

Dead Wood Meeting 2015

Participants & abstracts

Compiled and edited by Dmitry Schigel

Participants, their affiliations, e-mail addresses and abstracts (if submitted) are listed in an alphabetical order of last names. The abstract are displayed as submitted after obvious typos were corrected.

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Does connectivity matter for fungal conservation?

Among the factors that affect the conservation efficiency of protected areas, lack of connectivity is considered as one of the main problems. In this study, we aim to assess the influence of connectivity of European beech forest reserves on wood-inhabiting fungal communities, compared to influence of local factors. For addressing this topic, we used a data matrix consisting of 344 fungal species on 1571 resource units sampled in 42 European beech forest reserves. Our results show that connectivity has significant effects on wood-inhabiting fungal communities in European beech forest reserves, and that the effectiveness of reserves for maintaining the wood-inhabiting fungal diversity is compromised by habitat fragmentation. Connectivity at small scales (measured as the area of the reserve) had a strong influence on the occurrence of indicator species and was also critical for the number of species at resource level. Connectivity at larger scales (connectivity to surrounding beech forests) seemed to be particularly critical for the community composition both at resource and reserve levels. In line with previous research, other covariates such as resource quality (especially size of the resource units) and climate (especially annual temperature range in the reserve) influenced wood-inhabiting fungal communities. The effects of habitat fragmentation were especially strong in western and northern European regions where the smallest and more isolated reserves were located. We propose that an effective conservation strategy of wood-inhabiting fungi should focus on increasing the areas of the present reserves as well as conserving new reserves in the proximity of the existing ones.

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Saproxylic beetle conservation projects in Neuchâtel (Western Switzerland)

As in many countries, old trees and dead wood are rare in managed forests of Switzerland. Therefore, the government encourages the creation of forest reserves. There are two kinds of forest reserves: total forest reserves which are left unmanaged and special forest reserves in which management must aim at enhancing biodiversity. Both types of reserves raise interesting conservation issues. Distances between total forest reserves are too important to allow connections between them for low dispersal species such as saproxylic beetles. To conserve rare species in special forest reserves, managers must sometimes deal with species having opposite requirements. As in other countries too, cities sometime represent a refuge for threatened species. In this perspective, three saproxylic beetle conservation projects are presented: the first one aims at creating a network of old trees within a managed forest, the objective of the second one is to find a solution to manage a forest reserve, taking into account divergent species requirements. The third one shows examples of saproxylic beetle conservation in an urban context.

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The early stage of wood decay: volatile attraction

A previous study highlighted the oviposition preference of saproxylic xylophagous beetle *Rutpela maculata* (Cerambycidae) as in or within 10 mm of the white rot fungi *Stereum hirsutum* in fresh felled beech logs. Taking this further the present study investigated whether host volatiles form an important component in host searching behaviour by gravid *R. maculata*, through olfactometry and GC-EAG testing. Antennal response chemicals were analysed by GC-MS. Results showed a strong preference of combined host volatiles of beech with *S. hirsutum* in olfactometry and together with GC-EAG responses, indicate volatiles are important for host searching behaviour in ovipositing *R. maculata*. Identified volatile antennal responses included three sesquiterpenes, a monoterpene, an alkane and either 1-H-Inden-1-one or 1,8-dimethyltetralin. Without further testing of individual chemicals in olfactometry the EAG responses cannot be defined as repellent or attractive but the results of fungal plug ovipositing preference suggest they are attractants. This is further supported by *R. maculata* extension of the ovipositor and probing while in beech with *S. hirsutum* arms of the olfactometer but no other treatments.

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All Star Dead Wood Circus Home of 100 Wonders

In managed landscapes, dead wood pool constitutes of different fractions, some of which are retained in purpose and some of which are accidental leftovers. The volume of different kinds of dead wood fractions is constantly changing due to political and practical reasons. Additions to conservation network, variation in logging activity and actions like retention forestry, forest fuel harvesting and forest restoration change the dead wood pool. In my opinion, these activities create a dead wood circus where the stage is changing fast and the actors, the dead wood dependent species, have difficulties to follow. Unfortunately, no one knows how many will drop out. During this talk I will introduce different actions that are currently performed in managed landscapes and discuss their potential effects on dead wood dependent species based on the current literature.

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Methodological approaches to rearing from deadwood

Methodological approaches to research in dead wood dwelling larvae of fungus gnats. Among more than 800 species of fungus gnats recorded in Europe, rearing records exist for about half of them. For another half larval microhabitats are not indicated so far. Dead wood impregnated with fungal mycelia is a very important development site for certain fungus gnat species, but this substrate is still overlooked in comparison with fungal fruiting bodies. It is evident that a requirement is to develop methods of rearing adult flies from larvae living in dead wood. Here I present my experience in using different rearing techniques in Finland and Russian Karelia.

<https://helda.helsinki.fi/handle/10138/154736>.

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Communities of wood-inhabiting corticioid fungi in different boreal broadleaved forest types

Wood-inhabiting fungi can be considered the most important dead wood dependent species group, since they are responsible for majority of decaying processes. The earlier research on wood-inhabiting fungi has focused on the effects of forest management and species associated with large diameter dead wood (i.e. coarse woody debris, CWD). Nonetheless, it has been shown that a major part of wood-inhabiting fungi utilize (also) small dead wood particles (i.e. [very] fine woody debris, [V]FWD). It has also been indicated that each dead wood diameter fraction hosts unique, yet partially overlapping fungal assembly. Natural herb-rich forests are known to be species rich habitats for wood-inhabiting fungi, along with other taxa. Wood pastures, in the other hand, are traditional semi-natural habitats, which have very diverse vascular plant and ground fungi communities. Both are nowadays threatened habitat types. Afforested fields, in turn, are novel, manmade habitats, that host diverse ground fungi communities. Both wood pastures and afforested fields are novel habitats for inventorying wood-inhabiting fungi. This study compares the species richness and fungal community composition among the aforementioned habitat types, and takes into account wood-inhabiting fungi occupying all dead wood diameter fractions. The study was conducted in Central Finland. Corticioid and polyporoid fungi was surveyed from 67 130 dead wood particles in 4 natural herb-rich forests, 4 birch dominated wood pastures, and 4 birch dominated afforested field sites. Fungal community composition showed some divergence among different habitat types. Natural herb-rich forests and afforested fields had higher overall species richness than wood pastures. Also, many rare or rarely collected species were detected in each forest type. Surprisingly, afforested fields contained especially high amount of rare species. Conserving threatened natural habitat types and managing traditional landscapes is essential in order to maintain biodiversity. However, afforested fields and wood pastures may serve as surrogate habitats for many broad-leaved dead wood associated species.

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“data literacy” and principles for producing data for reproducible research. The use of standards, the concepts of data quality and fitness-for-use, Specimen Identifiers, Online resources – available to enhance the data, using one’s data skills and finally publishing you data and why.

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Phylogeny of *Skeletocutis nivea* species complex

The genus *Skeletocutis* (Polyporales) is a taxonomically difficult group of white-rot fungi, and *Skeletocutis nivea* represents a case where current taxonomy falls short of depicting the true species level diversity. *S. nivea* can be found on dead hardwoods from the temperate zone to southern parts of the boreal zone and montane forests of the tropics. The aim of my study was (1) to map out the DNA level diversity within *S. nivea* in order to outline previously overlooked species borders and (2) to clarify the relationship of morphologically similar *S. ochroalba* to *S. nivea* group. I also (3) tried to identify some ecological and morphological diagnostic features for distinguishing the species occurring in northern Europe. I included *S. nivea* specimens primarily from the temperate and boreal northern hemisphere with additional material from Africa, Southeast Asia, Australia and New Zealand. I conducted maximum likelihood and Bayesian phylogenetic analyses using ITS sequences supplemented with *tef1* sequences. The analyses revealed at least ten species within *S. nivea*. The interspecies relationships were for the most part left weakly resolved but *S. ochroalba* seems to be embedded within *S. nivea* group. Three of the recognized *S. nivea* species occur in northern Europe but no clear ecological differences can be perceived between them. They are also morphologically very similar. The differences in pore and spore sizes are hardly detectable due to overlaps in variation.

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Genomic organization of laccase multigene family of fungus *Phanerochaete avellanea* (Bres.) J.Erikss. et Hjortstam.

Wood is the main renewable material on Earth. Wood and other lignocellulosic materials are formed by three main polymeric constituents, cellulose, lignin, and hemicelluloses. Lignin is highly resistant towards chemical and biological degradation, and confers mechanical resistance to wood. Basidiomycetes are the main wood rotters due to their ability to degrade or modify lignin. They synthesize oxidoreductive lignin-modifying enzymes such as laccase, lignin peroxidase and manganese peroxidase. One of the key enzymes of the complex is a laccase (EC 1.10.3.2), belonging to the family of

copper oxidases. The biotechnological importance of this enzyme lies in its ability to oxidise both phenolic and non-phenolic lignin related compounds as well as highly recalcitrant environmental pollutants. It has been shown that in the genome of basidiomycetes laccase formed multigene family. Seventeen non-allelic laccase genes and one gene footprint are present in the genome of *Coprinopsis cinerea*. Previously in our laboratory experiment was made using a pyrosequencing method 454 for establishing the amount and partial sequences of various laccases basidiomycetes. One of selected fungi was *Phanerochaete avellanea* voucher LE<RUS>:2009, which was able to identify five genes of laccases and get their partial sequences. The presence of protein laccase was also proved by the separation of proteins by two-dimensional electrophoresis. The aim of my work was to determine the full-length coding sequences and exon-intron structure of each isoform laccase fungus *Phanerochaete avellanea*, and make phylogenetic analysis. Superficial liquid phase was carried out by culturing in glucose-peptone medium, graft mycelium was harvested for isolation of total RNA, which is then used to obtain the copy number of the DNA by RT-PCR and genomic DNA. To establish the sequence of the full transcripts we used RACE-PCR with gene-specific primers selected on the previously installed partial sequence 454. To establish the exon-intron structure primers on end portions of the protein-coding sequence (CDS) were chosen and PCR with genomic DNA as a template was made, followed by Sanger sequencing. As a result of this work nucleotide sequences of five full-length transcripts encoding laccase were identified. Also we have got the exon-intron structure of these genes. In silico analysis of the predicted amino acid sequences we have obtained the number of glycosylation sites, the signal peptide length, the molecular weight and the isoelectric point of protein. To obtain amino acid and nucleotide sequences we made the phylogenetic analysis. Sequences were submitted to GenBank and we get their identification numbers: LacA-KR109250; LacB-KR109251; LacC-KR109252; LacD-KR109253; LacE-KR109254 It is planned to test the presence of laccase activity in these enzymes.



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Białowieża National Park as biodiversity hotspot in Europe

The Białowieża Forest World Heritage Site straddles the border of the Republic of Poland and the Republic of Belarus. It is the unique temperate deciduous forest of primeval character with additional mixed and pure coniferous stands. This is the remnant core of the forests which prevailed in Europe in the past. The natural processes have been running here unbroken for thousands of years. The Forest is famous for the presence of rare fauna of forest dwelling birds, saproxylic invertebrates and fungi. It is the last place where the largest terrestrial mammal of Europe, the European bison, survived in wild until the beginning of the 20th century. The size of the Forest ensures that all stages of natural forest development are present. The mosaic of natural phenomena and its' dynamic as well as the rich and diverse habitats are of outstanding international importance as an essential habitat for numerous species typical of natural forest ecosystems of temperate climate zone.

Dead wood holds the vital importance for forest carbon budgets as well as is invaluable wildlife resource. Dead wood appears in many forms, sizes and positions including standing dead trees, dead branches in the canopy trunks and branches on the ground. Decomposition of a tree is a process that leads to disappearance of the habitat of some species. To persist, the decomposer species must be able to disperse to a new habitat patch within a proper time-scale. In forests under natural disturbance dynamics without human exploitation of wood, the input of dead wood is more or less constant in relation to the life-spans and dispersal abilities of decomposer species. Białowieża Forest is also renown for exceptional dimensions and age of trees. Most of the old growth tree species present here are distinct from their counterparts in Europe in terms of their height and breast-height diameter. The trees live here until natural death and the forest stands have a characteristic uneven-age and multi-layered structure. Despite a relatively good knowledge of the biological diversity of Europe, new species of fungi or invertebrate fauna are still discovered in the Białowieża Forest. The Forest is also home to a whole range of ungulates present in Poland, large predators such as lynx and wolf as well as typical forest dwelling birds. The Forest has a large population of woodpeckers, among which the white-backed woodpecker and the three-toed woodpecker, which are typical species of old and natural tree stands, are particularly interesting.

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New next generation sequencing based method for exploration of laccase multigene family in basidiomycetes fungi

Here we present a new next generation sequencing (NGS) based method for obtaining information about DNA sequences of fungal laccase multigene families (MGF) members. This new method thought as a good alternative to traditional cloning-based methods both in terms of cost and labor. Essential part of this new method is replacement of cloning procedure by Polony PCR. In our study multiple laccase genes were identified in all investigated fungi (14 different fungal species). Phylogenetic analysis using obtained partial gene sequences reveals that members of MGF from the same fungus do not have tendency to aggregate into the same clade. However, aggregation is observed at the family level Phanerochaetaceae and Polyporaceae genes appear as two distinct clades on the tree. Interesting exception from the general tendency can be observed for *Phanerochaete avellanea* which genes reside in both Phanerochaetaceae and Polyporaceae clades. Developed in this study method can be used in primary search for new perspective genes for catalysts, screening of environmental samples and fast characterization of laccase MGF in newly identified fungal species.

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Characterisation of lignocellulose-degrading complex of a white-rot fungus *Phanerochaete avellanea*

White rot fungi are well known lignin degraders in forest fungal communities. Comparative study of extracellular enzymes facilitates their use in different fields of biotechnology. We performed secretome analysis of white rot fungus *Phanerochaete avellanea* using 2D electrophoresis followed MALDI-TOF/TOF mass-spectrometry to determine enzyme sets under different cultivation conditions. 28 proteins were identified in secretomes derived. The largest group of secreted enzymes consisted of dye-decolorizing peroxidases (DyP), alcohol oxidases, glyoxal oxidases, as well as cellulose-degrading glycoside hydrolases (families 5,10,79) and polysaccharide lyases, also several proteases were identified. Lignin peroxidases (LiP) and manganese peroxidases (MnP) were not found, suggesting that cultural conditions used are not efficient for production of these enzymes, or their proportion is insufficient for the effective

identification. On the other hand, one of the enzymes produced turned to be laccase, which is not typical for other fungi from *Phanerochaete* genus, including model fungi *Phanerochaete chrysosporium*. Concluding the results obtained, we suggest that *Phanerochaete avellanea* releases both extracellular hydrolytic and oxidative enzymes for lignocellulose degradation. Addition of Cu²⁺ or wheat straw induces laccase production, whereas DyP, alcohol oxidase and glyoxal oxidase could be identified almost under all conditions studied.

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The link from traits to occurrences in wood decaying fungi

A fundamental aim of community ecology is to understand what determines the identities and abundances of species in space and time. Key processes include community assembly from global to local species pools, and how environmental conditions and biotic associations affect them. Today these processes are seen more as stochastic than deterministic, so that our knowledge about the characteristics of species, their environment, and their biotic interaction networks influence the likelihoods of certain community compositions rather than dictate them deterministically. Species functional traits are characteristics that affect the performance of species in a given space and time, related to both environmental conditions as well as biotic interactions. The communities of dead wood inhabiting fungi can consist of tens to hundreds of highly interactive species that form spatially relatively distinguishable communities inside individual decaying logs. Within the dead wood inhabiting fungal community, phylogenetically different species have developed similar qualitative and quantitative traits.

How are species occurrences and responses to their environment influenced by morphological, functional, and life-history traits? And how do traits relate to species interaction patterns? I will illustrate how these questions can be addressed with a newly emerging statistical modelling framework, and some results for a dead wood inhabiting fungal community data set collected from beech forests in the Basque country.

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Should we do fruit-body inventories, sequencing, or both?

In animals and plants, the adult life stage is often easy to survey in the field, whereas reproductive effort is difficult to observe. The opposite is true for fungi, as fruit bodies are often conspicuous, but other life stages difficult to observe. As a consequence, knowledge on fungal ecology, e.g. on resource use and species distributions, is often based on data on the fruit body stage. A deeper understanding of fungal ecology (including its implications for conservation) calls for knowledge on how distributional patterns build up from the underlying processes, such as dispersal, mycelial growth and competition, and formation of fruit bodies. Sampling these cryptic life-history stages has become increasingly feasible with next generation sequencing (NGS). We (Ovaskainen et al., ISME 2013) combined NGS sequencing with fruit body inventory to study simultaneously mycelial and fruit body occurrences. As examples of the results, we showed that species that have high mycelial abundance also have a high fruiting rate and produce large fruit bodies, leading to a positive feedback loop in their population dynamics. Further, we showed that some of the rare and red-listed species are more abundant as mycelium in wood than what could be expected from their occurrence as fruit bodies, and thus they may not be considered equally rare from the view point of the mycelial population.

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Effects of forest restoration by fire on polypores – A case study from Finland based on a 23-year monitoring period

Information on the impacts of fire on wood-inhabiting fungi is scanty, and long-term studies on the effects are almost totally lacking. Here we present results from a long-term field study conducted in eastern Finland in 1988-2011. Two pine-dominated boreal forest stands, a seminatural and a managed one, were intentionally burnt in 1989. We inventoried polypores one year before the fire, in the year of burning, and 1, 2, 6, 13 and 22 years after the fire. The short-term effects of fire were destructive for polypore communities. However, species

numbers recovered to the pre-fire level six years after the fire. After 13 years, the number of species was clearly higher than before the fire, due to the large input of fire-killed dead trees. The number of red-listed species was strikingly high (18 species) in the seminatural stand 13 years after the fire including several species which have earlier been considered as old-growth forest indicators, and remained at high level (17 species) still 22 years after the fire. The number of red-listed species was much lower in the formerly managed stand (6 and 8 species, respectively). We conclude that burning of stands can be a very effective method to create habitats for red-listed polypore species, at least if the stand is located close to high-quality source areas and contains a sufficient amount of large-diameter trunks of different tree species. **Reference:** Penttilä, R., Junninen, K., Punttila, P. and Siitonen J. 2013. Effects of forest restoration by fire on polypores depend strongly on time since disturbance - a case study from Finland based on a 23-year monitoring period. *Forest Ecology and Management* 310: 508-516.

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Nematodes of Ulmaceae wood vectored by *Scolytus* spp. beetles

A.Y. Ryss, Polyamina K.

Dutch elm disease *Ulmus* spp. resulted in the death of plantings in the parks of St. Petersburg and the Leningrad region, including historic parks palaces-museums. This wilt is caused by the fungus *Ophiostoma novo-ulmi* (Brasier, 1991) carried by the beetles *Scolytus scolytus* (Fab., 1775) and *S. multistriatus* (Marsh., 1802). The pathogenesis of this wilt disease (DED) is similar to the wilt of woody species, caused by the Association of nematodes, fungi, and insect vectors (pine wilt disease PWD, wilt poplar (SAD). Therefore, the objective was to study the species composition of nematodes in diseased elms, in beetle vectors *Scolytus scolytus* and *S. multistriatus*, and the correlation of nematode species found in the wood corresponding to the found forms of entomophilous dauer larvae with clarifying rooms transmissible stage larvae of each species of nematodes.

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Lessons from species specific fruiting phenologies

Old-growth forests are globally rare and one of the most threatened ecosystems in the world due to fragmentation, habitat destruction and forest management. For the species associated with old-growth forest and dead wood, there is a hurry to gain knowledge in order to design their conservation and management. Wood-inhabiting fungi are key providers of ecosystem functions and highly sensitive to environmental changes. However, the majority of wood-inhabiting fungal species, especially species producing poorly detectable fruit bodies, still remain ecologically and taxonomically poorly known, or undiscovered. Our research aims to investigate and give new information about the biodiversity, detectability and habitat requirements of poorly known fungal species, especially Ascomycetes, in the fruiting wood-inhabiting fungal communities of boreal forests. We will also survey the effects of different forest management actions on these communities. As conservation and management decisions considering fungi rely mostly on datasets in which the occurrence of species are based on observations of their fruit bodies, the surveys considering species specific fruiting characteristics are surprisingly scarce. We conducted a highly intensive fruit body survey, in which the same wood-inhabiting fungal communities were repeatedly investigated during one growing season. We then combined the gained species specific information on timing and longevity of the fruiting with other fruiting phenology characteristics, such as the morphology and size of the fruit bodies. In this presentation I am going to present the main findings of this study and discuss the usage of this information in performing fungal surveys of wood-inhabiting fungal species, giving special emphasis on the poorly know fungal groups.

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Introduction to the study of the relationship between volatile organic compounds (VOCs) emitted by tree species *Q. pyrenaica* and the saproxylic beetles assemblages

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Saproxylic fauna is one of the fundamental components of temperate deciduous European forests. Currently, many species of this saproxylic fauna are seriously threatened due to a wide range of factors, most of them derivatives of human action. Saproxylic beetles tend to shape very complex assemblages, which determine both landscape- and local-scale forest structure. That is why they are known as the architects of the ecosystem. Given its importance, it is necessary to deepen the study of physical, chemical and biotic factors that are influencing the formation of these assemblages. In the case of chemical factors, previous studies have shown that the tree, which can act as a potential host for these organisms, releases a big amount of volatile organic compounds (VOCs). Moreover, saproxylic beetles have the ability to detect these chemical signals and develop a behavioural response. Based on the above, the aim of this study is (1) to analyse whether there are significant differences in the set of volatile organic compounds released by specimens of *Q. pyrenaica* with different size and (2) try to figure out how these compounds are conditioning the composition and species richness of saproxylic beetles associated with this tree species. Preliminary results obtained so far show differences in both the VOCs emission levels and the structure of saproxylic beetles assemblages between specimens of *Q. pyrenaica* with different size. Financial support was provided by the Spanish Minister of Science (CGL 2012-31669) and the Valencian Gener.



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Xylobiont nematodes of Moscow & Saint Petersburg regions: associations, life cycles, refuges and threat risks to parks and forest plantations.

Summer heat and drought of 2010 with the temperatures for 7 °C higher than climatic norm, reaching 40-41 °C, led to devastation of the forest plantations in 2011-2014 in giant areas of the Russian Federation (RF). The following five regions showed the highest damage: River Volga area; Moscow and surrounding regions; Black-Soil Belt at Ukrainian border (Voronezh and Belgorod reg.), East Siberia

(Buryatia and Altai), Primorye (i.e. Southern Pacific area). Survey of xylobiont nematodes in Moscow and St Petersburg regions ((2013-2014 33.) resulted in significant increase of frequency of records of the plant pathogenic wood inhabiting nematodes: *Bursaphelenchus*, *Aphelenchoides*, *Ruehmaphelenchus*, *Ektaphelenchoides*, *Ektaphelenchus*, *Laimaphelenchus*, *Sychnotylenchus*, *Neoditylenchus*, *Nothotylenchus*. The question to be answered: whether the infections are moved to the above-mentioned areas from the South or the local refugees of infections wake up because of the global warming? To light the problem it is necessary to study the life cycles of nematodes and their associations with woody trees and insect vectors. The most convenient way to study the nematode life history(LH), is to use laboratory cultures; for the pathogenic wood nematodes (genus *Bursaphelenchus*) time of reproduction on the fungus *Botrytis cinerea* (egg to egg) varied from 3 to 7 days at 22 °C. LH includes ii) two propagative generations feeding either on fungi or on a tree host, when the plant dying the nematode transfer their nutrition target from phloem or resin canals in wood, to fungi that occupying the dying tree; ii) transmission (=spreading) generation with rudimentary pharynx and stoma vectored by wood and bark-inhabiting beetles (Coleoptera: Scolytidae).

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Dmitry Schigel, PhD, is working as Programme Officer for Content Analysis for [Global Biodiversity Information Facility](#) and is based Copenhagen, Denmark. Dmitry is docent of mycology in the University of Helsinki, and he maintains close connection with the [Metapopulation Research Centre](#) and with [LUOMUS](#) – Finnish Museum of Natural History through research projects and student supervision. Dmitry is interested in biodiversity informatics, dead wood (see Dead Wood Movie [trailer](#)), species interactions, entomology and mycology, and also in molecular ecology and metagenomics, molecular identification and systematics, host selection and adaptations of fungivorous Coleoptera, wood-decaying fungi, databases, nature conservation, boreal and montane ecosystems, and successions, see his [ResearchGate page](#) for contributions. Funded by [SIU](#), Dmitry runs the **Nordic-Russian Boreal Forest Biodiversity Education Network** with four events: Biodiversity in Dead Wood lecture course, Helsinki 2013; Preparing samples for fungal community sequencing, lab course Uppsala 2014; Forest biodiversity and ecosystems in Finland & Russia, field course Tver’ 2014; the Dead Wood Meeting, Lammi 2015.

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Probabilistic taxonomic classification

We have developed a computational classification method, PROTAX, which gives probabilistic taxon assignments for DNA sequences. In order to make it work, user needs to provide a taxonomy structure, a set of representative sequences with known taxonomic labels, and a method for calculating sequence similarities, e.g. BLAST. These are used for estimating the parameters of the model after which new sequence data can be classified. The plan is to make our software publicly available. In this presentation we describe the method and show some preliminary results.

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This presentation will discuss conditions that govern patterns for the assembly of fungal communities with particular reference to wood decay fungi. The integrity of woody substrate is largely controlled by the tree while still alive. Pathogen recognition and defence mechanism against microorganisms together with the low oxygen levels inside the interior of a tree trunk will make most fungi suppressed in the living tree. Some species may still establish as endophytes or as pathogenic root rots or slightly less pathogenic heartrots. Death of the tree however opens up a large wood resource for colonisation either from the already established mycelia or from newly arrived spores in primary resource capture. Spores dispersal and delivery to the substrate may be facilitated by bark and wood feeding insects that are attracted to dying trees. Later on in the decomposition process, most of the wood is occupied by fungal mycelia and new arrivals have to establish by replacing the earlier fungi in secondary resource capture. With time, the quality of the wood gets increasingly recalcitrant as easily degradable molecules get depleted. Species of wood decay fungi tend to establish in assemblages that are non-random. An interesting trade off between early establishment/fast decay rate and combative capacity has been observed in some experiments. The importance of priority effects, combative strength and substrate quality requirements are still not completely understood. The concepts will be illustrated with results from field observations, experimental work, and community analyses using isolation of fungal mycelium and high throughput sequencing.

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Fungal community shifts in structure and function across a boreal forest fire chronosequence

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Wildfire is a common natural disturbance in forested ecosystems. It is crucial to understand the responses of soil fungal communities to wildfire as fungi contribute to biogeochemical cycling in soil, by e.g. degrading soil organic matter (SOM) and releasing nutrients from organic sources. Using high-throughput sequencing of the ribosomal RNA gene markers, coupled with functional gene array, we investigated fungal community structure and its potential function across a boreal forest fire chronosequence (2-152 years post-fire). Our analyses revealed that boreal forest soil harbored the most diverse fungal community two years after fire and that its diversity subsequently decreased with increasing time since fire. Differences in fungal community structure were primarily driven by changes in the abundance of Basidiomycetes and Ascomycetes. Ectomycorrhizal (ECM) fungi contributed to the increase of basidiomycetes over time, with OTUs representing *Cortinarius* and *Piloderma* dominating. The sites with different post-fire time formed site-specific clusters indicating potential differences in essential biogeochemical processes in soil. The site with highest biological diversity had also the most diverse gene pool. In the mature forest where ECM fungi were the most abundant, the genes involved in the organic matter degradation were as common as in the site where saprotrophic fungi had higher abundance. This supports the hypothesis that ECM fungi could play a role in soil organic matter decomposition and organic N transformations.

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Alexandra Tokareva, an undergraduate student from SpbSU (Russia), interested in dead wood ecology and mostly in polypores. This summer and autumn going to work with some species of polypores for future research.

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The Saproxylic Fauna of Wytham Woods

The poster will outline the TCV Natural Talent UK scheme and present the projects that I will be carrying out over the 2015 survey season at Wytham Woods in Oxfordshire, England. This will include historical museum records and modern day sampling, public engagement work to promote better understanding and appreciation of saproxylic habitats and setting up a re-run of a long running saproxylic ecological project.