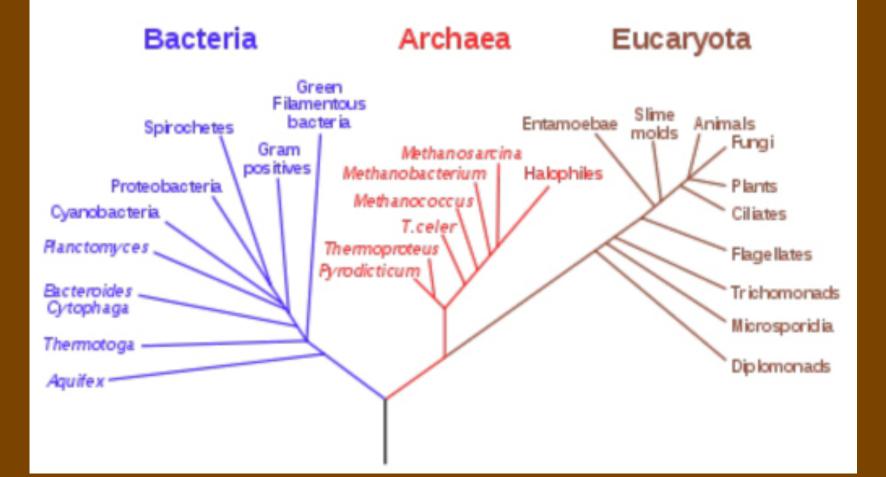
Introductory Mycology BI 432/532 Lecture 2: Overview of Fungi



Phylogenetic Tree of Life



Fungi are:

- Microbes (mostly)
- Eukaryotic, heterotrophic organisms that obtain nutrients by <u>absorption</u> and reproduce by <u>spores</u>.

Extracellular enzymes act on complex substrates, low molecular weight breakdown products are absorbed through the fungal cell wall.

Fungi live in their food.

Nutrition

- Heterotrophs (chemoheterotrophs)
- Aerobes, facultative anaerobes (except Neocallimastix)
- Absorptive nutrition
- Secrete extracellular enzymes that act on complex substrates
- Saprobes: decay dead organic matter
- **Parasites**: biotroph, necrotroph



Reproduce by **spores**

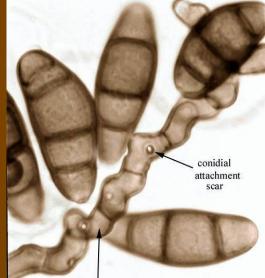
Reproduction, dissemination or survival structures

A differentiated structure that may be specialized for dissemination, a resistant structure produced in response to adverse conditions, and/or produced during or as a result of a sexual or asexual reproductive process.

Spores may be one-celled or multicelled, colorless or pigmented (brown)







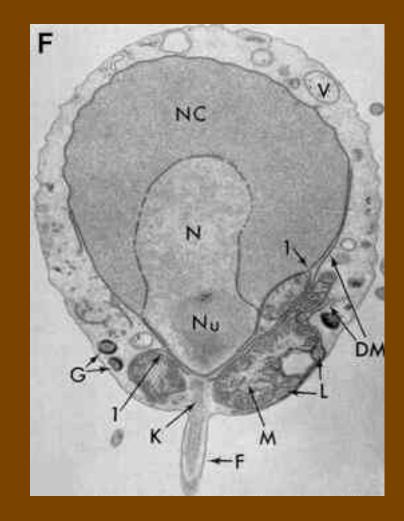
Fungal spores



Spores of some true fungi (chytrids), and funguslike taxa (Oomycetes) are motile zoospores



Chytrid zoospores have a single posteriorly directed flagellum



Oomycetes

fungus-like organisms more closely related to plants than to true fungi

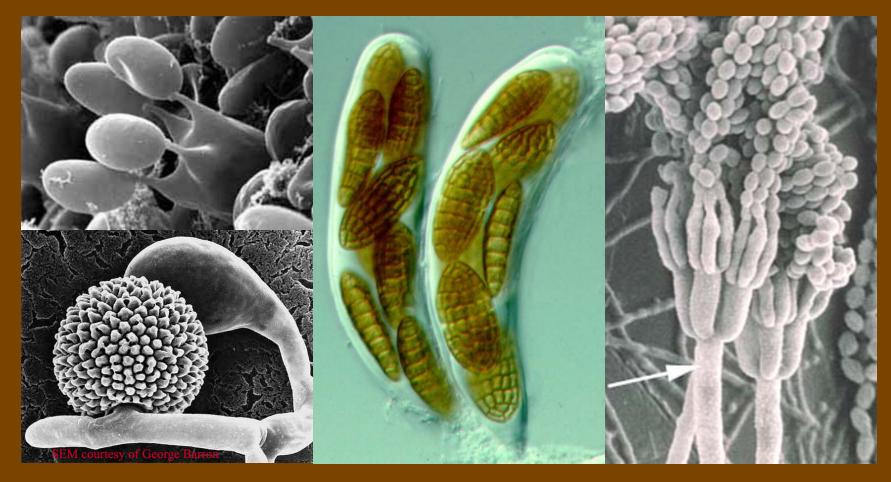


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Oomycete zoospores have two flagella, one anteriorly directed and one posteriorly directed Spores of "higher fungi"—zygomycetes, ascomycetes, basidiomycetes are non-motile

Spores of fungi may result from sexual (meiotic division) or asexual (mitotic division) processes

Major groups of fungi (phyla) mainly based on how sexual spores are formed



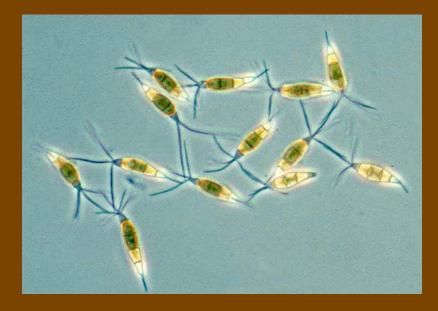
Asexual spore diversity





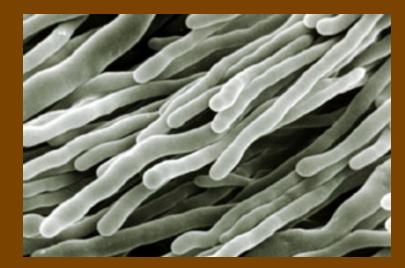






Cellular structures

- Simple organization, vegetative (thallus) and reproductive structures (sporocarps, sporangia)
- The somatic body of most fungi is a thallus composed of hyphae (sing. hypha) that elongate by tip growth
- unicellular (yeast), filamentous, or both (=dimorphic)
- **Hypha** (pl. hyphae) is the basic "cellular" unit in filamentous fungi; they may be septate or coenocytic (aseptate); collectively a **mycelium**





200 years of research on hyphae

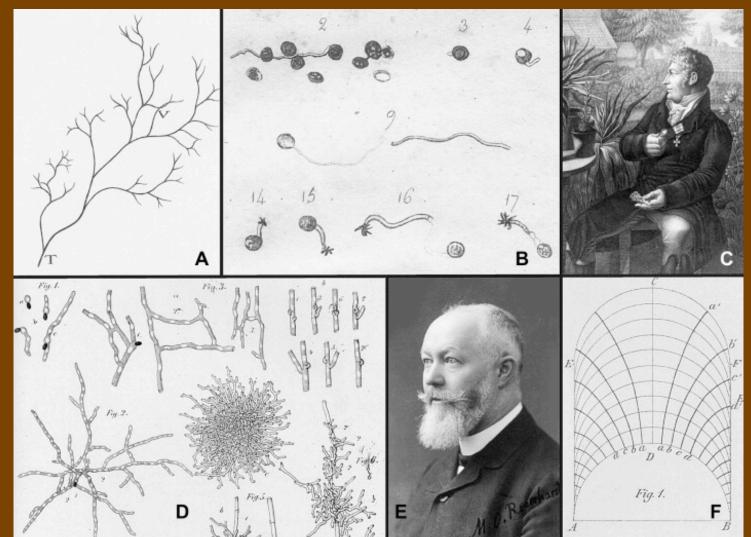
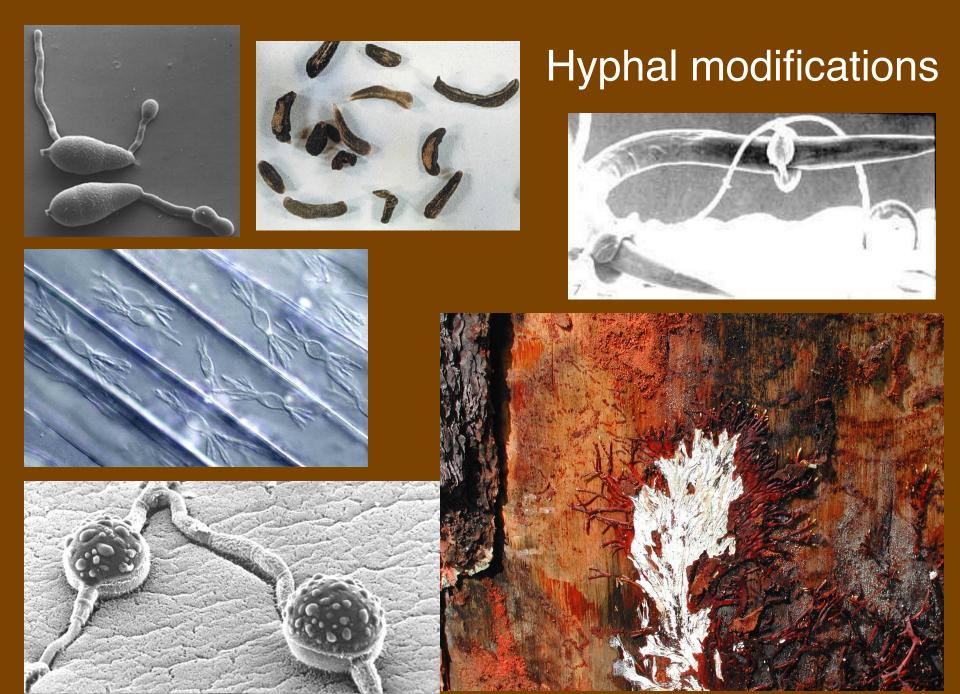


Fig 1. Early research on hyphae. (A) The first illustration of hyphae from Malpighi's (1675–1679) Anatome Plantarum. (B) Detail from classic illustration of spore germination in Tilletia caries by Prévost (1807). (C) Carl Ludwig Willdenow (1765–1812), the scientist who coined the term 'hypha' in 1810. (D) Illustration of spore germination and hyphal development by Oscar Brefeld (1872). (E) Max Otto Reinhardt (1854–1935). (F) Diagram of hyphal apex showing trajectories of points on the surface of the extending cell wall from Reinhardt (1892).

Hyphal modifications: variations on a simple structure

infection structures appressoria, haustoria, rhizomorphs survival structures sclerotia, chlamydospores dispersal structures conidia – asexual spores trapping structures nematode traps, nets, adhesive knobs



Reproduction

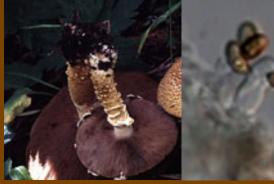
- Sexual reproduction: spores have meiotically derived nuclei
- Monoecious or dioecious: reproductive structures of one or both mating types may be present in the same individual
- Homothallic (self fertile/compatible)
- Heterothallic (obligately outcrossing)
- Genetic mating system MAT loci in ascomycetes, single locus, two allele

Tetrapolar or bipolar systems in basidiomycetes--1 to hundreds of "sexes"

- Asexual reproduction
 - Spores with mitotically derived nuclei







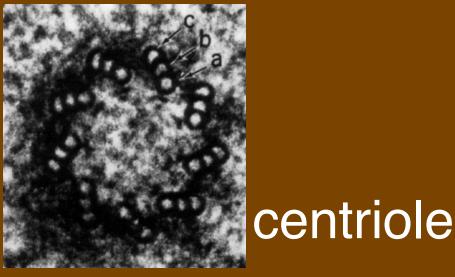


Different fungi may have sexual, asexual, or both modes of reproduction in life cycle

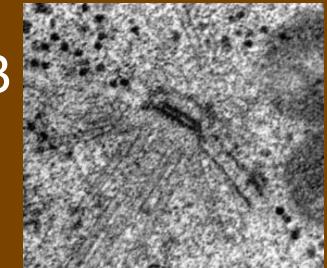
sexual reproduction: nuclei derived from meiotic division, sometimes called meiospores (ascospores, basidiospores, zygospores)

asexual reproduction: nuclei derived from mitotic division, sometimes called mitospores (conidia, sporangiospores)

- Mitosis
 - intranuclear: nuclear membrane doesn't break down until late in mitosis
 - centric in flagellated forms; typical centrioles of eukaryotes
 - noncentric in nonflagellated forms; possess spindle pole bodies (SPBs); differ from centrioles in lacking microtubular component



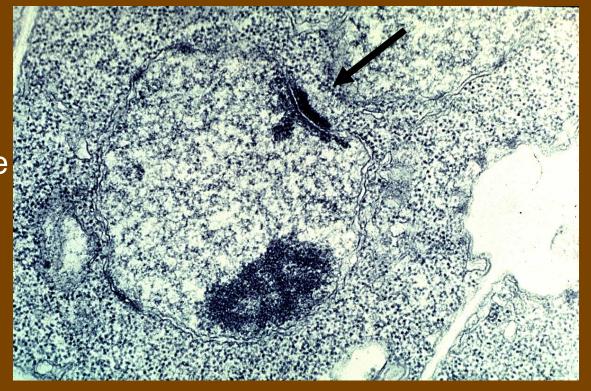
SPB



Spindle pole bodies (SPB)

Nucleus associated structure, function like centriole

Function as microtuble organizing centers in nuclear divisions Duplicates during prophase, move to opposite sides of dividing nucleus Spindle apparatus develops



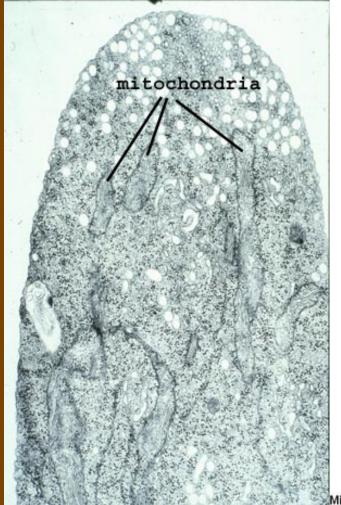
Organelles

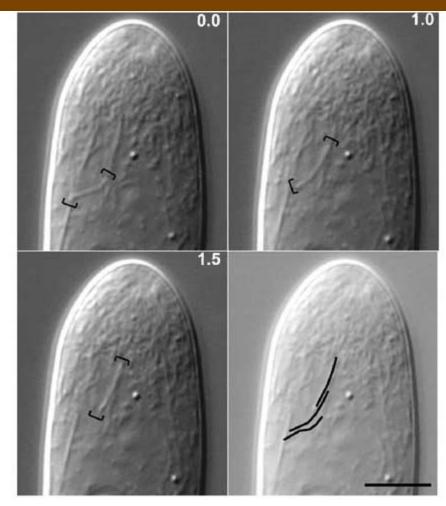
- typical eukaryote assemblage of organelles + fungal specific ones (e.g. chitosomes)
- mitochondria
- endoplasmic reticulum
- dictyosome cisternae (=golgi apparatus)
- vacuoles
- microbodies

function in fatty acid degradation, SOD dissipation, N metabolism

Mitochondria

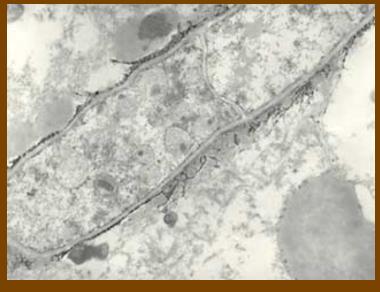
Most organelles aggregated behind hyphal tip; cytoplasm more distant behind tip becomes vacuolate, inactive.

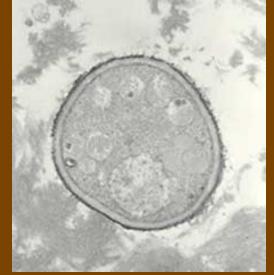


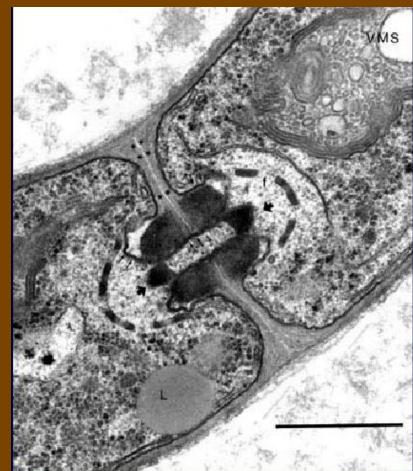


Mitochondrion movement in region IIA: McDaniel and Roberson, Fungal Genetics and Biology (in press)

Fungal cells have cell walls

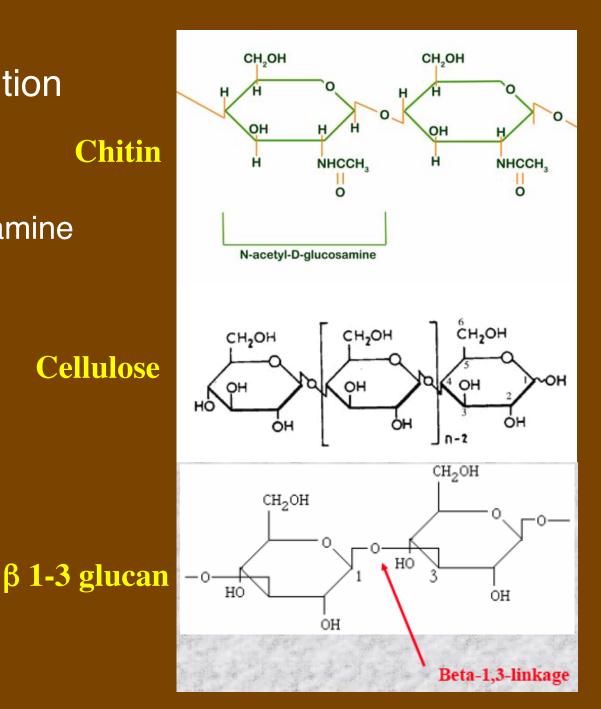






Cell Wall Composition

- chitin
- β1-4 n-acetyal glucosamine
- β-glucans
 polymers of glucose
- β1-3 gluc
- cellulose in few
- β 1-4 glucose



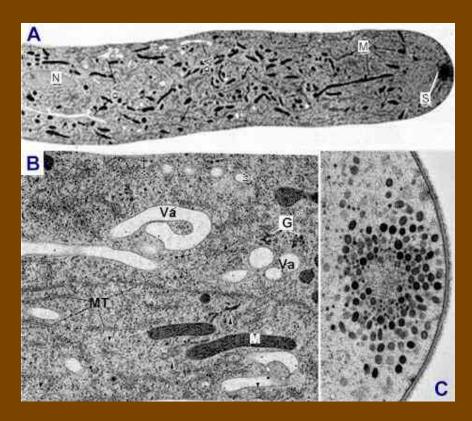


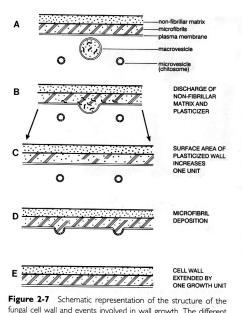


•fungal specific organelles involved in cell wall growth **Spitzenkörper** associated with growing hyphal tips in septate fungi

chitosome

microvesicles transporting chitin synthases to growing cell wall

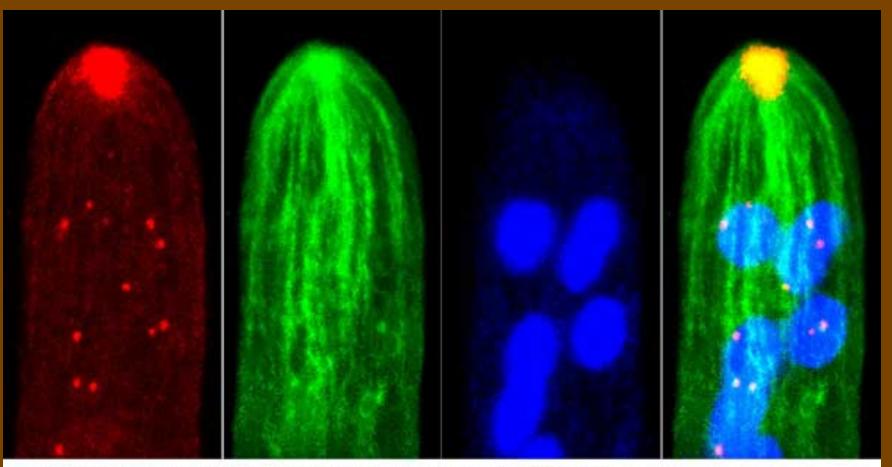




fungal cell wall and events involved in wall growth. The different events are depicted in consecutive steps (A–E) for the sake of clarity but are presumed to occur simultaneously.

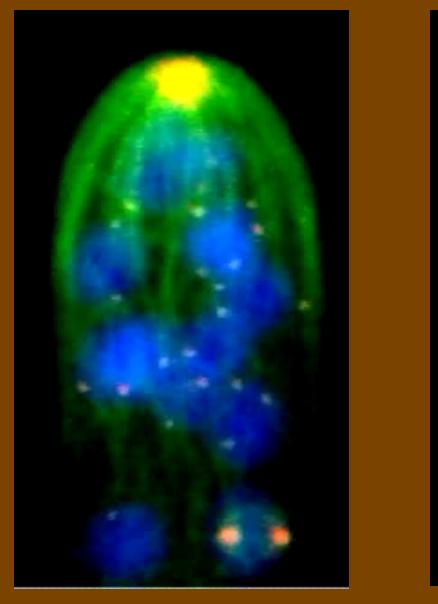
Cytoskeleton

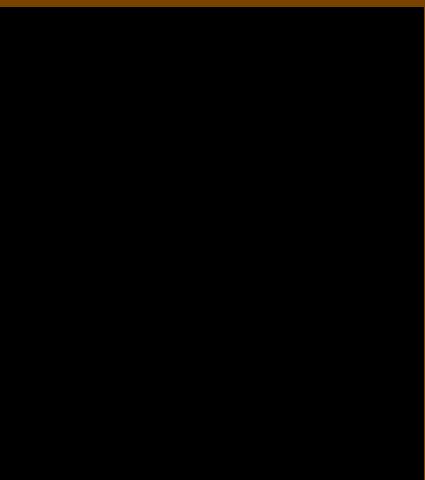
Micotubule (tubulin) and actin filaments, an internal scaffold system Hyphal growth is polar – extension at the hyphal tip Vesicles move along cytoskeleton to deposit wall synthesis materials



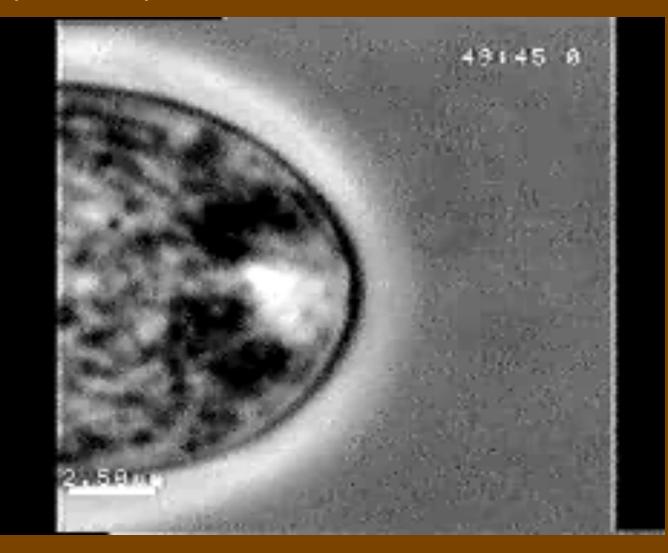
γtubulin, α-tubulin, nuclei: McDaniel and Roberson 1998 Protoplasma 203:118-123

The Spitzenkörper Vesicles, chitosomes actin filaments





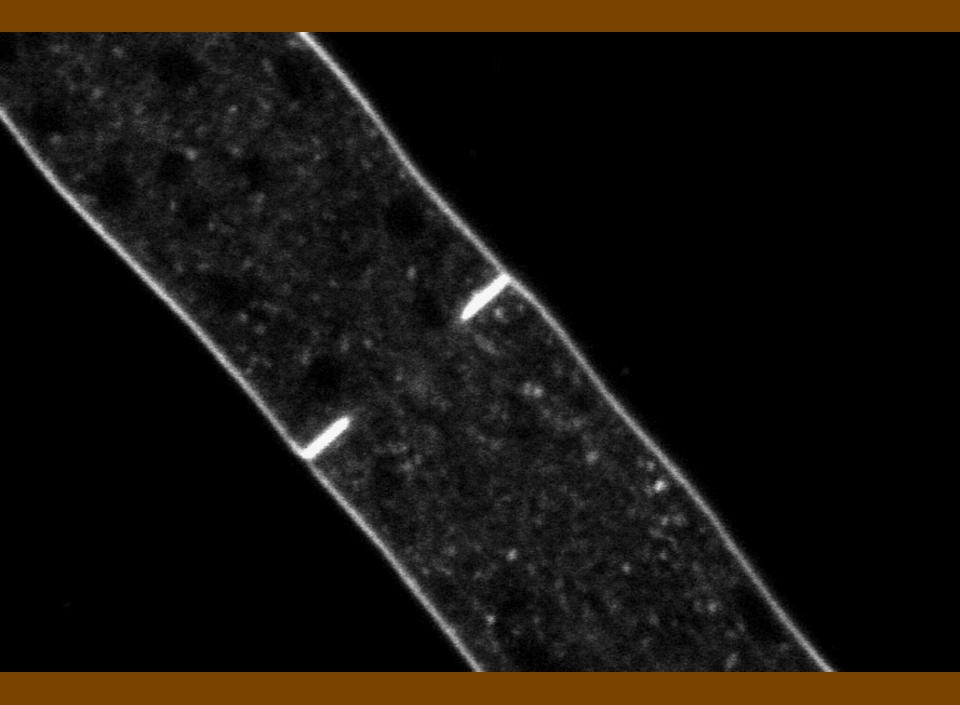
Cell wall synthesis materials are produced behind the hyphal tip and transported on the cytoskeletal scaffold to the Spitzenkörper



SECONDERVISION CONTRACTOR









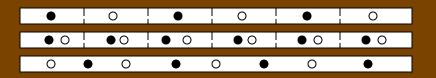
Fungi vary in number of nuclei and sometimes types of nuclei in cells

- Uni, bi- or multinucleate, depending on phylum/order
- Haploid, diploid (uncommon)
- Monokaryon, homokaryon

All nuclei are identical, there may be mutliple nuclei per hyphal compartment (cell)

• Dikaryon, heterokaryon

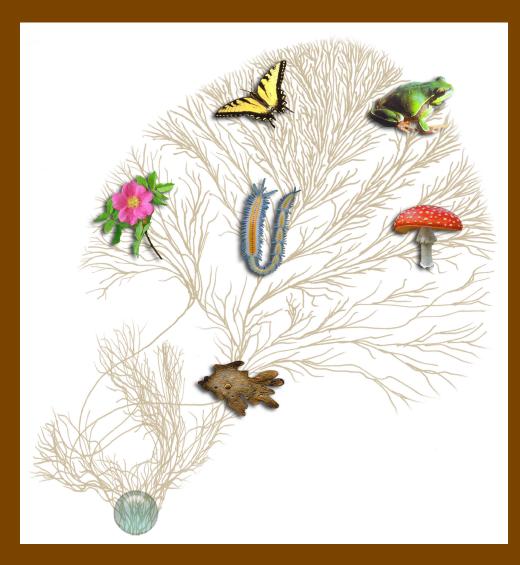
Unique to fungi, 2 different, compatible haploid nuclear types pair and divide synchronously; delay between fusion of gametes and fusion of nuclei



Different dikaryon types

Phylogeny

- Phylogeny, phylogenetics: the study of evolutionary relationships
- Whittaker (1969) proposed 5 kingdoms:
 - Prokaryotes, Eukaryotes (Animals, Plants, Fungi, Protists)
- At least 7 kingdoms are now recognized:
 - Eubacteria
 - Archaebacteria
 - Animalia
 - Plantae
 - Eumycota (Fungi)
 - Stramenipila (Chromista)
 - Protoctista (Protozoa, Protista)



Phylogenetics: inferring evolutionary relationships, lineages

Prior to PCR & gene sequencing, phylogenetic relationships were inferred from:

Morphology: structure, subcellular structure
Biochemistry: synthetic pathways, composition of cell components
Shared life history traits
Ecological characteristics
Reproductive structures and mechanisms

all subject to errors, evolutionary convergence

Traditional phylogenetics (morphology/ecology) Recognition of Fungi as a separate kingdom Whittaker (1969) predated gene sequencing, molecular phylogenetics.

Fungi were recognized as a distinct evolutionary lineage based on:
filamentous structure
reproduction by spores
absorptive, heterotrophic nutrition
Major groups, phyla, within the fungi were also well established prior to
DNA sequencing, based on details of structures, reproduction, cell wall
composition, biochemical pathways, cellular organelles, ecology.
TRUE Fungi comprise a separate lineage, but not all organisms formerly

classified as Fungi are part of the same lineage

Fungal phyla: Ascomycota Basidiomycota Zygomycota Chytridiomycota Oomycota—later shown to belong to the plant lineage

Molecular phylogenetics

Since 1990s, development of polymerase chain reaction (PCR), rapid **DNA** sequencing and computing capacity, phylogenetic inferences have increasingly been based on comparisons of gene sequences.

			20	30	40	50	60	70	80	90	100	110
A.flavus	:	TCGTCCCTCAACGT	CAGTTTTTACA	TAGAAGGATG	CCTTCGCCGTTAC	C-AGTCCTT	CTGGTATCA	AA-GTATTTC	ATCCCTACTC	CA(GAAATTCTTC	CTTCTC
A.fumigatus	:	TCGTCCCTCAACGT	CAGTTTTTACA	TAGAAGGATG	CCTTCGCCGTTAC	C-AGTCCTT	CTGGTATCA	AG-GTATTTC	ATCACTACTC	CA(GAAATTCTTC	CTTCTC
A.niger A.ochraceus	:	TCGTCCCTCAACGT TCGTCCCTCAACGT										
A.penicilloides	÷	TCGTCCCTCAACGT	CAGTTTTTACA	TAGAAGGATG	CCTTCGCCGTTAA	C-AGTCCTT	CTGGTATTA	AA-GTATTCT	ATCACTACTC	CA(GAAATTCTTC	CTTCTT
A.silverticus	:	TEGTCCCTCAAEGT	CAGTTTTTACA	TAGAAGGATG	CCTTCGCCGTTAC	C-AGTCTCT	CTGAGATTA	TTCATATTAA	ATCACTACTC.	CA(GARATTCTTC	CTCETT
A.versicolor	:	TCGTCCCTCAACGT	CAGTTTTTACA	TAGAAGGATG	CCTTCGCCGTTAC	C-AGTCTCT	CTGAGATTA	TTCATATTAA	ATCACTACTC	CA(GAAATTCTTC	CTCOTT
E.herbariorum	:	TCGTCCCTCAACGT	CAGTTTTTACA	TAGAAGGACG	CCTTCGCCGTTAT	C-AGTCCTT	CTGGTATTA	AAA-TATTCT	ATCACTACTC	CA(GAAATTCTTC	CTTCTC
P.commune	:	TCGTCTCTCAACGT	CAGTTATTACA	TAGAAGGACG	CCTTCGCCGTTGA	C-AGTCCTC	CTGGTATCA	TCA-AATTTT	ATCTCTACTC	CA(GAAATTCTTC	CTTCTC
P.frequentans P.italicum	:	TCGTCTCTCAACGT TCGTCTCTCAACGT	CAGITATTACA	TAGAAGGACG	COTTOGOCOTTGA	C-AGTCCTC	CTCCTATCA	ACA-AATTCI	ATCTCTACTC	CAJ	CARAFTCTTC	CTTCTC
P.brevicompactum		TCGTCTCTCAACGI	CAGTTATTACA	TAGAAGGACG	CCTTCGCCGTTGA	C-AGTCCTC	CTGGTATTA	AC-GAATTCT	ATCTCTACTC	CA(GGAATTCTTC	CTTCTC
P.variotii		TCGTCCCTCAACGT										
M.plumbeus	:	TOGTACCTCAGOGT	CAGTGTTTAGT	TAGAAAGAAG	CCTTCGCCTTAAG	CG-GTCTTC	CGAGGATCA	ACAG-ATTCC	ATCCCTACTC	TC(GGAGTTCCTC'	TTTCCT
R.microsporus	:	TCGTACCTCAGCGT TCGTACCTCAGCGT	CAGTGTTTAGT	тадалалаб	CCTTCGCCTTAAG	CG-GTCTTC	CGAAGATCA	ACAG-ATTTC	ATCCCTACTT	TC(GGAGTTCCTT'	TTTCCT
R.rhizopodi	:	TCGTACCTCAGCGI	CAGTGTTTAGT	TAGAAAAAAG	CCTTCGCCTTAAG	CG-GTCTTC	CGAAGATCA	ACAG-ATTTC	ATCCCTACTT	TC(GGAGTTCCTT	TTTCCT
S.chartarum S.dichroa	:	TCGTCCTTTAACGT TCGTCCTTTAACGT										
S.kampalensis		TCGTCCTTTAACGT										
S.oenanthes	:	TCGTCCTTTAACGT	CAGTTGTGACC	TAGAGAGCTG	CCTTCGCATTAAC	CGAGTCCCT	TTGGTATAA	AC-GGATTTT	ATCCCTCCTC	CT1	TAAGTACTGT	TCTCTT
T.harzianum	:	TCGTCCTTTAACGT	CAGTTTTCACA	TAGAGGGCTG	CCTTCGCCTTTAC	CGAGTCCCT	TTGGTATCA	TA-GAATTTC	ATCTCTCCTC	CT(CAAGTACTGC	CCTOTT
T.pseudokoniigi	:	TCGTCCTTTAACGT										
T.reesei	:	TCGTCCTTTAACGT	CAGTTTTTACA	TAGAAGGCTG	CCTTCGCCTTTAC	CGAGTCCCT	TTGGTATCA	TA-GAATTTC	ATCTCTCCTC	CT(CAAGTACTGC	CCTCTT
T.víríde C.elatum	:	TCGTCGTTTAACGT	CAGTTTTTACA	TAGAAGGCTG	CCTTCGCCTTTAC	CGAGTCCCT	TTGGTATCA	TA-GAATTTC	ATCTCTCCTC	CT(CAAGTACTGC	CCTCTT
C.sphaerospermum		TCGTCCCTCAACGT TCGTCCCTCAACGT	CAGITATIACA	TAGAGGTTTG	COTTOGCCGTTAT	C-GTCCCA	TTAGTATCA	AAA-CATTTT	ATCTCTACTC	CAATGGTT	CTAATATTTT	CTUTC
C.cladosporioide	s :	TCGTCCCTCAACGT	CAGTTATTACA	TAGAGGTTTG	CETTEGECGETAT	CC-GTCCCA	TAAGTATCA	AAA-CATTTT	ATCTCTACTC	CAATGGTT	CTAATATTTT	CCTCTC
C.vaiabile	:				CCTTCGCCGCTAT							
C.oxysporum	:	TEGTECCTCAAEGT	CAGTTATTACA	TAGAGGTTTG	CCTTCGCCGCTAT	CC-GTCCCA	TTAGTATCA	AAA-CATTTT	ATCTCTACTC	CAATGGTTO	CTAATATTTT	CCTETC
C.cucumerinum	:	TCGTCCCTCAACGT TCGTCCCTCAACGT	"CAGTTATTACA	TAGAGGTTTG	CCTTCGCCGCTAT	CC-GTCCCA	TTAGTATCA	AAA-CATTTT	ATCTCTACTC	CAATGGTT	CTAATATTTT	CCTCTC
C.macrocarpum	:	TCGTCCCTCAACGT	CAGTTATTACA	TAGAGGTTTG	CCTTCGCCGTTAT	CC-GTCCCA	TTAGTATCA	AAA-CATTTT	ATCACTACTC	CAATGGTT	CTAATATTTT	CCTCTC
C.herbarum	:	TCGTCCCTCAACGT TCGTCCCTCAACGT	CAGTTATTACA	TAGAGGTTTG	CCTTCGCCGTTAT	CC-GTCCCA	TTAGTATCA	AAA-CATTTT	ATCACTACTC	CAATGGTT	CTAATATTTT(CCTCTC
C.effusum C.cladosporides	, :	TCGTCCCTCAACGT	CAGITATTACA	TAGAGGTTTG	COTTOGOCOTTAT	CC-GTCCCA	TTAGTATCA TTAGTATCA	AAA-CATTTT	ATCACTACTC	CAATGGTT	CTAATATTTT	CTOTC
pisicola		100100010101001			001100000001111	ec precen						
			-	-				o-TaqMan prob				
		Clado-1	aqMan-PF				Cla	ado-SYBRG-P	F			
		120	130	140	150	160	170	190	190	20.0	210	220
		120	130	140			170	180	190	200	210	220
	:	ACATAAAACTCTAG	TAAAAAGT		ACTCATTTAG	.	. λG-Τͳ	TAATTTACC	TCTAGGTACC	CTTTAAAC	CTAATAAAGA	I
A.fumigatus	:	ACATAAAACTCTAG	 ТААААААGT ТАААААААGT		ACTCATTTAG ACTCATTTAG		 AG-TT AG-TT	TAATTTACCG	TCTAGGTACCO	CTTTAAACO	 CTAATAAAGA' CTAATAAAGA'	IGACTA IGACTA
A.flavus A.fumigatus A.niger	:	ACATAAAACTCTAG ACATAAAACTCTAG	TAAAAAAGT TAAAAAAGT		ACTCATTTAG ACTCATTTAG	.	AG-TT AG-TT	TAATTTACCG	TCTAGGTACCO	CTTTAAAC	CTAATAAAGA' CTAATAAAGA' CTAATAAAGA'	IGACTA IGACTA
A.fumigatus A.niger A.ochraceus	:		TAAAAAAGT TAAAAAAAGT TAAAAAAAGT TAAAAAAAGT		ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCATTTAG		AG-TT AG-TT AG-TT AG-TT	TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG	TCTAGGTACCO TCTAGGTACCO TCTAGGTACCO TCTAGGTACCO	CTTTAAACO CTTTAAACO CTTTAAACO	CTAATAAAGA' CTAATAAAGA' CTAATAAAGA' CTAATAAAGA'	ГGАСТА ГGАСТА ГGАСТА ГGАСТА
A.fumigatus A.niger A.ochraceus A.penicilloides	:	АСАТААААСТСТАС АСАТААААСТСТАС АСАТААААСТСТАС АСАТААААСТСТАС ТСАТААААСТСТАС ТТАТААААСТСТАС	 TAAAAAAGT TAAAAAAGT TAAAAAAGT TAAAAAAGT		ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCAATTAG ACTCAATTAG		AG-TT AG-TT AG-TT AG-TT AG-TT	TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG	TCTAGGTACCO TCTAGGTACCO TCTAGGTACCO TCTAGGTACCO TCTAGGTACCO	CTTTAAACO CTTTAAACO CTTTAAACO CTTTAAACO	CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA	IGACTA IGACTA IGACTA IGACTA IGATTA
A.fumigatus A.niger A.ochraceus A.penicilloides A.silverticus	:		Г ТААААААGT ТААААААGT ТААААААGT ТАААААААGT ТААААААААТ ТАААСААGT ТАААСААGT		ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCAATTAG ACTCATTTAG ACTCATTTAG ACTCATTTAG			TAATTTACC TAATTTACCC TAATTTACCC TAATTTACCC TAATTTACCC TAATTTACCC TAATTTACCC TAATTTACCC	I I. TCTAGGTACCO TCTAGGTACCO TCTAGGTACCO TCTAGGTACCO TCTAGGTACCO TCTAGGTACCO	CTTTAAAC CTTTAAAC CTTTAAAC CTTTAAAC CTTTAAAC CTTTAAAC CTTTAAAC	I I CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA	II FGACTA FGACTA FGACTA FGATTA FGATTA FGATTA
A.fumigatus A.niger A.ochraceus A.penicilloides A.silverticus A.versicolor E.herbariorum	:	АСАТААААСТСТАС АСАТААААСТСТАС АСАТААААСТСТАС ТСАТААААСТСТАС ТТАТАААСТСТАС АСАТААААСТСТАС АСАТААААСТСТАС ССАТААААСТСТАС			ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCATTTAG		AG-TT AG-TT AG-TT AG-TT AG-TT AG-TT AG-TT	TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG	TCTAGGTACCI TCTAGGTACCI TCTAGGTACCI TCTAGGTACCI TCTAGGTACCI TCTAGGTACCI	CTTTAAAC CTTTAAAC CTTTAAAC CTTTAAAC CTTTAAAC CTTTAAAC CTTTAAAC	II. CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA	I I IGACTA IGACTA IGACTA IGACTA IGACTA IGATTA IGATTA
A.fumigatus A.niger A.ochraceus A.penicilloides A.silverticus A.versicolor E.herbariorum P.commune		АСАТ АЛА АСТСТВО АСАТ АЛА АСТСТВО АСАТ АЛА АСТСТВО ТСАТ АЛА АСТСТВО ТТАТ АЛА АСТСТВО АСАТ АЛА АСТСТВО ТСАТ АЛА АСТСТВО ТСАТ АЛА АСТСТВО ТСАТ АЛА АСТСТВО ТСАТ АЛА АСТСТВО	ТААААААGT ТААААААGT ТААААААGT ТААААААGT ТАААААААТ ТАААААААТ ТАААСААGT ТАААСААGT ТААААААGT ТААААААGT ТААААААGT		ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCATTTAG ACTCATTTAG		AG-TT AG-TT AG-TT AG-TT AG-TT AG-TT AG-TT AG-TT	TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG TAATTTACCG	TCTAGGTACCI TCTAGGTACCI TCTAGGTACCI TCTAGGTACCI TCTAGGTACCI TCTAGGTACCI TCTAGGTACCI TCTAGGTACCI	CTTTAAACC CTTTAAACC CTTTAAACC CTTTAAACC CTTTAAACC CTTTAAACC CTTTAAACC CTTTAAACC CTTTAAACC	II. CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA CTAATAAAGA	I I TGACTA TGACTA TGACTA TGATTA TGATTA TGATTA TGATTA TGACTA
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Clado-TaqMan PR

Molecular phylogenetics

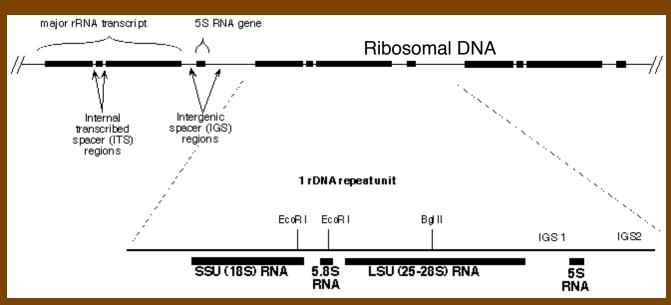
Advantages of direct gene sequence comparisons:

- •each base position in gene sequence an independent character
- possible to have hundreds of characters to compare in a gene sequence, together with invariant base positions that allow sequence alignment
- •can compare shared genes/sites across multiple taxa
- •it is quantitative; relative probabilities can be estimated, statistical tests applied
- neutral mutations can be used

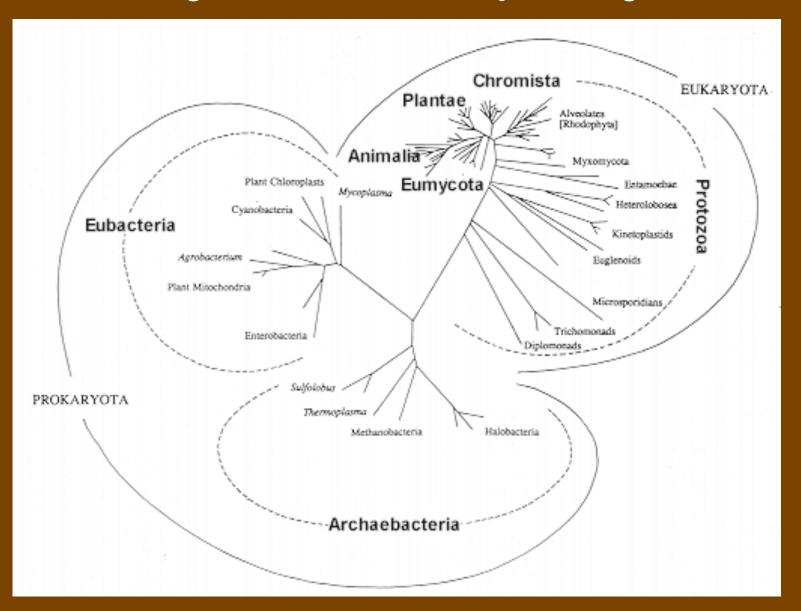
•allow quantitative tests of monophyly (a single evolutionary lineage having a common ancestor, a natural evolutionary group) vs polyphyly (an unnatural group, arising from different evolutionary ancestry)

Molecular phylogenetic analysis

- •Has used mainly ribosomal genes (ITS, LSU, SSU, IGS)
- •Can be used across all eukaryote taxa
- •Nuclear genes
- •Multiple copies in the genome, arranged as a series of repeating units
- •Variable and conserved regions, amenable to testing closely or distantly related taxa
- •Various other genes also used, multigene analyses
 - translation elongation factor (tef 1)
 - •beta tubulin
 - histone



Fungi are one of the "crown eukaryote" groups that diverged about 1 billion years ago



Molecular phylogenetics

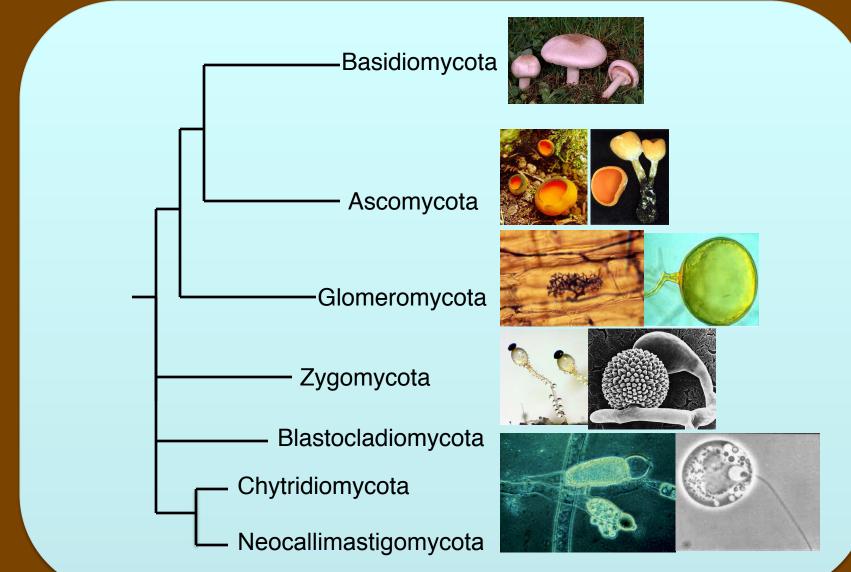
Has helped to settle some long standing questions, and provide new insights concerning evolutionary relationships in the fungi:
•Fungi as traditionally constituted (at least by some mycologists) is polyphyletic.

•The phylum Oomycota has a different ancestry than the true fungi, Eumycota.

•True fungi, Eumycota, are more closely related to animals than to plants. The Oomycota however are a part of the kingdom Chromista (or Stramenopila), together with the Hyphochytridiomycota and Labyrinthulomycota.

•Floridean hypothesis disproved. Hypothesis on evolutionary origin of fungi was that they shared a common ancestry with the red algae (Rhodophyta), based on similarities of reproduction, alternation of diploid sporophyte and haploid gametophyte generations, filamentous growth, parasitism in both groups.

Phyla of Fungi



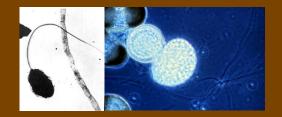
Phylogenetic Classification of Fungi

- Dikarya- Ascomycota+Basidiomycota septate hyphae, complex sporocarps
- Glomeromycota (4 orders, 10 genera) aseptate hypha, lack of meiosis (?)
- Zygomycota (14 orders, ~175 genera)
 mostly aseptate hyphae, zygosporangium
 Dimargaritales
 Endogonales
 Entomophthorales
 Mucorales
 Zoopagales
 Kickxellales
- Chytridiomycota (4 orders, ~110 genera) aseptate hyphae, zoospore Chytridiales Monoblepharidales Spizellomycetales









Recently Recognized Phyla

- Blastocladiomycota (2001; 1 order, 14 genera) Blastocladiales
- Neocallimastigomycota (2007; 1 order, 5 genera) Neocallimastigales

Both formerly orders in Chytridiomycota

Lungi Eumycota, Kingdom, monophyletic

<u>f</u>ungi Eumycota plus fungus-like organisms, polyphyletic

Chromista (Stramenopila) Phyla: Oomycota Hyphochytriomycota Labyrinthulomycota Protists (Protoctists) Phyla: Plasmodiophoromycota Dictyosteliomycota Acrasiomycota Myxomycota

"-mycota" because these groups were traditionally studied by mycologists, not because they are related to Fungi

Some characters that separate the the Kingdom Fungi from "Chromistan fungi

Kingdom Fungi

mitochondria:

cristae flattened

motile cells:

no motile cells or posterior flagellum



Chromistan fungi

cristae tubular

motile cells with anterior or lateral heterokont flagella

cell wall carbohydrate:

 β -glucans, chitin, chitosan



-glucans, cellulose

lysine biosynthesis: alpha-aminoadepic acid (AAA)

storage compound: glycogen, α 1,4 glucan

sterols ploidy

ergosterol haploid in somatic cells

Phyla: (covered in class)

Chytridiomycota Zygomycota Glomeromycota Basidiomycota Ascomycota

mycolaminarins, β 1,3 glucan

fucosterol diploid in somatic cells

diaminopimelic (DAP)

Oomycota Hyphochytridiomycota Dictyosteliomycota Myxomycota

General characteristics of the Phyla of the Kingdom Fungi

Chytridiomycota & Blastocladiomycota: (900 spp.)
•unicellular to mycelial (coenocytic)
•zoospores with single posterior whiplash flagellum
•aquatic & terrestrial

Zygomycota: (1100 spp.)
•generally coenocytic mycelium
•production of zygosporangia & zygospores

Glomeromycota: (170)
formerly part of Zygomycota (Glomales)
coenocytic mycelium
no known sexual reproduction
arbuscular mycorrhizae (Glomerales)

