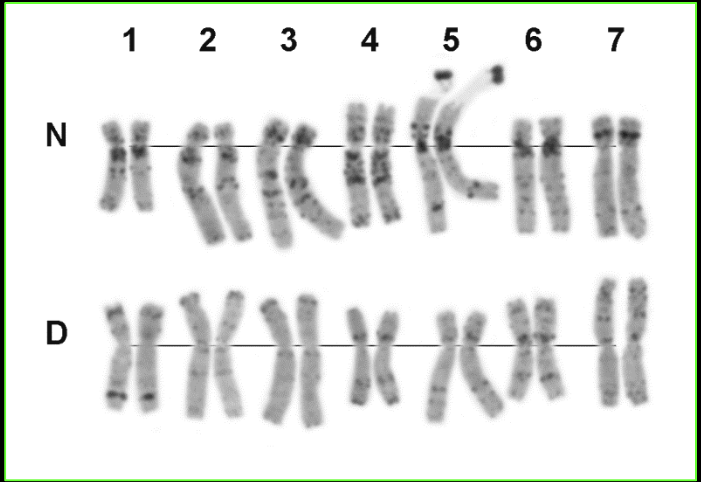
Ae. ventricosa

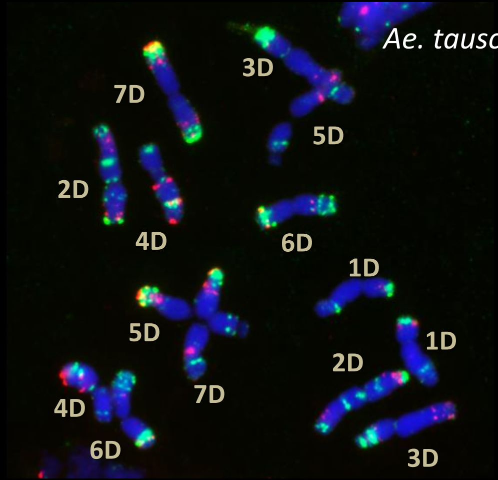
All chromosomes of *Ae. ventricosa* are modified compared to the parental species. The D^v-genome is more similar with the D-genome of *Ae. crassa* than the D-genome of *Ae. tauschii.* The 45S rDNA locus on the chromosome $5D^v$ is deleted.

The level of chromosome modifications is lesser for the N^v-genome. We however found some differences both in C-banding and labeling patterns of some N^v-genome chromosomes of *Ae. ventricosa* compared to *Ae. uniaristata*

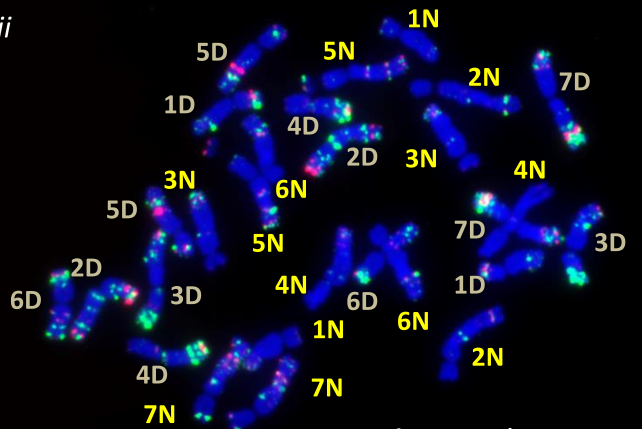


Ae. uniaristata

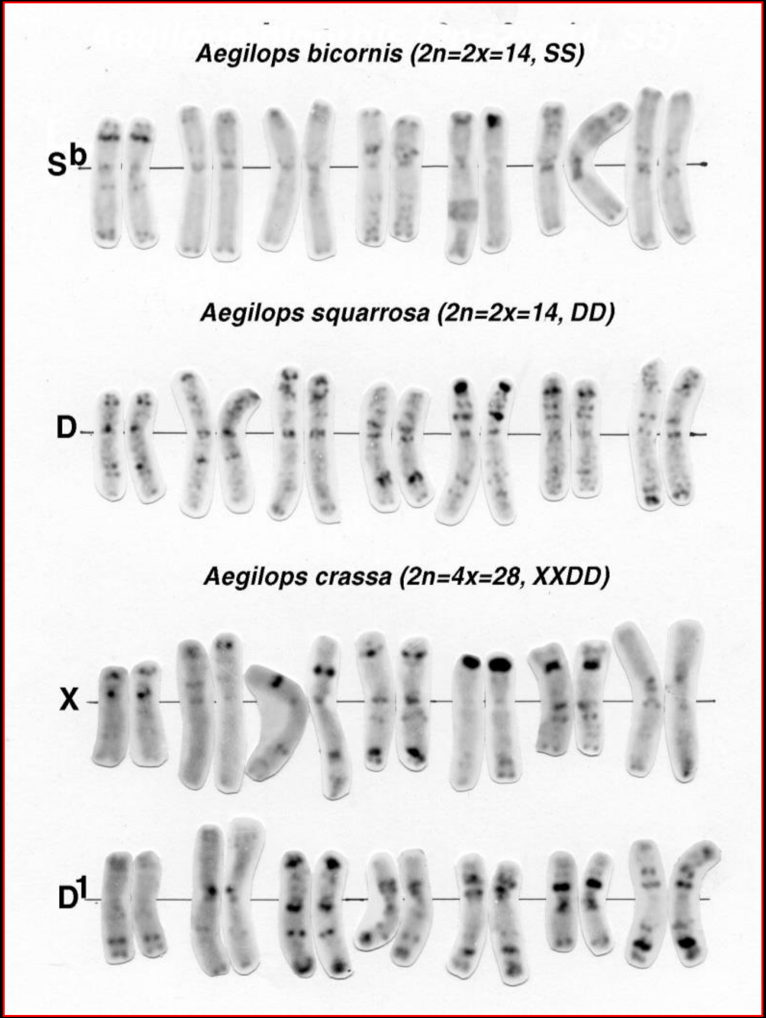




Ae. tauschii

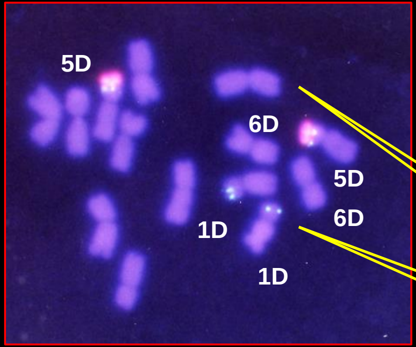


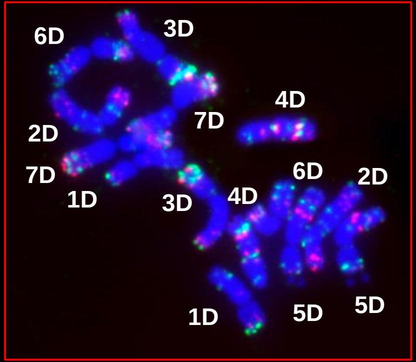
Ae. ventricosa

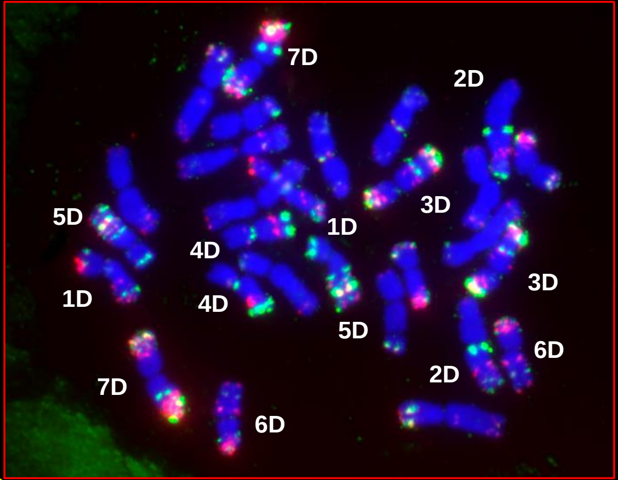


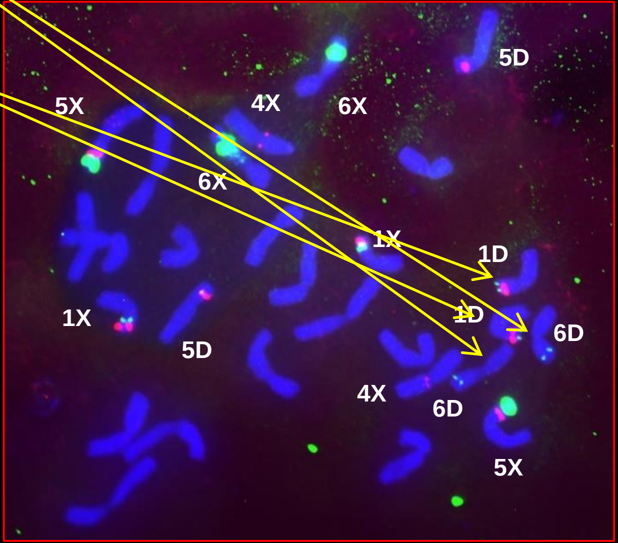
Aegilops crassa

Tetraploid *Ae. crassa,* the most ancient polyploid *Aegilops* species, was probably originated from hybridization of *Ae. tauschii* with an extinct diploid species of the Sitopsis group.



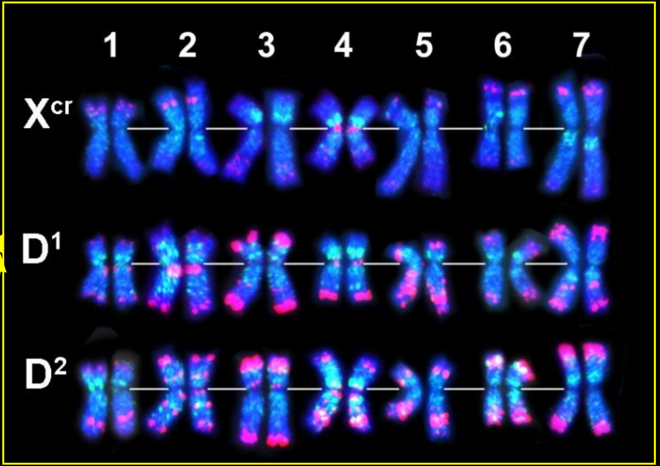


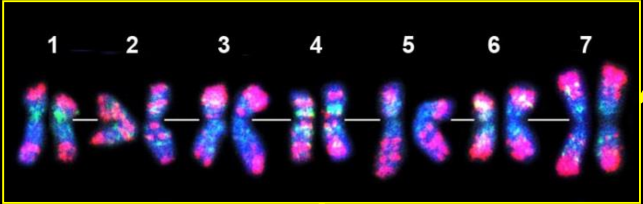




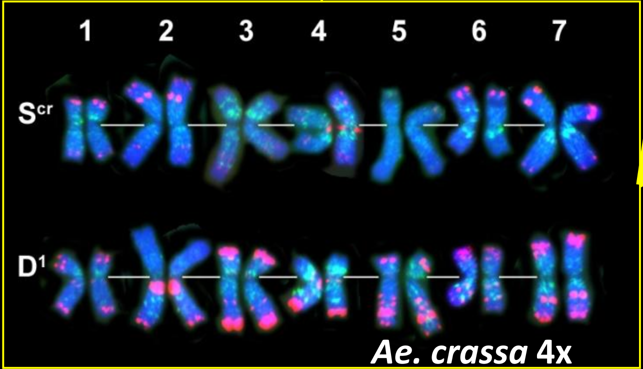
Evolution of *Aegilops* species belonging to complex Crassa

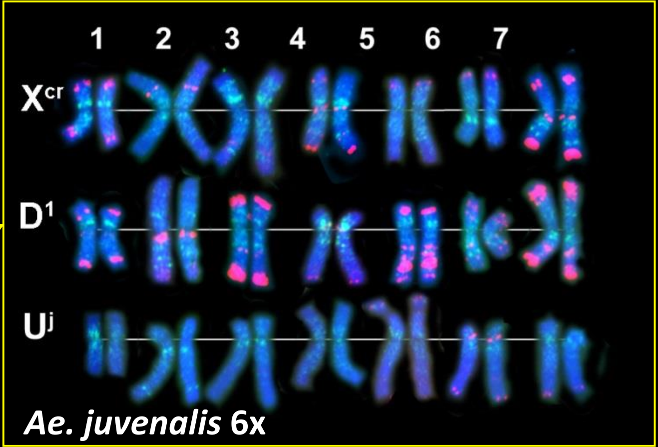
The tetraploid *Ae. crassa* is the parental form of three hexaploid species - *Ae. crassa* (genome $D^1X^{cr}D^2$), *Ae. vavilovii* (genome $D^1X^{cr}S$) and *Ae. juvenalis* (genome $D^1X^{cr}U$). FISH analysis reveals that labeling patterns of the hexaploid *Ae. crassa* and *Ae. vavilovii* chromosomes are the same to what is seen in the parental species. In contrast, we found significant alterations in the distribution of the *Fat* probe on the chromosomes of all three genomes of *Ae. juvenalis,* some of which are likely to be due to chromosomal rearrangements that have occurred over the course of evolution (Badaeva *et al.* 2002).

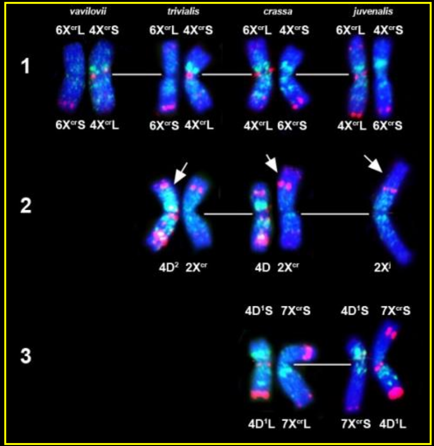




Ae. tauschii

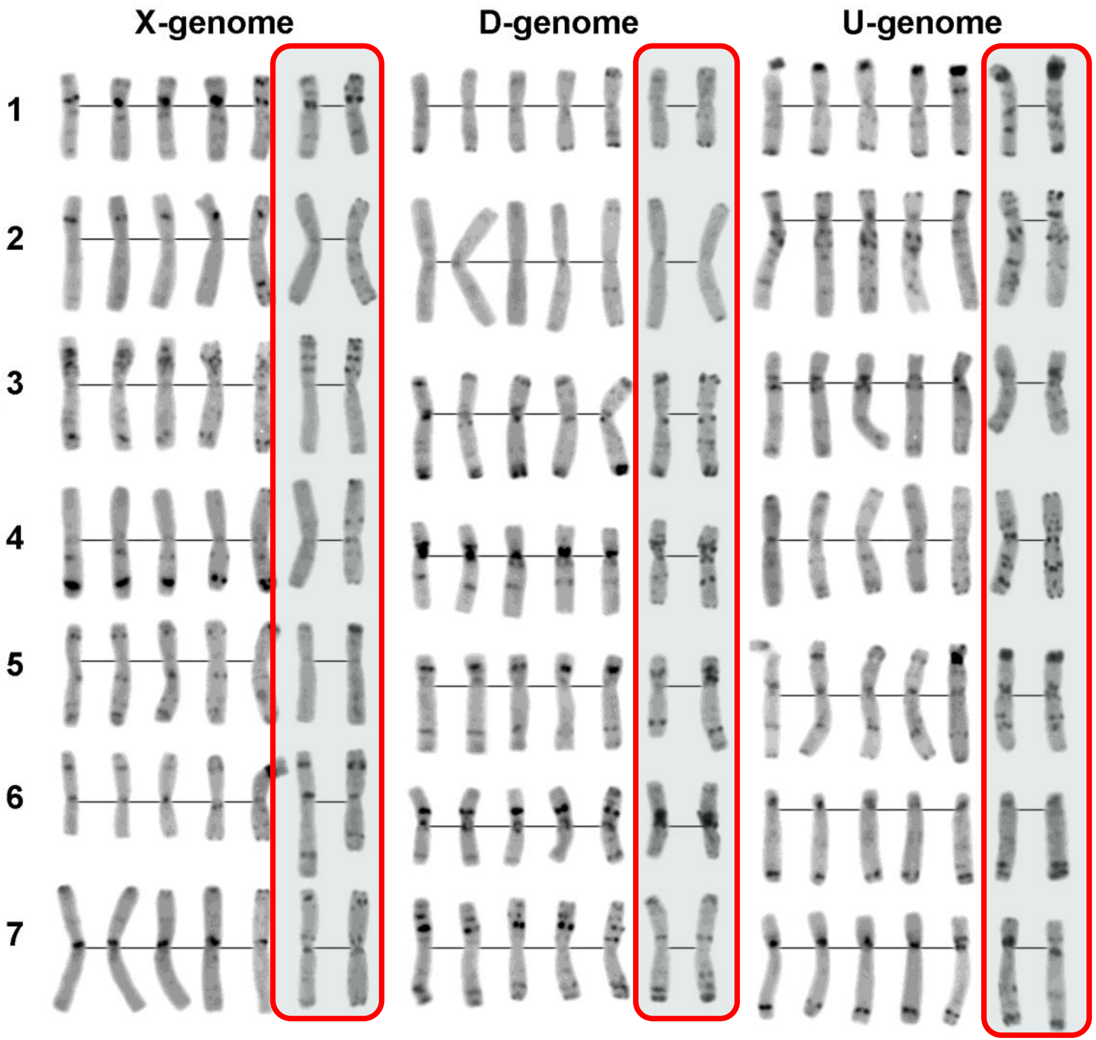




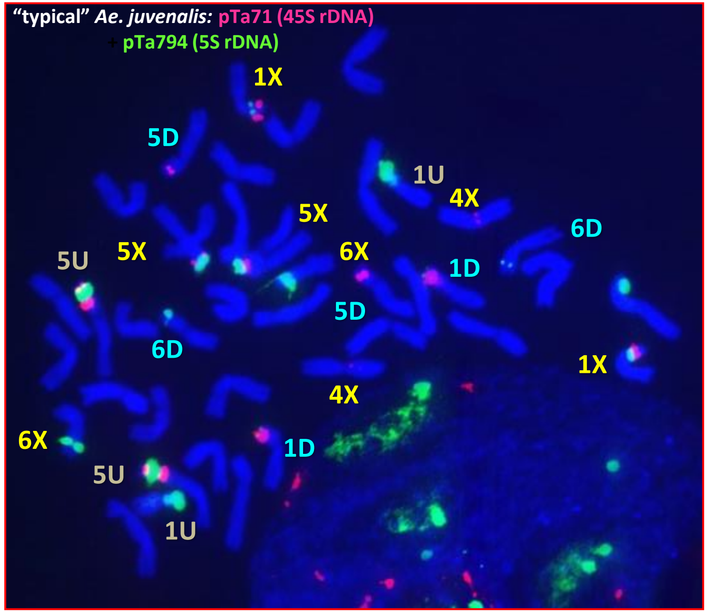


Chromosomal rearrangements in polyploid species of complex Crassa:

1. T4X^{cr}:6X^{cr} (*Ae. crassa,* 4x and *Ae. juvenalis*),
2. T4D^2:2X^{cr} (*Ae. crassa,* 6x) and 2X^{cr}:? (*Ae. juvenalis*),
3. T4D^1:7X^{cr} (*Ae. juvenalis*).



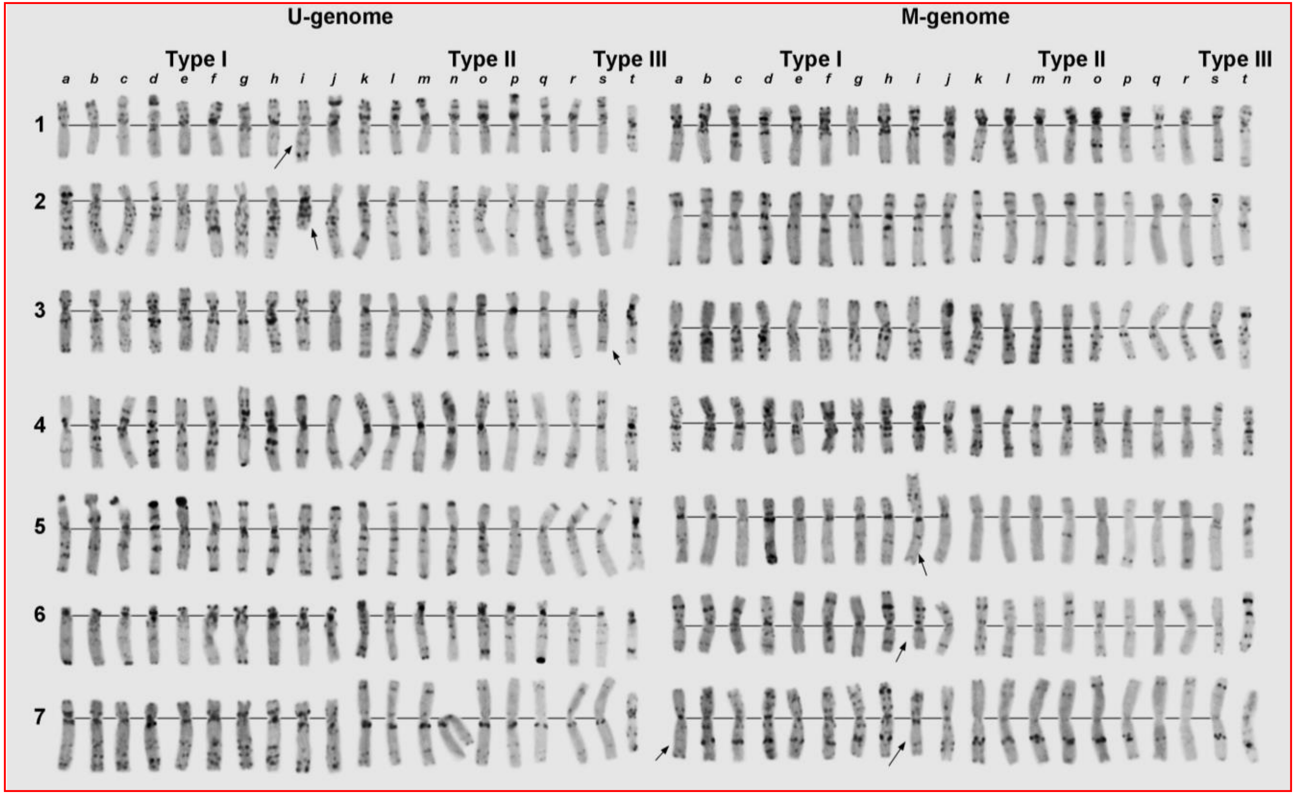
C-banding analysis divided *Aegilops juvenalis* into two groups. The first – "typical" group is non-polymorphic and it is broadly distributed. The chromosomes are highly rearranged compared to the parental species. The second group includes two accessions. Karyotypically they do not differ from parental species and probably, derived recently from new hybridization event between *Ae. crassa x Ae. umbellulata.*



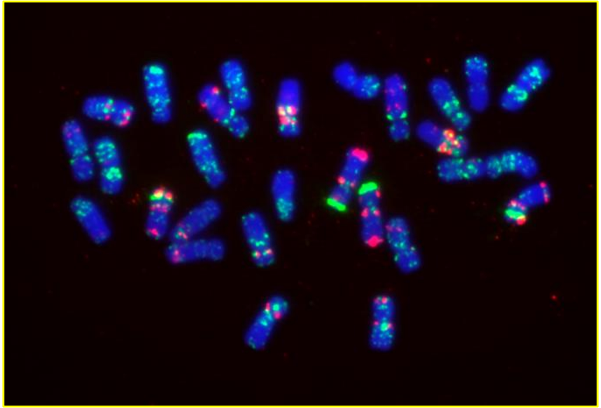
Polyploid *Aegilops*: U-genome cluster

Aegilops biuncialis - UUMM

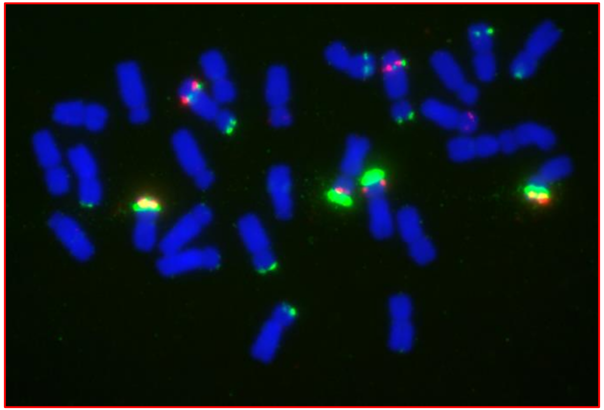
We found differences between the three groups of *Ae. biuncialis* also in labeling patterns of *pSc119.2 pAs1, pTa-535,* and *Fat* probes, 5S and 45S rDNA. These differences could be caused by chromosomal rearrangements. Alternatively, they can reflect multiple origins of the species.



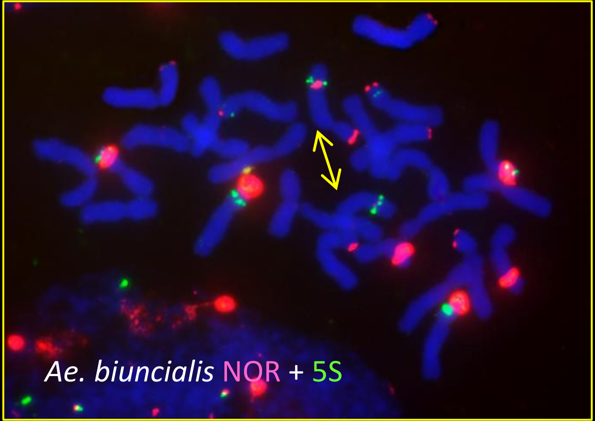
C-banding analysis subdivided *Ae. biuncialis* into three unequal groups. The first one is widespread and found in all regions of species distribution, the second is restricted to Cyprus and Israel, and the third is found in one accession from Libya. Representatives of these groups differ in karyotype structure and C-banding patterns of most chromosomes.



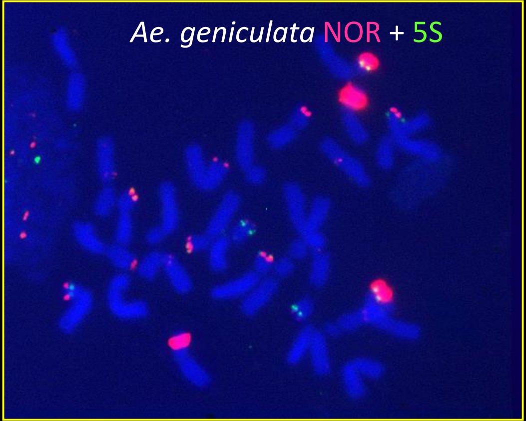
Ae. biuncialis pAesp_SAT86 + GAA



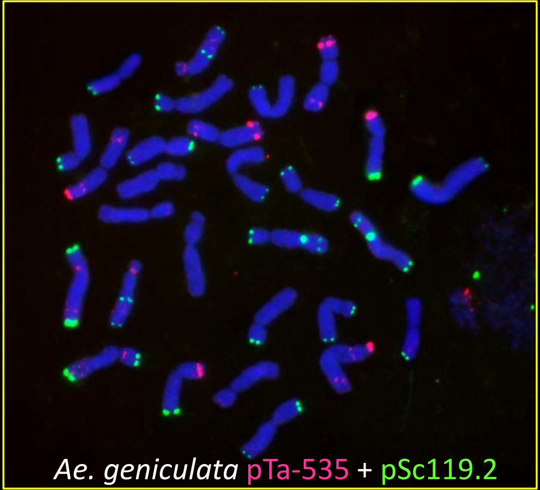
Ae. biuncialis NOR + 5S



Ae. biuncialis NOR + 5S



Ae. geniculata NOR + 5S

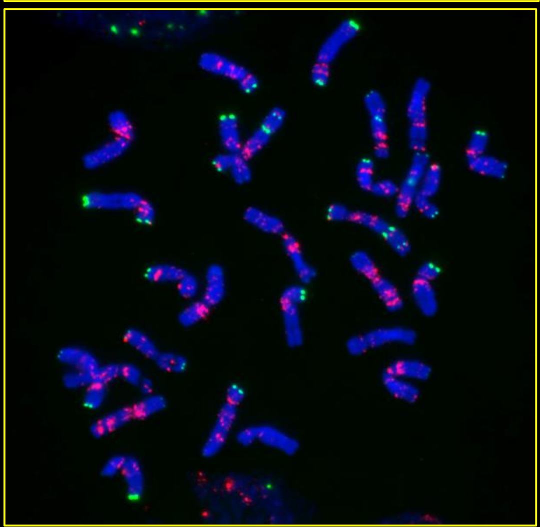


Ae. geniculata pTa-535 + pSc119.2

Ae. comosa NOR + 5S

Ae. umbellulata NOR + 5S

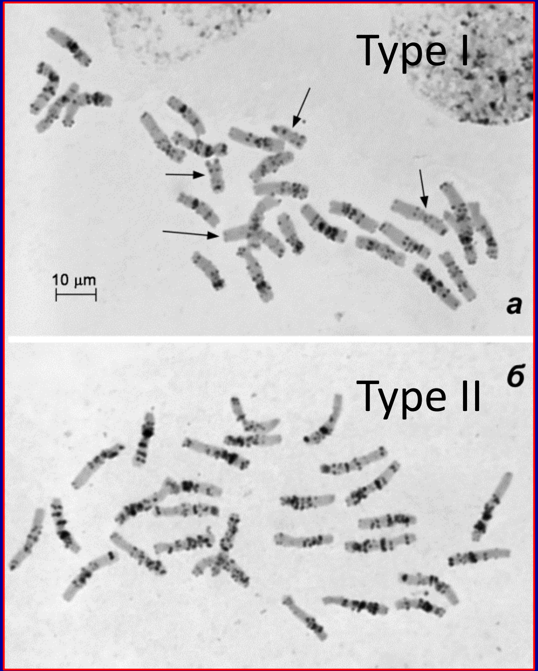
The results of FISH analysis with 45S and 5S rDNA probes showed that *Ae. geniculata* is more similar to the parental species *Ae. comosa* and *Ae. umbellulata* than *Ae. biuncialis* in the number and location of rDNA loci. This indicates that formation of *Ae. biuncialis* was accompanied with significant changes of parental genomes which led, in particular, to the transition of 5S rDNA locus and minor NOR from short to the long arm of chromosome 5M. Many minor NORs on the M-genome chromosome were lost. In both species all functional NORs are located on the U-genome chromosomes, whereas the NORs of the M-genome chromosomes are suppressed. These species show distinct hybridization patterns with pSc119.2, pAs1, pTa-535, pAesp_SAT86, and FAT DNA sequences

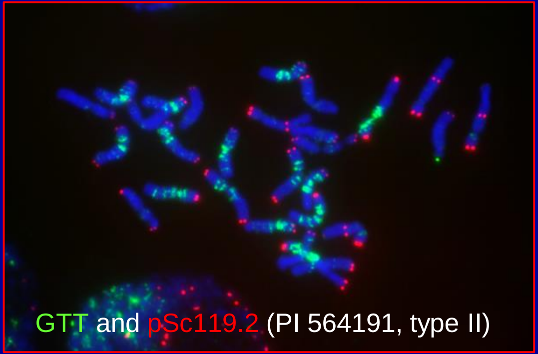


Ae. geniculata CTT + pSc119.2

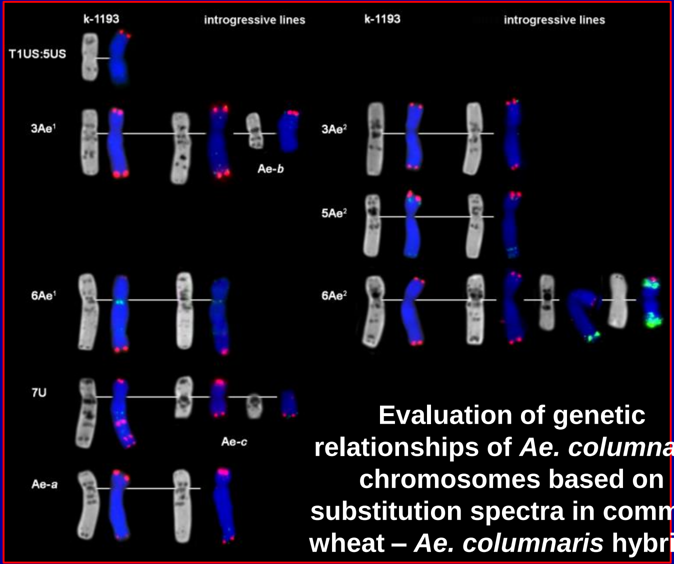
Aegilops columnaris

Two chromosomal types are distinguished in *Ae. columnaris*. They differ significantly in karyotype structure, C-banding patterns, FISH with pSc119.2 and pAs1 probes, the number and location of 5S and 45S rDNA loci. Type I is dominant and found in different areas of species distribution, the type II is identified in four Turkish accessions. These two types are probably derived from different hybridization events.

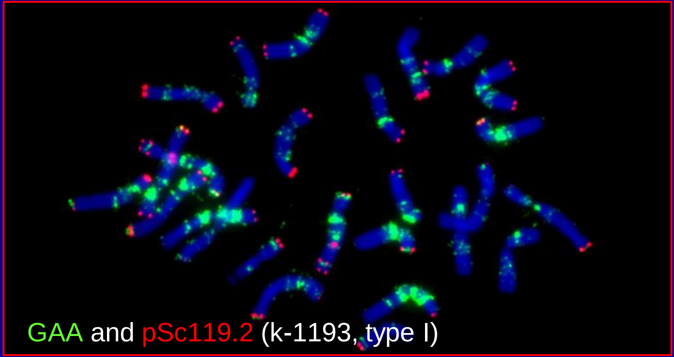




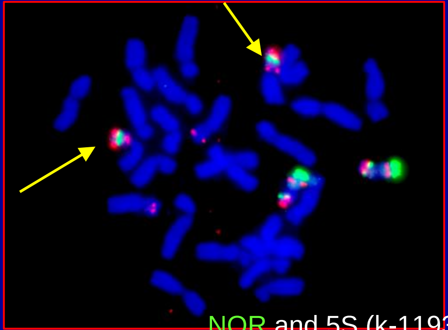
GTT and pSc119.2 (PI 564191, type II)



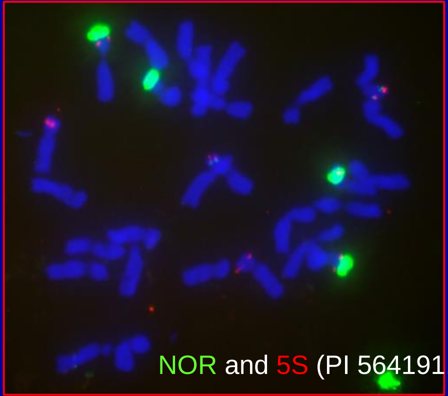
Evaluation of genetic relationships of *Ae. columnaris* chromosomes based on substitution spectra in common wheat – *Ae. columnaris* hybrids.



GAA and pSc119.2 (k-1193, type I)

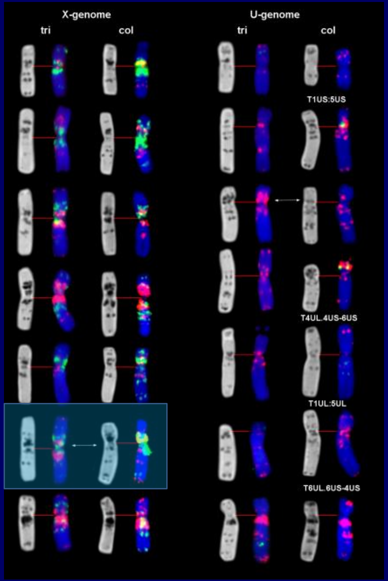


NOR and 5S (k-1193, type I)



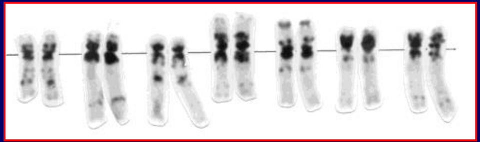
NOR and 5S (PI 564191, type II)

Aegilops triaristata- Ae. recta

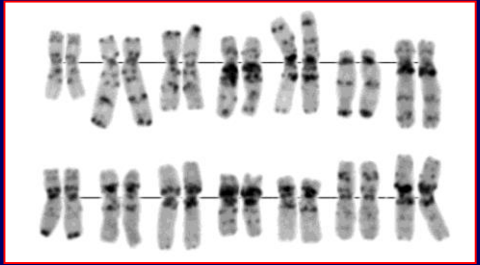


Ae. triaristata is similar with *Ae. columnaris,* type I in karyotype structure, C-banding patterns, the number and distribution of 5S and 45S rDNA loci. No intraspecific divergence has been observed in this species. Genomes of *Ae. recta* are not modified compared to genomes of the parental species. Specific chromosomal type – Spanish, which differs from normal in the presence of intergenomic translocation can be distinguished in *Ae. recta.* Formation of this hexaploid species is not associated with any gross chromosomal changes.

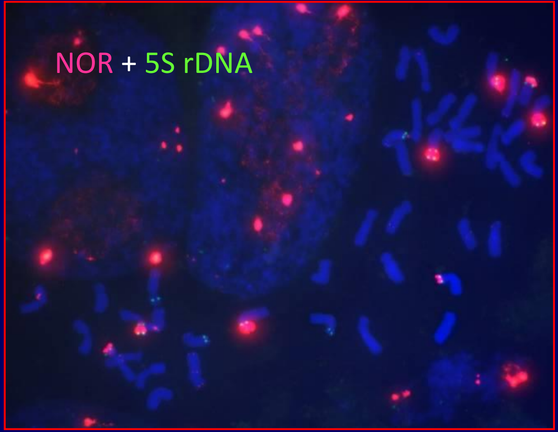
Ae. uniaristata

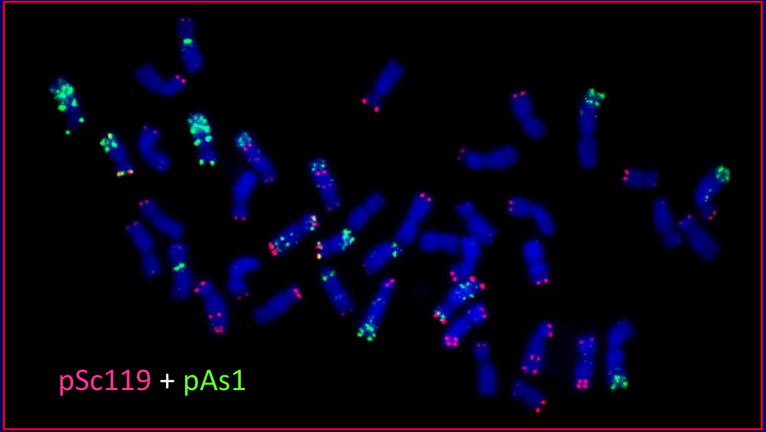


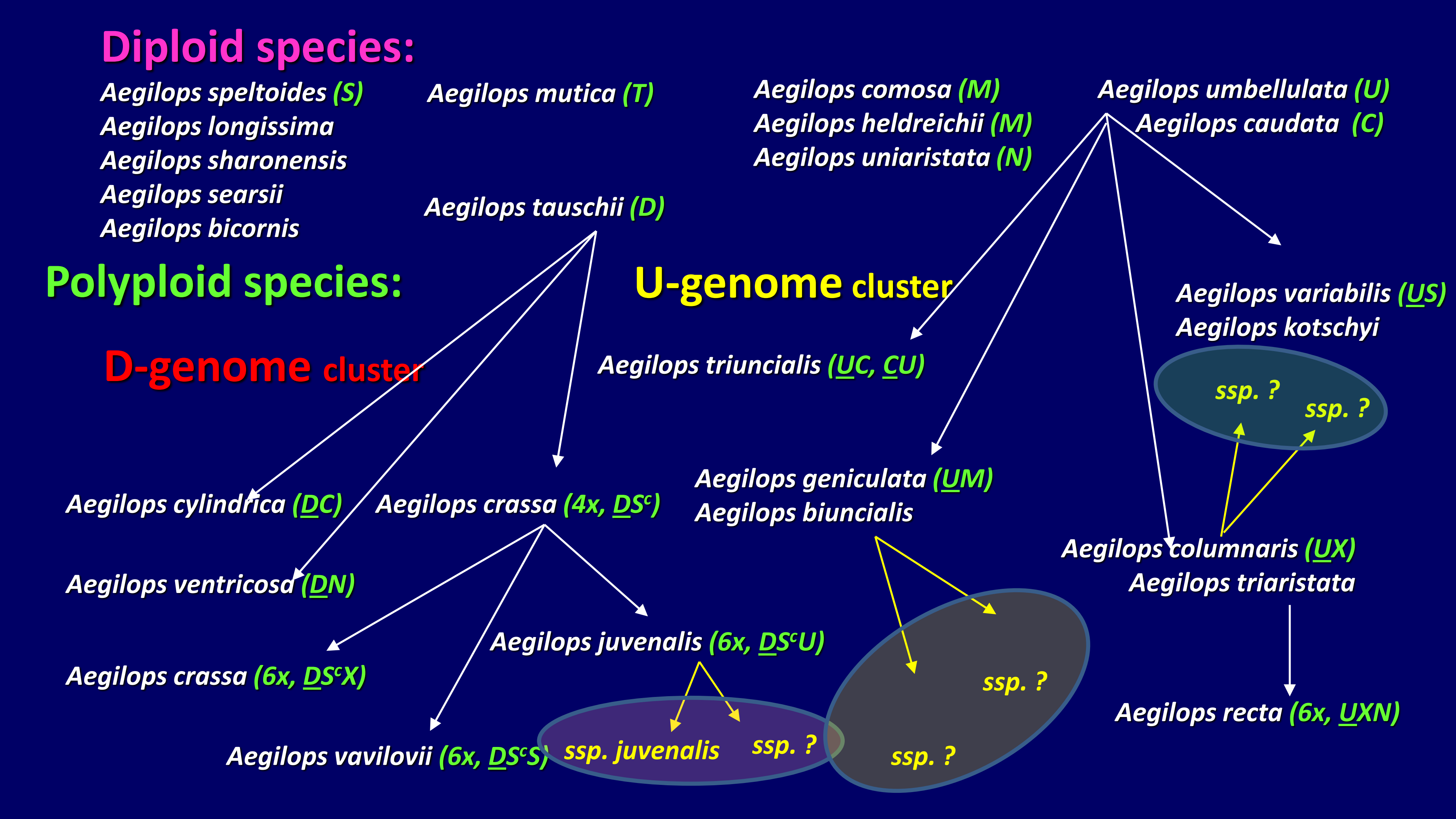
Ae. triaristata



K-1469, *Ae. recta*






Diploid species:
Aegilops speltoides (S)
Aegilops longissima
Aegilops sharonensis
Aegilops searsii
Aegilops bicornis
Aegilops mutica (T)
Aegilops tauschii (D)
Aegilops comosa (M)
Aegilops heldreichii (M)
Aegilops uniaristata (N)
Aegilops umbellulata (U)
Aegilops caudata (C)
Polyploid species:
D-genome cluster
U-genome cluster
Aegilops variabilis (US)
Aegilops kotschyi
ssp. ?
ssp. ?
Aegilops triuncialis (UC, CU)
Aegilops cylindrica (DC)
Aegilops crassa (4x, DS^c)
Aegilops geniculata (UM)
Aegilops biuncialis
Aegilops columnaris (UX)
Aegilops triaristata
Aegilops ventricosa (DN)
Aegilops juvenalis (6x, DS^cU)
Aegilops crassa (6x, DS^cX)
ssp. ?
Aegilops recta (6x, UXN)
Aegilops vavilovii (6x, DS^cS)
ssp. juvenalis
ssp. ?
ssp. ?

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WGGRC, KSU, U.S.A.
ICARDA, Aleppo, Syria
Institute of Evolution, University of Haifa, Israel
Weizman Institute of Science, Rehovot, Israel
Kyoto University, Japan
IPK, Gatersleben, Germany
ICG, Novosibirsk, Russia
Institute of Botany, Erevan, Armenia

Thank you for attention!