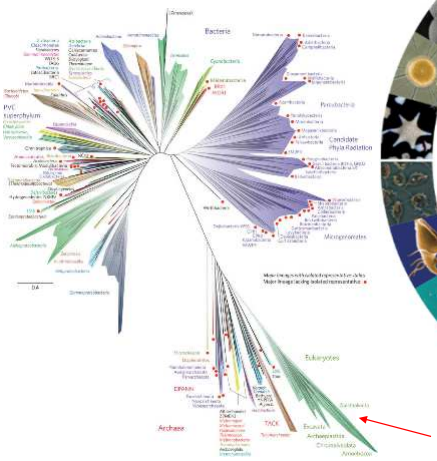
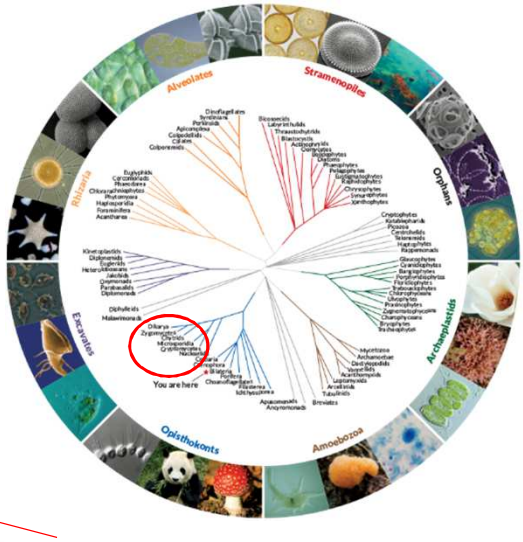
Introduction to fungi in dead wood

Diversity, life-cycles, life-history traits and more..

Håvard Kauserud, University of Oslo

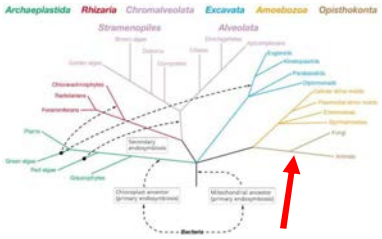
Fungi - phylogenetic placement



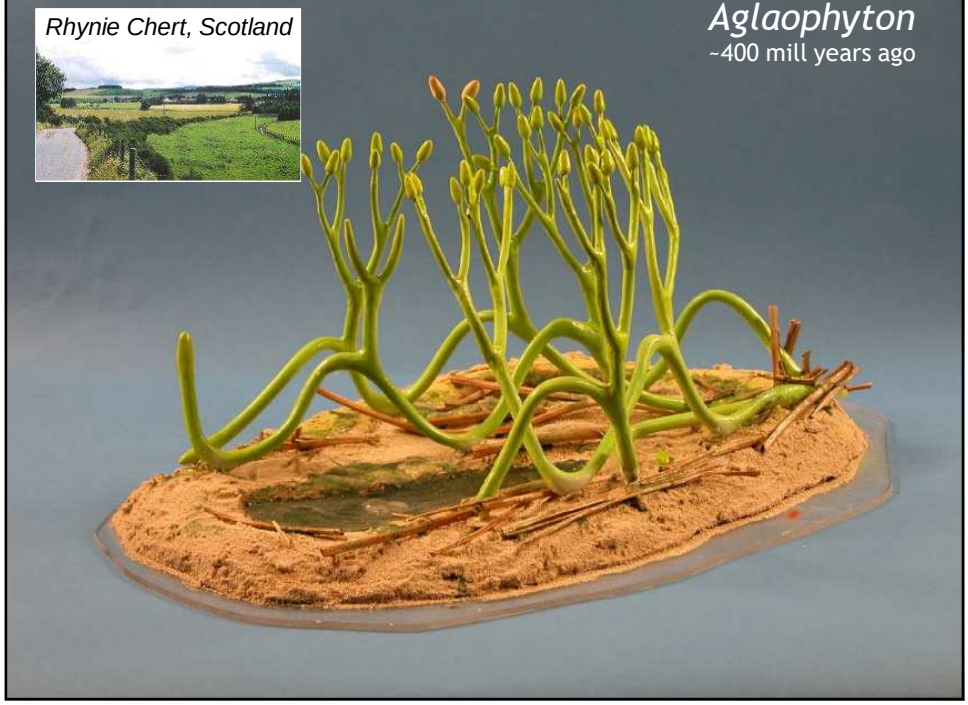


LETTER

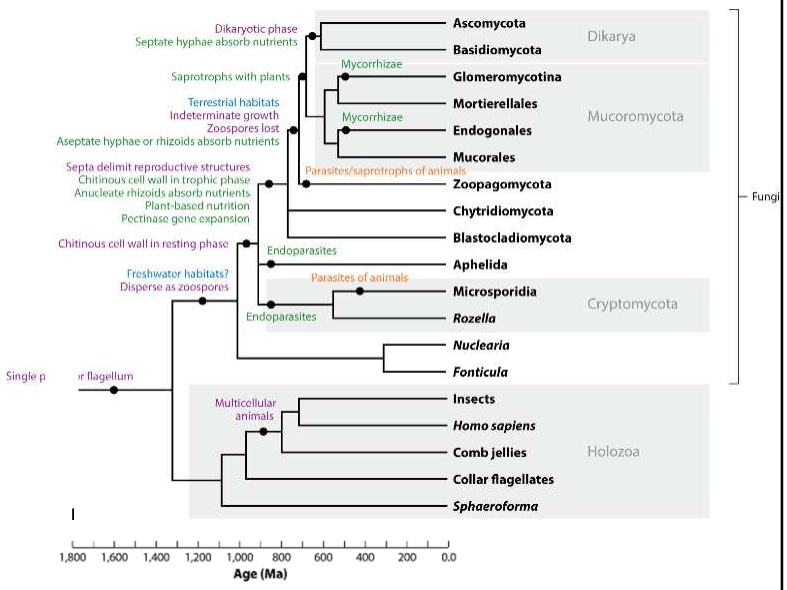
Early fungi from the Proterozoic era in Arctic Canada



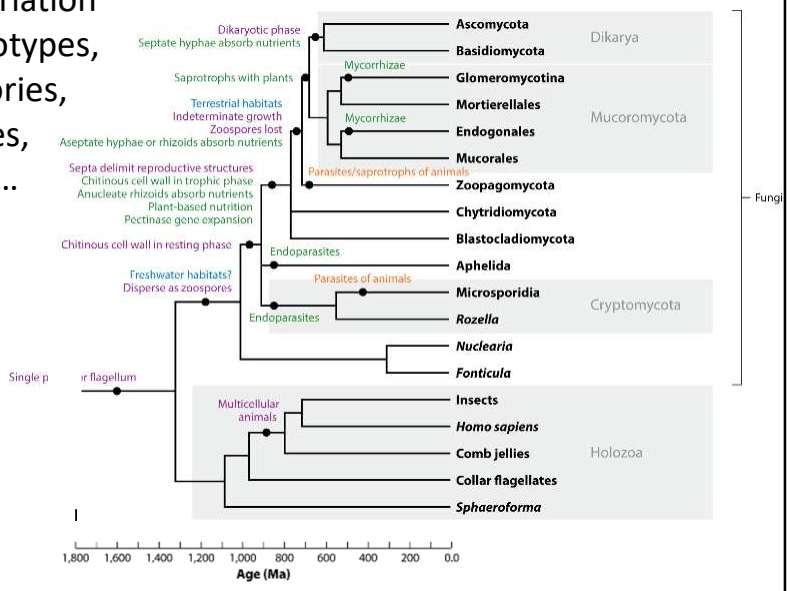
- Originated approximately 1.5 billion years ago
- One of the oldest eukaryotic lineages
- Established in terrestrial habitats together with the plants ~470 mill years ago
- Fungi have always posed a strong selection pressure on plants!

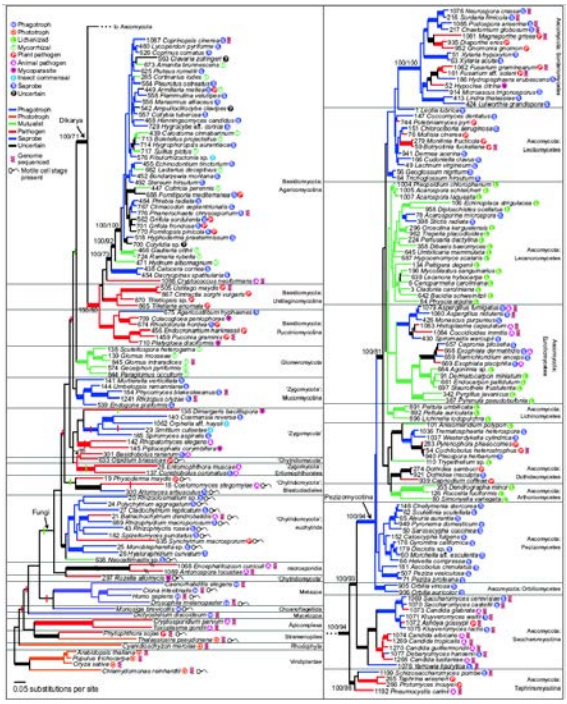


Fungal tree of life



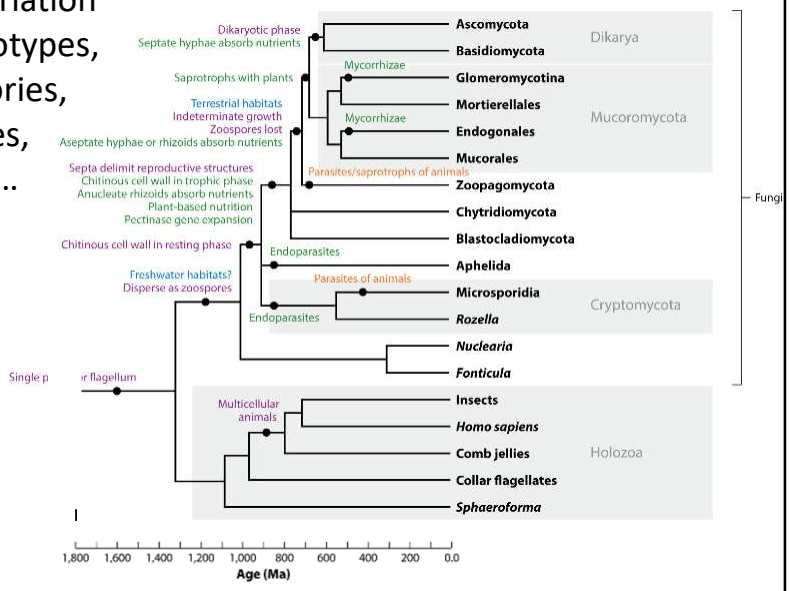
Wide variation in phenotypes, life histories, life cycles, ecology…

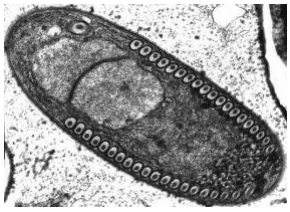




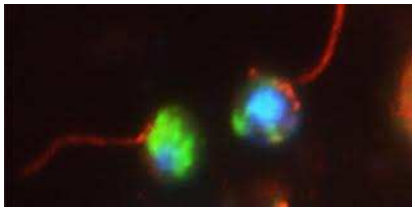
James et al. Nature

Wide variation in phenotypes, life histories, life cycles, ecology…

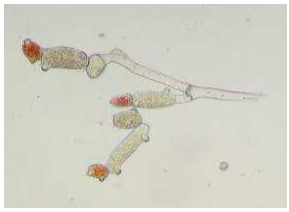




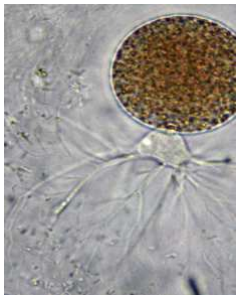
Microsporidia



Cryptomycota (Rozellamycota)



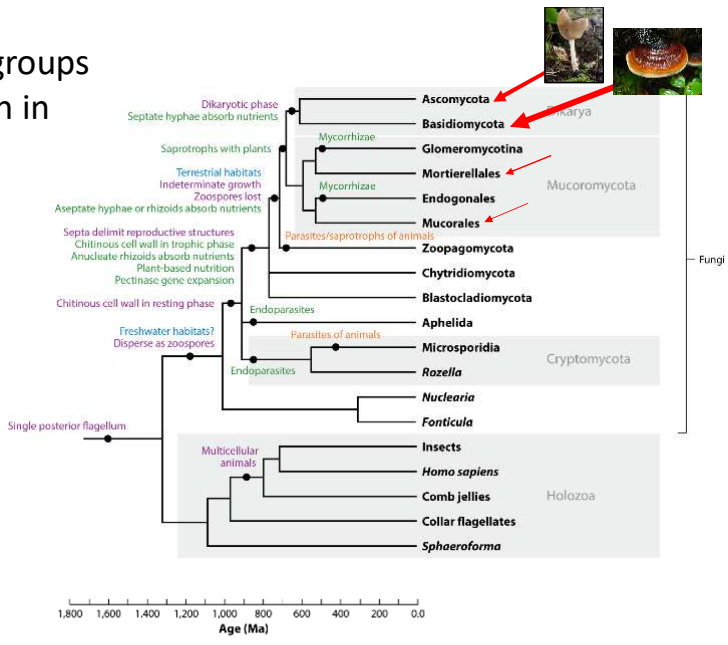
Blastocladiomycota

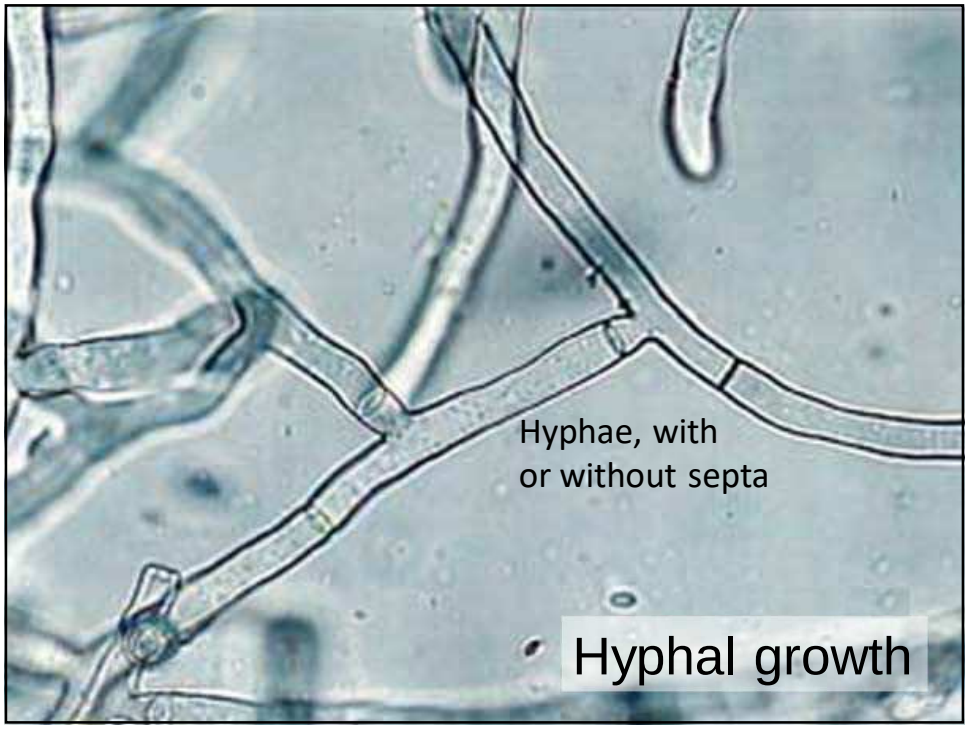


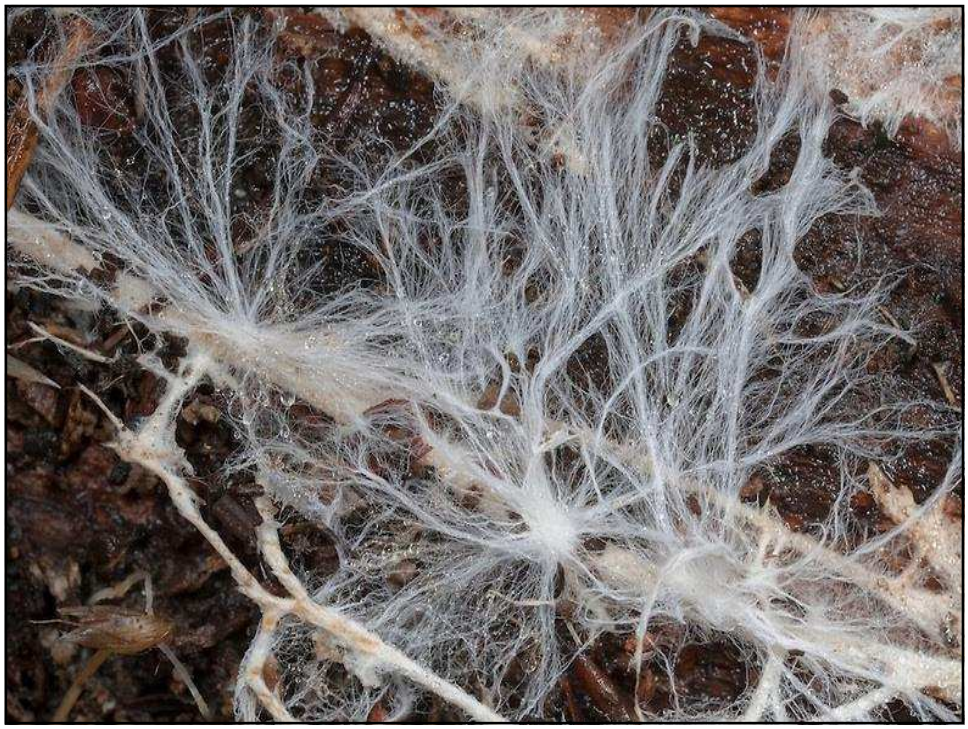
Chytridiomycota

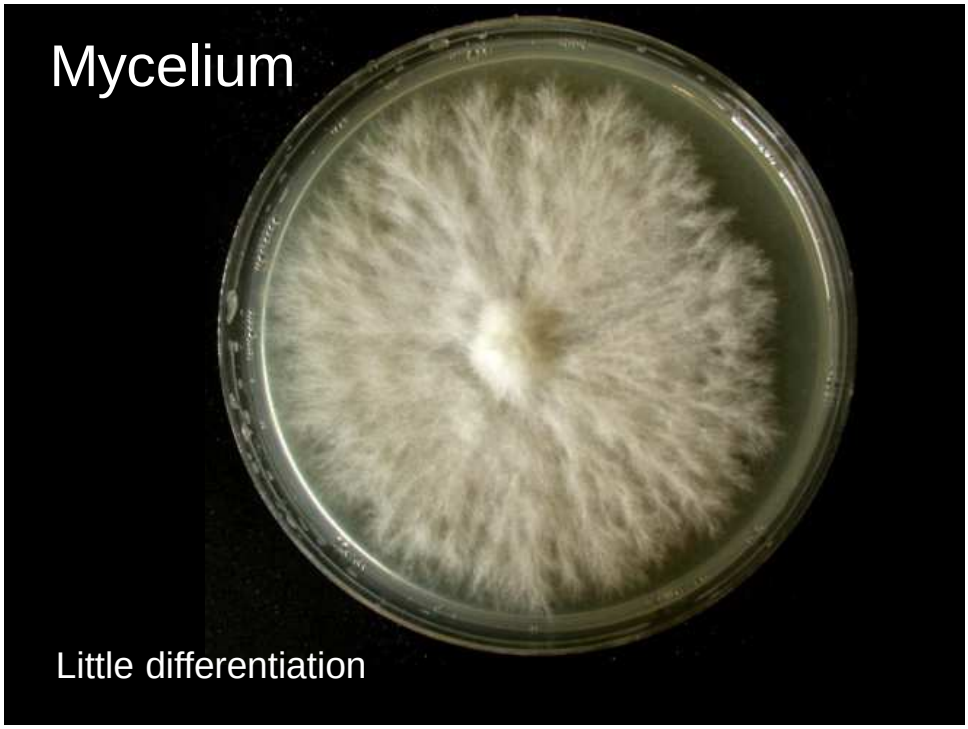
- Some of the basal groups are single-celled, flagellated, and does not form hyphae and mycelia
- These groups are not widespread in wood

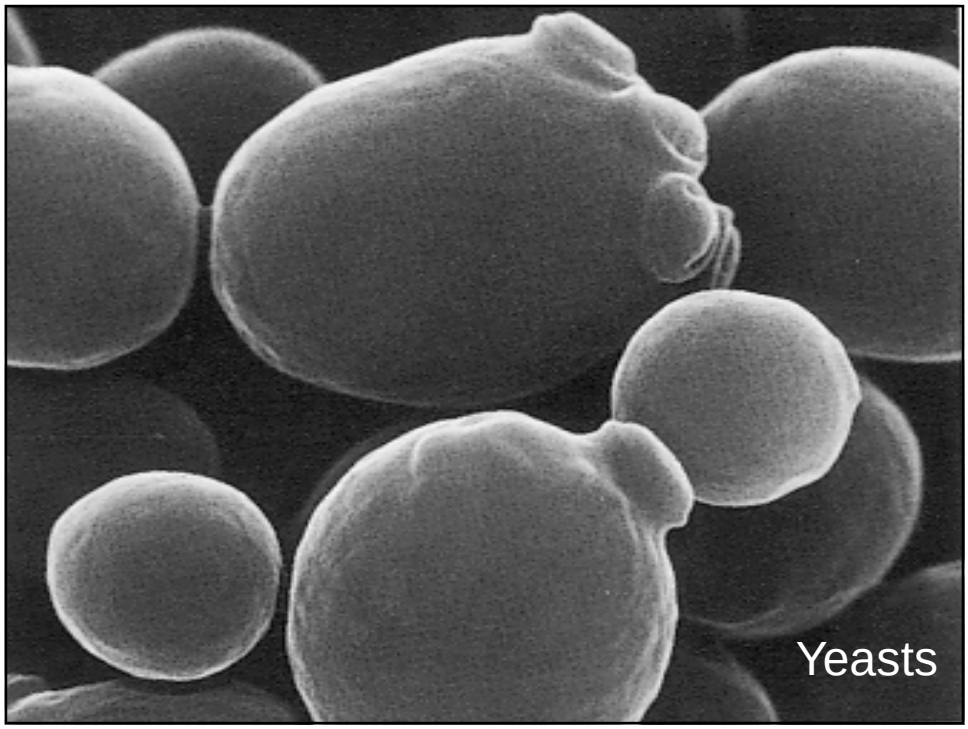
Fungal groups common in wood

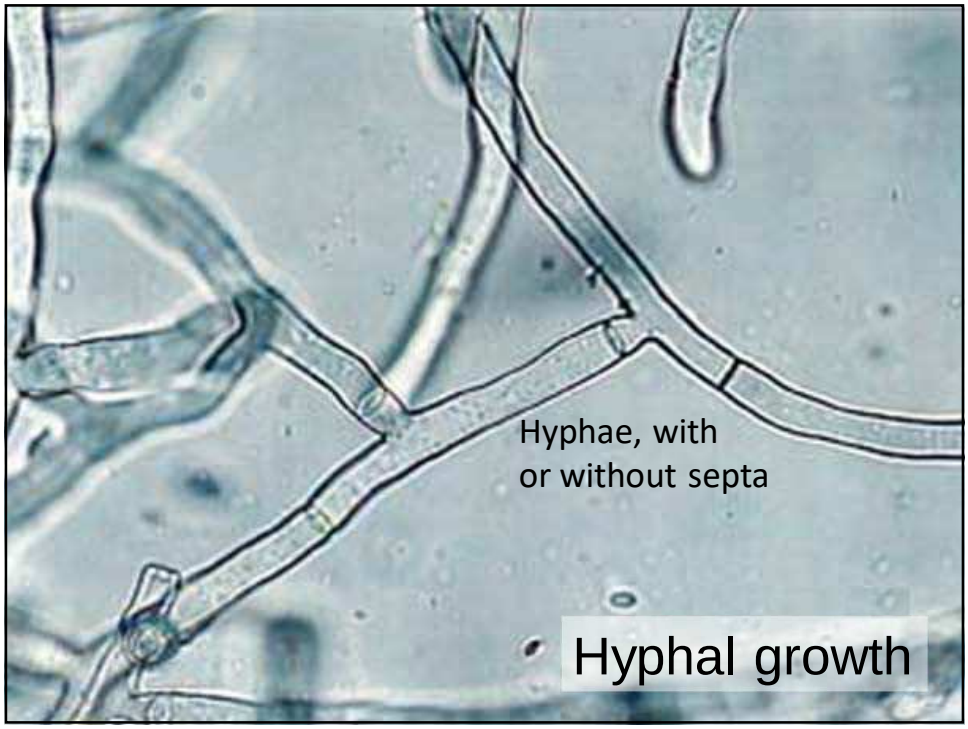



Hyphae, with
or without septa
Hyphal growth

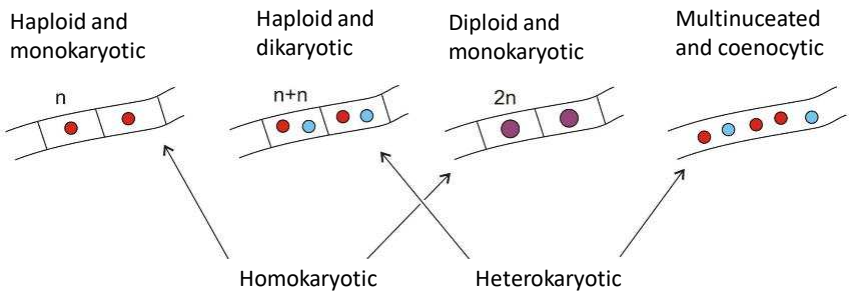



Mycelium
Little differentiation

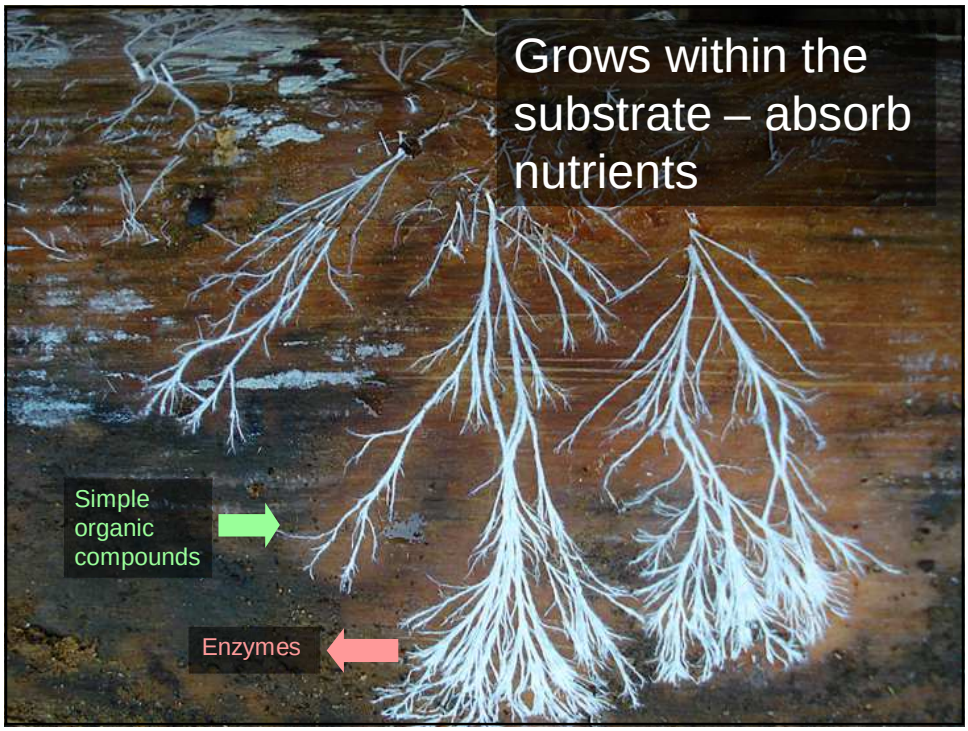

Yeasts



Different karyotypes and «genetic makeup»



Heterotrophic organisms



White-rot fungi

- Decompose both the lignin + cellulose/ hemicellulose → white colour
- Fungi one of few organismal groups able to decompose lignin using e.g. laccases + peroxidases

Fomes fomentarius

Armillaria

Brown-rot fungi

- Decompose cellulose + hemi-cellulose → brown colour
- Important in boreal forests

Fomitopsis pinicola

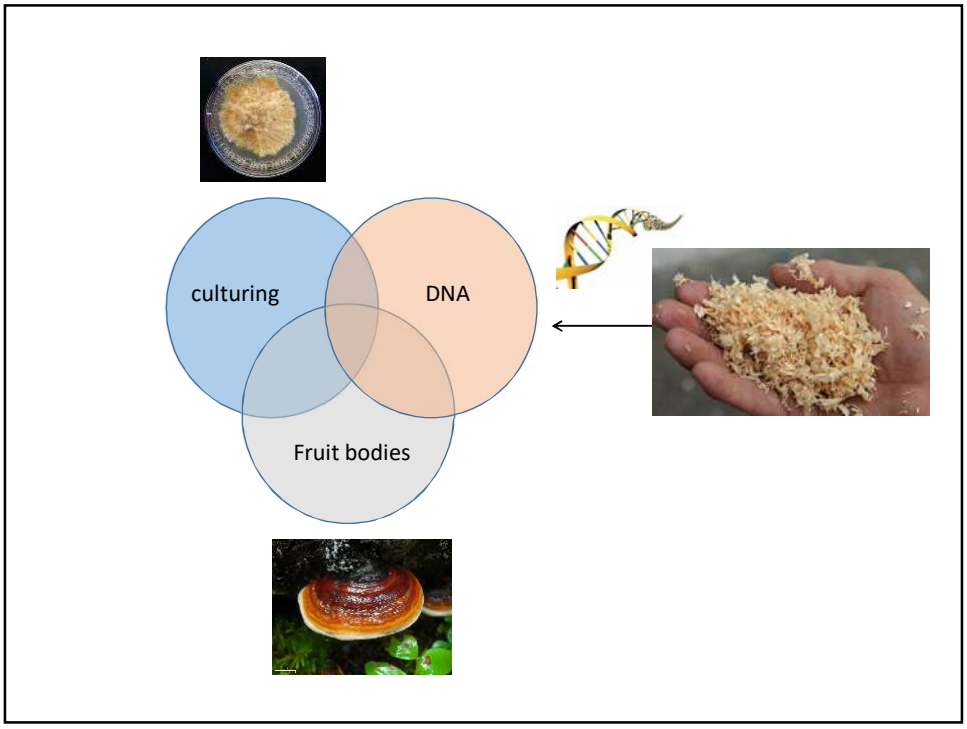
Wood decay fungi are essential for nutrient and C cycling

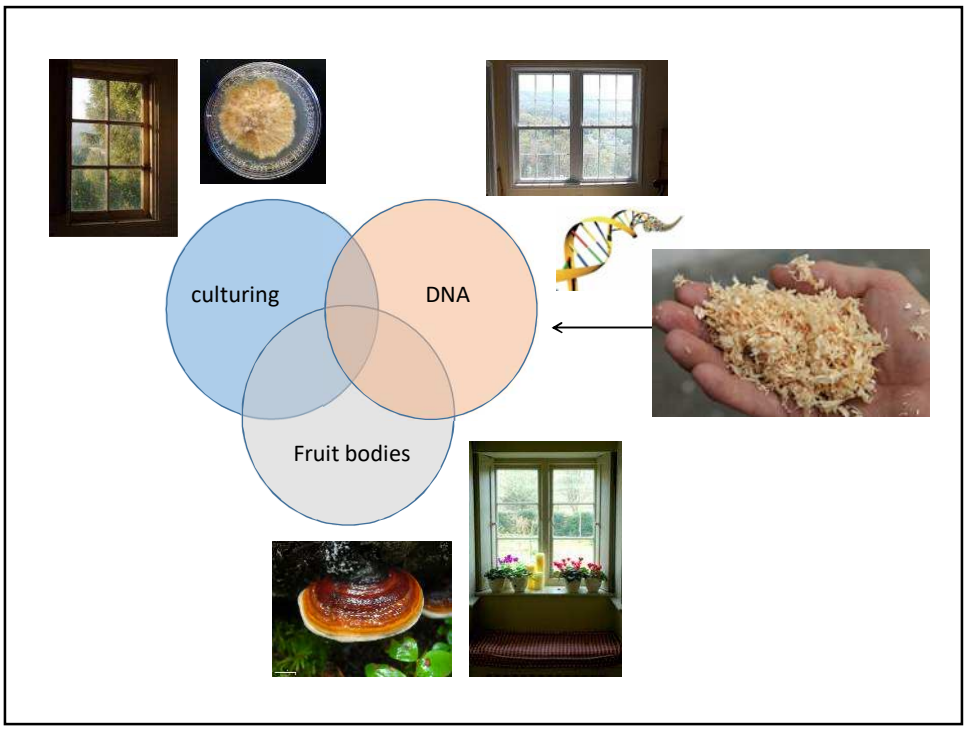
- Much carbon is bound in dead plant litter – wood decay fungi are among the main decomposers
- Important player in the global carbon budget: Far more carbon would have accumulated if not wood decay fungi were around

Fungal diversity

- Only ~100.000 described
- Between 1.5 and 7 million species have been estimated
- But, basically we have no clue..
- .. but if more or less all plants and animals harbour specific fungi, the diversity could be immense!

How can we assess fungal diversity in wood?


culturing
DNA
Fruit bodies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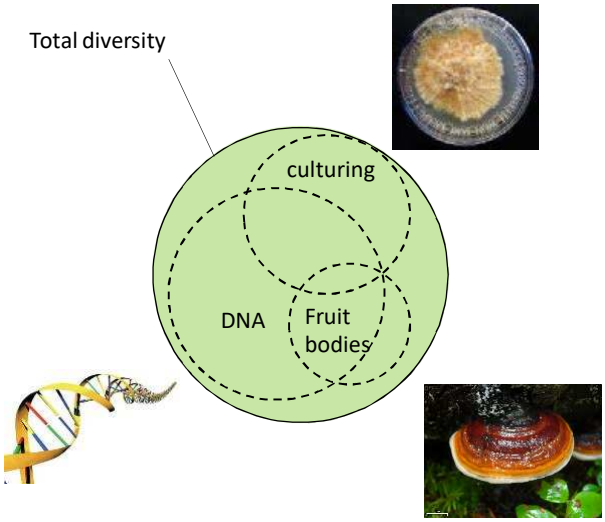
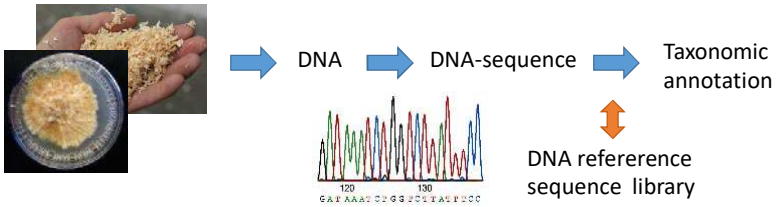


Sanger sequencing

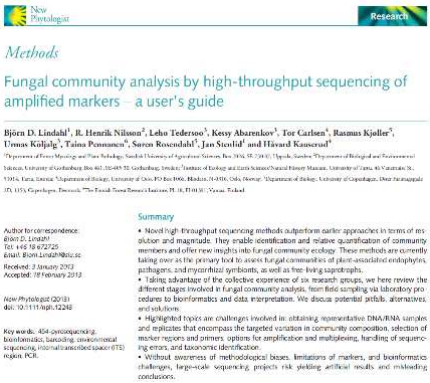
- During the 1990's PCR and Sanger sequencing was established in fungal ecology
- Possible to extract DNA from substrates, PCR amplify, DNA sequence and obtain knowledge about which fungi that occur in environmental samples
- Depends on comparison to known sequences!



- The environmental sequencing studies typically included only a few hundred Sanger sequences in maximum
- By this, could still only get at glimps into the extant fungal diversity/ecology

High throughput sequencing

- About 2005 – new DNA sequencing techinques emerges (second generation techniques)
- Now possible to generate >100.000 sequences in a single study
- Enables both a qualitative and, to some degree, quantitative assessment. Possible to investigate fungal ecology on 'a larger scale'



New Phytologist — Research

Methods

Fungal community analysis by high-throughput sequencing of amplified markers – a user's guide

Björn D. Lindahl[1], R. Henrik Nilsson[2], Leho Tedersoo[3], Kessy Abarenkov[3], Tor Carlsen[4], Rasmus Kjøller[5], Urmas Kõljalg[3], Taina Pennanen[6], Søren Rosendahl[7], Jan Stenlid[1] and Håvard Kauserud[8]

Summary

- Novel high-throughput sequencing methods outperform earlier approaches in terms of resolution and magnitude. They enable identification and relative quantification of community members and offer new insights into fungal community ecology. These methods are currently taking over as the primary tool to assess fungal communities of plant-associated endophytes, pathogens, and mycorrhizal symbionts, as well as free-living saprotrophs.
- Taking advantage of the collective experience of six research groups, we here review the different stages involved in fungal community analysis, from field sampling via laboratory procedures to bioinformatics and data interpretation. We discuss potential pitfalls, alternatives, and solutions.
- Highlighted topics are challenges involved in: obtaining representative DNA/RNA samples and replicates that encompass the targeted variation in community composition, selection of marker regions and primers, options for amplification and multiplexing, handling of sequencing errors, and taxonomic identification.
- Without awareness of methodological biases, limitations of markers, and bioinformatics challenges, large-scale sequencing projects risk yielding artificial results and misleading conclusions.

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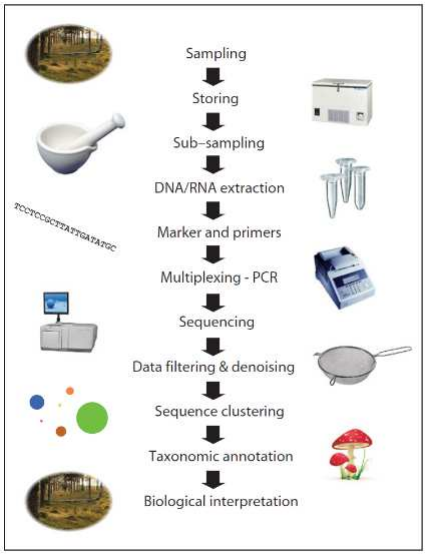
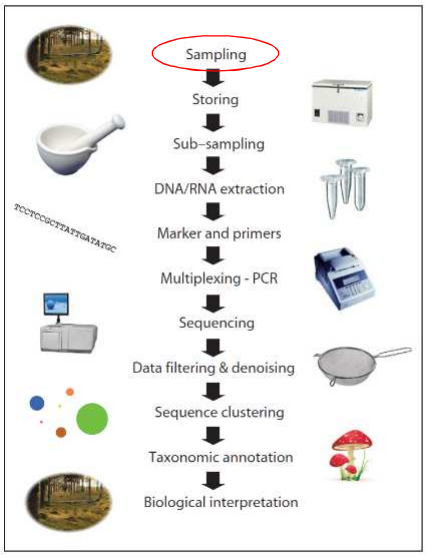
Key words: 454-pyrosequencing, bioinformatics, barcoding, environmental sequencing, internal transcribed spacer (ITS) region, PCR.

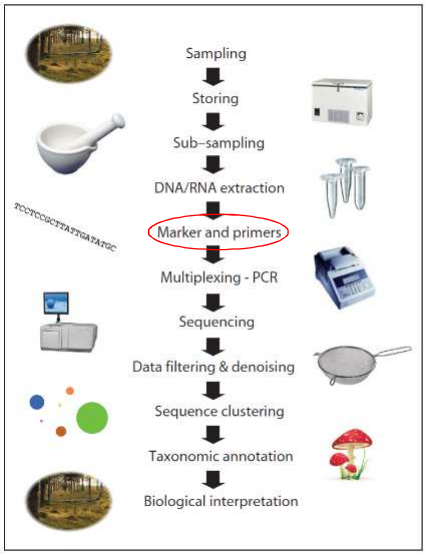
High throughput sequencing

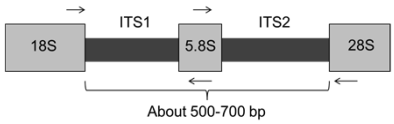


High throughput sequencing

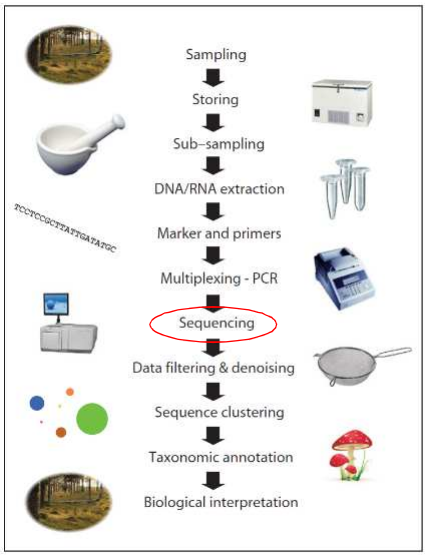


High throughput sequencing

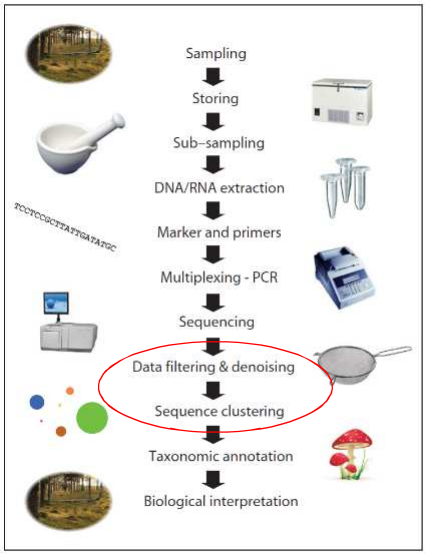


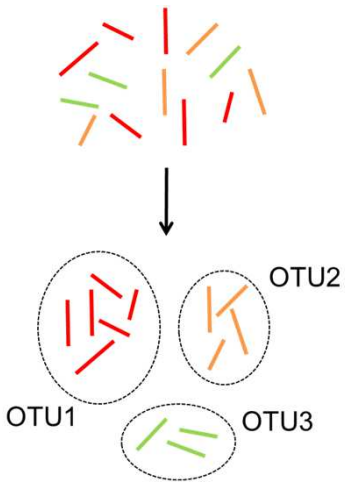


High throughput sequencing

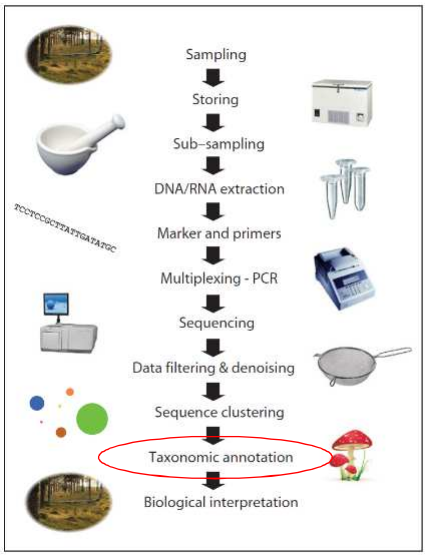


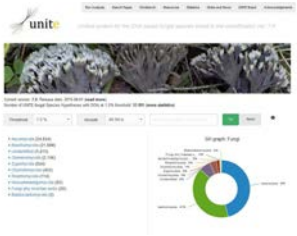
High throughput sequencing



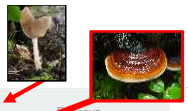


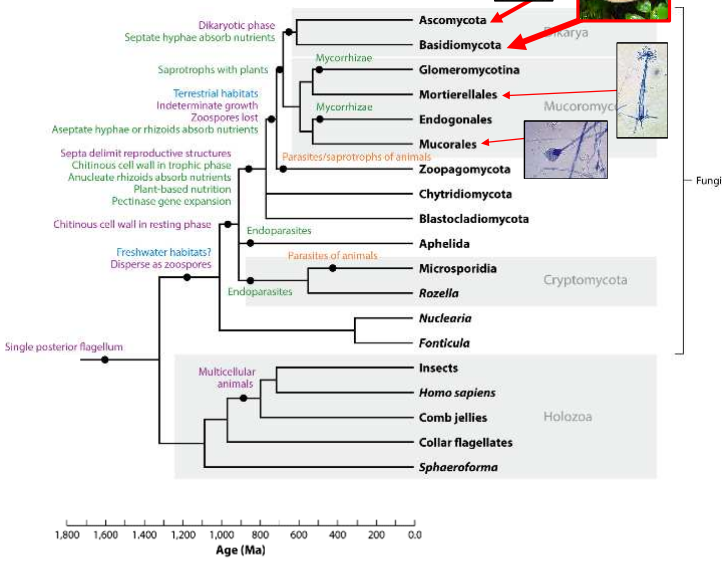
High throughput sequencing



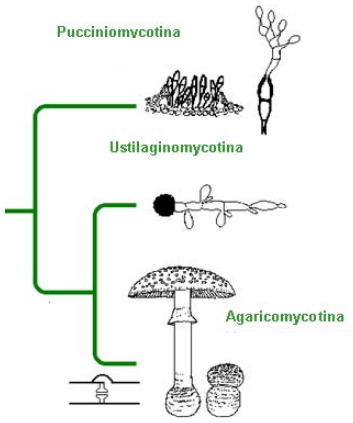


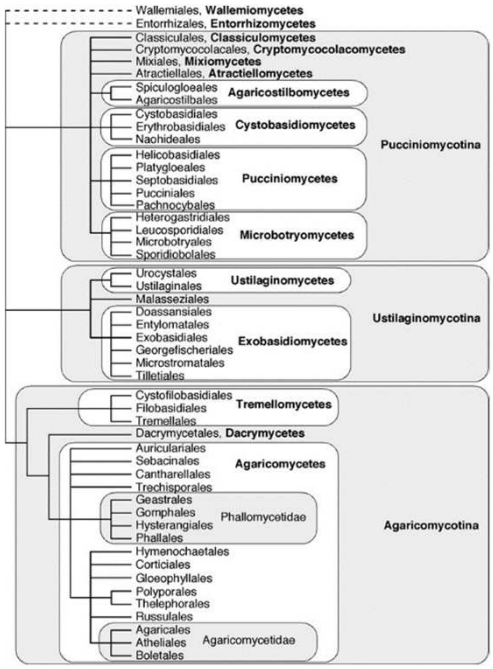
Major fungal groups growing in wood



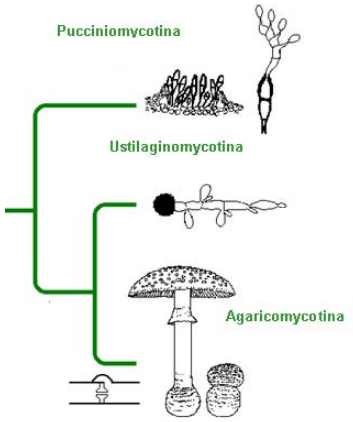


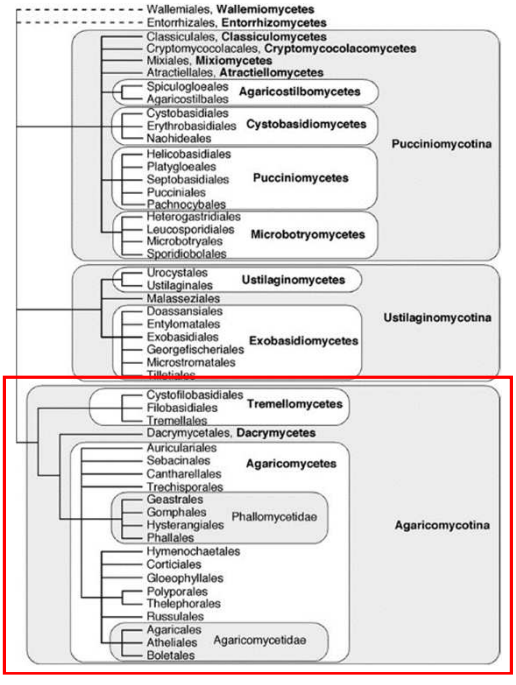
Basidiomycota



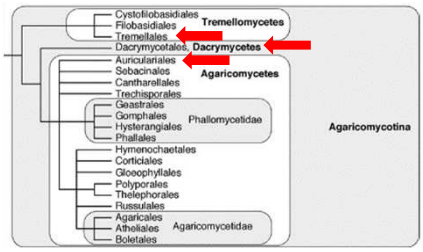


Basidiomycota





Tremellales, Dacrymycetales, Auriculariales



«Jelly fungi»

Tremella

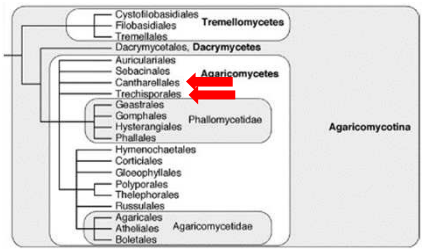
Dacrymyces

Calocera

Auriculariales

Basidiodendron

Cantharellales and Trechisporales



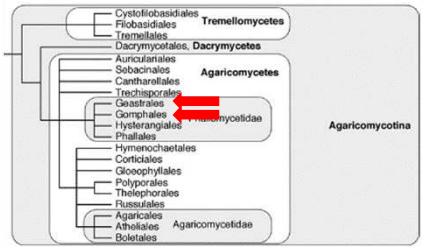
Trechispora

Tulasnella

Botryobasidium

Many «corticoids»

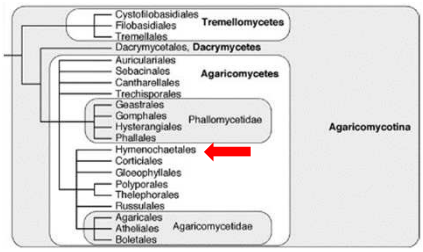
Phallomycetidae

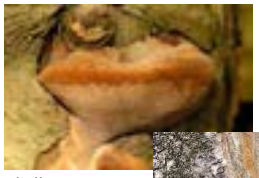


Geastrum

Lentharia

Hymenochaetales





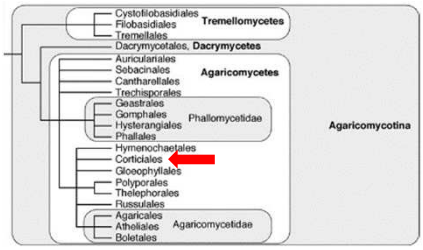
Phellinus

Inonotus

Schizopora

Hymenochaete

Corticiales

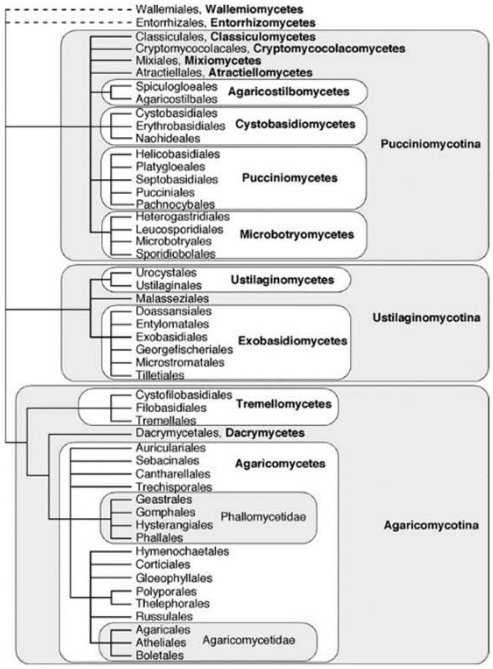


Vuilleminia

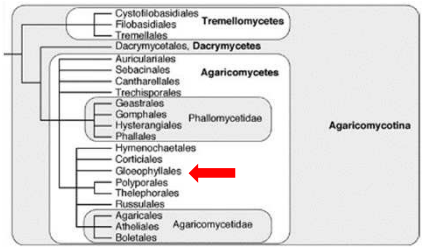
Punctularia

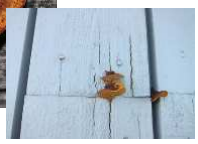
Corticium

- The old Corticiaceae – extremely polyphyletic
- Collapsed when using DNA based phylogeny
- Fruit body form says little about phylogenetic placement in the fungal kingdom!!



Gloephyllales

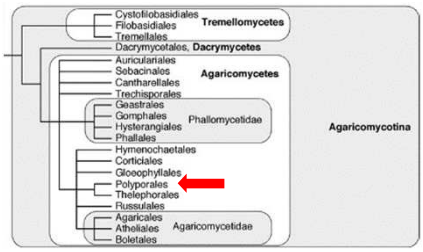




Gloeophyllum

Neolentinus («Train wrecker»)

Polyporales



Ganoderma

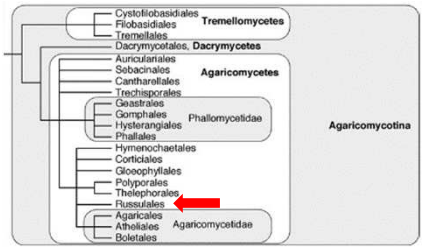
Fomitopsis

Crustomyces

Teraneae

Merulius

Russulales



Stereum

Peniophora

Auriscalpium

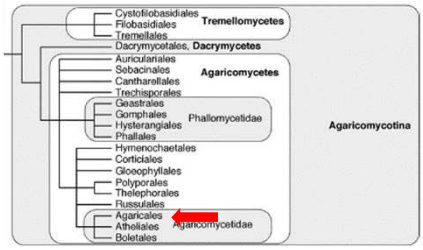
Hericium

Heterobasidion

Heterobasidion

Butt rot

Agaricales



Chondrostereum

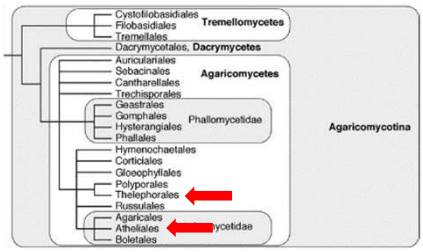
Mycena

Schizophyllum

Hypholoma

Pleurotus

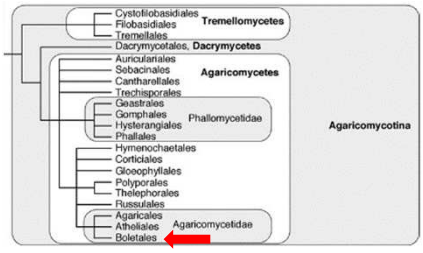
Thelephorales and Atheliales



Amaurodon

Hypochnella

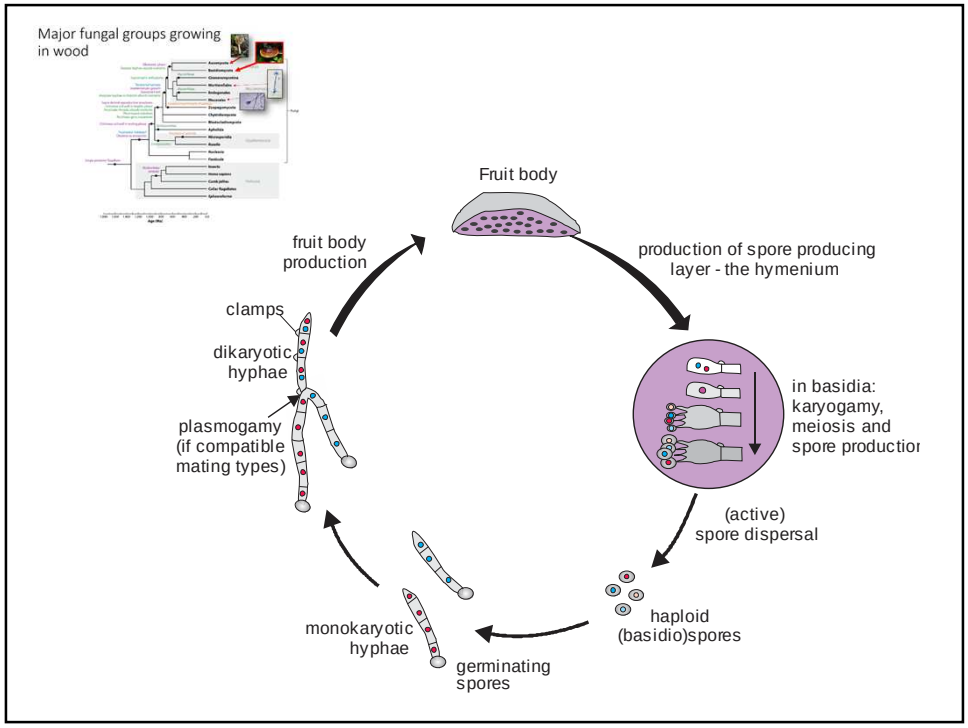
Boletales

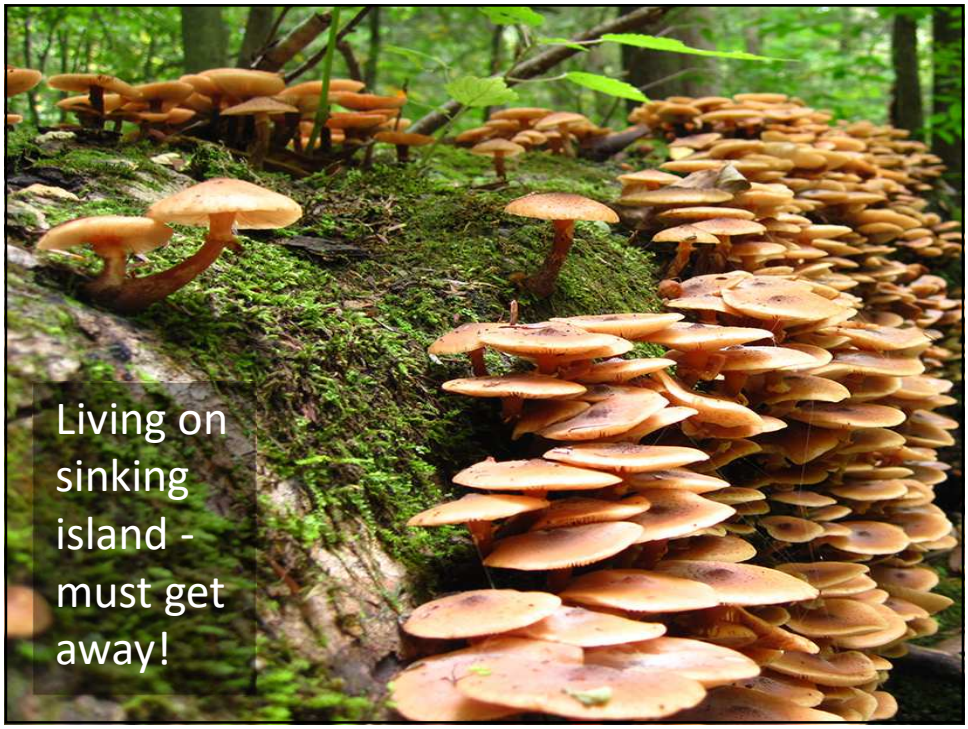


Tapinella

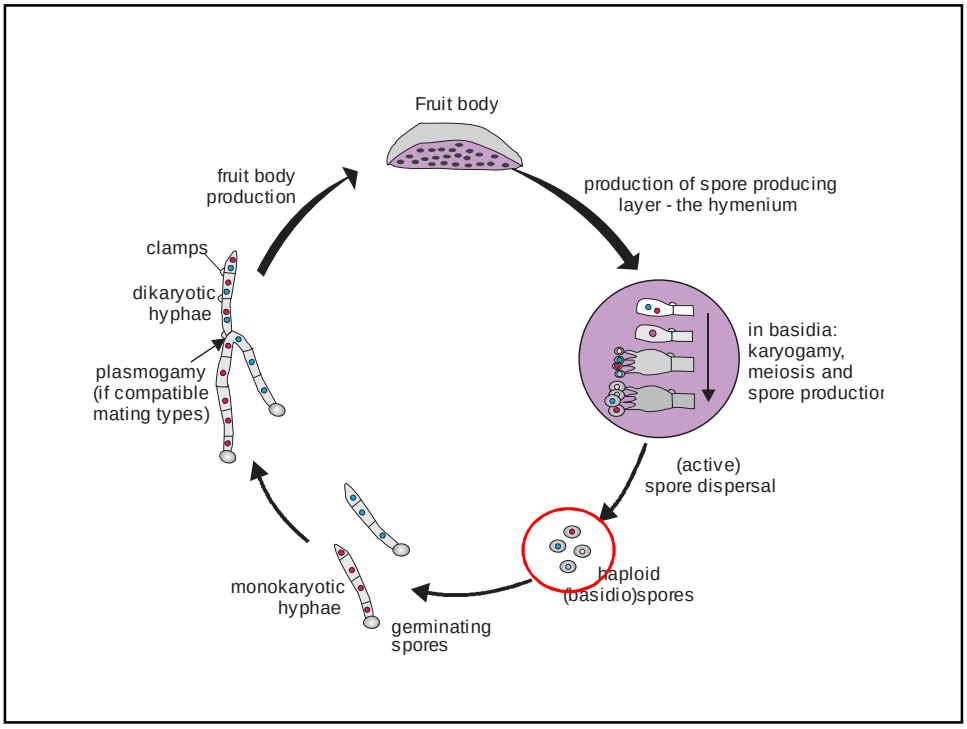
Coniophora

Serpula


Major fungal groups growing in wood
Fruit body
production of spore producing layer - the hymenium
in basidia: karyogamy, meiosis and spore productior
(active) spore dispersal
haploid (basidio)spores
germinating spores
monokaryotic hyphae
plasmogamy (if compatible mating types)
dikaryotic hyphae
clamps
fruit body production


Living on sinking island - must get away!


Disperse mainly by spores


Fruit body
production of spore producing layer - the hymenium
in basidia: karyogamy, meiosis and spore productior
(active) spore dispersal
haploid (basidio)spores
germinating spores
monokaryotic hyphae
plasmogamy (if compatible mating types)
dikaryotic hyphae
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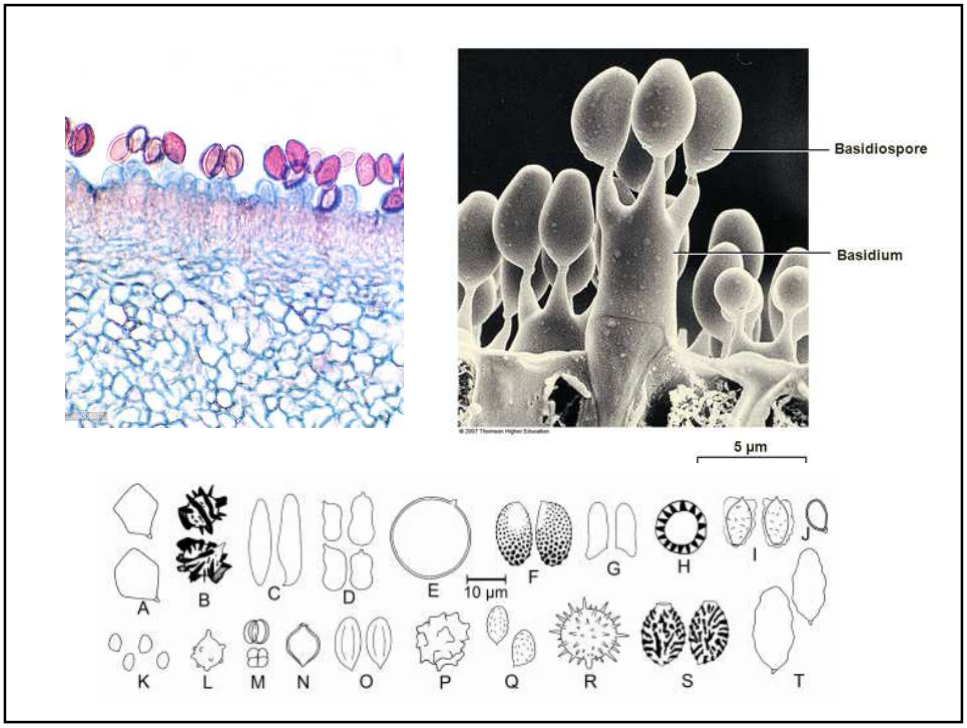
fruit body production


Basidiospore
Basidium
5 µm
10 µm
A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P
Q
R
S
T

Oikos 121: 961–974, 2012
doi: 10.1111/j.1600-0706.2012.20052.x

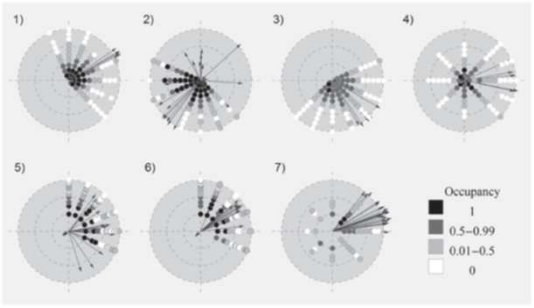
Subject Editor: Dries Bonte. Accepted 13 January 2012

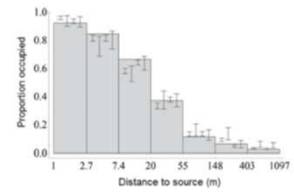
Dispersal may limit the occurrence of specialist wood decay fungi already at small spatial scales

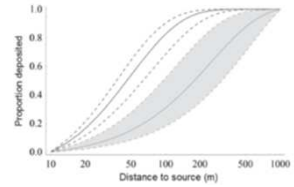
Veera Norros, Reijo Penttilä, Mai Suominen and Otso Ovaskainen

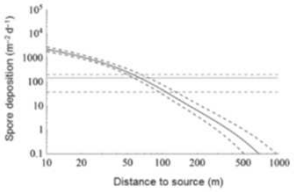
V. Norros (veera.norros@helsinki.fi) and O. Ovaskainen, Dept of Biosciences, PO Box 65, FI-00014, University of Helsinki, Finland. – R. Penttilä, Finnish Forest Research Inst., PO Box 18, FI-01301, Vantaa, Finland. – M. Suominen, School of Forest Sciences, Univ. of Eastern Finland, PO Box 111, FI-80101 Joensuu, Finland.

~20,000 spore traps!!!!









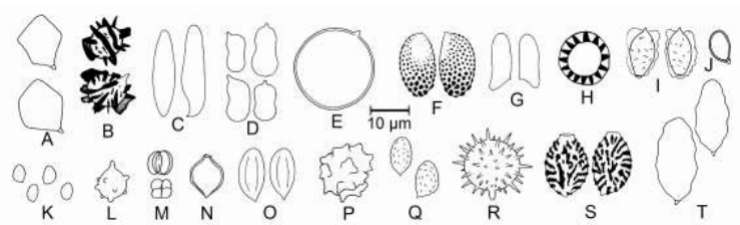
Ecology, 95(6), 2014, pp. 1612–1621

Do small spores disperse further than large spores?

VEERA NORROS,[1,2,5] ÜLLAR RANNIK,[3] TAREQ HUSSEIN,[3,4] TUUKKA PETÄJÄ,[3] TIMO VESALA,[3] AND OTSO OVASKAINEN[1]

[1]*Metapopulation Research Group, Department of Biosciences, P.O. Box 65, FI-00014, University of Helsinki, Helsinki, Finland*
[2]*Marine Research Centre, Finnish Environment Institute, P.O. Box 140, FI-00251, Helsinki, Finland*
[3]*Department of Physics, P.O. Box, FI-00014, University of Helsinki, Helsinki, Finland*
[4]*The University of Jordan, Department of Physics, Amman 11942 Jordan*

« Our results suggest that by evolutionary adjustment of spore size, release height and timing of release, fungi and other organisms with microscopic spores can change the expected distribution of dispersal locations markedly. »



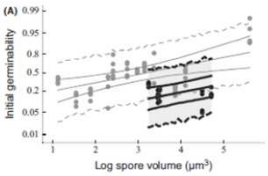
Ecology and Evolution

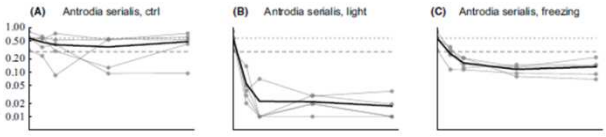
Open Access

Spore sensitivity to sunlight and freezing can restrict dispersal in wood-decay fungi

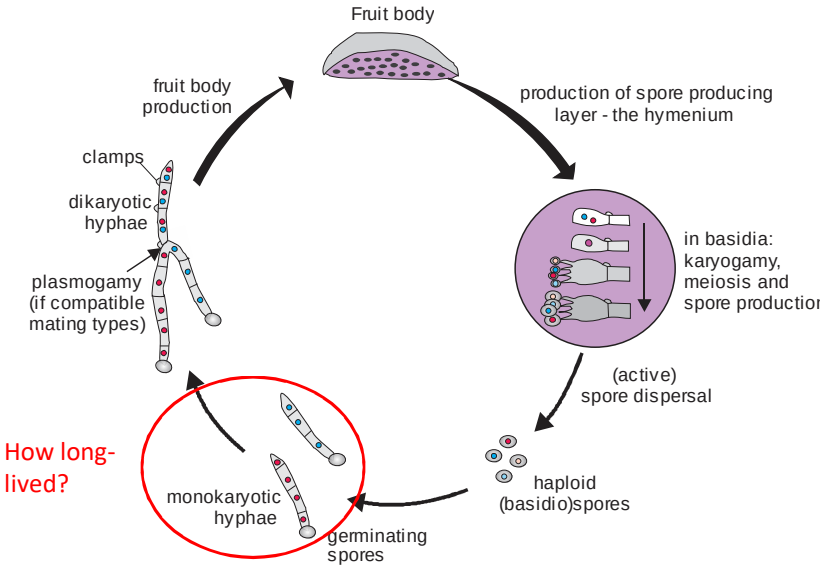
Veera Norros[1,2], Elina Karhu[1], Jenni Nordén[3,4], Anssi V. Vähätalo[5] & Otso Ovaskainen[1]

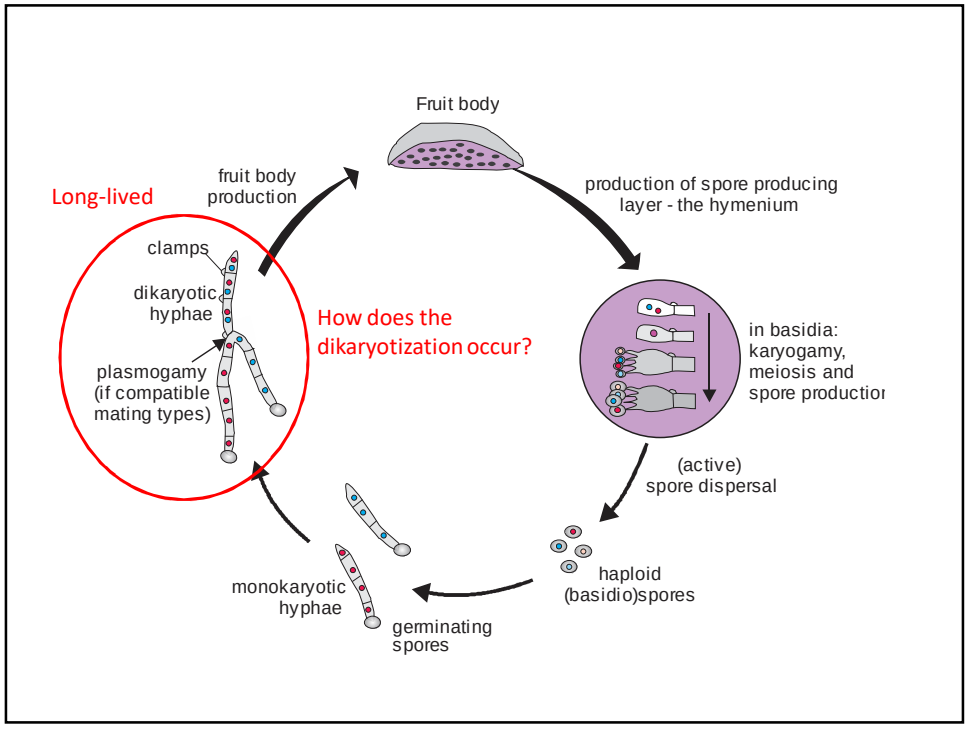
[1]Department of Biosciences, Metapopulation Research Centre, University of Helsinki, P.O. Box 65, FI-00014 Helsinki, Finland
[2]Marine Research Centre, Finnish Environment Institute, P.O. Box 140, FI-00251 Helsinki, Finland
[3]Natural History Museum, University of Oslo, P.O. Box 1172 Blindern, NO-0318 Oslo, Norway
[4]Section for Genetics and Evolutionary Biology, Department of Biosciences, University of Oslo, P.O. Box 1066 Blindern, NO-0316 Oslo, Norway
[5]Department of Environmental Sciences, University of Helsinki, P.O. Box 65, FI-00014 Helsinki, Finland





Both treatments but especially sunlight markedly reduced spore germinability in most species, and species with thin-walled spores were particularly light sensitive. Extrapolating the species' laboratory responses to natural irradiance conditions, we predict that sunlight is a relevant source of dispersal mortality at least at larger spatial scales. In addition, we found a positive effect of spore size on spore germinability, suggesting a trade-off between dispersal distance and establishment.



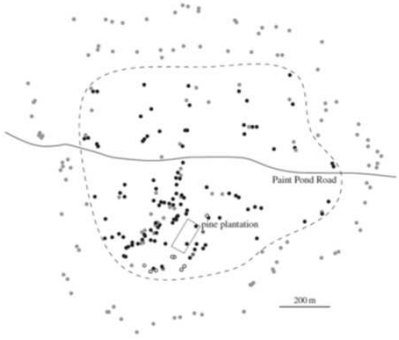

Fruit body
fruit body production
production of spore producing layer - the hymenium
Long-lived
clamps
dikaryotic hyphae
plasmogamy (if compatible mating types)
How does the dikaryotization occur?
in basidia: karyogamy, meiosis and spore productior
(active) spore dispersal
haploid (basidio)spores
monokaryotic hyphae
germinating spores

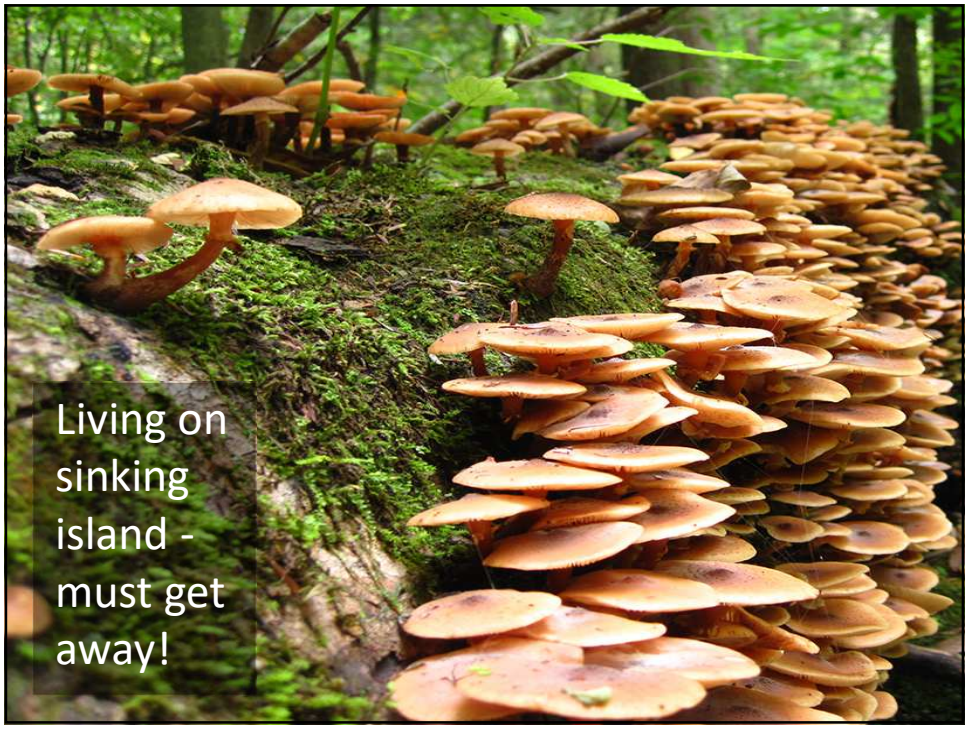
Serpula lacrymans

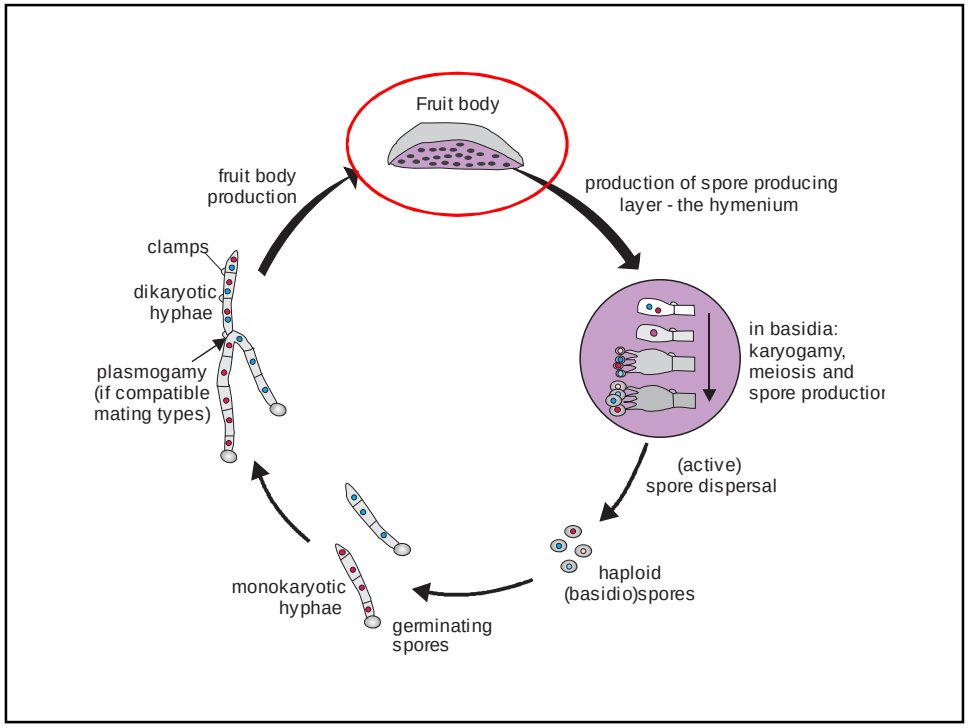
Clonal evolution and genome stability in a 2500-year-old fungal individual

James B. Anderson[1], Johann N. Bruhn[2], Dahlia Kasimer[1], Hao Wang[3,4], Nicolas Rodrigue[3,4] and Myron L. Smith[3]

«The humongous fungus»




Living on sinking island - must get away!


Fruit body
production of spore producing layer - the hymenium
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(active) spore dispersal
haploid (basidio)spores
germinating spores
monokaryotic hyphae
plasmogamy (if compatible mating types)
dikaryotic hyphae
clamps
fruit body production

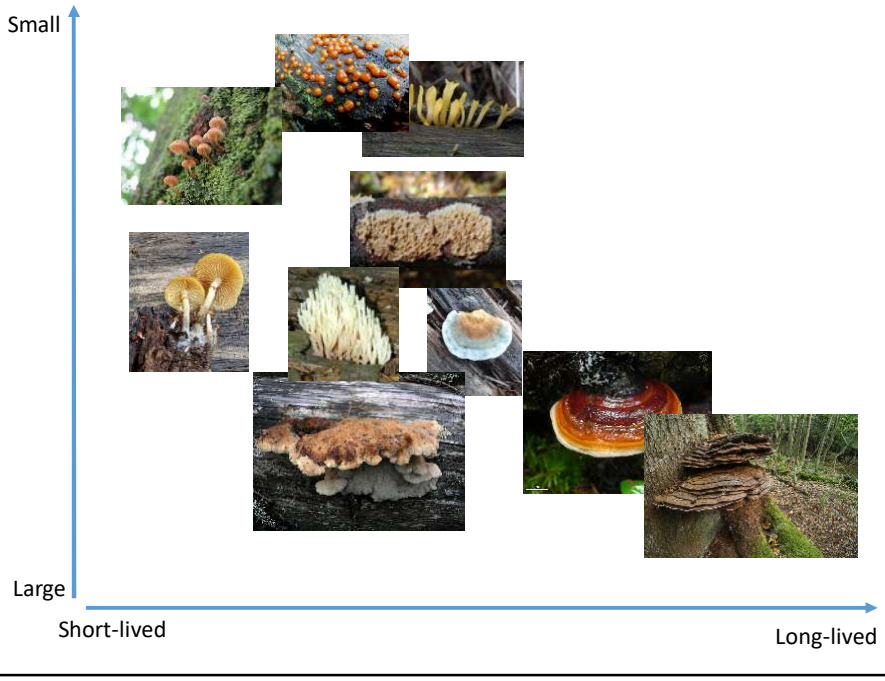
«Jelly fungi»


Corticoid

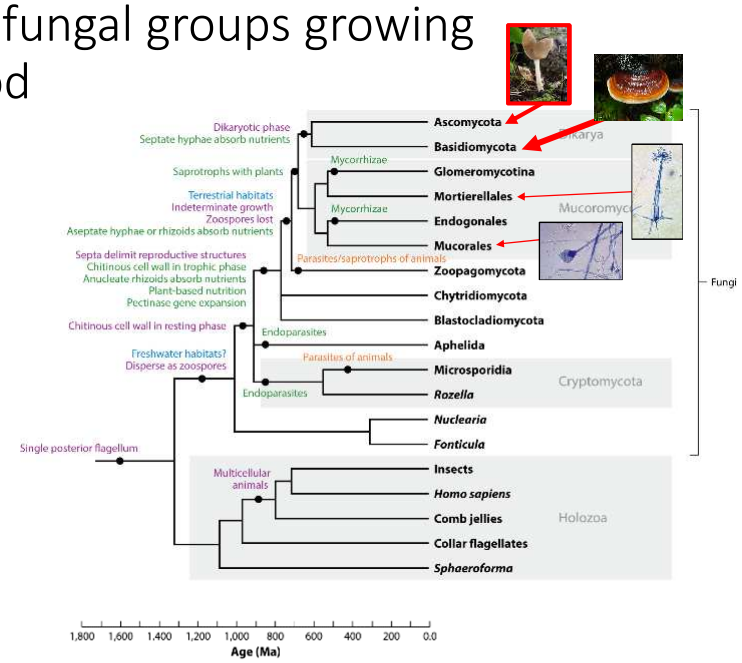

Agaricoid


Polyporoid

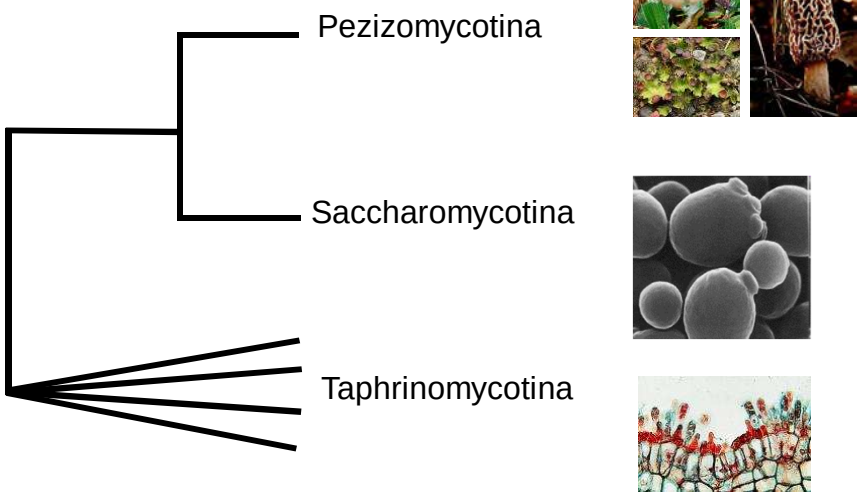

Corraloid



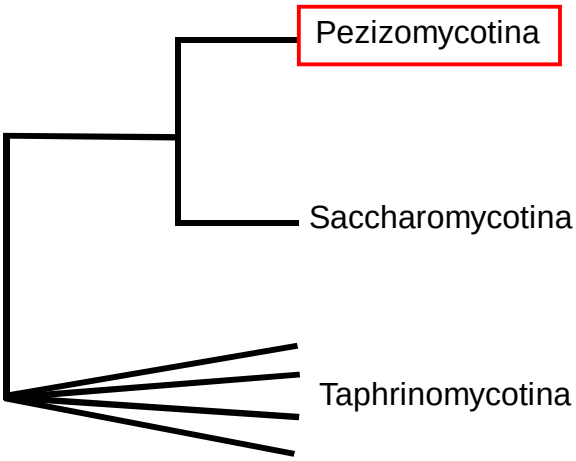
Major fungal groups growing in wood

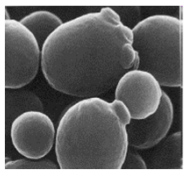


Ascomycota

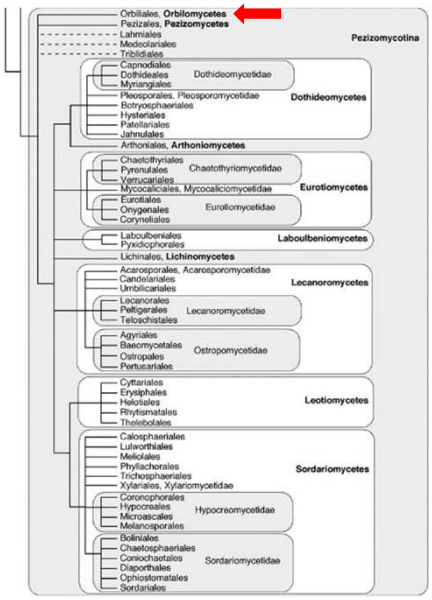


Ascomycota

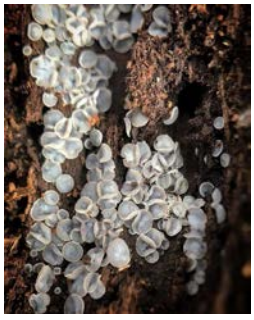




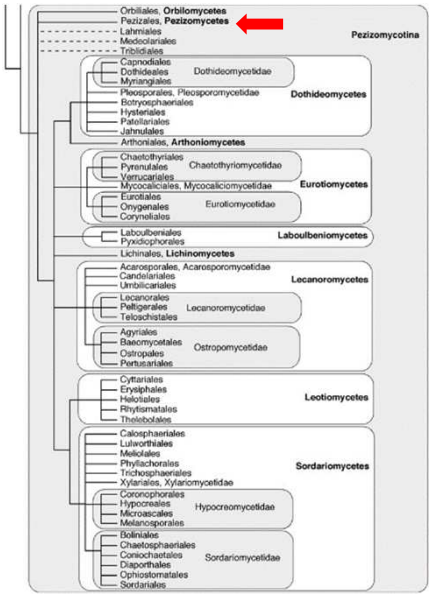
Orbiliomycetes



Orbilia



Pezizales

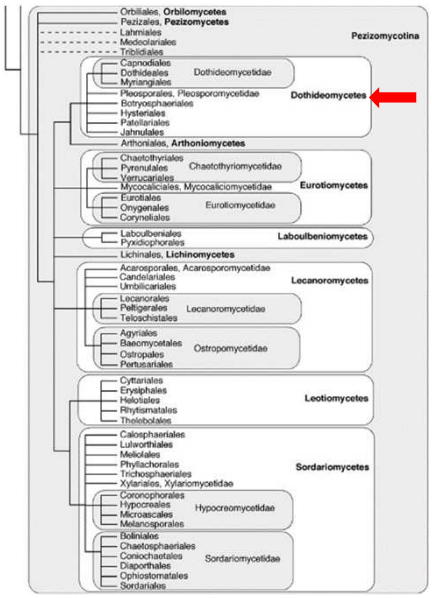


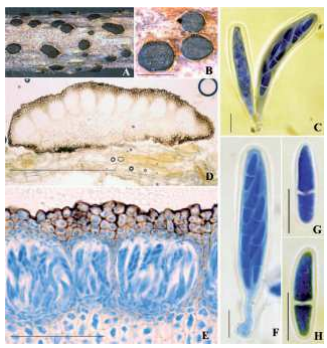
Sarcoscypha

Gyromitra

Scutellinia

Dothideomycetes

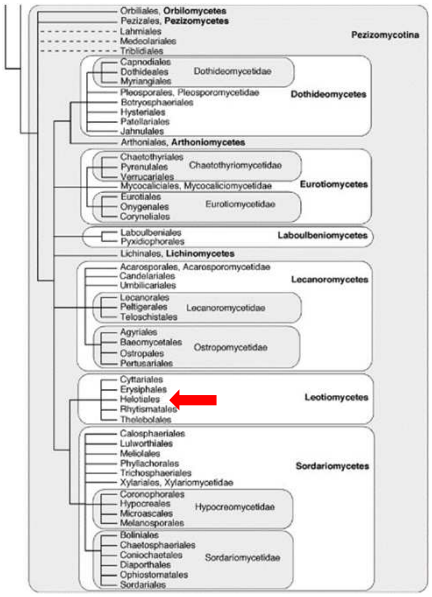




Dothidea

Pleospora

Helotiales

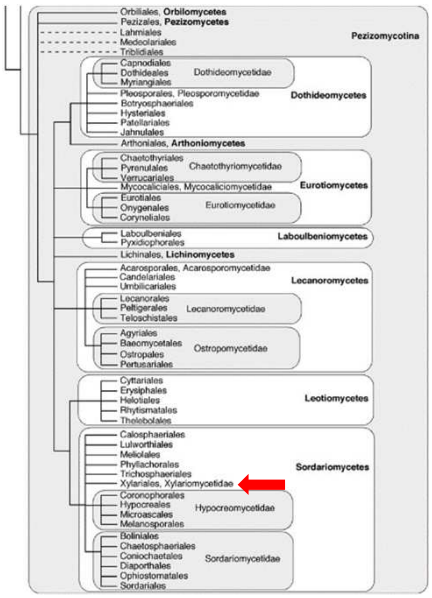


Chlorociboria

Bisporella

Ascocoryne

Xylariales



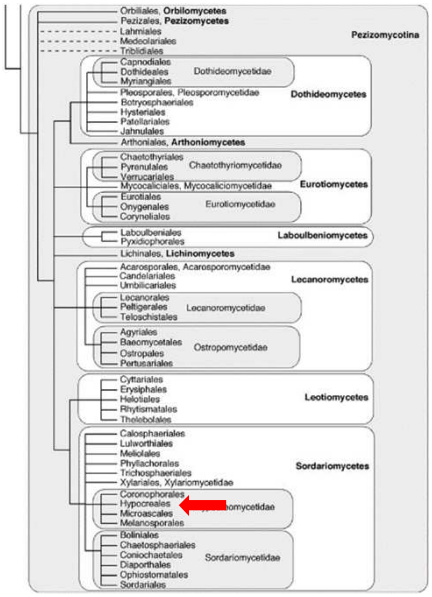
Xylaria

Hypoxylon

Daldinia

Anthostoma

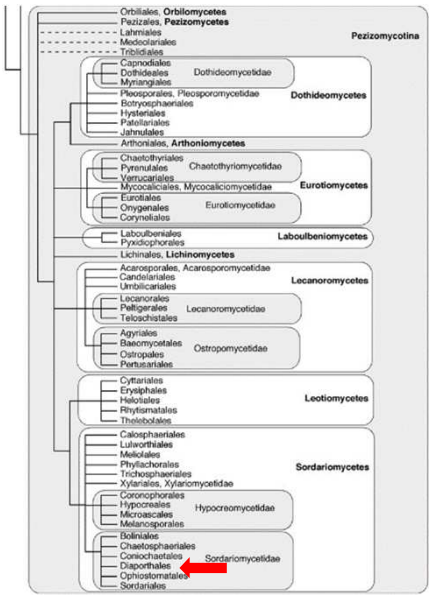
Hypocreales



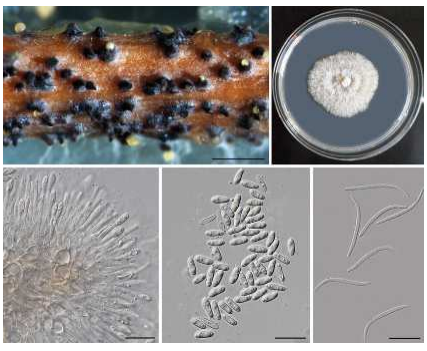
Hypocrea

Hypocreopsis

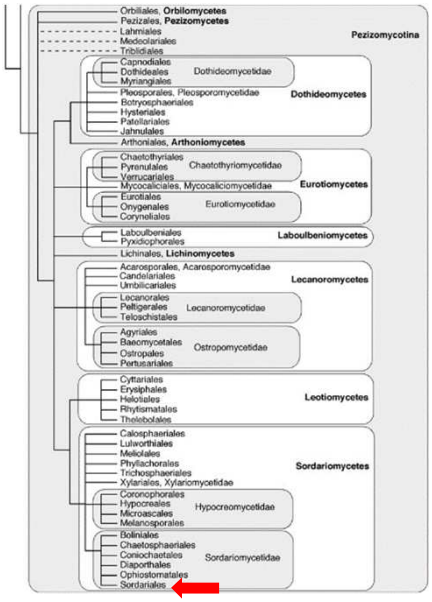
Diaporthales



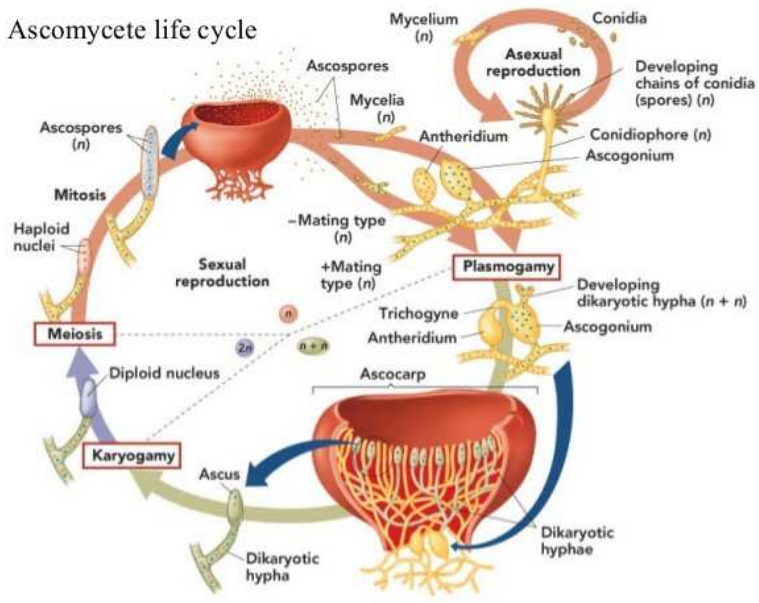
Diaporthe

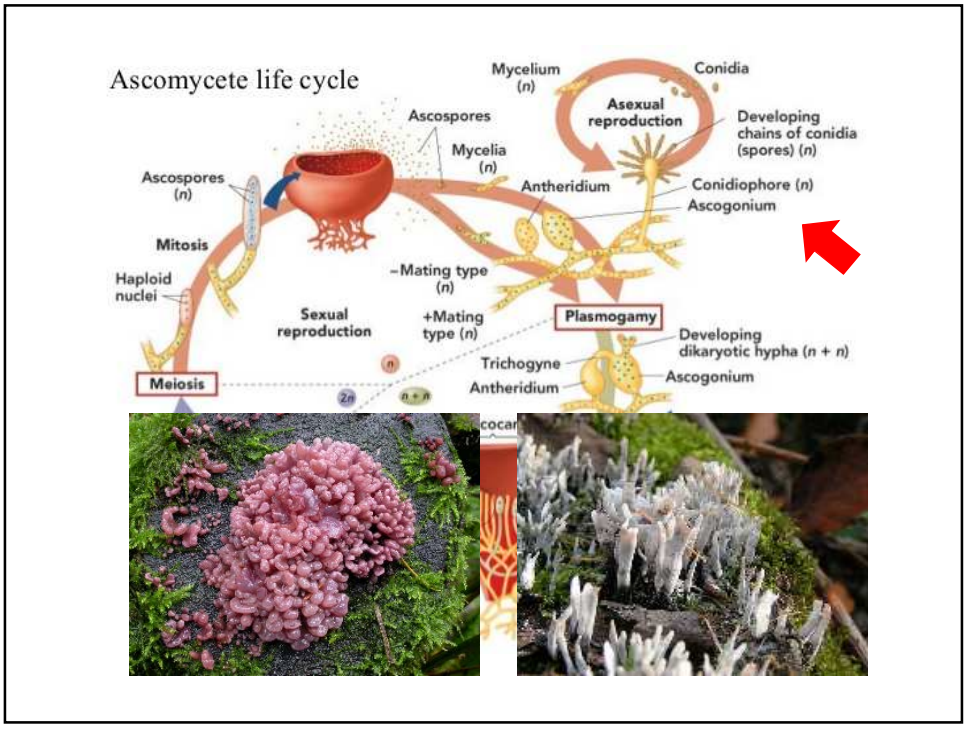


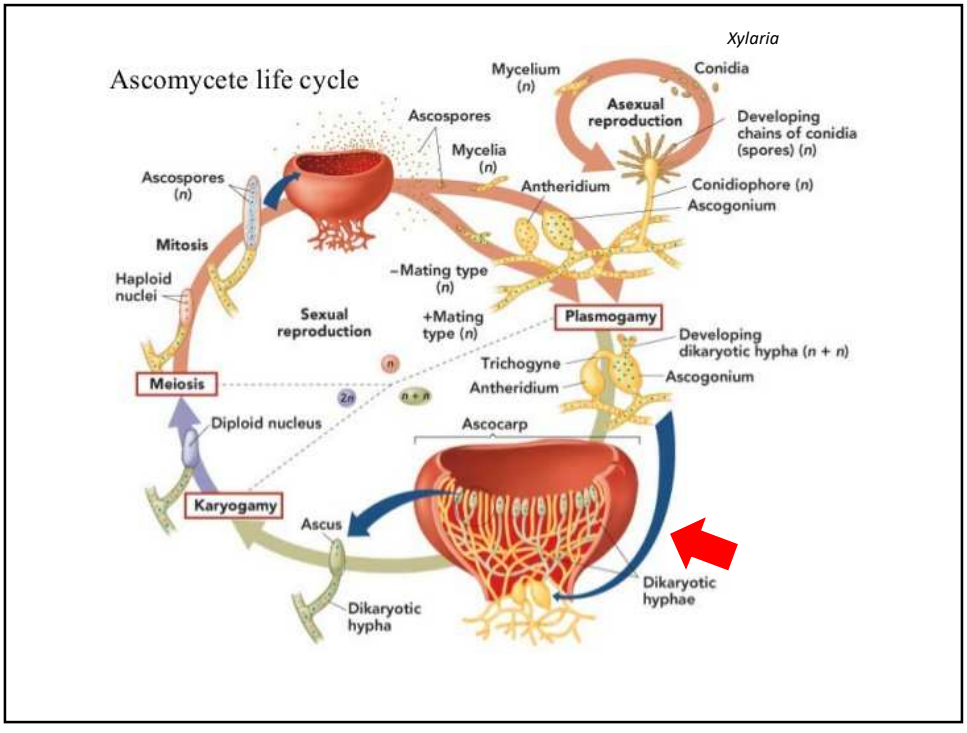
Sordariales

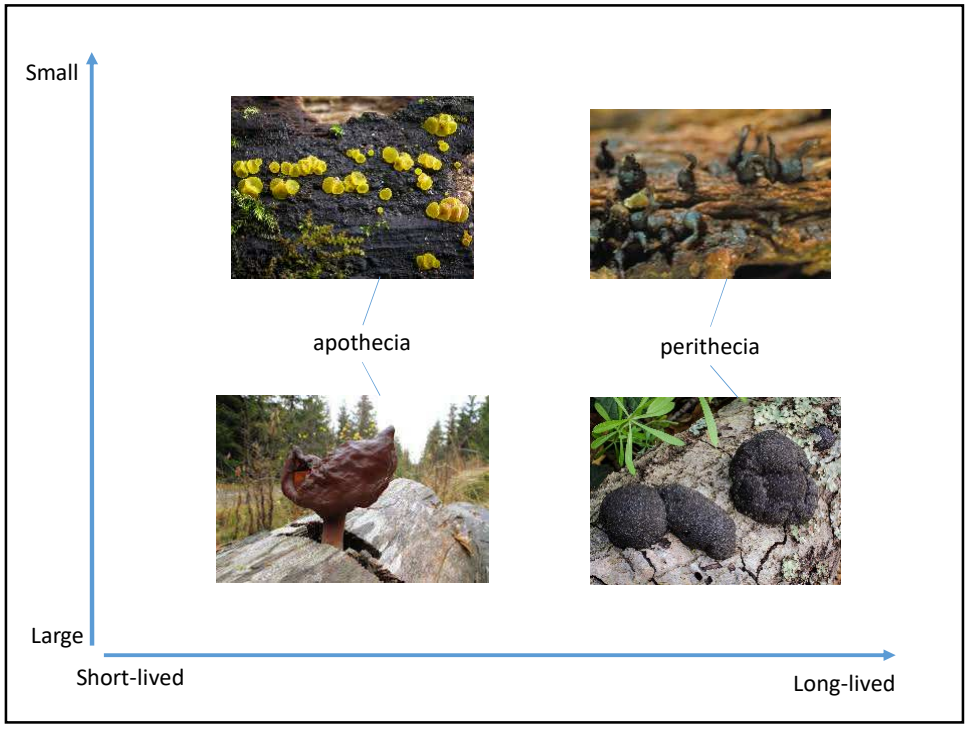


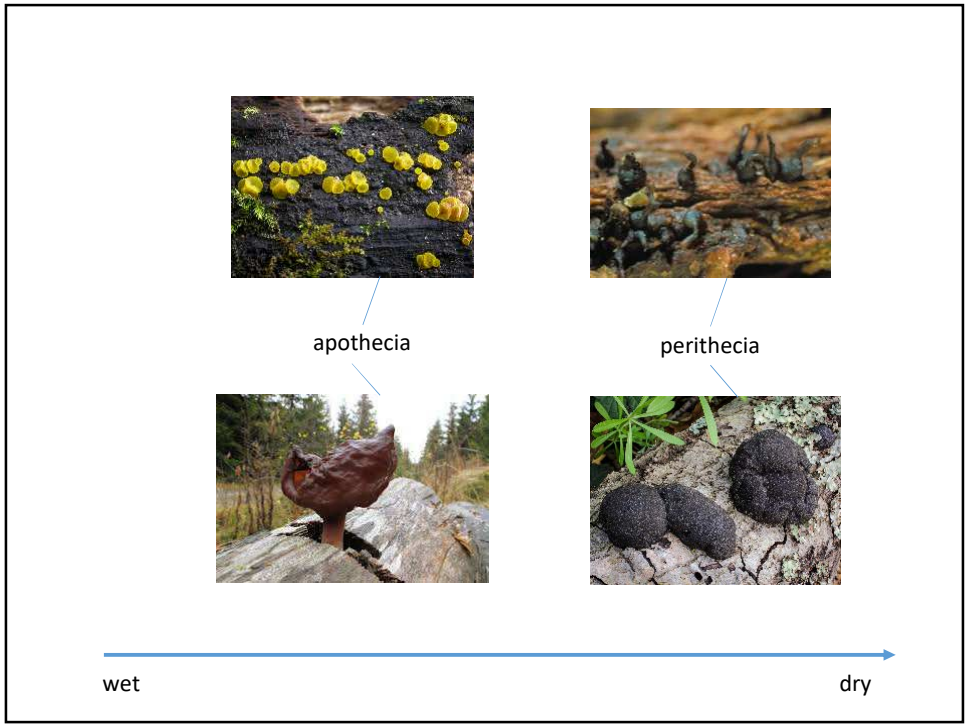
Neurospora



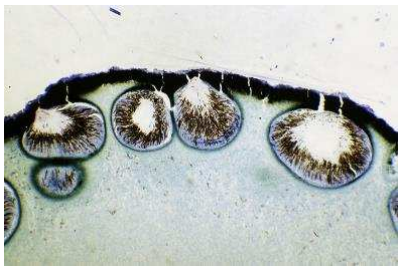

Ascomycete life cycle
Mycelium (n)
Conidia
Asexual reproduction
Developing chains of conidia (spores) (n)
Ascospores
Mycelia (n)
Ascospores (n)
Antheridium
Conidiophore (n)
Ascogonium
Mitosis
Haploid nuclei
–Mating type (n)
Sexual reproduction
+Mating type (n)
Plasmogamy
Developing dikaryotic hypha (n + n)
Trichogyne
Antheridium
Ascogonium
Meiosis


Xylaria
Ascomycete life cycle
Mycelium (n)
Conidia
Asexual reproduction
Developing chains of conidia (spores) (n)
Ascospores
Mycelia (n)
Ascospores (n)
Antheridium
Conidiophore (n)
Ascogonium
Mitosis
Haploid nuclei
–Mating type (n)
Sexual reproduction
+Mating type (n)
Plasmogamy
Developing dikaryotic hypha (n + n)
Trichogyne
Antheridium
Ascogonium
Meiosis
Diploid nucleus
Ascocarp
Karyogamy
Ascus
Dikaryotic hypha
Dikaryotic hyphae


Small
apothecia
perithecia
Large
Short-lived
Long-lived

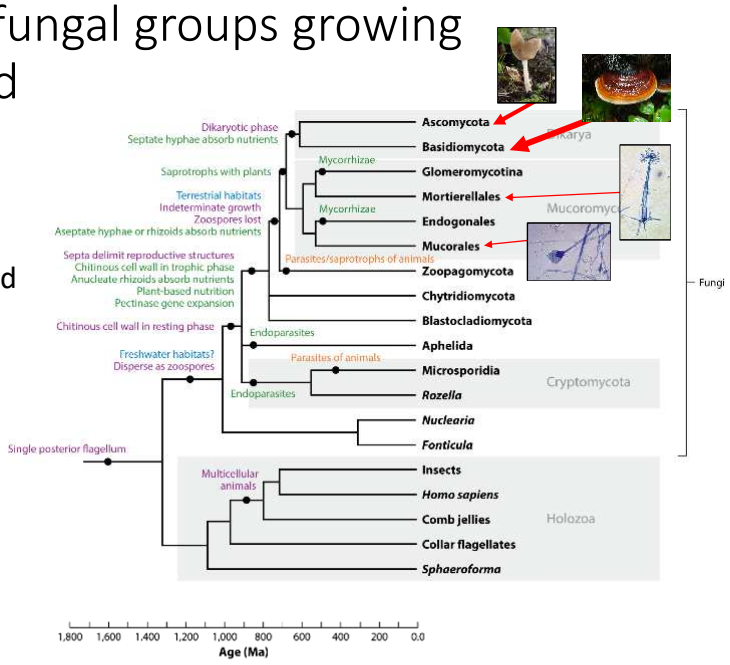

apothecia
perithecia
wet
dry

Perithecia – an adaptation to dry habitats



Major fungal groups growing in wood

Current knowledge to large extent based on fruit bodies..

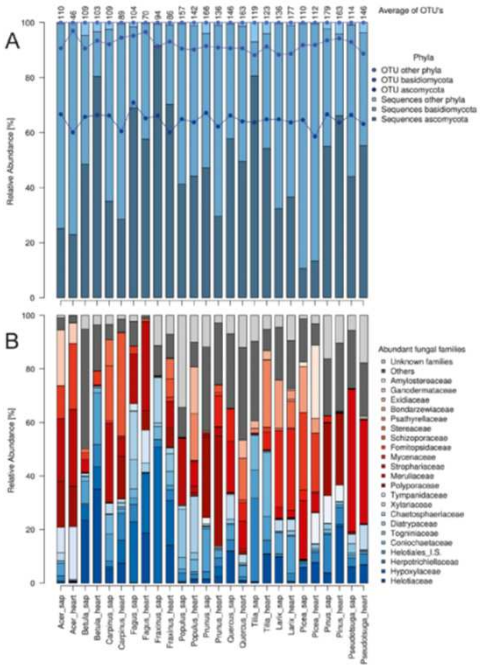


RESEARCH ARTICLE

Molecular fungal community and its decomposition activity in sapwood and heartwood of 13 temperate European tree species

Sabrina Leonhardt[1*], Björn Hoppe[2,3*], Elisa Stengel[4], Lisa Noll[5], Julia Moll[2], Claus Bässler[6], Andreas Dahl[7], Francois Buscot[2,8], Martin Hofrichter[1], Harald Kellner[1]

- 13 temperate tree species
- DNA based assessment after ~6 years decay



RESEARCH ARTICLE

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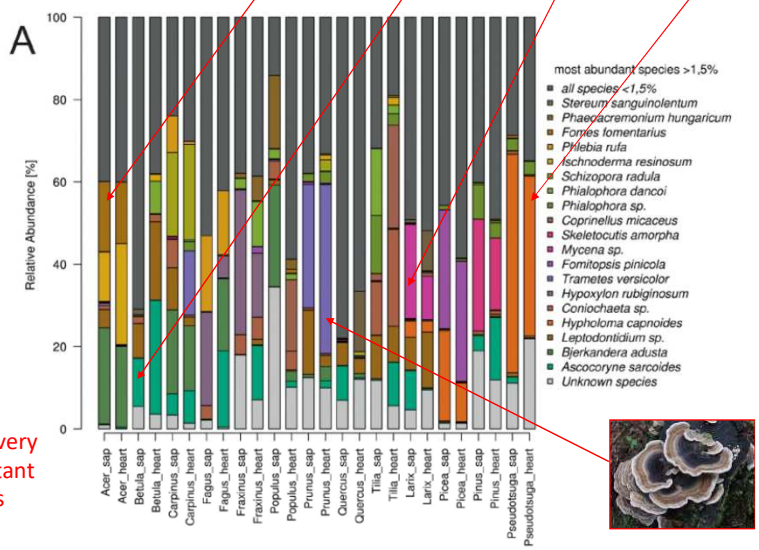

Some very important players

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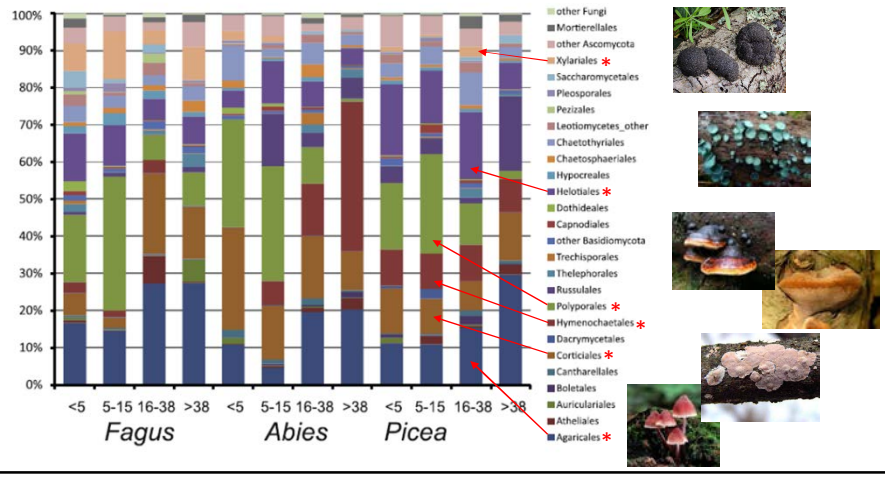
journal homepage: www.elsevier.com/locate/funeco

Fungi associated with decomposing deadwood in a natural beech-dominated forest

Petr Baldrian [a,*], Petra Zrůstová [a], Vojtěch Tláskal [a], Anna Davidová [a], Věra Merhautová [a], Tomáš Vrška [b]



The ISME Journal (2013) 7, 1696–1709

ORIGINAL ARTICLE

Combining high-throughput sequencing with fruit body surveys reveals contrasting life-history strategies in fungi

Otso Ovaskainen[1], Dmitry Schigel[1], Heini Ali-Kovero[1], Petri Auvinen[2], Lars Paulin[2], Björn Nordén[3,4] and Jenni Nordén[1,3,5]

Combined approach

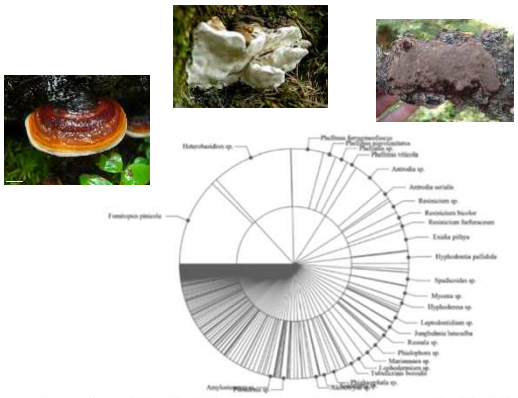


Figure 2 Species and genera of fungi identified from 454-sequencing data in 100 Norway spruce logs. The wheel shows the distribution of those sequences that were identified either to the genus level or to the species level with at least 90% probability of correct identification. The inner part of the wheel represents the genera and outer part the species. For the sake of readability, species names are shown only for those cases, which yielded at least 4000 sequences. For the data on all species, see Supplementary Information.

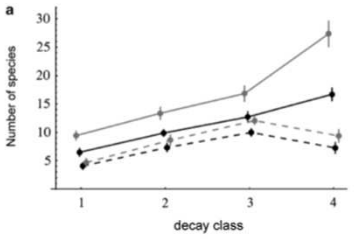


Figure 3 Patterns of mycelial (as detected from DNA) and fruit body occurrence. (a) Shows the mean number of species detected as DNA (continuous lines) or as fruit bodies (dashed lines), either for the target species community (black) or for all observed species (grey). The error bars show ±1 s.e.

Pellopilus nigrolimitatus

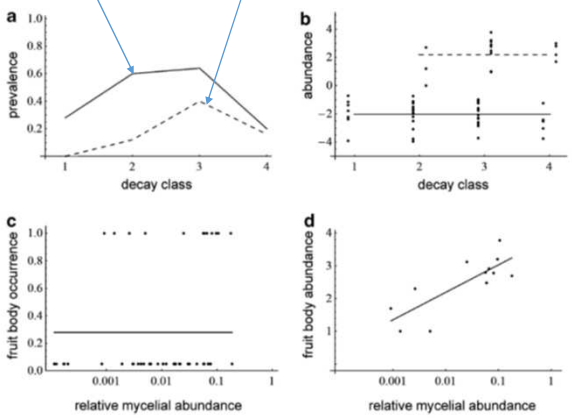


Figure 5 As Figure 4, but for *Phellinus nigrolimitatus*. Nonsignificant regression models are shown as horizontal lines. For corresponding figures for 28 other species, see Supplementary Information.

Succession of fungi during wood decay

Succession of fungi during wood decay


Stereum sanguinolentum


Trichaptum abietinum


Fomitopsis pinicola


Pellopilus nigrolimitatus

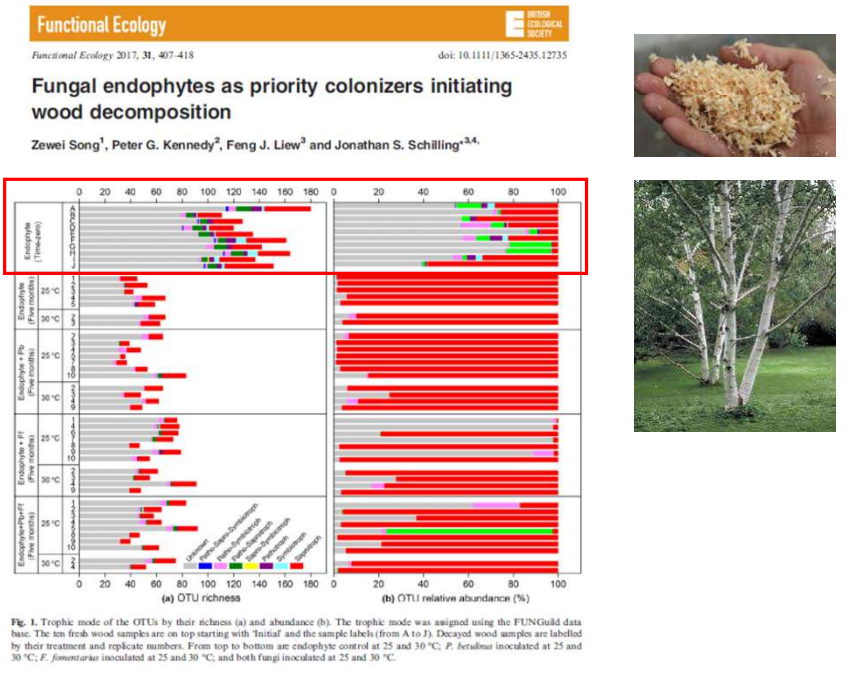

Piptoporus betulinus


Cylindrobasidion evolvens


Fomes fomentarius


Ganoderma applanatum

Primary colonizers Main wood decayers Late stage decayers



Functional Ecology

Functional Ecology 2017, **31**, 407–418 doi: 10.1111/1365-2435.12735

Fungal endophytes as priority colonizers initiating wood decomposition

Zewei Song[1], Peter G. Kennedy[2], Feng J. Liew[3] and Jonathan S. Schilling[3,4]

(a) OTU richness (b) OTU relative abundance (%)

Fig. 1. Trophic mode of the OTUs by their richness (a) and abundance (b). The trophic mode was assigned using the FUNGuild data base. The ten fresh wood samples are on top starting with 'Initial' and the sample labels (from A to J). Decayed wood samples are labelled by their treatment and replicate numbers. From top to bottom are endophyte control at 25 and 30 °C; *P. betulinus* inoculated at 25 and 30 °C; *F. fomentarius* inoculated at 25 and 30 °C; and both fungi inoculated at 25 and 30 °C.

The ISME Journal (2017) 11, 1964–1974

OPEN

ORIGINAL ARTICLE

Interactions between soil- and dead wood-inhabiting fungal communities during the decay of Norway spruce logs

Raisa Mäkipää[1], Tiina Rajala[1,4], Dmitry Schigel[2], Katja T Rinne[1], Taina Pennanen[1], Nerea Abrego[3] and Otso Ovaskainen[2,3]
[1]Natural Resources Institute Finland (Luke), Helsinki, Finland; [2]Department of Biosciences, University of Helsinki, Helsinki, Finland and [3]Department of Biology, Centre for Biodiversity Dynamics, Norwegian University of Science and Technology, Trondheim, Norway

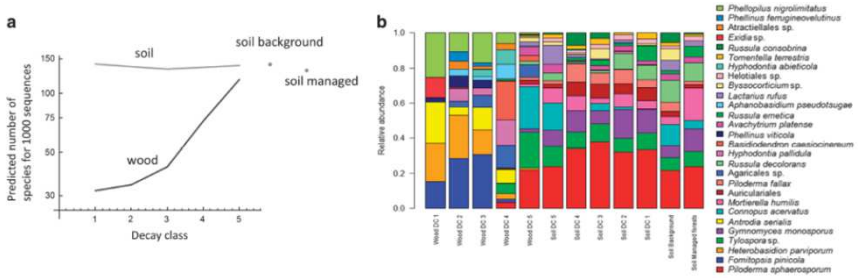


Figure 2 Species richness and species identity in wood and soil substrates. (**a**) The predicted fungal species richness in different substrates and (**b**) the RA of 30 most abundant operational taxonomic units in each substrate type. For constructing (**a**), the response variable in the underlying linear model was the log-transformed number of operational taxonomic units (OTUs) identified for each sample, and the explanatory variables were the log-transformed number of sequences (a continuous covariate) and the sample group (a categorical variable).

The ISME Journal (2017) 11, 1964–1974

OPEN

ORIGINAL ARTICLE

Interactions between soil- and dead wood-inhabiting fungal communities during the decay of Norway spruce logs

Raisa Mäkipää[1], Tiina Rajala[1,4], Dmitry Schigel[2], Katja T Rinne[1], Taina Pennanen[1], Nerea Abrego[3] and Otso Ovaskainen[2,3]
[1]Natural Resources Institute Finland (Luke), Helsinki, Finland; [2]Department of Biosciences, University of Helsinki, Helsinki, Finland and [3]Department of Biology, Centre for Biodiversity Dynamics, Norwegian University of Science and Technology, Trondheim, Norway

Table 1 Fungal species found exclusively in soil, exclusively in dead wood, and in both substrate types

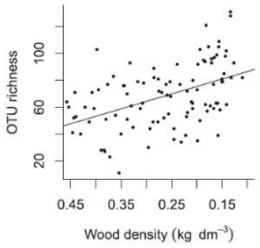
Unique to soil (793)	*Both in soil and wood (608)*	*Unique to wood (589)*
Piloderma sp. (OTU 00094)	*Piloderma sphaerosporum* (OTU 00310)	*Fomitopsis pinicola* (OTU 00001)
Russula sp. (OTU 00048)	*Heterobasidium parviporum* (OTU 00003)	*Antrodia serialis* (OTU 00004)
Russula vesca (OTU 00178)	*Tylospora* sp. (OTU 00005)	*Phellopilus nigrolimitatus* (OTU 00006)
Tretomyces lutescens OTU 00211)	*Gymnomyces monosporous* (OTU 00011)	*Phellopilus nigrolimitatus* (OTU 00022)
Amanita sp. (OTU 00174)	*Connopus acervatus* (OTU 00017)	*Phellinus viticola* (OTU 00014)
Pseudotomentella sp. (OTU 00189)	*Mortierella humilis* (OTU 00009)	*Phellopilus nigrolimitatus* (OTU 00019)
Cortinarius caperatus (OTU 00180)	Auriculariales sp. (OTU 00029)	*Exidia* sp. (OTU 00037)
Cortinarius rubellus (OTU 00088)	*Piloderma fallax* (OTU 00024)	*Atractiellales* sp. (OTU 00033)
Rhodocollybia sp. (OTU 00128)	Agaricales sp. (OTU 00010)	*Phellinis ferrugineovelutinus* (OTU 00020)
Cortinarius traganus (OTU 00212)	*Russula decolorans* (OTU 00025)	*Coniophora puteana* (OTU 00007)
Trechisporales sp. (OTU 00308)	*Hyphodontia pallidula* (OTU 00012)	*Basidioascus* (OTU 00039)
Pseudotomentella humicola (OTU 00308)	*Basidiodendron caesiocinereum* (OTU 00012)	*Pseudeurotiaceae* sp. (OTU 00044)
Cortinarius sp. (OTU 00319)	*Avachytrium platense* (OTU 00015)	*Sistotrema brinkmannii* (OTU 00041)
Piloderma sphaerosporum (OTU 00310)	*Russula emetical* (OTU 00038)	*Hyphoderma* sp. (OTU 00055)
Mortierella sp. (OTU 00097)	*Aphanobasidium pseudotsugae* (OTU 00013)	*Stereum sanguinolentum* (OTU 00026)

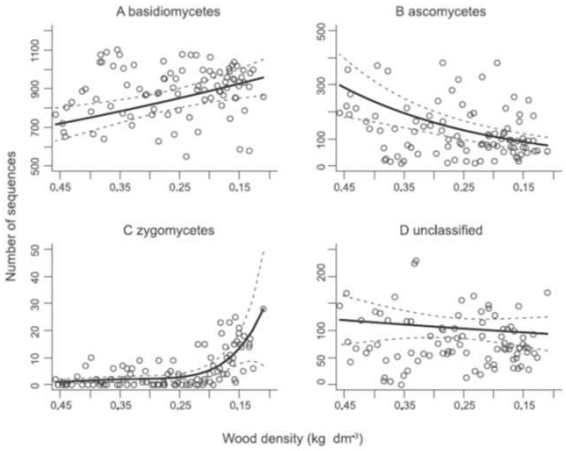
The 15 most abundant species are listed, and the numbers in brackets indicate the total number of species found.

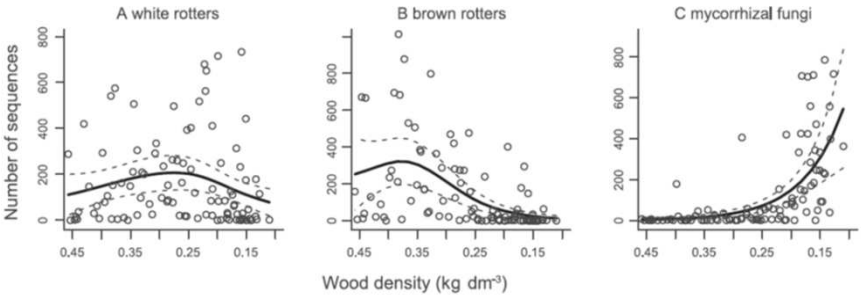
Contents lists available at ScienceDirect
Fungal Ecology
journal homepage: www.elsevier.com/locate/funeco

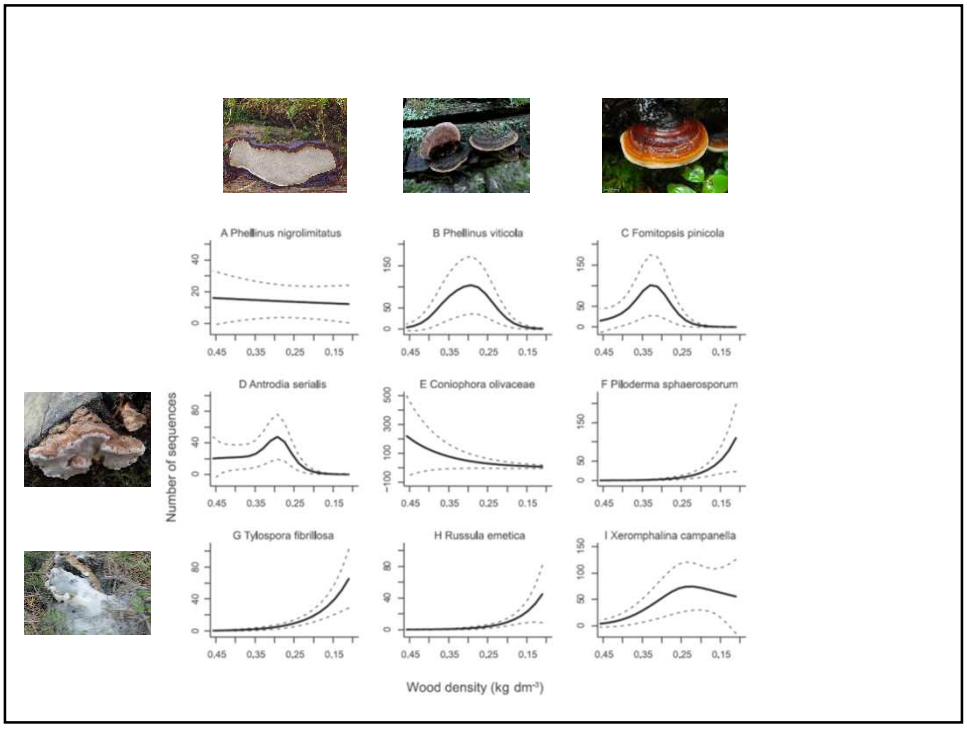
Habitat models of wood-inhabiting fungi along a decay gradient of Norway spruce logs

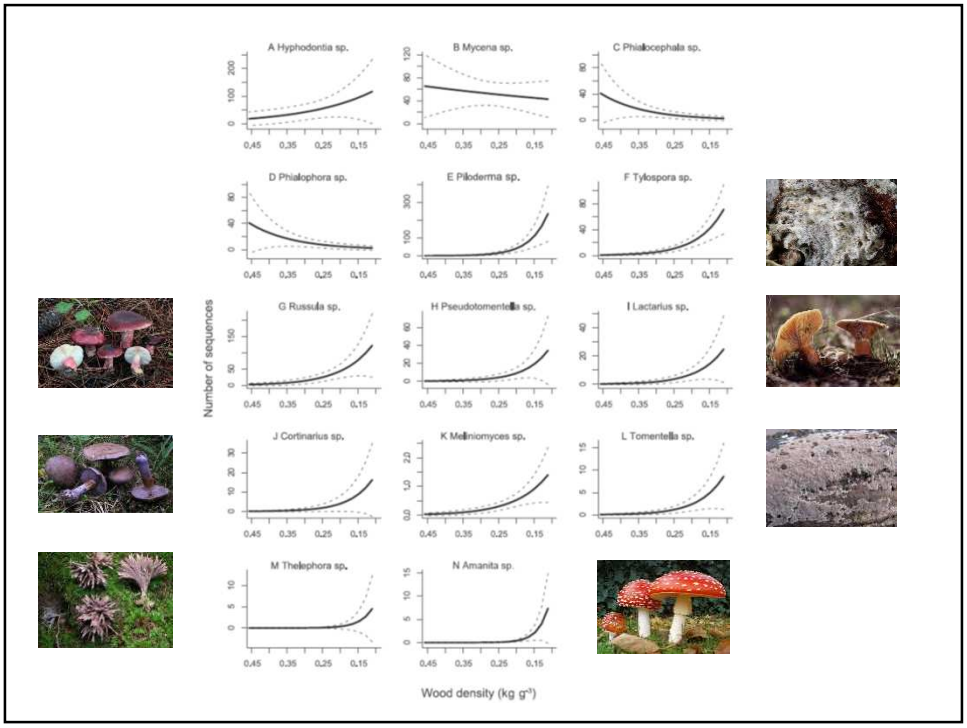
Tiina Rajala [a], Tero Tuomivirta [b], Taina Pennanen [b], Raisa Mäkipää [b,*]








A Phellinus nigrolimitatus
B Phellinus viticola
C Fomitopsis pinicola
D Antrodia serialis
E Coniophora olivaceae
F Piloderma sphaerosporum
G Tylospora fibrillosa
H Russula emetica
I Xeromphalina campanella
Number of sequences
Wood density (kg dm⁻³)


A Hyphodontia sp.
B Mycena sp.
C Phialocephala sp.
D Phialophora sp.
E Piloderma sp.
F Tylospora sp.
G Russula sp.
H Pseudotomentella sp.
I Lactarius sp.
J Cortinarius sp.
K Meliniomyces sp.
L Tomentella sp.
M Thelephora sp.
N Amanita sp.
Number of sequences
Wood density (kg g⁻³)

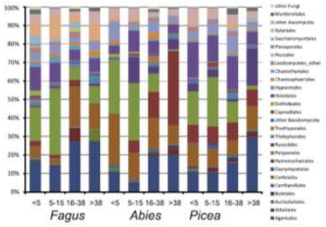
Contents lists available at ScienceDirect

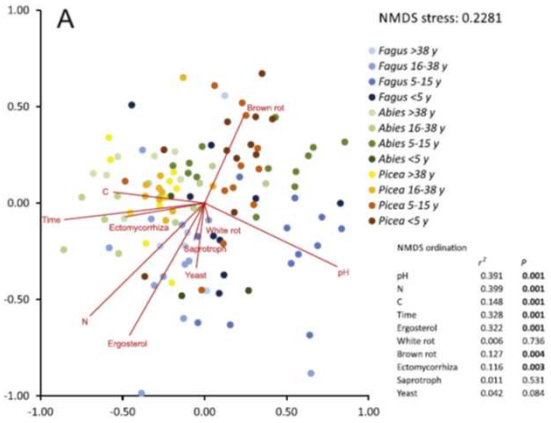
Fungal Ecology

journal homepage: www.elsevier.com/locate/funeco

Fungi associated with decomposing deadwood in a natural beech-dominated forest

Petr Baldrian [a,*], Petra Zrůstová [a], Vojtech Tláskal [a], Anna Davidová [a], Věra Merhautová [a], Tomáš Vrška [b]





NMDS ordination

	r^2	P
pH	0.391	**0.001**
N	0.399	**0.001**
C	0.148	**0.001**
Time	0.328	**0.001**
Ergosterol	0.322	**0.001**
White rot	0.006	0.736
Brown rot	0.127	**0.004**
Ectomycorrhiza	0.116	**0.003**
Saprotroph	0.011	0.531
Yeast	0.042	0.084

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Fungi associated with decomposing deadwood in a natural beech-dominated forest

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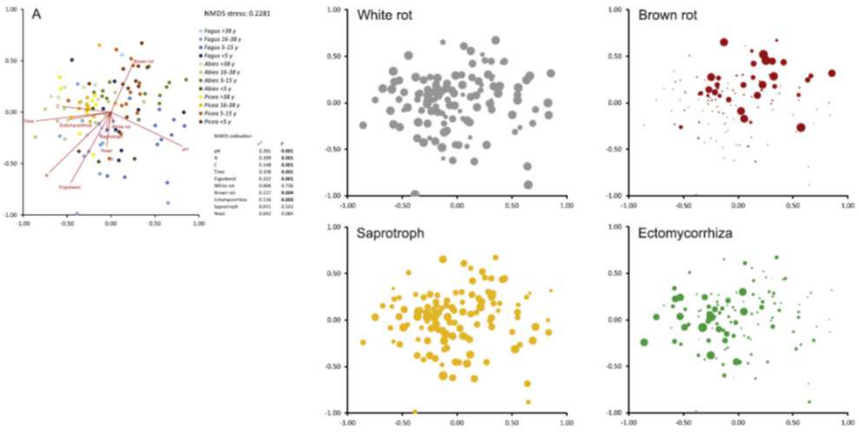

Succession of fungi during wood decay


Stereum sanguinolentum


Trichaptum abietinum


Fomitopsis pinicola


Pellopilus nigrolimitatus


Piptoporus betulinus


Cylindrobasidion evolvens


Fomes fomentarius


Ganoderma applanatum

Primary colonizers Main wood decayers Late stage decayers

Pellopilus nigrolimitatus

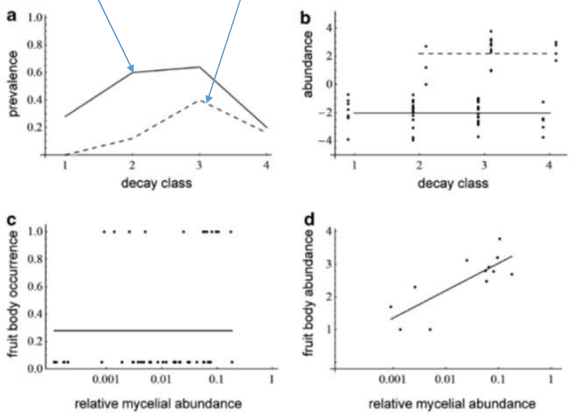

Figure 5 As Figure 4, but for *Phellinus nigrolimitatus*. Nonsignificant regression models are shown as horizontal lines. For corresponding figures for 28 other species, see Supplementary Information.

Not only wood decay fungi!

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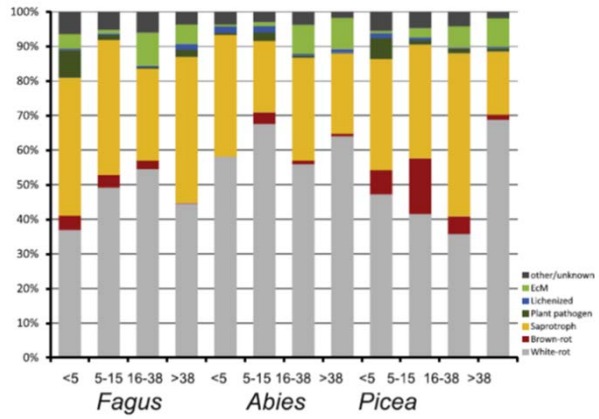
Fungi associated with decomposing deadwood in a natural beech-dominated forest

Petr Baldrian [a,*], Petra Zrůstová [a], Vojtech Tláskal [a], Anna Davidová [a], Věra Merhautová [a], Tomáš Vrška [b]

[a] Laboratory of Environmental Microbiology, Institute of Microbiology of the CAS, Vídeňská 1083, 14220 Praha 4, Czech Republic
[b] Department of Forest Ecology, The Silva Tarouca Research Institute for Landscape and Ornamental Gardening, Lidická 25/27, 602 00 Brno, Czech Republic

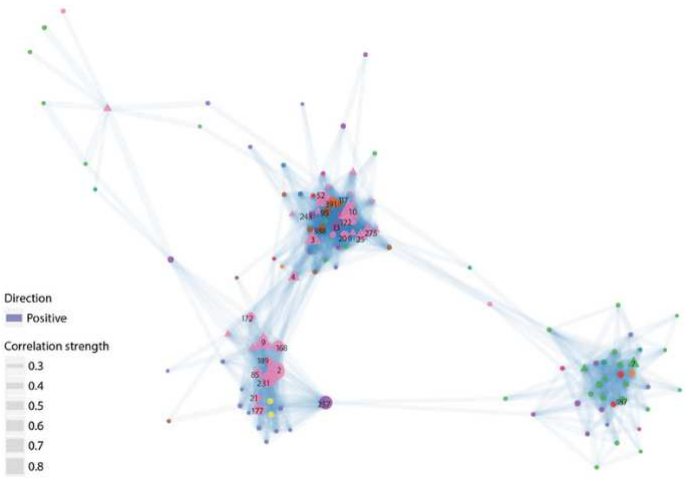


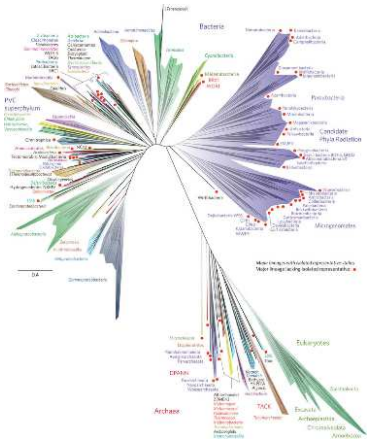
General model for fungal sucession

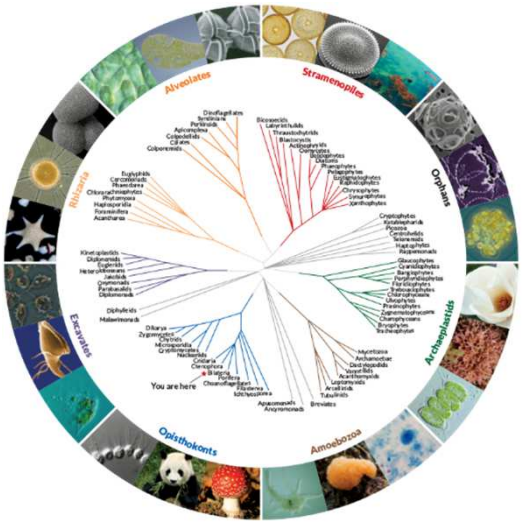
- Endophytes / parasites
- Wood decayers – brown rot
- Wood decayers – white rot
- Ectomycorrhizal fungi

- Ascomycetes
- Basidiomycetes

Biotic interactions in wood





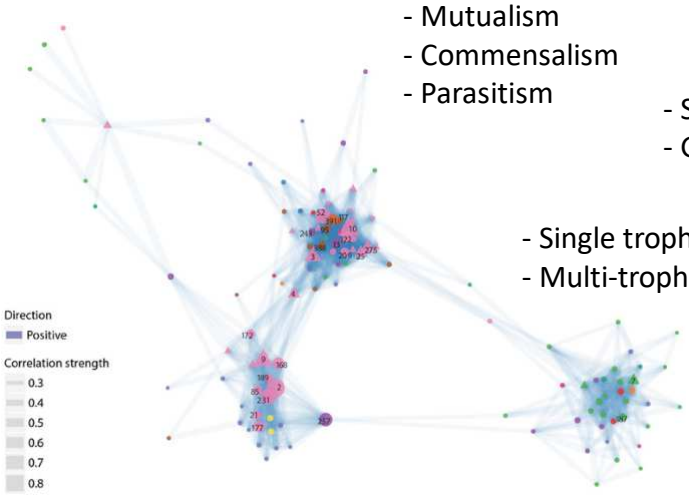


Biotic interactions in wood

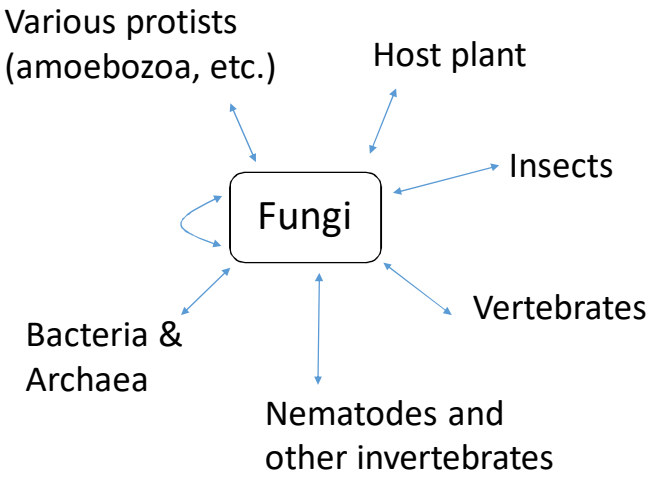
- Mutualism
- Commensalism
- Parasitism

- Specific
- General

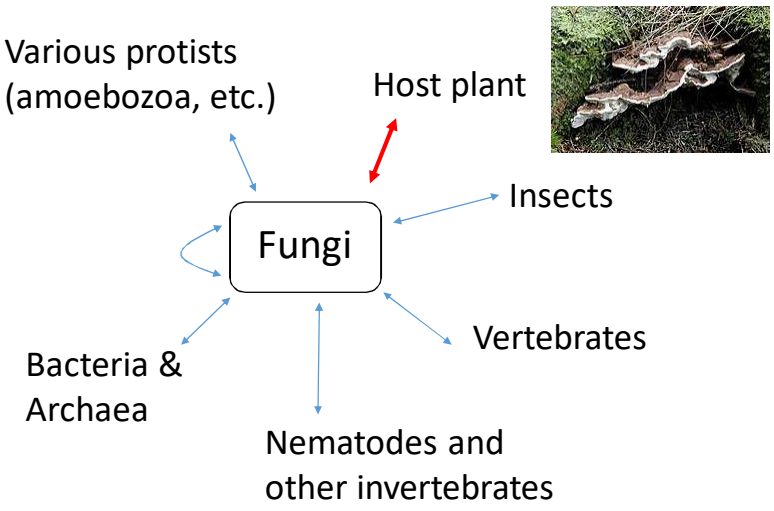
- Single trophic level
- Multi-trophic



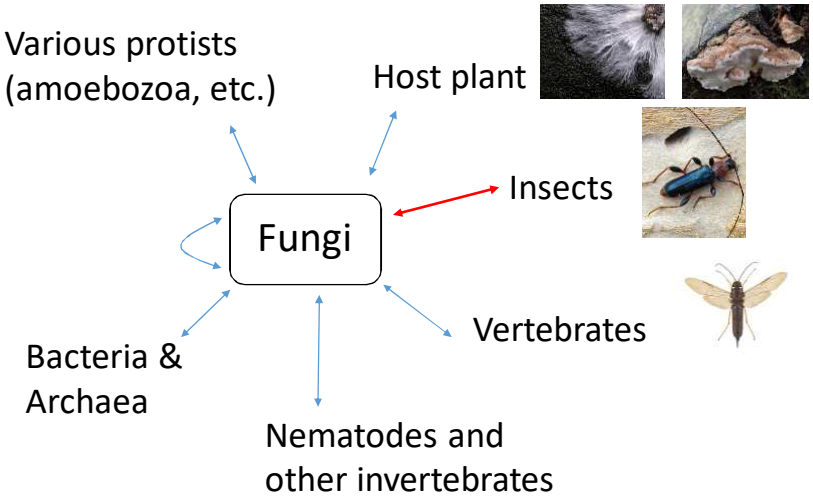
Biotic interactions in wood



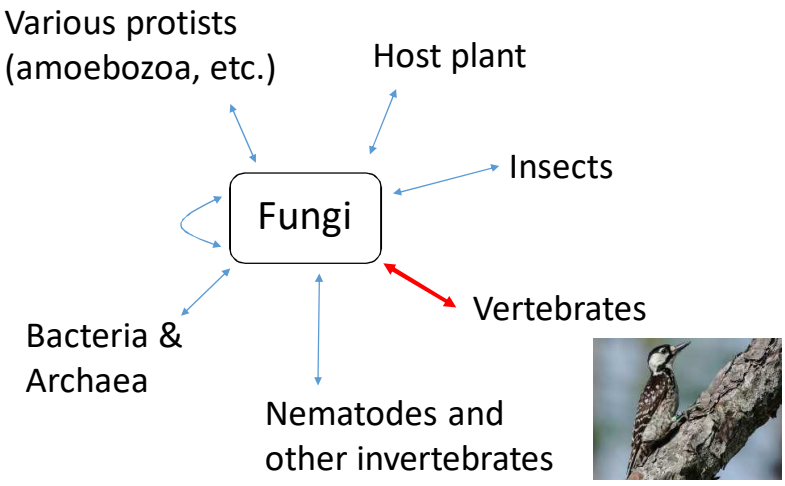
Biotic interactions in wood



Biotic interactions in wood



Biotic interactions in wood



PROCEEDINGS B

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Research

Experimental evidence of a symbiosis between red-cockaded woodpeckers and fungi

Michelle A. Jusino[1,2], Daniel L. Lindner[1], Mark T. Banik[1], Kevin R. Rose[2,3] and Jeffrey R. Walters[2]

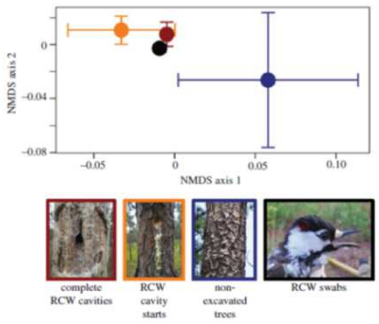


Figure 1. NMDS ordinations of the communities of Basidiomycota fungi found on RCWs and in RCW cavities, RCW cavity starts, and non-excavated trees. The dots in the centre represent the means of the points on the two NMDS axes, and the bars represent 1 s.e. from the mean. NMDS stress = 0.0069, two dimensions.

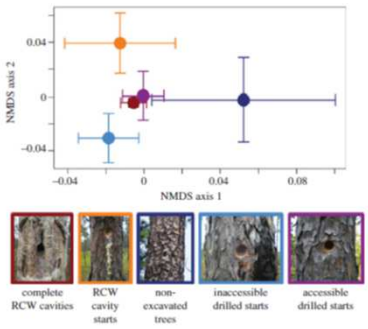
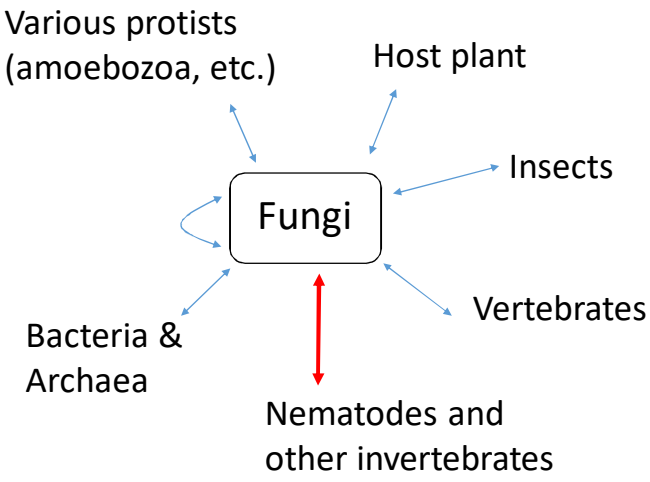
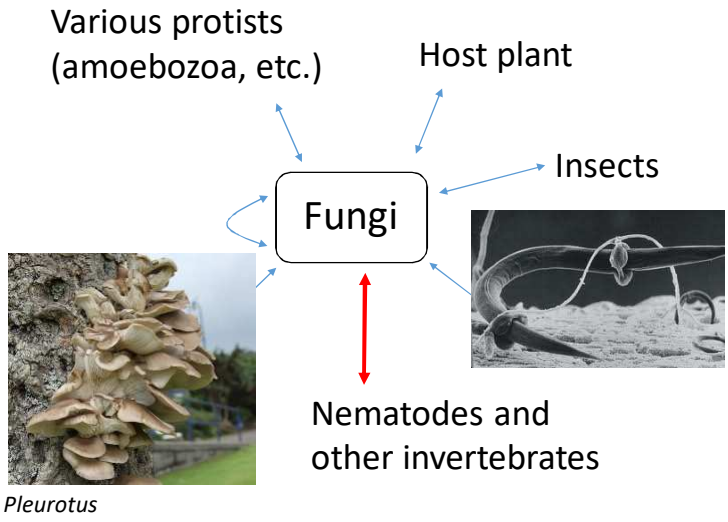


Figure 2. NMDS ordinations of communities of Basidiomycota fungi found in completed RCW cavities, RCW cavity starts, non-excavated trees, drilled starts accessible to RCWs, and drilled starts inaccessible to RCWs. The dots in the centre represent the means of the points on the two NMDS axes, and the bars represent 1 s.e. from the mean. NMDS stress = 0.0062, two dimensions.

Biotic interactions in wood

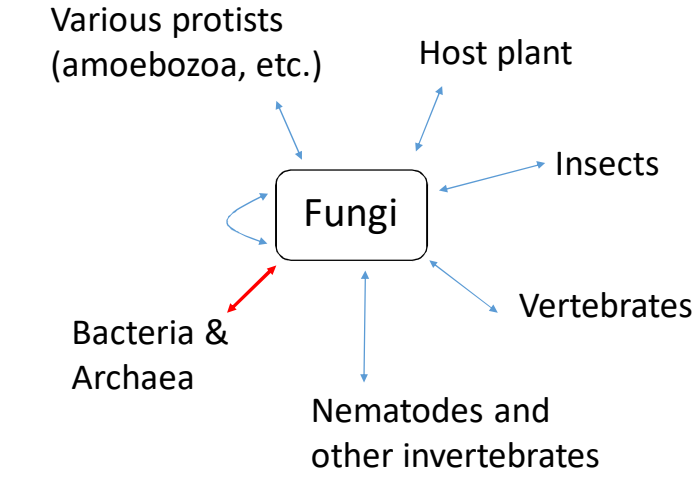


Biotic interactions in wood



Pleurotus

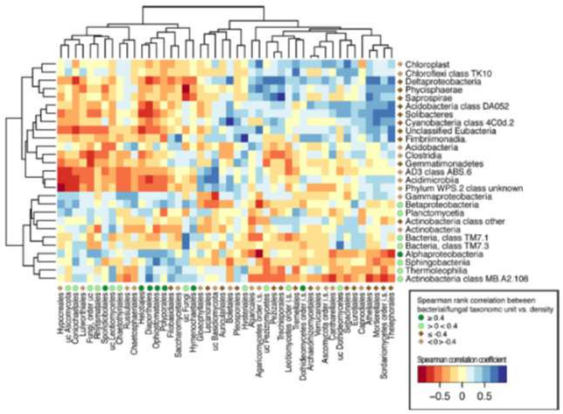
Biotic interactions in wood



RESEARCH ARTICLE

Natural decay process affects the abundance and community structure of Bacteria and Archaea in *Picea abies* logs

J. M. Rinta-Kanto[1,*], H. Sinkko[1], T. Rajala[2,†], W. A. Al-Soud[3], S. J. Sørensen[3], M. V. Tamminen[4] and S. Timonen[1]



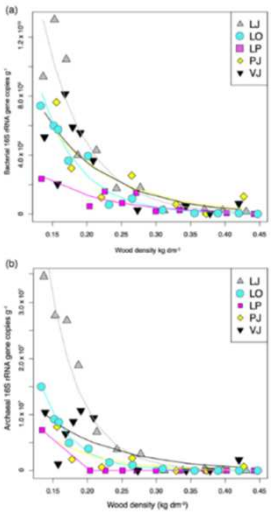


Figure 4. Co-occurrence patterns of fungal orders and bacterial classes in relation to wood density. Spearman rank correlations were calculated between relative abundances of bacterial classes and fungal orders. The *P*-value is ≤ 0.05 if the absolute value of the correlation coefficient is ≥0.536 and *P* ≤ 0.01 if the absolute value of the correlation coefficient is ≥0.732. Symbols after taxonomic IDs represent Spearman rank correlations between relative abundance of the taxonomic unit and wood density.

MINIREVIEW

Bacteria in decomposing wood and their interactions with wood-decay fungi

Sarah R. Johnston*,†, Lynne Boddy and Andrew J. Weightman

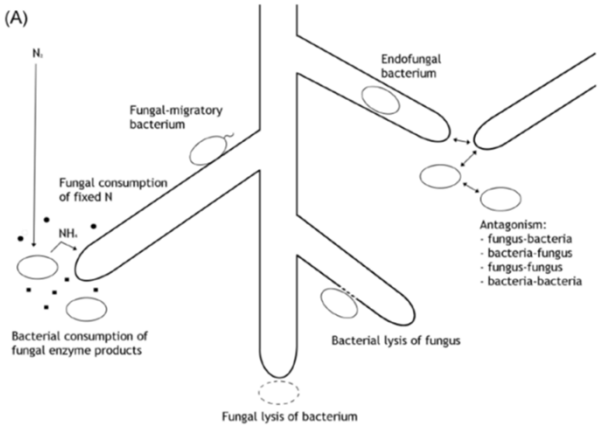
Cardiff School of Biosciences, Cardiff University, Museum Avenue, Cardiff, CF10 3AX, UK

*Corresponding author: Cardiff School of Biosciences, Cardiff University, Museum Avenue, Cardiff, CF10 3AX, UK. Tel: 07906199939; E-mail johnstonar@cardiff.ac.uk

One sentence summary: Bacteria and fungi both live in wood, but not much is known about how they interact—this article reviews what is already known about them and what is yet to be found out.

Editor: Gerard Muyzer

†Sarah R. Johnston, http://orcid.org/0000-0002-3806-3416



Functional Ecology

Functional Ecology 2017, 31, 530–541 doi: 10.1111/1365-2435.12734

Accumulation rates and sources of external nitrogen in decaying wood in a Norway spruce dominated forest

Katja T. Rinne*, Tiina Rajala†, Krista Peltoniemi, Janet Chen, Aino Smolander and Raisa Mäkipää

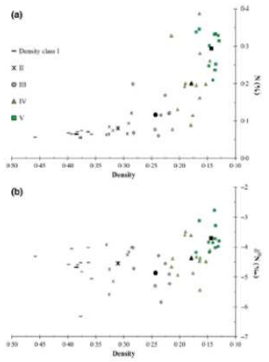


Fig. 1. The N% (a) and $\delta^{15}N$ (b) values of the 49 decayed wood samples of Lapinjärvi. The results are shown separately for each density class, and the average of each class is indicated (the five larger symbols).

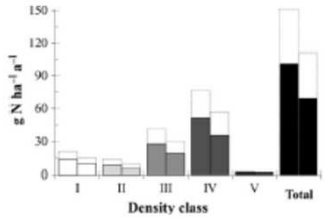
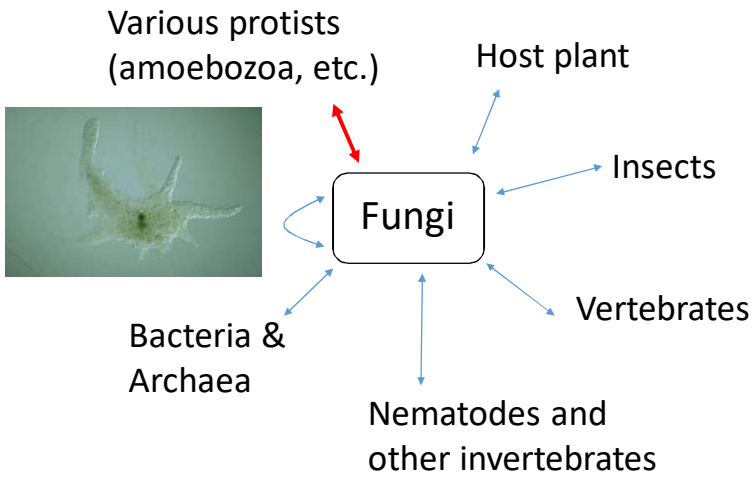
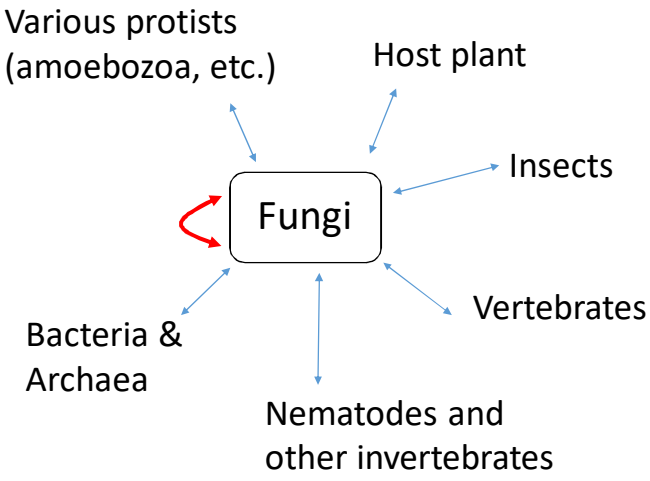


Fig. 4. The annual levels of N_2 fixation of fallen spruce logs in Lapinjärvi. The results are shown separately for each decay class and for two consecutive years. The total per year is also indicated. The dotted lines indicate the estimated N_2 fixation rate at the climate warming scenario RCP 4-5 (Ruosteenoja *et al.* 2013).

Biotic interactions in wood



Biotic interactions in wood



Many unknown biotic interactions between fungi in wood

Fomitopsis pinicola

Pycnoporellus fulgens

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Modeling species co-occurrence by multivariate logistic regression generates new hypotheses on fungal interactions

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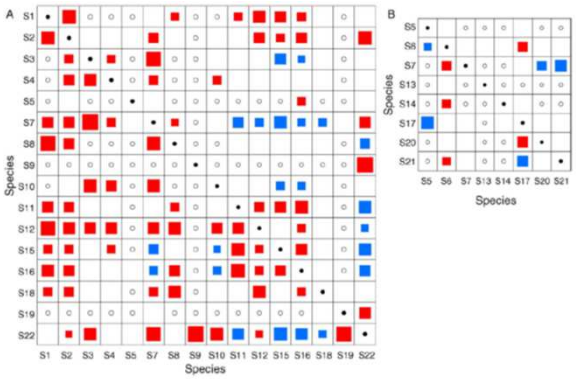

FIG. 2. The estimated species-to-species correlation coefficients on dead-wood fungi inhabiting (A) spruce and (B) birch logs. Upper diagonals correspond to the model M2(**R**) which accounts for the substrate variables; lower diagonals to the model M1(**R**) which assumes that all substrate units are equal. Red refers to positive and blue to negative correlations, and the size of the colored rectangle corresponds to the median estimate for the absolute value of the correlation coefficient. The estimates are averaged among the sites, including only cases in which the posterior probability for a positive (negative) correlation was at least 90%. Species pairs that were never included in the same analyses are shown by empty circles.

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ARTICLES

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Diversity begets diversity in competition for space

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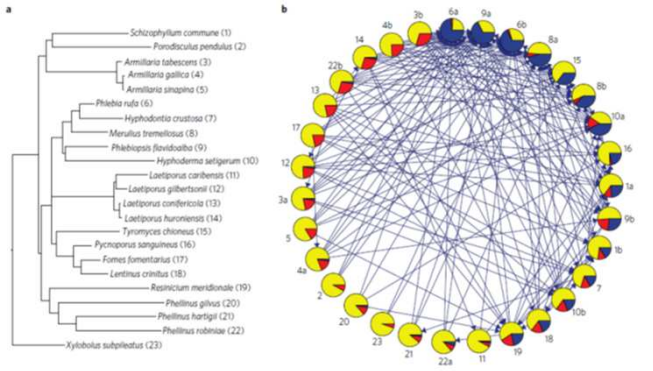

Figure 1 | The 23 fungal species used in the pairwise competition experiments. a, The molecular phylogenetic tree including all species. **b**, The competitive network structure for 31 of the 37 colonies (not shown are six *Armillaria gallica* colonies). Blue arrows point to the winner of each competition, and a lack of an arrow indicates deadlock. Numbers in **b** correspond to species numbers in **a**, and letters denote different isolates within species. Species are ranked in order of competitive ability (see Methods), with the most dominant species (6a) at the top, moving clockwise towards the least dominant species (3b). Pie charts indicate the proportion of wins (blue), losses (red) and deadlocks (yellow) for each isolate.

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LETTER

Outcomes of fungal interactions are determined by soil invertebrate grazers

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Abstract

Saprotrophic fungal community composition, determined by the outcome of competitive mycelial interactions, is one of the many key factors affecting soil nutrient mineralisation and decomposition rates. Fungal communities are not generally predicted to be regulated by top-down factors, such as predation, but rather by bottom-up factors, including resource availability. We show that invertebrate grazers can exert selective pressures on fungal decomposer communities in soil, reversing the outcomes of competitive interactions. By feeding selectively on the cord-forming fungus *Resinicium bicolor*, isopods prevented the competitive exclusion of *Hypholoma fasciculare* and *Phanerochaete velutina* in soil and wood. Nematode populations also reversed the outcomes of competitive interactions by stimulating growth of less competitive fungi. These represent two opposing mechanisms by which soil fauna may influence fungal community composition and diversity. Factors affecting soil invertebrate communities will have direct consequences for fungal-mediated nutrient cycling in woodland soils.