Introduction to fungi in dead wood

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

Håvard Kauserud, University of Oslo

Fungi - phylogenetic placement
• 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!

Aglaophyton
~400 mill years ago

Rhynie Chert, Scotland
Fungal tree of life

Wide variation in phenotypes, life histories, life cycles, ecology...
Wide variation in phenotypes, life histories, life cycles, ecology...
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
Hyphal growth

Hyphae, with or without septa
Mycelium

Little differentiation

Yeast
Hyphal growth

Different karyotypes and «genetic makeup»
Heterotrophic organisms

Grows within the substrate – absorb nutrients

Simple organic compounds

Enzymes
• Cellulose
• Hemicellulose
• Lignin
• (Pectin ++)

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 + hemicellulose → brown colour
• Important in boreal forests

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?
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 techniques 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’
High throughput sequencing
High throughput sequencing

[Diagram of high throughput sequencing steps]

High throughput sequencing

[Diagram with OTU1, OTU2, and OTU3]
High throughput sequencing

Major fungal groups growing in wood
Basidiomycota
Tremellales, Dacrymycetales, Auriculariales

«Jelly fungi»

- Tremella
- Dacrymyces
- Calocera
- Basidiadendron
- Auriculariales

Cantharellales and Trechisporales

- Tulasnella
- Botryobasidium
- Trechispora
- Many «corticoids»
Phallomycetidae

Geastrum

Hymenochaetales

Phellinus

Inonotus

Schizopora

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

- **Gloephyllum**
- Neolentinus («Train wreckers»)

Polyporales

- **Crustomyces**
- **Teraneae**
- **Merulius**
- **Ganoderma**
- **Fomitopsis**
Boletales

Tapinella

Coniophora

Serpula

Serpula lacrymans
haploid (basidio)spores

germinating spores

monokaryotic hyphae

plasmogamy (if compatible mating types)
dikaryotic hyphae

clamps

fruit body

production of spore producing layer - the hymenium

in basidia: karyogamy, meiosis and spore production

(active) spore dispersal
Living on sinking island - must get away!

Disperse mainly by spores
haploid (basidio)spores

Spore dispersal

germinating spores

Fruit body

production of spore producing layer - the hymenium

clamps
dikaryotic hyphae

plasmogamy (if compatible mating types)

monokaryotic hyphae

in basidia: karyogamy, meiosis and spore production

(active) spore dispersal

haploid (basidio)spores

Fruit body production

Basidiospore

Basidium
~20,000 spore traps!!!!
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.
haploid (basidio)spores

Fruit body

production of spore producing layer - the hymenium

in basidia: karyogamy, meiosis and spore production

Long-lived

clamps
dikaryotic hyphae

plasmogamy (if compatible mating types)

monokaryotic hyphae

germinating spores

Fruit body production

How does the dikaryotization occur?

haploid (basidio)spores

(active) spore dispersal
Serpula lacrymans

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

James B. Anderson, Johann N. Brune, Dahlia Krämer, Hao Wang, Nicolas Rodríguez and Myron L. Smith

«The humongous fungus»
Living on sinking island - must get away!

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

Fruit body
Major fungal groups growing in wood

Ascomycota

- Pezizomycotina
  - Taphrinomycotina

- Saccharomycotina
Ascomycota

- Pezizomycotina
- Saccharomycotina
- Taphrinomycotina

Orbiliomycetes

- Orbilia
Helotiales

Chlorociboria

Bisporella

Ascoscyne

Xylariales

Xylaria

Hypoxylon

Daldinia

Anthostoma
Perithecia – an adaptation to dry habitats

Major fungal groups growing in wood

Current knowledge to large extent based on fruit bodies..
• 13 temperate tree species
• DNA based assessment after ~6 years decay

Some very important players

- Fomes
- Ascocoryne
- Hypholoma
- Fomitopsis
Combined approach
Succession of fungi during wood decay
Succession of fungi during wood decay

Primary colonizers
- 
Piptoporus betulinus
- 
Cylindrobasidium evolvens

Main wood decayers
- 
Stereum sanguinolentum
- 
Trichaptum abietinum
- 
Fomitopsis pinicola

Late stage decayers
- 
Fomitopsis pinicola
- 
Pellopilus nigrolimitatus
- 
Piptoporus betulinus
- 
Cylindrobasidium evolvens
- 
Fomes fomentarius
- 
Ganoderma applanatum

Fungal endophytes as priority colonizers initiating wood decomposition

Fig. 1: Enzyme activity of the OTUs by their relative richness and abundance. (a) The orange scale was assigned using the R1750A300 data set. The dark blue scale was assigned using the RNAseq data set. Each fungal species is represented with a different color. Differences were calculated between the mean of the cold (4 °C) and the mean of the warm (23 °C and 36 °C) decay temperatures.
original article
Interactions between soil- and dead wood-inhabiting fungal communities during the decay of Norway spruce logs

Benoit Makimäki, Tyya Rohmu, Donald Sjögren, Kaija T Erviä, Tekla Penttinen, Naama Avishai and Ole Økland
Natural Resource Institute Foundation, Helsinki, Finland. Department of Biosciences, University of Helsinki, Helsinki, Finland. Department of Mathematics, University of Helsinki, Helsinki, Finland. 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).

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

<table>
<thead>
<tr>
<th>Unique to soil (788)</th>
<th>Both in soil and wood (808)</th>
<th>Unique to wood (389)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Pleurotus</em> sp. (OTU 00004)</td>
<td><em>Pleurotus sphaerocephalus</em> (OTU 00010)</td>
<td><em>Fomitopsis pinicola</em> (OTU 00001)</td>
</tr>
<tr>
<td>Russula sp. (OTU 00009)</td>
<td><em>Heterobasidion parvum</em> (OTU 00003)</td>
<td><em>Amanita verna</em> (OTU 00004)</td>
</tr>
<tr>
<td>Russula sp. (OTU 00007)</td>
<td><em>Tylospora</em> sp. (OTU 00000)</td>
<td><em>Phaeolus niglerianus</em> (OTU 00006)</td>
</tr>
<tr>
<td><em>Trametes</em> hirsuta (OTU 00021)</td>
<td><em>Gymnocorymbus sanguineus</em> (OTU 00011)</td>
<td><em>Phaeolus niglerianus</em> (OTU 00022)</td>
</tr>
<tr>
<td><em>Auricularia fluviatilis</em> (OTU 00172)</td>
<td><em>Ganoderma lucidum</em> (OTU 00017)</td>
<td><em>Phaeolus sikkimensis</em> (OTU 00014)</td>
</tr>
<tr>
<td><em>Gyrinella auriculata</em> (OTU 00030)</td>
<td><em>Auricularia auriculata</em> (OTU 00009)</td>
<td><em>Phaeolus niglerianus</em> (OTU 00019)</td>
</tr>
<tr>
<td><em>Coriolus</em> rhododendri (OTU 00008)</td>
<td><em>Pleurotus fallicus</em> (OTU 00024)</td>
<td><em>Exidia</em> sp. (OTU 00002)</td>
</tr>
<tr>
<td><em>Hypholoma</em> sp. (OTU 00005)</td>
<td><em>Ganoderma lucidum</em> (OTU 00019)</td>
<td><em>Atrabilis</em> sp. (OTU 00003)</td>
</tr>
<tr>
<td><em>Hypholoma</em> sp. (OTU 00006)</td>
<td><em>Ganoderma lucidum</em> (OTU 00019)</td>
<td><em>Phlebia serrulata</em> (OTU 00014)</td>
</tr>
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<td><em>Trametes</em> hirsuta (OTU 00021)</td>
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<td><em>Phlebia serrulata</em> (OTU 00014)</td>
</tr>
</tbody>
</table>

The 15 most abundant species are listed, and the numbers in brackets indicate the total number of species found.
Fungi associated with decomposing deadwood in a natural beech-dominated forest

Petr Rabaján, Petra Zvézda, Vojtech Švábk, Anna Bandylová, Věra Mekhanrova, Tomáš Voška

NMDs stress: 0.2281

A

NMDS ordination

<table>
<thead>
<tr>
<th>F</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>pH</td>
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</tr>
<tr>
<td>N</td>
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</tr>
<tr>
<td>C</td>
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<tr>
<td>Tr</td>
<td>0.001</td>
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<tr>
<td>Exp</td>
<td>0.001</td>
</tr>
<tr>
<td>White rot</td>
<td>0.001</td>
</tr>
<tr>
<td>Brown rot</td>
<td>0.001</td>
</tr>
<tr>
<td>Scopulariopsis</td>
<td>0.001</td>
</tr>
<tr>
<td>P. t.</td>
<td>0.001</td>
</tr>
</tbody>
</table>

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

Petr Rabaján, Petra Zvézda, Vojtech Švábk, Anna Bandylová, Věra Mekhanrova, Tomáš Voška

White rot

Brown rot

Saprotroph

Ectomycorrhiza
Succession of fungi during wood decay

Primary colonizers: Cylindrobasidion evolvens, Piptoporus betulinus, Stereum sanguineolentum

Main wood decayers: Fomitopsis pinicola, Trichaptum abietinum

Late stage decayers: Pellopilus nigrolimitatus, Piptoporus betulinus, Stereum sanguineolentum

**Figure 5** As Figure 4, but for *Pellopilus nigrolimitatus*. Non-significant regression models are shown as horizontal lines. For corresponding figures for 28 other species, see Supplementary Information.
Not only wood decay fungi!
General model for fungal succession

- 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

Various protists (amoebozoaa, etc.)

Host plant

Fungi

Insects

Vertebrates

Bacteria & Archaea

Nematodes and other invertebrates
Biotic interactions in wood

- Various protists (amoebozoa, etc.)
- Host plant
- Bacteria & Archaea
- Insects
- Vertebrates
- Nematodes and other invertebrates

*Figure 1: NMDS ordination of the communities of Basidiomycota fungi found in red-cockaded woodpecker cavities, with trees in complete cavities, on non-excavated trees, and on 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 = 0.0006, two dimensions.*

*Figure 2: NMDS ordination of communities of Basidiomycota fungi found in completed RCOW cavities, on non-excavated trees, and on 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 = 0.0006, two dimensions.*
Biotic interactions in wood

- Various protists (amoebozoans, etc.)
- Host plant
- Insects
- Fungi
- Nematodes and other invertebrates
- Bacteria & Archaea
- Vertebrates

*Pleurotus*
RESEARCH ARTICLE

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


MONOGRAPH

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

Sarah R. Johnstone1, Lynne Bodd and Andrew J. Weightman

Cardiff School of Biosciences, Cardiff University, Rumney Avenue, Cardiff, CF10 3XJ, UK

Supporting information is available online at www.rspb.royalsocietypublishing.org.

1. How can we be sure that the bacteria and fungi found in the wood are the same? There is no evidence for this.

2. Is there any information about the organisms in the lake? There is no information about this.
Biotic interactions in wood

Various protists (amoebozoa, etc.)

Host plant

Insects

Fungi

Vertebrates

Bacteria & Archaea

Nematodes and other invertebrates
Biotic interactions in wood

Various protists (amoebozoa, etc.)

Host plant

Insects

Vertebrates

Nematodes and other invertebrates

Fungi

Bacteria & Archaea
Many unknown biotic interactions between fungi in wood

Fomitopsis pinicola  Pycnoporellus fulgens
Diversity begets diversity in competition for space

Daniel S. Maynard*, Mark A. Bradford, David L. Lindner, Linda T. A. van Diepen, Serita D. Frey, Jessica A. Glaser* and Thomas W. Crowther*

Figure 1: The 27 fungal species used for the pairwise competition experiments. A. The molecular phylogenetic tree including all species. B. The competitive network structure for 10 of the 27 species and shown at six American oak sites. Blue arrows point to the winner of each competition, and a lack of an arrow indicates deadlock. Numbers in the corresponding 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 out at the top, moving clockwise towards the least dominant species). The pie charts indicate the proportion of wins (blue), losses (red) and deadlocks (yellow) for each isolate.

ECOLOGY LETTERS

Outcomes of fungal interactions are determined by soil invertebrate grazers

Harry W. Bradford, Luke Hardy and Paul W. Lewis

Abstract

Hypothetical fungal-mycorrhizal interactions are determined by the intensity of competition mediated interactions. In this study, we observed the effects of soil fauna on soil fungal communities and the mycorrhizal colonization of roots. Fungal communities are not generally optimal for fungal interactions, as in previous studies, but optimal for fungal colonization. Mycorrhizal colonization was altered by soil fauna, as soil fauna promoted the colonization of fungal species that are beneficial for plant growth. These results suggest that soil fauna are important for fungal community dynamics and ecosystem functioning.