



Deutsche Gesellschaft für Mykologie e.V.
German Mycological Society

DGFM MEETING Bernried

Lectures 12.-15.09.2016

Time	MONTAG	Ecology and plant/fungus Interactions Chairs Claus Bässler/Derek Peršoh
14:00-14:45	Community assembly and decomposition processes in angiosperm wood	<u>Lynne Boddy</u>
14:45-15:05	The influence of anthropogenic stressors on fungal freshwater guilds	<u>Oliver Röhl</u> , Jens Boenigk, Vasco Elbrecht, Florian Leese, Julia Nuy, Moritz Mittelbach, Derek Peršoh and Dominik Begerow
15:05-15:35	When mycorrhizal fungi meet leaf-endophytes: Fungal communities in decaying plant litter	<u>Derek Peršoh</u> , Marco Guerreiro, Dominik Begerow
15:35-16:00	Break	
16:00-16:20	Mapping a 'cryptic kingdom': Performance of LiDAR derived environmental variables in modelling the occurrence of forest fungi	<u>Claus Bässler</u> and Maiju Peura
16:20-16:40	Urban mycology: ectomycorrhizal fungi associated with exotic and native tree species	<u>Anja Schneider</u> , Torsten Bernauer, Markus Scholler
16:40-17:00	The rare polypore <i>Antrodiella citrinella</i> and its special phenology in the Black Forest National Park (Germany)	<u>Max Wieners</u> , Anne Reinhard, Markus Scholler
17:00-17:20	Break	
17:20-17:40	First multilocus phylogeny for the order Phyllachorales	<u>Melissa Mardones</u> , Tanja Trampe, Sophie Oster, Meike Piepenbring
17:40-18:00	Resource diversity is more important than resource amount and microclimate for wood-inhabiting fungal diversity	<u>Franz-Sebastian Krah</u> , Jörg Müller, Sebastian Seibold, Petr Baldrian, Hanno Schäfer, Claus Bässler
18:00-19:00	POSTER SESSION	
	DIENSTAG	GBOL2 Chairs Martin Kemler/Markus Scholler
14:00-14:30	German Barcoding of Life (GBOL): Fungal pathogens & necrotic fungi in orchards	<u>Martin Kemler</u> , Julia Steffen, Ben Bubner, Ulrike Damm, Ursula Eberhardt, Gerhard Rambold,

		Markus Scholler, Marc Stadler, Dominik Begerow
14:30-14:50	Host specificity of ectomycorrhizal fungi: a case study with the <i>Laccaria laccata</i> species complex	<u>Ben Bubner</u> , Markus Scholler, René Jarling
14:50-15:10	Organisation of regional taxon lists for research projects: Examples from the DGfM and the GBOL project	<u>Konstanze Bensch</u> , Tanja Weibulat, Frank Dämmrich, Juan Carlos Monje, Dagmar Triebel
15:10-15:40	Break	
15:40-16:00	Work- and Dataflow of the EcoChip Development and Application	<u>Janno Harjes</u> , Gerhard Rambold
16:00-16:20	Filling gaps in the DNA barcode reference library of macrofungi growing in forests and orchards (GBOL-Pilze)	<u>Ursula Eberhardt</u> , Cornelia Krause
16:40-17:00	A molecular evidence for correlated species in the rust genus <i>Tranzschelia</i>	M. Catherine Aime, Matthias Lutz, <u>Markus Scholler</u>
17:00-17:20	Break	
17:20-17:40	Fungi associated with wood necrosis of stone fruit trees in Germany	<u>Steffen Bien</u>
17:40-18:00	Expanding the Ceraceosorales, an enigmatic order of smut fungi	<u>Marcin Piątek</u> , Matthias Lutz, Kai Riess, Dariusz Karasiński, Teeratas Kijpornyongpan, M. Catherine Aime
18:00-18:20	Neomyceten, gebietsfremde Pilze in der Schweiz	<u>Ludwig Beenken</u> , Beatrice Senn-Irlet
18:20-19:00	POSTER SESSION	
	MITTWOCH	LOEWE IPF, Chairs Meike Piepenbring/N.N. (Vorschlag Marc José!)
14:00-14:30	More verticillium-like hyphomycetes reclassified	<u>Walter Gams</u> and Rasoul Zare
14:30-14:50	Are the interactions between fungal root endophytes and plants context-dependent?	<u>Sevda Haghi Kia</u> , Sascha Pallesch, Jose G. Maciá-Vicente
14:50-15:10	Comparison of Fungal Diversity in Comprehensive-Taxa Inventories	<u>Stefanie Rudolph</u> , Hermine Lotz-Winter, Meike Piepenbring
15:10-15:45	Break	
15:45-16:10	Unravelling molecular and morphological diversity in <i>Subulicystidium</i> (Trechisporales, Basidiomycota)	<u>Alexander Ordynets</u> , Karl-Henrik Larsson, Ewald Langer
16:10-16:30	<i>Agrocybe aegerita</i> as a model basidiomycete for fruiting body formation	Robert Herzog, Irina Solovyeva, Deepak Kumar Gupta, Rahul Sharma, Martin Rühl, Marco Thines, <u>Florian Hennicke</u>
16:30-16:50	A transformation system for the black poplar mushroom <i>Agrocybe aegerita</i>	<u>Robert Herzog</u> , Irina Solovyeva, Michael Bölker, Florian Hennicke
16:50-17:10	Intraspecific genetic variability in root-endophytic fungi and implications on dispersion dynamics and environmental adaptation	<u>Kyriaki Glynou</u> , Jose G. Maciá-Vicente
17:10-17:30	Break	
17:30-17:50	News on the diversity and distribution of <i>Tricholoma</i> spp.	<u>Kai Reschke</u> , Flavius Popa, Zhu L. Yang, Gerhard Kost
17:50-18:10	Insights into the Taxonomy of Philippine Mangrove Oomycetes	<u>Reuel Bennett</u> , Marco Thines*
	Gesellschaftsabend	

	DONNERSTAG	Applied mycology/miscellaneous Chairs Kathrin Wittstein/Marc Stadler
14:00-14:45	Fungal secondary metabolites from plant pathogenic fungi and their impact on plant/pathogen-interactions	<u>Eckhard Thines</u>
14:45-15:05	Bioactive secondary metabolites from <i>Laxitextum incrustatum</i> – a tropical fungus	<u>Cynthia Mudalungu</u> , Christian Richter, Kathrin Wittstein, Josphat Matasyoh, Roderich D. Süßmuth, Marc Stadler
15:05-15:25	Studies on the secondary metabolite production of <i>Rosellinia</i> spp.	<u>Kathrin Wittstein</u> , Arne Cordsmeier, Jennifer Weber, Chollaratt Boonlarpradab, Simone Heitkämper, Marc Stadler
15:25-15:50	Break	
15:50-16:10	A multigene phylogeny within the Xylariaceae	<u>Lucile Wendt</u> , Eric Kuhnert, Derek Peršoh, Janet Jennifer Luangsa-ard, Marc Stadler
16:10-16:30	Contributions to pleurotin biosynthesis – isolation and characterization of novel derivatives	<u>Birthe Förster</u> , Benjarong Thongbai, Frank Surup, Marc Stadler
16:30-16:50	New secondary metabolites from <i>Hypoxylon lienhwacheense</i>	<u>Simone Heitkämper</u> , Frank Surup, Eric, Kuhnert, Marc Stadler
16:50-17:10	Break	
17:10-17:30	Studies on <i>Amanita</i> species in Northern Thailand	<u>Benjarong Thongbai</u> , Rodham E. Tulloss, Steven L. Miller, Kevin D. Hyde, Jie Chen, Ruilin Zhao & Olivier Raspé
17:30-17:50	Nerve Growth- and Brain-Derived Neurotrophic Factor inducing metabolites from <i>Hericium</i> spp.	<u>Zeljka Rupcic</u> , Kathrin Wittstein, Monique Rascher, Eduard Löwen, Reinhard W. Köster, Marc Stadler
17:50-18:10	What do we learn from cultures and High-throughput sequencing for the same samples?	<u>Abu Bakar Siddique</u> , Anis Mahmud Khokon, Martin Unterseher

Posters

Biodiversity of cultivable fungi after an artificial flooding of the soil habitat	<u>Anja Feige</u> , Oliver Röhl, Dominik Begerow
Host preference and sorus location correlate with parasite phylogeny in the evolution of the genus <i>Microbotryum</i>	<u>Martin Kemler</u> , Dominik Begerow, Matthias Lutz
Heterospecific infections with <i>Microbotryum</i> (Pucciniomycotina) show lower disease rate than homospecific infections	<u>Sebastian Klenner</u> , Britta Bükler, Dominik Begerow
Flight characteristics of teliospores of <i>Urocystis</i> species	<u>Magnus Wolf</u> , Sascha Lotze-Engelhard, Dominik Begerow
Selection of <i>Alnus glutinosa</i> for resistance against the causal agent of alder decline, <i>Phytophthora x alni</i>	Ben Bubner, Jasmin Seven, Volker Schneck, Stefan Wagner, Sabine Werres
Effect of nutrient availability on the interaction between root endophytes and plants	Sascha Pallesch, Sevda Haghi Kia, Kyriaki Glynou, Meike Piepenbring, Jose G. Maciá-Vicente
Monitoring der natürlichen Waldentwicklung im Nationalpark Schwarzwald	<u>Flavius Popa</u> , Stefanie Gärtner, Sönke Birk, Jörn Buse, Sandra Calabro, Esther del Val Alfaro, Christoph Dreiser, Raffael Kratzer, Marc Förschler
Diagrams showing the importance of fungi in ecosystems for teaching and environmental education	Meike Piepenbring
A thorough revision of the genus <i>Hebeloma</i> (Agaricales) in Europe	<u>Ursula Eberhardt</u> , Henry J. Beker, Jan Vesterholt †
Fungal vitality under anaerobic conditions	<u>Asli Ekizoglu</u> , Oliver Röhl, Dominik Begerow
Pesticide effects on stream fungi in a realistic apple-crop exposure scenario	<u>Steffen Carl</u> , Silvia Mohr, Mark O. Gessner, René Gergs, Christiane Baschien5

DGFM MEETING Bernried 2016

Plenary Lectures, Monday 12 September 2016

Community assembly and decomposition processes in angiosperm wood

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The way in which initial wood decay communities develop depends on the environmental conditions when the resource becomes available for colonisation, ranging between low and high stress. Under low stress, e.g. felled wood, community development begins with species having relatively ruderal (R-selected) characteristics (including rapid germination and growth, and early and extensive commitment to production of spores). In contrast, under high stress, e.g. heartwood of trees containing allelopathic compounds, or recently living attached branches, the earliest colonisers have appropriate stress tolerant (S-selected) characteristics sometimes combined with R-characteristics. In the natural situation, the earliest colonisers of standing trunks, attached twigs and branches usually arise from propagules latently present in functional sapwood. Whether in standing, attached, felled or fallen wood, the composition of the community usually changes with time, i.e. early colonisers are subsequently replaced by other species. Changes are brought about particularly by combative, antagonistic interactions, and also by extrinsic and intrinsic changes in the abiotic conditions within wood (including temperature, pH, gaseous regime, physical and chemical structure). Antagonistic interactions include: (1) antagonism at a distance; (2) hyphal interference; (3) mycoparasitism; and (4) gross mycelial interaction; fungi employ enzymes, volatile organic compounds (VOCs) and diffusible organic compounds (DOCs). The overall outcome of interactions can be deadlock – where neither antagonist makes any headway, replacement – where one fungus takes the territory of another, and also partial and mutual replacement. These outcomes vary between species combinations and fungal strains, and are altered by the biotic and abiotic environment.

Fungi that arrive first can dictate the subsequent pathway of community development (i.e. there are priority effects) by altering the physical and chemical composition, and as a result of their antagonistic activity. Priority effects may depend on the available air spora and soil-borne spores and mycelia. These effects are linked to biochemical alteration of the resource and combative ability of the predecessor. The communities that develop clearly also depend on available air spora and soil-borne spores and mycelia, so the communities that follow a specific primary coloniser vary between sites and times.

The influence of anthropogenic stressors on fungal freshwater guilds

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Freshwater fungi obtain a crucial role in decomposition of organic material in aquatic ecosystems. Nevertheless their group remains poorly investigated compared to habitats like soil. Especially the community response to anthropogenic caused stressors is addressed in a very limited number of publications only.

Therefore we created a mesocosm experiment along an artificial sidearm of a freshwater stream in Germany, to test the effects of three applied stressors on the community composition. 64 mesocosm were equipped with litterbags (filled with leaf litter from riparian vegetation) and former sterilized ceramic tiles, which serve as a standardized sampling area for biofilm communities. An initial period of two weeks for colonization of respective compartments was followed by two weeks with stressor exposure. As stressors we chose fine sediment, salt and a reduction of flow velocity (single stressors) and their respective combinations (three double stressors and one triple stressor). Each stressor was applied in eight replicates. In contrast to the majority of hitherto published fungal freshwater studies we did not use morphological criteria to assess fungal communities but used a metagenomic barcode approach of the ITS nrDNA marker.

Clustering of raw reads into Operational Taxonomic Units (OTUs) with CD-HIT-OTU and usearch revealed highly identical results between the two different algorithms. However, the detected 570 OTUs exceed the number of species detected with morphology-based methods by factor three to ten. The unique study design with two different compartments enabled the identification of three different ecological guilds according to their compartment preferences. The first guild represents aquatic fungi, the second comprises amphibious fungi, while the third contains terrestrial fungi. Each guild is characterized by a unique stressor response supporting the idea to divide the total community into specific sub-communities. While aquatic and terrestrial fungi show now visible effect caused by the applied stressors, the amphibious fungi respond significantly towards the enriched salt concentrations. However we assume this signal to be a secondary effect since the amphibious fungi are highly correlated to algae communities, which are more prone to applied stressors than the fungal communities.

When mycorrhizal fungi meet leaf-endophytes: Fungal communities in decaying plant litter

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The decomposition of plant litter is a key process in nutrient cycling and thus for ecosystem functioning. Our current understanding is that the process of decomposition is linked to the succession in the fungal decomposer community in forest ecosystems, i.e. successive degradation of the major plant compounds entails a shift from an Ascomycota to a Basidiomycota dominated decomposer community. This shift is supposed to be due to faster growth of the former in the presence of easily utilizable compounds while the latter are better equipped for degradation of recalcitrant compounds, such as lignin. Mineralized nutrients, the final product of litter degradation, are supposed to be provided to the plant by mycorrhizal fungi, which colonize the plant roots. This widely accepted picture has, however, been challenged recently.

We present evidence that endophytic fungi, which already colonize living plants, persist in fallen leaves for more than one year and shape the decomposer community. Indigenous saprotrophic soil fungi only play a minor role in the early stages of decomposition. Furthermore, litter is already colonized by mycorrhizal fungi less than one year after leaf-abscission. Accordingly, plant-associated fungi are key players throughout the decomposition process. The implications of these findings and the interaction among the different fungal guilds involved in litter decomposition will be discussed.

Mapping a ‘cryptic kingdom’: Performance of LiDAR derived environmental variables in modelling the occurrence of forest fungi

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Fungi are crucial to forest ecosystem function and provide important provisioning, regulating, supporting, and cultural ecosystem services. As major contributors to biomass decomposition, fungi are important to forest biogeochemical cycling and maintenance of vertebrate animal diversity. Many forest plant species live in a symbiotic relationship with a fungal partner that helps a host plant to acquire nutrients and water. In addition, edible fungi are recreationally as well as economically valuable. However, most fungi live in very cryptic locations (e.g. in soils and interior plant tissues) and are only visible when their ephemeral fruiting bodies are produced, making fungal occurrence difficult to detect and predict. While remote sensing has been used increasingly to identify and scale many forest characteristics (e.g. structure, function, and species diversity) related to myriad ecosystem services, the use of remotely sensed data in modelling the occurrence of fungi is largely unknown. We compared the performance of airborne lidar derived structural variables, including those associated with single tree detection, with variables derived from field inventories to model overall fungal species abundance as well as specific fungal guilds (i.e. a range of edibility from highly edible to very poisonous, and the number of fruiting bodies of saprotrophic and mutualistic ectomycorrhizal species) based on fruiting body sampling in a low range mountain forest (Bavarian Forest National Park). Lidar derived variables performed better than variables derived from field measurements to explain the abundance of all guilds combined, as well as the guilds of soil saprotrophic and ectomycorrhizal fungi, and the yield of highly edible fungi. Variables derived from field measurements performed better than lidar derived variables in explaining the yield of very poisonous fungi. Upscaling of yield and abundance of fruiting bodies to the whole study area opens the avenue for managers to identify areas of high interest by mushroom pickers, as opposed to those of potential danger to people and those that co-occur with sensitive species and habitats of conservation relevance. Moreover, the strong, guild-specific relationships found between the occurrence of fungi and lidar derived variables opens new avenues for scaling to large areas the occurrence of members of this cryptic kingdom.

Urban mycology: ectomycorrhizal fungi associated with exotic and native tree species

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Exotic trees from warmer regions are preferentially grown in urban central European environments because they - at least initially - lack natural antagonists and often are more heat- and drought-tolerant. In Karlsruhe (SW Germany) *Platanus x hispanica*, *Aesculus* spp. and *Robinia pseudoacacia* represent a great proportion of urban trees and have been grown for many decades in public green areas (e.g. parks, avenues, cemeteries). In the meantime, however, especially *Platanus* and *Aesculus* spp. are attacked by several fungal and animal parasites that succeeded from the trees native area. Therefore, these trees are no longer suitable for urban habitats.

In addition, *Aesculus*, *Platanus* and *Robinia* do not form ectomycorrhizae and are one reason for losses of macrofungal diversity in Karlsruhe. Thus, there is a need for exotic ectomycorrhizae-forming trees suitable for the expected global warming and for general urban conditions. In this project supported by the state of Baden-Württemberg (Klimopass Campaign) six exotic tree species of the genera *Quercus*, *Tilia* and *Corylus* are compared with native species of the same genera with respect to ectomycorrhizae associations (epi- and hypogeous fungus species). In our presentation we give an account of the first results and introduce typical urban species.

The rare polypore *Antrodiella citrinella* and its special phenology in the Black Forest National Park (Germany)

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Within the framework of a mycological inventory of the old-growth spruce-fir forest “Wilder See”, a protected zone of the Black Forest National Park, the phenology of two associated polypore species on *Picea abies* logs, *Fomitopsis pinicola* and the rare red data list species *Antrodiella citrinella* were studied. For our investigation we combined detailed field studies and temperature-dependent in-vitro growth studies. Whereas perennial fruitbodies of *F. pinicola* developed from late spring to autumn, the annual *A. citrinella* fruitbodies were almost only formed in late autumn (October, November) and again in spring (April and May). Growth studies on agar media confirm that *A. citrinella* grows faster at lower temperatures (5–10 °C), whereas *F. pinicola* is clearly superior in growth rate between 15 °C and 25 °C. This indicates that *A. citrinella* is a generally rare, but locally common species that may have been overlooked because of its special phenology.

The “Wilder See” area seems to be an important retreat for the species. Previously it was shown in Bavaria that *A. citrinella*'s existence depends on dense woody debris. We additionally found that high humidity and the co-existence of *F. pinicola* in close neighborhood are necessary as well. A presumed parasitic relationship between the two polypores is part of the discussion.

First multilocus phylogeny for the order Phyllachorales

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Phyllachorales (Pezizomycotina, Ascomycota) are an order of biotrophic, obligate plant parasitic ascomycetes with a tropical distribution and high host specificity. Two families are recognized within the order: Phyllachoraceae and Phaeochoraceae, based mostly on morphological and host characteristics. There are no recent taxonomic studies and no molecular studies of this group and the evolutionary relationships within and among them are largely unknown. We have used new molecular data from recent collections mainly from Neotropical regions to elucidate their relationships within Sordariomycetes as well as their family classification. We analyzed 53 DNA sequences representing 29 species of tar spot fungi, of five gene regions, nrLSU rDNA, nrSSU rDNA, ITS rDNA, and the protein coding genes *RPB2*, and *TEF1* (EF-1 α), to obtain a high resolution phylogenetic tree of Phyllachorales, using maximum likelihood and Bayesian inference analyses. The position of Phyllachorales nested in the subclass Sordariomycetidae (Sordariomycetes) is confirmed, as well as the monophyly of the order. The traditional family and generic classification based on morphological characteristics was not reflected by our molecular phylogenies. The family Phaeochoraceae is supported as a monophyletic group, while the family Phyllachoraceae and the genus *Phyllachora* are not monophyletic. Sequences of Phyllachorales included in the analysis cluster into three major clades with high BPP and BS support: Clade I containing the type species of *Phyllachora*, *P. graminis*, other species on grasses as well as members of the genera *Camarotella* and *Cocodiella*, Clade II containing species of Phaeochoraceae on palms, and Clade III containing species of tar spot fungi with immerse perithecia and infecting species belonging to many different plant families, but not Poaceae. Ancestral state reconstructions based on Likelihood Ancestral States Method indicate that the ancestor of Phyllachorales most likely had a monocotyledonous host plant, immersed perithecia, and a black stroma.

Resource amount is more important than resource heterogeneity for wood-inhabiting fungal diversity

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Several theories were suggested predicting biodiversity in dead wood, like the species-energy (resource amount) and habitat-heterogeneity hypothesis. Among saproxylic species, wood-decay fungi stand out by the exceptional feature to depend entirely upon woody compounds in all states of their lifecycle. However, independent effects of availability and heterogeneity of resources were not tested, but would allow overcoming the trade-off between timber use and the maintenance of fungal diversity and related ecosystem processes in commercial forests.

We set up a large field experiment using *c.* 800m³ dead-wood altering combinations of amount and heterogeneity (amount class diversity, tree species diversity) of dead-wood in shady and sunny conditions (microclimate) and aggregated additional dead wood. This design allowed us to disentangle the independent effects of dead-wood amount versus dead-wood heterogeneity accounting for microclimate conditions and local dead-wood (accumulation) on fungal species diversity on plot level. On object level we additionally disentangled the habitat effect, asking for the contributions of amount class and tree species accounting for microclimate conditions based on a surface standardization.

On plot level we found an overall stronger effect of amount than heterogeneity of dead wood. However, heterogeneity had also a significant independent effect. Microclimate affected community composition but not species richness on plot level. Local accumulation of dead wood had no effect. On log level we found that habitats that come along with the amount class have a stronger effect on species richness than tree species, succession and microclimate. Surface accumulation curves showed that coarse woody debris (CWD) is substitutable to some extent by fine woody debris (FWD) since FWD has higher species richness per surface volume.

To maintain fungal diversity, we recommend forest managers to enrich dead-wood amount in pure stands while in mixed stands the focus should be on different tree species within dead-wood, though applying logging techniques which provides gaps into the canopy.

DGFM MEETING Bernried 2016

Plenary Lectures,

Tuesday 13 September 2016

German Barcoding of Life (GBOL): Fungal pathogens & necrotic fungi in orchards

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Fungi are key species in terrestrial ecosystems and fungal biodiversity is heavily involved in most ecosystem services. Despite their importance and the enormous effort of many excellent researchers, the total number of fungal species and their diversity for Germany are unknown. Although some groups, such as mushrooms, are well described and documented in literature, many microfungal species are still awaiting description or discovery. Most species have been described on a morphological base, making it difficult to estimate species richness for a certain area at a given time point, as fruiting bodies are often missing. This shortcoming has become prominent especially with the advent of massive parallel sequencing (i.e. NGS) of marker DNA of fungal communities. These methods thereby represent the only realistic approach at the moment to understand fungal diversity of habitat or ecosystems. However, species inventories using NGS methods heavily rely on databases with complete sequence coverage. The rDNA Internal Transcribed Spacer (ITS) region is the most widely used DNA sequence for fungal identification and has recently been accepted as the barcode DNA marker

for Fungi. Barcoding initiatives have been established for many organismal groups and have been shown to reliably identify species in many ecosystems. The German Barcoding Initiative has been established in 2011 by the Bundesministerium für Bildung und Forschung and has entered its second phase in 2016 (GBOL II). Within this framework a barcoding initiative for assessing fungal diversity associated with fruit trees was started. The goal of this project is to exemplify fungal species diversity within a defined habitat, to provide a database of the identified fungi, to test its usefulness for re-identification of species in NGS data and additionally raise awareness of the impact of fungal diversity on agricultural production in Germany.

Host specificity of ectomycorrhizal fungi: a case study with the *Laccaria laccata* species complex

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Ectomycorrhizal fungi can have broad or narrow host ranges, *viz.* generalists versus host-specific fungi. Molecular methods allow direct determination of the fungal species colonizing a mycorrhized root tip of a certain tree species. Therefore, the sequence of a fungal barcode gene marker, being usually the Internal Transcribed Spacer (ITS), obtained from a mycorrhized root tip has to be compared with entries from a reference database containing sequences of morphologically determined fruiting bodies. However, the quality of species determination using this approach mainly depends on the integrity of the database, *i.e.* the fungus of interest must be deposited with the correct name.

In a previous study on ectomycorrhizal biodiversity in mixed and pure stands of Scots pine (*Pinus sylvestris* L.) and beech (*Fagus sylvatica* L.) a fungus was found, whose ITS sequence matched 100% to UNITE and Genbank entries of *Laccaria laccata* (Scop.) Cooke. Its ectomycorrhizas were exclusively present on beech roots, even in close proximity to Scots pine roots. This contradicts literature reports about *L. laccata* as a generalist colonizing both, deciduous trees and conifers. A phylogenetic analysis of all database entries of "*Laccaria laccata*" revealed that these do not form a monophyletic group within the genus. Hence, "*L. laccata*" likely constitutes a species complex of taxa with different host specificity.

In order to further clarify the status of the *Laccaria* taxon from the ectomycorrhizal study, fruiting bodies collected in Berlin and Brandenburg as well as all "*L. laccata*" specimens from the herbarium KR were ITS sequenced. Many of these sequences are identical to that of the taxon found during the ectomycorrhizal biodiversity study. The fruiting bodies of this taxon usually grow close to beech but also with oak (*Quercus* spp.) and hazelnut (*Corylus avellana* L.), but never beneath conifers. This indicates that *L. laccata* as commonly described in German literature is a morphospecies consisting of at least two different host-specific taxa. Future studies in the *L. laccata* complex (including related species like *L. proxima* and *L. bicolor*) will be concentrated on collections with absolutely certain tree species relations. Can you say anything on *Laccaria* associated with *Pinus*?

Organisation of regional taxon lists for research projects: Examples from the DGfM and the GBOL project

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Monitoring initiatives, biodiversity research and nature conservation projects often rely on their own name backbones and concepts, i.e. regional species checklists or taxon reference lists. They are essential as underlying name and classification vocabularies for data entry and quality control, for human-readable web presentation services (e.g. as scroll lists), for machine-readable web services, and as standard name backbones for mobile apps and analysis tools in research and nature conservation projects. Such lists can be managed in SQL database installations of DiversityTaxonNames (= DTN) on a publicly accessible server of the IT Center of the Staatliche Naturwissenschaftliche Sammlungen Bayerns (SNSB) (ER model, Hagedorn et al. 2011).

The activities to organize and publish such regional DTN lists started in 2012 as a cooperation between the DiversityMobile/IBF project (http://www.diversitymobile.net/wiki/IBF_Project) and the German Barcoding of Life (= GBOL) project (<https://www.bolgermany.de>). Since 2014, the services are provided through the German Federation for Biological Data (= GFBio) project with involvement of the Staatliches Museum für Naturkunde Stuttgart, the Staatliche Naturwissenschaftliche Sammlungen Bayerns and the Zoologisches Forschungsmuseum Alexander Koenig.

Checklists often contain regionalised and domain-specific information on the taxa (e.g. red list categories, indication of status information, ecological parameters assigned to the taxon). The more than 50 currently published lists mainly cover taxa occurring in Germany or in certain regions of the country. They are actively curated by taxonomists with specific expertise. Each checklist has its own history and objectives, is managed independently having its own higher hierarchical classification. Basic information on more than 100,000 taxon names in use, synonyms, classification and German vernacular names of animals, fungi and plants are delivered. The data flow (import via DTN import wizard, management in the databases with rich clients of the Diversity Workbench, export as csv-files) is demonstrated with examples, one of them being the ‘Taxon list of fungi and fungal-like organisms from Germany compiled by the DGfM’, which is the largest list for a single organism group including 30,000 names with 11,700 of these treated as synonyms.

The lists are provided via a REST web service (Seifert et al. 2015) and published via GBIF with DOI assignment (see Dämmrich 2015, 2016). They are available for the DiversityMobile App to facilitate field work (see <http://www.diversitymobile.net/>).

Dämmrich F (2015 onwards) Taxon list of fungi and fungal-like organisms from Germany compiled by the DGfM. DWB REST Webservice for Taxon Lists. – Accessed via

<http://services.snsb.info/DTNtaxonlists/rest/v0.1/static/api-doc.html> on 2016-07-28.

Dämmrich F (2016 onwards) Taxon list of fungi and fungal-like organisms from Germany compiled by the DGfM. – Accessed via <http://www.gbif.org/dataset/155b33d2-84b1-4a31-9287-9d9e900bc6c8> on 2016-07-28. Data publisher: Staatliche Naturwissenschaftliche Sammlungen Bayerns. doi:10.15468/gtvmjw.

Hagedorn G, Weiss M & Triebel D (2011) DiversityTaxonNames information model (version 2.4). – http://www.diversityworkbench.net/Portal/TaxonNamesModel_v2.4.

Seifert S, Rulik B, Morinière J, Spelda J, Holstein J, Monje J C, Weibulat T & Triebel D (2015, onwards) (eds.) DWB REST Webservice for Taxon Lists. – Accessed via <http://services.snsb.info/DTNtaxonlists/rest/v0.1/static/api-doc.html> on 2016-07-28.

Work- and Dataflow of the EcoChip Development and Application

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Phytopathogenic fungi are capable of causing significant costs when populating economically relevant trees. Since the symptoms of fungal infections in plants are often difficult to distinguish, or even undetectable to the human eye, molecular tools for diagnosis provide the possibility of an efficient way to screen for fungal diseases. In this context, the development of a microarray-based screening method to detect phytopathogenic infections in trees, grown for fruit or wood production, aims to improve the accuracy and efficiency of disease control in plantations and to shift the focus from prophylactic treatment with broadband fungicides to a more targeted approach. The development of an EcoChip-like microarray chip will include a dual probe set, combining a set of probes to screen for phylogenetic gene markers and a set of probes to screen for functional genes, which are associated with the expression of pathogenicity factors (Peršoh et al. 2012). Applying this technique provides the advantage that information about the community composition and function can be collected simultaneously. Since microarray data supply quantitative information, the expression levels of functional genes from chosen metabolic pathways can be displayed (Weig et al. 2013). The development of this EcoChip will include three generations, during which the different probes, as well as the layout of the chip, will be assessed and optimized. Whereby the first generation aims to optimize the use of the phylogenetic probes, which are derived from Internal Transcribed Spacer (ITS) sequences, obtained either from already accessible sequences entries from public databases or from the partners from the GBOL project, including NGS datasets. The NGS datasets can furthermore be used to assess the reproducibility of the microarray chip test results, as these also provide information on the community profiles from the sampled trees. The second generation of the microchip will include additional phylogenetic markers, in order to compensate for the lack of resolution of the ITS probes. This can be observed as sometimes closely related species differ in only a few nucleotide positions in the ITS sequences (Nilsson et al. 2008). The third generation of the microchip aims to optimize the inclusion of the probe set screening for functional genes. Additionally the application of an automated statistical analysis tool will be refined during the last 2 generations, in order to provide a fully operational diagnostic tool as the final product.

Peršoh D, Weig A, Rambold G (2012) A transcriptome-targeting EcoChip for assessing functional mycodiversity. *Microarrays*. **1**: 25–41, doi:10.3390/microarrays1010025.

Weig A R, Peršoh D, Rambold G (2013) EcoChips für die Erforschung mikrobieller Lebensgemeinschaften. *BIOspektrum*. **19**(4): 382–385, doi:10.1007/s12268-013-0326-9.

Nilsson R H, Kristiansson E, Ryberg M (2008) Intraspecific ITS variability in the Kingdom Fungi as expressed in the international sequence databases and its implications for molecular species identification. *Evol Bioinform Online*. **4**: 193-201.

Filling gaps in the DNA barcode reference library of macrofungi growing in forests and orchards (GBOL-Pilze)

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More than 500,000 good quality fungal ITS sequences were available beginning of this year (<https://unite.ut.ee/repository.php>, visited Aug. 2016; Kõljalg et al. 2013) that can be used for fungal identification by ITS sequence comparison. However, this figure includes not only data from well identified and documented material that fulfils the so-called barcode standard (Eberhardt et al. 2014) and the taxonomic coverage is patchy. A small portion of the funding in GBOL-Pilze, roughly covering the costs of 1500-1800 sequences, is dedicated to classical specimen-based DNA barcoding of macrofungi for filling gaps in the available reference data. Such gaps can be

- the total lack of reference data for a taxon;
- the lack of sequences with cited reference material;
- the lack of sequences from Germany or adjacent areas;
- taxonomic ambiguity that can be diminished by obtaining sequence data from type materials.

For this project, we are looking out for resources – additional target groups, specimens already deposited in public collections, specimens made available to be utilized in the project and in the course deposited in a public collection, as well as persons with extraordinary taxonomic experience who are happy to contribute – that will help towards the completion of the global DNA barcode reference data and towards advancing the knowledge of the German funga.

Eberhardt U et al. (2014) DNA-Barcoding, Pilze und das German Barcode of Life-Projekt (GBOL). *Z Mykol* 80: 627–641.

Kõljalg U et al. (2013) Towards a unified paradigm for sequence-based identification of Fungi. *Mol Ecol* 22: 5271-5277.

A molecular evidence for correlated species in the rust genus *Tranzschelia*

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Heteroecism, i.e. alternation between two hosts, is a widespread phenomenon among rust fungi (Pucciniales). In addition to heteroecism, the rust fungi have evolved elaborate life cycles culminating in the five-spore stages of macrocyclic species, with many variations down to microcyclic species that may produce as few as two of these stages to complete their life cycles. Considering the large number of nearly 8000 species and a high proportion of these that are host-alternating, heteroecism is obviously a successful strategy for these fungi. However, the cost of maintaining a heteroecious strategy with respect to spore production and population development must be high. Correlated species in Pucciniales are proposed pairs consisting of a macrocyclic host-alternating and microcyclic non-host-alternating species that share a common host. In this study we examined correlated species in the rust genus *Tranzschelia* concentrating on *T. pruni-spinosae* and its proposed micro-form species *T. fusca*. Molecular phylogenetic data, some of which retrieved within the German Barcode of Life project (GBOL), reveal that there are at least three pairs of correlated species within the *Tranzschelia pruni-spinosae/T. fusca* complex. Findings show that the life cycle mode does not reflect phylogenetic relationships within *Tranzschelia*. Additionally, it is shown that species with micro-cycles, other non-host-alternating life cycle forms, and finally host-alternating species all derive initially from host-alternating species. Consequently, heteroecious species are the starting point of speciation in many different directions, i.e. to other host-alternating and to non-host-alternating species.

Expanding the Ceraceosorales, an enigmatic order of smut fungi

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Until recently the enigmatic order Ceraceosorales, belonging to the Ustilaginomycotina, contained the single genus *Ceraceosorus* with only one species *Ceraceosorus bombacis*, parasitic on *Bombax ceiba* (Malvaceae) in India. In 2016, a second *Ceraceosorus* species was described from West Africa, namely *Ceraceosorus africanus*, parasitic on *Bombax costatum* (Malvaceae) in Benin, Ghana and Togo (Piątek et al. 2016). In the same time, the third species, *Ceraceosorus guamensis* was described from the South Pacific Island of Guam (Kijpornyongpan & Aime 2016). This species was isolated from healthy dicot leaf and represents the first nonparasitic yeast anamorph in the order Ceraceosorales. The putative fourth and unnamed species was isolated from healthy dicot leaf in Louisiana, USA.

In the presentation we will include historical overview of *Ceraceosorus*, *Ceraceosorus bombacis* and the Ceraceosorales, discuss the morphological and molecular characters of *Ceraceosorus africanus* and *C. guamensis* and delineate differences compared to *Ceraceosorus bombacis*. Additionally, we will merge all available sequence and biogeographical data on the Ceraceosorales, provide a hypothesis on the phylogenetic position of the order and delineate future challenges for the Ceraceosorales.

This work was supported by the W. Szafer Foundation for Polish Botany, National Science Centre (NCN) of Poland (project no. N N303 414037), the German Research Foundation (DFG; project no BA 75/3-1), and the Volkswagen Foundation.

Piątek M et al. (2016) Integrative analysis of the West African *Ceraceosorus africanus* sp. nov. provides insights into the diversity, biogeography, and evolution of the enigmatic Ceraceosorales (Fungi: Ustilaginomycotina). *Org Divers Evol*: DOI 10.1007/s13127-016-0285-3

Kijpornyongpan T & Aime MC (2016) Rare or rarely detected? *Ceraceosorus guamensis* sp. nov.: a second described species of Ceraceosorales and the potential for underdetection of rare lineages with common sampling techniques. *Antonie van Leeuwenhoek* 109: 1127–1139.

Fungi associated with wood necrosis of stone fruit trees in Germany

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Germany is counted among the major producer regions for sweet cherry, sour cherry as well as plum worldwide. Extensive analysis about fungi associated with wood necrosis in stone fruit trees come from South Africa and North America. As part of the GBOL-Project an analysis of the diversity of fungi associated with wood necrosis of commercially used *Prunus* trees from Saxony, Lower Saxony and Baden-Württemberg is introduced. First results based on morphological determination and ITS-analysis are presented and show considerable differences to results from South Africa and North America. In addition to the samples obtained from orchards in the above mentioned regions an inclusion of samples provided by private *Prunus* tree owners is desired. Therefore a short explanation for sample procedure is given.

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More verticillium-like hyphomycetes reclassified

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The morphologically little differentiated group of phialidic verticillium-like hyphomycetes is characterized and history and taxonomy are briefly reviewed. Molecular studies show that *Verticillium s.str.* and a few others belong to the Plectosphaerellaceae, (Glomerellales, Sordariomycetes), and others to five families of the Hypocreomycetidae: three of which formerly called Clavicipitaceae, now Cordycipitaceae, Clavicipitaceae and Ophiocordycipitaceae, as well as Hypocreaceae and Bionectriaceae (besides some others). A group of verticillium-like taxa with erect conidiophores is distributed over these families and some novelties are presented in each of these families. This classification is corroborated by morphology, ecology and ribosomal DNA analysis.

Zare, R. & Gams, W. (2016). More white verticillium-like anamorphs with erect conidiophores. – Mycological Progress, in press.

Gams, W. (2016). An annotated checklist of epithets published in *Verticillium* and *Acrostalagmus*, some similar genera, and teleomorphs associated with verticillium-like anamorphs. – Nova Hedwigia, in press.

Are the interactions between fungal root endophytes and plants context-dependent?

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The outcomes of the interaction between plants and fungal endophytes are varied in nature. This variation can be partly explained by factors external to the symbionts, including abiotic conditions as well as biotic interactions with other extant organisms. This context dependency can influence to a different extent the outcome of symbioses, either positively or negatively for each partner. Yet, we lack the understanding of how plant–endophyte associations are affected by environmental variables. In this study, we aimed to better understand the context-dependency of these particular symbioses. For this, we assessed the effect of abiotic and biotic factors on the interaction between a selection of fungal endophyte strains and different plant species. In the first case, we assessed how gradients of nutrient availability, light intensity, or pH of the substratum, affected the growth responses of different plant species (*Arabidopsis thaliana*, *Microthlaspi erraticum* and *Hordeum vulgare*) to inoculation with 23 individual strains. To test the effect of biotic factors, we studied the *in planta* interaction between pairwise combinations of strains from different species using quantitative PCR, and assessed their joint effects on the growth of *A. thaliana*. We did not find an overall significant effect of abiotic factors on the outcome of interactions, although a few strains showed an increased parasitism under particular nutrient or light regimes. Preliminary results from co-inoculation experiments show that the root colonization by most strains, and their effects on plant growth, are influenced by the presence of co-occurring endophytes. Altogether, our findings suggest that plant–endophyte symbioses are highly variable under controlled conditions. Moreover, biotic factors seem to have a greater effect than abiotic factors on the outcome of interactions.

Comparison of Fungal Diversity in Comprehensive-Taxa Inventories

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Fungi are an important component of every ecosystem but hardly considered in biodiversity monitoring projects. This work aims at characterizing fungal diversity, with an emphasis on epigeous fungi, encompassing different biogeographic zones. The compared sites are situated in Germany (two sites), in Austria, Spain and Panama (one site each; for Panama see Piepenbring et al. 2012). All areas were investigated with a standardized sampling protocol focusing on macroscopically evident fungi and vascular plants using a time-restricted transect design.

The fungal species richness of single sampling events was highest in the mountainous regions in Spain and Austria, which showed the highest altitude and precipitation from the European areas. However, the highest precipitation was recorded for Panama, but the direct comparison revealed greater species numbers in Europe. The plant:fungus ratio was similar between the European areas, but differed strongly between Germany and Panama. This supports the hypothesis that the plant:fungus ratio is comparable on regional but not on global scale.

A comparison of the sampling areas revealed similar patterns on high taxonomic scale of divisions, notwithstanding their differences in vegetation and geographical location. Except during the mushroom season in autumn, when basidiomycetes dominated fungal diversity in Europe, the number of Ascomycota was usually higher, followed by Basidiomycota and by a small number of slime moulds. At order level, members of Agaricales were recorded most frequently in almost all sampling areas. At sampling events during dry conditions, other orders were more frequent.

In contrast to the higher taxonomic levels, the species composition was different across sampling sites and the Panamanian area was most dissimilar compared to the European areas. No common fungal species were found in all sampling areas, but six species were recorded in the four European sampling sites. Only one species was shared between three European sites and Panama. All these species inhabit wood, which shows the importance of wood for fungal diversity recorded within the performed sampling design. Furthermore, the monitoring of many fungal groups including small and/or inconspicuous fruit bodies is essential for comparing different regions because some of the species, which were found in four different areas, develop only small fruit bodies.

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Unravelling molecular and morphological diversity in *Subulicystidium* (Trechisporales, Basidiomycota)

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The genus *Subulicystidium* Parmasto unites corticioid fungi of the order Trechisporales K.H. Larss. that are characterized by uniquely ornamented subulate cystidia. Currently, nine species are recognized within the genus based on morphological evidence. The genus remains poorly represented in molecular studies so far. Currently available public sequences are usually named to the genus level or even just as ‘Trechisporales’. Sequences from fruit bodies annotated to the species level are extremely rare (Volobuev 2016).

For many decades, mycologists were challenged to discriminate the species within *Subulicystidium*. Few morphologically distinct species were described (Oberwinkler 1977). For a number of collections no better solution was found than attributing them to a highly variable *S. longisporum* complex (Duhem & Michel 2001, Liberta 1980). This gave an impression that hidden *Subulicystidium* diversity should be looked for primarily in the material having acicular basidiospores, i.e. as those in *S. longisporum*.

In this study we report 11 new species of *Subulicystidium* with relatively short (e.g. non-acicular and often less than 10 µm long) basidiospores. These species are being described based on our and colleagues’ fruit body collections from Paleotropics (Réunion Island, Madagascar, Africa, South-East Asia) and Neotropics (Caribbean region, various countries of South America). This material has been collected since 1970-ies and preserved in O, KAS and FR herbaria. Type collections of *S. meridense* Oberw. (preserved in TUB), *S. nikau* (G. Cunn.) Jülich (PDD) were also involved in the study. We generated 41 ITS and 25 LSU rDNA sequences from this material. We present morphological and phylogenetic evidence for describing these 11 new species, and clarify the concepts of 5 previously known short-spored species. In addition to the size and shape of basidiospores, we demonstrate a high diagnostic value of cystidial morphology in *Subulicystidium*. A correlation of these morphological traits with the rDNA-based phylogenies will be discussed.

Duhem B., & Michel H. (2001). Contribution à la connaissance du genre *Subulicystidium* Parmasto 1968 (Basidiomycota, Xenasmatales). *Cryptogamie Mycologie* 22(3): 163-173.

Liberta A.E. (1980). Notes on the genus *Subulicystidium*. *Mycotaxon* 10: 409-412.

Oberwinkler F. (1977). Species and generic concepts in the Corticiaceae. The species concept in Hymenomycetes. *Cramer, Vaduz*, 331-348.

Volobuev S. (2016). *Subulicystidium perlongisporum* (Trechisporales, Basidiomycota) new to Russia, with notes on a molecular study of the species. *Nova Hedwigia* 102(3-4): 531-537.

Agrocybe aegerita as a model basidiomycete for fruiting body formation

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Beyond a detailed understanding of the molecular mechanisms driving the sophisticated developmental programme of fruiting body (mushroom) formation in Agaricomycetes, model basidiomycete-based research also aims at yield and quality increase in edible mushroom production. In order to directly come towards both goals, we decided to use the commercially cultivated top-quality edible mushroom *Agrocybe aegerita* as a model system which displays the extraordinary phenomenon of monokaryotic fruiting. Initially, we have selected a set of *A. aegerita* wildtype strains exhibiting a ‘text-book’ basidiomycete life cycle and other highly beneficial features such as abundant monokaryotic oidia production. This strain set comprises the parental dikaryon *A. aegerita* AAE-3 and a pair of AAE-3-derived mating-compatible monokaryons, *A. aegerita* AAE-3-13 and *A. aegerita* AAE-3-32. This pair of sibling monokaryons represents the extremes of the monokaryotic fruiting spectrum ranging from no formation of fruiting stages in *A. aegerita* AAE-3-13 to the formation of almost fully developed but low-sporulating fruiting bodies in *A. aegerita* AAE-3-32. Advantageously, both strains produce abundant oidia accessible to a dominant selection marker-based transformation procedure we developed relying on the transformation of oidia-derived protoplasts. All this taken together with the availability of the *in silico* annotated whole-genome sequence of the dikaryon *A. aegerita* AAE-3, we think that *A. aegerita* deserves a reappraisal as a modern model basidiomycete to study monokaryotic and normal dikaryotic agaricomycete fruiting body formation.

A transformation system for the black poplar mushroom *Agrocybe aegerita*

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Agrocybe aegerita, the black poplar mushroom, is both a model organism which is used to examine basidiomycete fruiting body formation and a commercially grown choice edible mushroom. Here, we report the establishment of a dominant selection marker-based transformation system for *A. aegerita* using the monokaryotic standard wild type strain *A. aegerita* AAE-3-13. The transformation procedure relies on the PEG-mediated transformation of protoplasts derived from monokaryotic oidia. Applying this procedure, at the same time, a homologous marker gene-based dominant selection marker was established first-time for *A. aegerita*, which is a resistance to the systemic fungicide carboxin (Cbx). Carboxin resistance (Cbx^R) was conferred to the Cbx sensitive strain *A. aegerita* AAE-3-13 by applying a single point mutation (His237 to Leu) to the *A. aegerita* gene *AaeSDII* encoding the iron-sulfur protein subunit of succinate dehydrogenase, which is then introduced into *A. aegerita* AAE-3-13. The linearised Cbx^R plasmid we used is supposed to integrate into the native *A. aegerita* *AaeSDII* locus. This dominant selection marker-based protoplast transformation protocol at hand, *A. aegerita* molecular genetics approaches can now be carried out in order to undertake a functional characterisation of *A. aegerita* candidate genes with a potential role for basidiomycete fruiting body development.

Intraspecific genetic variability in root-endophytic fungi and implications on dispersion dynamics and environmental adaptation

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Studying community dynamics of plant-associated fungi is necessary to unravel their interactions with hosts and their function in ecosystems. We aimed to identify how communities of root endophytic fungi change across environments and to associate these changes with the ability of fungi to disperse and adapt to different ecological conditions. A recent sampling revealed that only a few fungal groups, defined by their ITS rDNA sequences, dominate endophytic communities in roots of the non-mycorrhizal plant *Microthlaspi perfoliatum* s.l. across Europe. The groups had a widespread distribution across sampling sites but strains of these fungi displayed a broad phenotypic variability. We hypothesized that the widespread presence detected could be due to our reliance on the ITS region for the molecular identification of strains. The use of more sensitive molecular markers could unravel intraspecific genetic differences among geographic populations and explain the observed phenotypic variations. In that case, genetic differences between strains ought to increase with geographic distance between populations. We performed a multilocus analysis by sequencing three additional genetic loci (*TEF-1 α* , *TUB*, *ACT*) from 188 strains representative of the five most abundant fungal groups, and we also characterized them by AFLP profiling. We observed very little genetic variation within all fungal groups and no correlation with geography and environmental factors, indicating a large homogeneity irrespective of the sampling site. Our results suggest that endophytic fungi have very efficient dispersal capabilities. However further investigation of genes related to functional traits could reveal variabilities within fungal groups related to environmental adaptations.

News on the diversity and distribution of *Tricholoma* spp.

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Species of the genus *Tricholoma* (Fr.) Staude produce sizable and distinctive fruiting bodies and thus have been continuously studied since Fries. The genus includes the most expensive edible agaric mushroom, *Tricholoma matsutake* (S. Ito & S. Imai) Singer, which is of high economic importance in several parts of Asia. Though, several *Tricholoma* species produce toxic mushrooms which may cause fatal intoxications. Species of the genus are present in most of the temperate and boreal forests of the world, contributing to the function of ectomycorrhiza. *Tricholoma* species are also specific hosts to mycoheterotrophic plants of the Ericaceae subfamily Monotropoideae.

While the state of taxonomic knowledge on the genus is near satisfying in North-West Europe, the knowledge about the global diversity and distribution is scarce. In this study the diversity and distribution of species of the genus were analysed by morphological and molecular methods based on 61 collections from Yunnan, China, 45 collections from Central Europe, 32 collections from Colorado, USA, nine collections from Japan and three collections from Ukraine. A holarctic distribution limited by the host range is suggested for the first time for five species, based on ITS sequences. A new section of the genus is proposed, based on morphological and molecular characters. Six species are formally described as new species to science from Yunnan. Two further probably new species could not be delimited due to insufficient material. Generally, a lot remains to be done on the genus *Tricholoma*.

Insights into the Taxonomy of Philippine Mangrove Oomycetes

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The Republic of the Philippines is a biodiversity hotspot. They have both a high degree of species richness and endemism due to their tropical and archipelagic nature. Of the interesting groups of microorganisms in Republic of the Philippines, the mangrove-inhabiting oomycetes are poorly studied. The knowledge gap becomes evident considering the published Philippine directory of microbial strains, which does not list a single reference strain of collections or herbaria focused on marine oomycetes. The challenge now is to annotate, identify, and describe mangrove oomycetes using classical and molecular approaches on isolates obtained from fallen senescent mangrove leaves from selected areas in Republic of the Philippines. A total of 840 strains were isolated from 468 mangrove leaf samples. Of these, representative species from *Halophytophthora* s.l., *Phytophthora*, *Phytopythium*, *Pythium*, *Salisapilia*, and *Salispina* are herewith reported and discussed focusing on taxonomic changes and diagnostic descriptions.

DGFM MEETING Bernried 2016

Plenary Lectures,

Thursday 15 September 2016

Fungal secondary metabolites from plant pathogenic fungi and their impact on plant/pathogen-interactions

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The adaptation of fungal organisms to a distinct habitat and the ability to compete against other microorganisms is reflected by the exceedingly rich fungal secondary metabolism. Such natural compounds from fungal sources have in the past been very successful lead structures for pharmaceutical or agrochemical applications. Many of those compounds have been discovered by fermentation of organisms in axenic or static cultures in artificially defined media, which are poor surrogates for mimicking an organism's natural habitat. As a consequence only a small number of genes potentially involved in the biosynthesis of secondary metabolites are expressed under these conditions.

Magnaporthe oryzae is the causal agent of blast, a devastating fungal disease on cultivated rice. The fungus is known to produce secondary metabolites involved in plant/pathogen interaction, such as pyriculol and pyriculariol. Within the genome 20 genes encoding polyketide synthases have been identified by homology search, whereas qPCR experiments revealed that only four of them are transcribed in axenic culture. Apart from cultivation variation approaches molecular based techniques have become suitable methods in order to explore the products of silent secondary metabolite pathways.

In order to investigate regulatory elements of secondary metabolism and to identify new natural products many technologies can be applied. Several reverse genetics studies have successfully been conducted at the IBWF. For those studies gene deletion/gene disruption strains were generated, promoters were changed and transcription factors or other pleiotropic regulators were over- expressed. Furthermore epigenetic strategies were successfully applied in order to elucidate new secondary metabolites. The application of demethylase inhibitors led to the identification of novel polyketides from *M. oryzae* which have not been isolated from extracts of axenic cultures before.

Apart from the identification of new secondary metabolites and their potential role in pathogenicity the studies will provide insights into the regulation of phytotoxin biosynthesis in plant/pathogen-interactions. Profound knowledge concerning chemical communication in these interactions via secondary metabolites (phytoalexins/phytotoxins) can contribute to new prevention strategies in integrated plant protection strategies.

Bioactive secondary metabolites from *Laxitextum incrustatum* – a tropical fungus

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The fungal kingdom is one of the largest organism groups comprising of about 1.5 to 3 million globally described species (Hawksworth, 2012). To our knowledge, the phylum (Basidiomycota) a mushroom-forming organism has in the current past increasingly received overwhelming attention. The interest accrues not only because of the important roles they play in various ecosystems but majorly due to its endowed bio- and chemodiversity in the underexplored niches, as observed in less than 2% portion that has been studied so far. From the documented reports, this phylum has been proved to be a prolific source of novel secondary metabolites with unique and unusual biochemical pathways (Stadler and Hoffmeister, 2015). The search for novel metabolites was in our attempts focused to the investigation of the fungal strains from the tropical forest (Kakamega equatorial rain forest) in Kenya collected during field trips. The axenic fungal strains are subjected to bioactivity guided screening, followed by the analytical techniques that thereafter lead to the desired target molecules. For instance, new cyathanes molecules named laxitextines were obtained as first secondary metabolites from a culture of *Laxitextum incrustatum* collected in Kenya (Mudalungu et al., 2016). The isolation of these compounds provided a chemotaxonomic inference to the close phylogenetic relationship of the genus *Laxitextum* to *Hericium coralloides* and *H. erinaceus* (Thongbai et al. 2015), from which novel cyathanes and other terpenoids were isolated. The search for novel metabolites from the above mentioned region is therefore an ongoing project which is expected to yield many other unprecedented scaffolds.

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Thongbai B et al. (2015). *Hericium erinaceus*, an amazing medicinal mushroom. *Mycol Prog* 14(91):1-23.

Studies on *Amanita* species in Northern Thailand

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Amanita Pers. is an important genus of mushrooms that includes several species that are widely recognized as the most toxic mushrooms in the world. The *Amanitaceae* is characterized as those agarics having bilateral, divergent lamella trama and longitudinally acrophysalidic stipe context (Tulloss *et al.* 2016). *Amanita* is concisely characterized as the set of species of the *Amanitaceae* that exhibit schizohymenial development in their agaric and secotioid species (Tulloss and Yang 2016a, Tulloss *et al.* 2016). Most species in the genus are considered to be ectomycorrhizal (ECM) and their distribution in forests including (among others) *Betulaceae*, *Dipterocarpaceae*, *Fabaceae*, *Myrtaceae*, *Pinaceae*, and *Salicaceae* suggests that they play a critical role in forest ecosystems worldwide. Since 2010, mushroom diversity in northern Thailand has been investigated and high diversity has been found. There have been few studies on *Amanita*. Sanmee *et al.* (2008) reported 25 *Amanita* taxa from northern Thailand. However, during fieldwork, we observed many more species, which suggests that *Amanita* diversity is high, demonstrating the need for further study of this genus.

In recent studies, we provided morphological descriptions and distribution data for four taxa discovered for the first time in Thailand, *Amanita concentrica*, *Amanita rimosa*, *Amanita cf. rubromarginata* and *Amanita zangii* while, *Amanita atrobrunnea*, *Amanita castanea* and *Amanita strobilipesis* were described as new to science and compared with similar species. Species identifications are supported by both morphological and molecular phylogenetic analyses.

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A multigene phylogeny within the Xylariaceae

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The Xylariaceae is a hyperdiverse and large family of Ascomycota with over 1300 accepted species. Some of them have been described for the first time over 300 years ago, based on descriptions of “macromycete” genera and species that produce rather conspicuous stromata including *Xylaria*, *Hypoxylon* and *Daldinia*. However, only in the past decades it has become evident that the Xylariaceae are abundant as endophytes of various plants, and the number of DNA sequences derived from spurious endophytes that can be recovered from environmental samples is steadily increasing. The Xylariaceae have also proven to be of great economical importance. Aside from a few pathogens, they contain extremely prolific secondary metabolite producers and some species have recently been evaluated successfully as potential biocontrol agents (e.g. mycofumigants) or as producers of industrial enzymes. The respective strains that are often obtained from environmental samples cannot be safely identified based on the present classification system that largely relies in morphology of the sexual states. Therefore, there is a great need for a concise classification of these fungi and possible a taxonomic rearrangement based on a polyphasic approach.

Thus, a phylogenetic approach was performed using a high number of reference strains (including various type strains or such ones that would serve well for epitypification in the future) and the large subunit (**LSU**), internal transcribed spacer (**ITS**), β -tubulin (**TUB**) and second-largest subunit of nuclear RNA Polymerase II (**RPB2**) as molecular markers. Especially LSU data have been generated for a large number of representatives for the first time.

The calculated Maximum-Likelihood multigene genealogy reflected phylogenetic relationships within the Xylariaceae with highly supported clades, reinforcing hypotheses that had been based on morphological and chemotaxonomic data. The “Xylarioideae” and the “Hypoxyloideae” are rather distinctly separated. Moreover, the genus *Hypoxylon* appears paraphyletic, revealing six distant lineages, and *Daldinia* and allies are separated into two distant lineages as well. Furthermore, the multigene tree supports the further segregation of *Annulohypoxylon* and *Hypoxylon*.

Some previous phylogenies have rejected ITS data altogether, which is unfortunate as the ITS represents the bulk of information that can usually be obtained from molecular ecology studies. Our study revealed, on the one hand, that a phylogeny based on a combination of ribosomal DNA with “housekeeping genes” is largely in accordance with phenotype data, including morphological features and chemotaxonomic traits. On the other hand, it might be practical to sequence partial LSU together with ITS in order to achieve a more concise “molecular identification” of Xylariaceae in the environment than ITS only. The main problem that remains is the collection of reference data from reliably identified species, in particular from the tropics, because over 50% of the known species are not yet represented by such conclusive data in GenBank, and no genuine cultures of these taxa are available in public domain repositories as yet.

Contributions to pleurotin biosynthesis – isolation and characterization of novel derivatives

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Within the family of Pleurotaceae, Basidiomycota, is a genus of nematode-trapping fungi, *Hohenbuehelia*. Some species of the genus are characterized by the production of the secondary metabolite pleurotin. Pleurotin is an antibiotic agent discovered in 1947 (Robbins et al. 1947). It gained renewed interest for its potent inhibition of the thioredoxin-thioreductase system and a potential use in dermatophyte infections (Kunkel et al. 1997; Berdicevsky et al. 2008). The elucidation of pleurotin's biosynthetic pathways is of further interest for its potential in the treatment of many hypoxia-induced solid cancers (Welsh et al. 2002). Knowing the biosynthesis provides new possibilities of pleurotin production, compared to the current challenges that come with the fermentation of the respective fungi. To obtain more information on the biosynthesis, new *Hohenbuehelia* specimens were collected in Thailand and molecular genetically as well as morphologically analyzed. The secondary metabolite profile was checked for the production of pleurotin and its derivatives. By isolating new pleurotin derivatives, conclusions on the biosynthesis could be drawn. In addition, the isolation of cysteine-derived conjugates of pleurotin gave new insight into a glutathione detoxification in filamentous fungi.

Berdicevsky I et al. (2008) Preliminary study of activity of the thioredoxin inhibitor pleurotin against *Trichophyton mentagrophytes*: a novel anti-dermatophyte possibility. *Mycoses* 52: 313-317.

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Welsh SJ et al. (2002) The redox protein thioredoxin-1 (Trx-1) increases hypoxia-inducible factor 1alpha protein expression: Trx-1 over-expression results in increased vascular endothelial growth factor production and enhanced angiogenesis. *Cancer Res.* 62:5089-5095.

New secondary metabolites from *Hypoxyton lienhwacheense*

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The Xylariaceae is one of the largest families within the Ascomycota and with more than 500 known secondary metabolites this family belongs to one of the most prolific secondary metabolite producers within the fungal kingdom (Stadler & Hellwig 2005). The genus *Hypoxyton* is cosmopolitan, but has the highest diversity in the tropics and subtropics. The fruiting bodies (stromata) are usually found on dead wood of dicots and monocots. Some taxa are host-specific, but others have a wide substrate range (Ju & Rogers 1996).

This talk deals with the characterization of *Hypoxyton lienhwacheense* using a polyphasic taxonomic approach. The morphological characterization is described as well as the molecular phylogenetic investigation based on ITS (internal transcribed spacer) and partial β -tubulin DNA sequences. Five different secondary metabolites were isolated from stromata via preparative HPLC and the structures of four compounds could be elucidated by NMR (nuclear magnetic resonance) spectroscopy. Beside the known BNT (binaphthalene tetrol) and cordyanhydride B, a new maleic anhydride and a new maleic anhydride tropolone derivative were identified. Additionally, the secondary metabolite production of mycelial cultures of the species was investigated. This led to the isolation of another two new maleic anhydride derivatives and cordyanhydride B. The latter compound is the first secondary metabolite of a species of Xylariaceae, which could be found in culture as well as in the stromata as major component.

These results further illustrate the high diversity of secondary metabolites in stromata and cultures of hypoxyloid Xylariaceae and reflect the high potential for the discovery of new natural products within this family.

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Ju Y-M and Rogers JD. 1996. A Revision of the Genus *Hypoxyton*. *Mycologia Memoir* no. 20. APS Press, ST. Paul, MN.

Nerve Growth- and Brain-Derived Neurotrophic Factor inducing metabolites from *Hericium* spp.

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Antibiotic resistance and neurodegenerative diseases are two major medical issues we have to face and which will become even more serious in the future. In order to cope with them and to develop improved therapies new active compounds with different modes of action are needed urgently. *Hericium* spp. of the phylum Basidiomycota are producing interesting secondary metabolites, such as hericenones and erinacines, which have been isolated from fruiting bodies and cultured mycelium, respectively. Many of these compounds have been found to promote nerve growth factor (NGF) biosynthesis (Ma et al. 2010, Zhang et al. 2015, Thongbai et al. 2015).

In a current study we are investigating secondary metabolites from different species of the genus *Hericium* with focus on the identification of novel antimicrobial and neurotrophic compounds. After establishing the evaluation of secondary metabolites production of several *Hericium* species by HPLC-UV/Vis-MS, *H. erinaceus* was chosen for scale-up fermentations (10L and 70L). Afterwards, downstream processing was performed in terms of extraction and isolation/purification using different chromatographic techniques. Structure elucidation of the compounds was performed by mass spectrometry and NMR spectroscopy. Finally, the biological activity has been investigated by antimicrobial, cytotoxicity and PC12/1321N1 cell stimulation assays. Several known and new hericenone-type substances and erinacines have been isolated and characterized. A large scale production of erinacine C has been established to enable future drug formulation studies.

Screening and isolation procedures of the isolated and characterized compounds will be presented. Some of them are showing interesting neurotrophic activities in vitro and have been chosen for further investigations.

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Zhang CC, Yin X, Cao CY, Wie J, Zhang Q, Gao JM, Bioorg. Med. Chem. Lett. 2015, 25, 5078–5082.

Thongbai B; Rapior S; Wittstein K, Hyde KD; Stadler M, Mycol. Prog, 2015, 14(91):1-23.

Neomycetes, alien fungi in Switzerland

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Alien fungi, neomycetes, are the less well-investigated group of neobiota. However, they have the potential to harm the indigenous flora and fauna of a region and as a consequence the local ecosystems. Ash dieback and chestnut blight as well as the crayfish plague are examples for such dangerous introduced plant respectively animal diseases.

The present study fills this gap for plant associated neomycetes in Switzerland. 283 fungal species were identified as neomycetes based on literature, data bases and museum collections. Own fieldtrips completed this survey. All data were georeferenced and implemented into the online Distribution maps of Swiss fungi, the SwissFungi database (www.swissfungi.ch). 13 species of neomycetes are new reports for Switzerland, such as the rust fungus, *Coleosporium asterum*. It was found on the introduced gold rod, *Solidago gigantea*, as well as on the indigenous *Solidago virgaurea*. The introduced powdery mildew of plane trees, *Erysiphe platani*, was found firstly on the tree of heaven, *Ailanthus altissima*, an invasive neophyte. We could identify both host jumps of these fungi using DNA-sequencing of their ITS region of the rDNA.

Beenken L, Senn-Irlet B (2016) Neomyceten in der Schweiz - Stand des Wissens und Abschätzung des Schadpotentials der mit Pflanzen assoziierten gebietsfremden Pilze. WSL Berichte (in press). http://www.wsl.ch/dienstleistungen/publikationen/schriftenreihen/berichte/index_DE

What do we learn from cultures and High-throughput sequencing for the same samples?

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Comparative studies of fungal cultivation and high-throughput (HTS) sequencing have rarely been conducted in the past years. For the present contribution HTS and cultivation protocols were applied for the same leaf samples of European beech (*Fagus sylvatica*) in order to identify commonalities and distinctions, in other words, method-dependent patterns of observed mycobiomes, at two contrasting sites in Bavarian Alps, Germany (for experimental details see Siddique and Unterseher 2016, Unterseher et al. 2016).

Both approaches resulted in non-overlapping mycobiome composition and pronounced differences in taxonomic classification and ecological signals. However, both methods revealed similar correlations of the fungal communities with local environmental conditions. Our results suggest that the immense body of literature about cultivable endophytic fungi can be reliably used for the interpretation of environment-dependent community signals obtained from HTS studies. However, our cultivation approach revealed clear deficits for various aspects of biodiversity analysis.

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Unterseher M et al. (2016) Diversity and Composition of the Leaf Mycobiome of Beech (*Fagus sylvatica*) Are Affected by Local Habitat Conditions and Leaf Biochemistry. *PLOS ONE*, 11(4), e0152878.

DGFM MEETING Bernried 2016

Posters,

**Sessions in the afternoon/early evening of 12 and 13 September
2016**

Diagrams showing the importance of fungi in ecosystems for teaching and environmental education

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The presence of fungi with highly diverse physiological activities is indispensable for ecosystem functioning, especially for nutrient cycles, equilibrium of species, vigorous plant growth, and protection of soil against erosion, among other aspects (Dighton 2016). Fungi are essential for the long term survival of plants and animals. These facts are scientifically proven but largely ignored or neglected by most ecologists, at schools, and in the context of environmental education. Aspects to explain this situation may be a certain mycophobic societal tendency, the inconspicuous habit of most fungi, as well as a lack of attractive teaching materials.

In order to illustrate functions of fungi in ecosystems, schematic drawings of a tropical forest including several tree species with individuals of different ages and fungi representing different ecological groups (saprotrophs, mycorrhizal fungi, insect parasites, plant parasites) were elaborated with the program CoralDRAW. For each ecological group of fungi, one forest diagram showing only these fungi is presented followed by one or several diagrams showing the forest as it might look like in the absence of fungi of the respective group. The most striking effects are the accumulation of organic material in the case of lacking saprotrophs, reduced plant vigor and health without mycorrhizal fungi, insect pest without insect pathogens, and reduced plant species diversity without plant parasites.

These diagrams shall help teachers and guides in nature to explain the ecological importance of fungi. For mycologists, they are helpful to develop hypotheses that can lead to corresponding experiments to investigate specific fungal ecosystem functions that are complex and far from being known for specific ecological settings including further microorganisms and complex further biotic and abiotic factors that change over time.

The teaching diagrams are available open access by the portal "Digital Documents for Learning and Teaching Mycology" (URL 1, URL 2) and were elaborated in the context of conservation biology teaching in Latin America with collaboration by Tropica Verde e.V. and support by the German Academic Exchange Service.

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Biodiversity of cultivable fungi after an artificial flooding of the soil habitat

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Soil-associated organisms are influenced by frequently changing abiotic and biotic factors. In this context, this study examines the effect of artificial flooding of soil habitat on the biodiversity of cultivable fungi. A mesocosm experiment was conducted to observe shifts in community composition under controlled conditions. Soil samples collected within this project were collected from flooded (8 days) or unflooded samples and investigated using a fungal cultivation. The samples were taken before and directly after flooding and additionally 14 days after soil dehydration. At the same time, samples of the control were taken, which were unflooded. The diluted soil samples were incubated on different artificial media (YM with Lactat or Chloramphenicol, DG18, Azotobacter, YNB with Phenol and YM under anaerobic conditions) to obtain a high diversity of yeast and filamentous fungi. Colonies were differentiated morphologically and occurrence was recorded. DNA was isolated from either one or two colonies (when the morphotype was frequent) of every morphotype. Subsequently, clones were differentiated based on MSP-PCR patterns, the ITS region of remaining samples was sequenced and the blastn algorithm in NCBI was used for identification.

All in all, 96 species were obtained. Eighteen of these samples had no blast hit based on the ITS region and therefore might be unknown species or genotypes. In addition, the study indicates that selective media supports the growth of highly specialized species that do not occur in high nutrient media. A few generalists like *Mucor hiemalis* were observed on every media but with varying abundance. The different flooding regimes changed community patterns in different ways. With increasing drought, diversity decreased and drought resistance species (e.g. *Fusarium oxysporum*) dominated those communities. All dry samples had similar or the same number of colony forming units (CFU). This suggests that water limited the number of CFUs. After flooding the community changed too, however, species diversity increased. Possible explanation for this increase could be the invasion of alien species through the flooding water, or increased germination of soil-borne spores, with increasing moisture levels. Furthermore the results show that communities of dehydrated soil do not revert back to their original state. But the fact that the sample, which was taken after dehydration, and the sample of the control are very similar suggests an existence of a specific drought community.

Effect of nutrient availability on the interaction between root endophytes and plants

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Plants harbour a high abundance and diversity of non-mycorrhizal fungi in their roots that most probably affect plant fitness. However, knowledge about these effects is very limited. A better understanding of the symbioses between plants and their associated fungi could lead to the development of biologically-based fertilizers and pesticides that may be alternatives to agrochemicals. Here, we study how nutrient availability impacts the effect of root endophytic fungi on plant growth. We performed inoculation assays of the model plant *Arabidopsis thaliana* with six endophytic strains, belonging to species within *Fusarium*, *Alternaria* and *Cadophora* (two strains of each). These fungi are ubiquitously distributed in plant roots across Europe and have shown different effects on plant growth in previous *in vitro* tests. In our experiments, plants and fungal strains were co-cultivated in culture media in upstanding square Petri dishes, to allow gravitropic growth of roots. Nutrient availability treatments consisted in applying gradients in the content of either nitrogen, phosphorus, or carbon (sucrose) available for both organisms. Effects on plant development were quantified by measuring fresh shoot biomass and maximal root length, while fungal growth was scored as colony diameter. Preliminary results show different effects of nutrient concentrations on plant-fungus interactions. For example, all strains strongly inhibited root elongation only when sucrose was present in the growth medium. Our findings suggest that the effects of fungal root endophytes on plant growth are partially determined by the availability of nutrients in the surrounding substrate.

Flight characteristics of teliospores of *Urocystis* species

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Only little information is available on the aerial distribution of smut spores on global scales (Fröhlich-Nowoisky et al, 2012). However, information is available about the liberation and dispersal of fungal spores (Ingold 1971). Functional links between spore sedimentation rate and morphological characters of smut teliospores are expected but unstudied so far. Sedimentation rate should affect dispersal of fungal spores in air and water. As this influences fitness, spore characteristics should be a target for adaptation and selection. We choose members of the *Urocystidiaceae*, encompassing a high morphological variability of the spores, with single spores up to spore balls, as model group for our study.

We investigated the flight characteristics of different *Urocystis* species from different host groups. The spore balls varied in size and the number of attached sterile cells. Experiments were performed in a wind tunnel in which spores are caught with a spore trap and analyzed using light microscopy.

The results indicate that, beside spore size and surface, the number of sterile cells, which surround the fertile spores in *Urocystis*, have a major influence on flight characteristics. An increasing number of sterile cells result in a lower sedimentation within the wind tunnel. This is especially interesting as *Urocystis* species parasitizing members of Poaceae usually possess more sterile cells around the few fertile cells. This may be an adaptation to the open habitat of the anemophilous Poaceae where the lower sedimentation rate would support spore dispersal into more distant localities.

Fröhlich-Nowoisky, J. et al. (2012). Biogeography in the air: fungal diversity over land and oceans. *Biogeosciences*, 9(3), 1125–1136.

Ingold, C. T. (1971). *Fungal spores. Their liberation and dispersal*. Oxford University Press

Fungal vitality under anaerobic conditions

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Uniquely adapted organisms, fungi amongst others find their niche in extreme ecosystems. One of these ecosystems is represented by mofettes, where low oxygen levels and high CO₂ concentrations are common. Aim of this study was to compare the growth abilities of five representatives of Ascomycota, Basidiomycota and Zygomycota and their adaptations to hypoxia, i.e. elevated CO₂ or N₂ levels. So far the studies conducted to this topic address low oxygen levels but do not emphasize the stress due to elevated CO₂ or N₂ concentrations. Strains were precultivated for 10 days under normal atmosphere. Standardized amounts of fungal colonies were used to inoculate YM + Lac media for tests under anaerobic conditions. Strains were cultivated for eleven days within airtight plastic bags, flooded with N₂ or CO₂. Zygomycota showed the best growth abilities amongst the three phyla, while Ascomycota grew with decreased speed and Basidiomycota did not grow at all. After eleven days of anaerobic growth, cultures were exposed to normal atmosphere again and each culture grew without visual differences to the control. More comprehensive insights into the capability of anaerobic growth was achieved by the analysis of the proteome of *Mucor circinelloides*, which was extracted with a newly developed protein extraction protocol. SDS-PAGE was used to examine the differences of the proteome from different phyla. Visually detectable changes in the proteome bands show that the *Mucor circinelloides* can adapt to anaerobic conditions by changing protein expression. This implicates that Zygomycota might have a repertoire of genes, which allows them to handle anaerobic conditions.

Heterospecific infections with *Microbotryum* (Pucciniomycotina) show lower disease rate than homospecific infections

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Fungal pathogens are one of the major agents of plant diseases. Loss of crop yield and new emerging resistant fungal pathogens are challenging agriculture production worldwide. The basidiomycetous plant parasite *Microbotryum* is an established model organism in genetics, ecology and population biology and provides insight into evolutionary processes of host adaption in a non-agriculture background.

A total of 1088 *Silene* plants were examined in homospecific and heterospecific cross infection experiments to investigate the potential of host-shifts of *Microbotryum* species from various phylogenetic distance. Our focus was mainly on the viability and infection potential of hybrids formed between different *Microbotryum* species. Preliminary results indicate cross infected *Microbotryum* species as well as hybrid progeny perform infection at lower disease rates on *S. latifolia* than homospecific infection by *M. lychnidis-dioicae* which may contribute to host specific traits in *Microbotryum* affected by the pathogen's environment. Phylogenetic distantly related *Microbotryum* species are impaired to mate and form pathogenic hybrid progeny. In addition, this study points out that flowering pattern of different infected *Silene* species infected by *Microbotryum* is manipulated by the fungus.

Host preference and sorus location correlate with parasite phylogeny in the evolution of the genus *Microbotryum*

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Parasites often have very intimate associations with their respective host and both partners can influence the ecology and evolution of the other. *Microbotryum* is a fungal genus mainly known for being the causing agent of anther smut in Caryophyllaceae. Recurrently, monophyletic genera within the Caryophyllaceae have been colonized once, with subsequent radiation and specialization to many different host species. The host range of *Microbotryum* however is considerably larger than Caryophyllaceae and includes host species in many other plant genera and families. Additionally, other locations of sorus formation than anthers have evolved. In this study we present an updated phylogenetic approach using a denser sampling of species from different host families.

The questions of this study are: 1) What is the ancestral state of host genus parasitized by the genus *Microbotryum*? 2) What is the ancestral state of sorus location in the genus *Microbotryum*? 3) Are monophyletic clades of parasites found on monophyletic groups of hosts? Our results indicate and corroborate previous results that the ancestor of the genus evolved on Polygonaceae and that most likely it already formed its spores in inflorescences. As in the Caryophyllaceae, many monophyletic groups of hosts have been colonized once with subsequent radiation. These results will be discussed in the light of some life-history traits of hosts and parasites.

***Hyphodontia* s.l. (Hymenochaetales) – new combinations and new species**

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For a long time many new taxa were described in *Hyphodontia* that do not fit the original concept. Since the first phylogenetic tree (Larsson et al. 2006) was published, it is well-known that *Hyphodontia* s.l. consists of several different genera. Hjortstam and Ryvarden (e.g. 2009) started to define genera and combined many species new on morphological features.

The current study continues these efforts for a clearly understanding of this group.

7 genera (*Xylodon*, *Lyomyces*, *Hastodontia*, *Hyphodontia* s.s., *Kneiffiella*, *Lagarobasidium* and *Palifer*) with 118 species are accepted, 40 of them are new combined. A new phylogenetic tree is provided. It contains 12 sequences from species that have never been sequenced before, 7 of them are from holotype material.

Furthermore this study includes an investigation of *Hyphodontia* s.l. species from La Réunion Island (Mascarene archipelago, Indian Ocean). 10 well-known species and 13 new species are identified.

One of the new species, *Hyphodontia borbonica*, is already published. It is the first *Hyphodontia* s.s. species with a poroid hymenium (Riebesehl et al. 2015).

Hjortstam K, Ryvarden L (2009) A checklist of names in *Hyphodontia* sensu stricto – sensu lato and *Schizopora* with new combinations in *Lagarobasidium*, *Lyomyces*, *Kneiffiella*, *Schizopora*, and *Xylodon*. *Syn Fung* 26: 33-55

Larsson KH et al. (2006) Hymenochaetales: a molecular phylogeny for the hymenochaetoid clade. *Mycologia* 98(6): 926-936

Riebesehl J et al. (2015) *Hyphodontia borbonica*, a new species from La Réunion. *Mycol Progress* 14:

Monitoring der natürlichen Waldentwicklung im Nationalpark Schwarzwald

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Schlagworte: Monitoring, natürliche Waldentwicklung, Pilze, Nationalpark Schwarzwald, Prozessschutz

Mit diesem Beitrag möchten wir das naturwissenschaftliche Monitoringkonzept des Nationalparks Schwarzwald vor- und zur Diskussion stellen. Die Deutsche mykologische Tagung bietet dazu ein exzellentes Forum, da wir gerne zusammen mit verschiedenen Universitäten, Forschungsinstituten, aber auch Spezialisten die wichtigen wissenschaftlichen Fragen von heute, aber auch die von Morgen beantworten möchten. Das Monitoring Konzept ist hierfür eine der Grundlagen, die der Nationalpark Schwarzwald bietet.

Mithilfe der Inventur und deren periodische Wiederholung wird dokumentiert wie, sich das Gebiet durch den Prozessschutz „eine Spur wilder“ entwickelt. Neben der reinen Dokumentation der Veränderung, liegt der Schwerpunkt auf der Analyse von Habitat- und abiotischer Schutzfunktion der Waldlandschaft. Unser Ansatz ist sowohl skalen- als auch organismengruppen übergreifend. Die Waldstrukturentwicklung wird für das gesamte Gebiet mittels Fernerkundung erfasst, und abgestimmt mit anderen deutschen Nationalparks (z.B. NLP Berchtesgaden) analysiert. Kombiniert wird diese Landschaftsanalyse mit detaillierten feldökologischen Erfassungen.

Die Stratifizierung für die terrestrische Erfassung orientiert sich zum einen an den naturräumlichen Gegebenheiten der Mittelgebirgslandschaft und wird nach Regionalklima und geologischem Ausgangssubstrat in Anlehnung an die Forstliche Standortkartierung der FVA untergliedert. Zum anderen an Stichprobendesigns länger bestehender Nationalparke, z.B. ein Vergleich der Entwicklungen entlang der Höhengradienten (NLP Bayerischer Wald). Zur Lokalisierung der einzelnen Stichprobenpunkte innerhalb der Straten wird das permanente Stichprobennetz der Betriebsinventur (ForstBW) weitergenutzt. Diese Nutzung bestehender Infrastruktur wie auch die Anlehnung der Waldstrukturerfassung an die der Bannwälder Baden Württembergs (FVA) ermöglicht den Vergleich mit aktuellen und historischen Daten. Sonderstandorte, wie beispielsweise Kare und Blockhalden, werden mit zusätzlichen Punkten berücksichtigt. An den Aufnahmeflächen der Waldstruktur werden genestet die verschiedensten Organismengruppen (Gefäßpflanzen, Bryophyten, **Pilze** u. Flechten, Vertebraten und Invertebraten) erfasst was eine Analyse der Strukturentwicklung, und deren Einfluss auf und die Interaktion zwischen den funktionalen Gruppen des Ökosystems ermöglicht. Zusätzlich wird ein Einblick in die aktuell bekannte Pilz Diversität im NLP Schwarzwald gegeben und mit Hilfe einer Art-Areal Berechnung eine zu erwartende Diversität berechnet und diskutiert.

Mit dieser Vorstellung unserer Arbeit erhoffen wir uns neue Impulse und möchten gleichzeitig zu weiteren wissenschaftlichen Kooperationen einladen.

Selection of *Alnus glutinosa* for resistance against the causal agent of alder decline, *Phytophthora x alni*

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Alnus glutinosa (L.) Gaertn. is a common tree species of riparian ecosystems. In Europe it suffers a serious decline in various countries, including Germany since the 1990s. The causal agent is the fungus-like microorganism *Phytophthora × alni* ([Brasier & S.A. Kirk] Husson, Ioos & Marçais) which belongs to the oomycota and is a hybrid of the two less aggressive species *P. × multiformis* and *P. uniformis*. It causes tar spots at the stem basis and finally death of the plant. In Germany the use of plant protection against *Phytophthora* in natural stands is not authorised. Therefore the most promising approach to fight the pathogen is the selection of resistant trees.

Within a project funded by the German Agency of Renewable Resources resistant trees have been selected in the Oderbruch in northeastern Germany. These trees were survivors among infected trees and showed little (partial resistance) or no damage. *In vitro* cultures have been established directly from buds of adult trees and from seedlings of those trees. Establishment of *in vitro* cultures from seedlings proved to be more reliable but requires that the clones are being tested for resistance since the resistance is not inherited by all descendants of the original tree. In preliminary studies resistance was tested under greenhouse conditions on potted plants by applying 1 ml of zoospore suspension ($1-3 \times 10^5$ zoospores/ml) to the stem base. The zoospore suspensions are prepared from a selection of 14 isolates of *Phytophthora x alni* from the Oderbruch (single isolates or mixtures). The development of a standard method that can be used for the screening of the susceptibility of alder seedlings and *in vitro* propagated alders towards the alder *Phytophthoras* is in progress.

In addition progenies of 18 alder seed plantations have been tested in 2015. The seed plantations are situated mostly in the middle and western part of Germany. Only the progeny of the two stands close to the eastern border (Spreewald and Märkische Schweiz) have been affected by the *Phytophthora* isolates of the Oderbruch. Whether the close vicinity of the alder stands and the isolate origins is evidence for a locally expressed basic compatibility has to be confirmed by further resistant tests that are being performed in 2016. The ultimate goal of the project is the establishment of a seed plantation with resistant alder clones to support the reforestation of destroyed stands.