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(O-1) Mixed forest stands and biodiversity belowground: mycorrhizal infection and enzymatic activities

Claire Guerin^{1,2}, Sylvie Milin^{1,2}, Mark R. Bakker^{2,1}

¹ INRA, UMR 1391 ISPA, F-33140 Villenave d'Ornon, France

² Bordeaux Sciences Agro, UMR 1391 ISPA, F-33170 Gradignan, France

Phone: (+33) 5 57 12 25 2, fax: 25 15, e-mail: Mark.Bakker@bordeaux.inra.fr

We took advantage of a replicated block design with Pine (*Pinus pinaster*), Birch (*Betula pendula*) as pure stands, as 50% mixtures (half Pine, half Birch) and as 25 % mixtures (25% Pine, 25% Birch, 50% young oak of three different species) to investigate belowground functional diversity. Next to the two tree species, we included the dominant understory species Bracken (*Pteridium aquilinum*) and Molinia (*Molinia caerulea*). The fine root parameters considered were fine root length, number of apex (ectomycorrhizal or not over fungal morphotypes), fine root biomass and specific root length. Ectomycorrhizal infection was assessed on Pine and Birch roots without staining and endomycorrhizal infection on Bracken and Molinia using a staining method with black ink. The enzymatic activities measured were acid phosphomonoesterase (for P), urease (for N) and invertase (for C).

Results show a different root response of Birch and Pine to increased stand complexity. Birch root development decreases correlated with a decrease in stand density while its branching rate increased. The population of Pine root keeps a constant volume regardless of its density but seems to favour mycorrhizae that explore the soil at short distances when the stand complexity increases. In the understory, Molinia sees its root development increased in response to a more-varied tree cover, while Bracken is apparently not sensitive to this. Soil enzyme activities for C and N appear to be highest in stands of Birch in monoculture.

(O-2) Forest trees determine the composition of soil fungal and bacterial communities and drive their activity

Petr Baldrian¹, Lucia Žifčáková¹, Tomáš Větrovský¹, Jana Voříšková¹, Michaela Urbanová¹, Adina Chuang Howe², Rubén López-Mondéjar¹

¹*Laboratory of Environmental Microbiology, Institute of Microbiology of the ASCR, Prague, Czech Republic*

²*Michigan State University, East Lansing, USA*

Phone: +420 723770570, fax: +420 241062384, e-mail: baldrian@biomed.cas.cz

Trees are the dominant primary producers in forested ecosystems, responsible for the bulk of C fixation in forests and its allocation belowground. The production of litter as well as root exudates affects the community of microbial decomposers in forest soils, most importantly the decomposers and root-associated symbionts. We used microbial community analysis and shotgun metatranscriptomics to explore the differences in microbial communities among various trees and their activity throughout the year in a temperate forest where photosynthesis is limited to the vegetation season. Fungi were more specific to dominant tree species than bacteria both in the litter and soil when seven tree species were compared: 35-37% of dominant fungal taxa but only 0-3% of bacteria were restricted to 1 or 2 trees, while 15-45% of the fungi and 80% of the bacteria were associated to 6 or 7 trees (Urbanová et al. 2015). Fungi also highly contributed to the total microbial transcription in litter and soil. Proteobacteria, Acidobacteria and Actinobacteria were most transcriptionally active among bacteria. Notably, the share of fungal transcription decreased dramatically between summer and winter with the transcription of genes involved in mycorrhiza formation being most affected. In contrast, the relative activity of Acidobacteria increased in winter. The results show that the species composition of the forest stands largely affects the community composition and activity of forest soil microbes, in particular fungi.

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Urbanová M., Šnajdr J., Baldrian P. (2015) Composition of fungal and bacterial communities in forest litter and soil is largely determined by dominant trees. *Soil Biology and Biochemistry* in press, Doi:10.1016/j.soilbio.2015.02.011.

(O-3) Microbial biomass increases with tree species diversity in European forest soils

Monique Carnol*¹, Lander Baeten³, Bernard Bosman¹, Sandrine Malchair¹, Astrid Vanoppen², Hans De Wandeler², Bart Muys²

¹Laboratory of Plant and Microbial Ecology, University of Liège, Institute of Botany Bât. B22, Boulevard du Rectorat 27, 4000 Liège, Belgium, email: m.carnol@ulg.ac.be, phone: + 32 43663845

²Laboratory of Forestry, Ghent University, Geraardsbergsesteenweg 267, 9090 Melle-Gontrode, Belgium

³Division of Forest, KU Leuven, Nature and Landscape Celestijnenlaan 200 E, Box 2411, 3001 Leuven, Belgium

Increasing tree species diversity in forests might contribute to ecosystem-service maintenance, as well as to the reconciliation of regulating, provisioning and supporting services within the frame of multifunctional and sustainable forestry. Individual tree species influence biogeochemical cycling through element deposition (throughfall, litterfall), and through microbial activities in the soil. Yet, the influence of mixing tree species on these ecosystem processes is unclear, in particular concerning the microbial diversity and activity in soils.

Here we synthesize results from the Exploratory Platform of the FunDivEUROPE project (<http://www.fundiveurope.eu/>). This network of 209 comparative plots covering a tree diversity gradient of 1 to 5 tree species was established in existing mature forests in 6 European regions. These six focal regions represent a gradient of major European forest types from boreal to Mediterranean forests. We analysed the impact of tree species diversity and the role of other controlling factors on the metabolic diversity of soil bacteria (BIOLOG Ecoplate), soil microbial biomass (fumigation-extraction) and potential nitrification (shaken soil slurry) in the forest floor and the upper organo-mineral soil horizon.

Mean values of microbial biomass carbon ranged from 3264 (Italy) to 8717 (Finland) mg kg⁻¹ in the forest floor. Statistical models predict microbial biomass to increase in both horizons by 7-8% with each step increase in tree diversity. Increased proportion of conifers was linked to a decrease in the metabolic diversity of soil bacteria. These tree diversity effects could be linked to soil drivers, such as pH, total and labile carbon and nitrogen.

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(O-4) *Arthrobacter* survival in the holm-oak rhizosphere after a wildfire

A.J. Fernández-González, J.F. Cobo-Díaz, P.J. Villadas, N. Toro, **M. Fernández-López**

Genetics Ecology Group, Department of Soil Microbiology and Symbiotic Systems, Estación Experimental del Zaidín, CSIC, calle Profesor Albareda 1, E-18008 Granada.

Phone: 958181600 ext. 140, email: manuel.fernandez@eez.csic.es

Forest fires are one of the main factors reducing the taxonomic and functional diversity of soil microbial communities (Smith *et al.* 2008; Bárcenas-Moreno *et al.* 2011; Xiang *et al.* 2014). We have evaluated the microbial communities associated with holm-oaks 3 years after a forest fire, which occurred in 2005 in the Sierra Nevada National Park, Southeast Spain. This study has allowed us to understand the role of these rhizospheric communities in the forest recovery process and what are the key bacterial groups in that process. The Actinobacterial genera *Arthrobacter*, from the family *Micrococcaceae*, and *Blastococcus*, from the family *Geodermatophilaceae*, were the best bacteria adapted to the burnt soils and the genus *Bradyrhizobium*, from the phylum *Proteobacteria*, was the most negatively affected by fire.

The metabolic functions of the rhizospheric communities were analyzed by Illumina sequencing of 180 million of reads. These data allowed us to build a virtual pan-genome of the *Arthrobacter* genus. The study of the pan-genome lets us know what features allow it to better adapt to the conditions of a disturbed soil after a wildfire. In this case, the most abundant enzyme, among the gene sequences of the population of *Arthrobacter*, was a heme-peroxidase. Could this heme-peroxidase allow *Arthrobacter* to survive through the degradation of lignocellulosic compounds as alternative carbon source? Some *Arthrobacter* species have already shown this capacity (Brown *et al.* 2011).

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(O-5) Modeling ectomycorrhizal forest: A plant-microbe system perspective

Oskar Franklin¹, Torgny Näsholm², Peter Högberg², Mona N Högberg²

¹IIASA- International Institute for Applied Systems Analysis, A-2361 Laxenburg, Austria;

² Department of Forest Ecology and Management, Swedish University of Agricultural Sciences, SE-901 83 Umeå, Sweden

Phone: +432236807251, e-mail: franklin@iiasa.ac.at

Ectomycorrhizal symbiosis is omnipresent in boreal forests, where it is assumed to benefit plant growth. However, experiments show inconsistent benefits for plants, which calls for a re-evaluation of the presumed role of this symbiosis (Näsholm et al. 2013). We reconciled these inconsistencies by developing a model that demonstrates how mycorrhizal networking and market mechanisms shape the strategies of individual plants and fungi to promote symbiotic stability at the ecosystem level. In line with observations in field-scale isotope labeling experiments (Näsholm et al. 2013), the model explains why ectomycorrhizal symbiosis does not alleviate plant nitrogen limitation. Instead, market mechanisms may generate self-stabilization of the mycorrhizal strategy via nitrogen depletion feedback, even if plant growth is ultimately reduced. This feedback mechanism may maintain the strong nitrogen limitation ubiquitous in boreal forests (Franklin et al. 2014).

We also discuss how the market mechanisms delineated by this game-theoretic model can be approximated by simpler supply and demand based model of fungal N – tree C exchange. This would facilitate extension of the model and still retain the essence of the original model – individual fitness maximization and market competition. By complementing this model with soil N and C dynamics and additional soil organisms we can obtain full ecosystem framework that accounts for interaction adaptation of plants and the soil community adaptation under long-term environmental changes.

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(O-6) Soil microbial community changes at the windthrow plots in Tatra Mts. (Slovakia)

Erika Gomoryova, Peter Fleischer, Dusan Gomory

Technical University in Zvolen, Faculty of Forest Sciences, TG Masaryka 24, SK-960 53 Zvolen, Slovakia

Phone: +421 455 206 214, e-mail: gomoryova@tuzvo.sk

The study focused on the responses of soil microbiomes to different management regimes on disturbed windthrow areas. The study was performed at four research plots -- a/ reference plot with spruce stand not affected by windthrow; b/ windthrow plot with extracted fallen trees; c/ windthrow plot damaged by wildfire; d/ windthrow plot without extraction of fallen trees left for spontaneous succession. Soil samples were taken from the mineral A-horizon during the vegetation period since 2006 until now. In soil samples, standard physico-chemical characteristics and characteristics of microbial community (microbial biomass, basal respiration, SIR, N-mineralisation, richness and diversity of microbial functional groups based on Biolog assay) were determined. The results indicate a gradual recovery of microbial community at all windthrow plots. Although there are some differences in microbial activity between plots, it seems that the influence of mesoclimate on microbial communities is more important than the differences in microclimatic conditions due to management differences. Richness and diversity of microbial functional groups did not differ between plots, but they exhibited clear temporal shifts. Abundances of some microbial functional groups as measured by specific substrate utilisation also showed temporal trends: while the utilisation of α -cyclodextrin declined from year to year, the utilisation of other substrates (L-arginine, L-asparagine, D-mannitol, etc.) increased with time.

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(O-7) Soil microbial community and their role in ecosystem functioning

Paola Grenni¹, Martina Di Lenola¹, Anna Barra Caracciolo¹

¹*Water Research Institute, National Research Council of Italy*

Phone: +39 06 90672785, fax: +39 06 90672787, e-mail: grenni@irsa.cnr.it

Microbial communities are fundamental living components in soil and thanks to their enormous genetic pool, catabolic versatility and potential high tolerance to stress are the main factor responsible for soil ecosystem homeostatic capabilities. Soil fertility is regulated by microbial communities through decomposition of organic matter into nutrients readily available for plants, thus directly contributing to plant productivity. Microbial communities may also limit or promote plant growth in the rhizosphere. Conversely, plants can strongly influence microorganism activity and community composition in the vicinity of their roots. Finally, soil microorganisms can induce plant defence responses to aboveground pests and herbivores and aboveground interactions can feed back in a variety of ways to the biodiversity, abundance and activities of soil organisms.

Microorganisms are also able to degrade organic contaminants, including xenobiotics, thus restoring soil quality. Consequently, microbial activities and their related functions provide several regulation ecosystem services. Pollution and intensive cultivation of agricultural land may influence soil quality and productivity, but little is known of their effects on soil microbial communities, and consequent impacts on key soil functioning. To give an example, some microbial populations can degrade a contaminant, but this fact does not exclude other populations disappearing or been inhibited by it, with a consequent loss of some ecosystem functioning.

The relationships between microbial diversity, ecosystem stability, productivity and sustainability need to be considered and studied more thoroughly to develop a predictive understanding of response to environmental disruptions and improve knowledge about forest and tree crop management.

(O-8) ECM community in conifer stands on peat soils 12 years after wood ash treatment

Darta Klavina¹, Taina Pennanen², Talis Gaitnieks¹, Dagnija Lazdina¹, Andis Lazdins¹, Sannakajsa Velmala², Audrius Menkis³

¹ Latvian State Forest Research Institute "Silava", Rigas 111, Salaspils, LV-2169, Latvia. e-mail address: darta.klavina@silava.lv

² Natural Resources Institute Finland (Luke), Vantaa Research Centre, P.O. Box 18, 01301 Vantaa, Finland

³ Department of Forest Mycology and Plant Pathology, Uppsala BioCenter, Swedish University of Agricultural Sciences, P.O. Box 7026, SE-75007 Uppsala, Sweden

Utilization of wood ash and methods to increase forest productivity are topics of high interest. The aim of this study was to get more knowledge about fertilization effect on fine root status and mycorrhization in forest stands on deep peat soils. This experiment characterises case of extreme fertilization regime as applied wood ash dosages in sample plots were high (50 t / ha⁻¹) and strong fertilization effect was still present (soil pH in fertilized plots and control sites was 7.1 and 3.5, on average).

To evaluate fine root biomass, vitality (living / dead root ratio) and ectomycorrhizal (ECM) community we sampled fertilized and control plots of three close located conifer stands representing different forest types (63 samples, in total). ECM community was assessed by morphotyping and sequencing of fungal ITS region.

There was a tendency observed that fine root biomass was higher in fertilized plots of all forest types analysed. However, ratio of living fine roots in control sites of two forest types was higher than in fertilized sites. Analysis of ECM community resulted in 50 fungal species; only 8 ECM species were observed in both fertilized and control sites. Species richness and Shannon diversity index tend to be higher in fertilized sites than in control. Dominant species in fertilized sample plots were *Amphinema byssoides* (17.8%) and *Tuber cf. anniae* (12.2%) but in control plots - *Tylospora asterophora* (18.5%) and *Lactarius tabidus* (20.3%). Fungal genus *Tylospora*, *Lactarius* and *Russula* were much more common in control than in wood ash fertilized plots but *Amphynema*, *Tuber* and *Inocybe* - in fertilized plots.

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(O-9) Exploring the drivers of post-disturbance soil CO₂ efflux in the Austrian Alps

Mathias Mayer¹, Bradley Matthews¹, Hans Göransson¹, Boris Rewald¹, Klaus Katzensteiner¹,
Douglas Godbold¹

¹*Institute of Forest Ecology, Department of Forest and Soil Sciences, University of Natural Resources and Life Sciences – BOKU, Vienna, Austria*

Phone: 0043 47654 4143, e-mail: mathias.mayer@boku.ac.at

Forest disturbance plays a major role in the global carbon (C) cycle; the effects on soil CO₂ efflux (F_s) and related driving mechanisms in mountainous regions are however poorly documented. We therefore utilized a windthrow chronosequence in the Austrian Alps in order to explore disturbance impacts on soil C dynamics. A variety of different soil and plant parameters (e.g. C and N stocks, temperature, roots, ectomycorrhizal (EM) activity) together with F_s were measured during a campaign in 2013. Structural equation modelling was conducted in order to reveal direct and indirect mechanisms driving F_s . Beside temperature and moisture, it could be shown that the activity of trees was an important driver of F_s , both directly via root biomass and related EM activity and indirectly by influencing soil micro-climate. Furthermore, it was determined that quality rather than quantity of soil C stocks was influencing F_s . In addition to the results of this study, we would also like to present a follow-up project, within which an *in situ* manipulation experiment will begin this spring. Girdling, trenching, and clear cut treatments will be established in order to separate abiotic and biotic drivers of initial post-disturbance soil C processes. As well as receiving helpful feedback regarding the planned experiment, we hope that the meeting will open the door for collaboration with other research groups interested in utilizing such an experimental infrastructure.

(O-10) The tripartite interaction olive-*Pseudomonas fluorescens* PICF7-*Verticillium dahliae* as study system to unravel biocontrol performance of an endophytic bacterium and plant genetic responses to root colonization

Carmen Gómez-Lama Cabanás, M. Mercedes Maldonado-González, David Ruano-Rosa, Rafael Sesmero, Antonio Valverde-Corredor, **Jesús Mercado-Blanco**

Department of Crop Protection, Institute for Sustainable Agriculture (CSIC), Campus 'Alameda del Obispo' s/n, Apdo. 4084, 14080 Córdoba, Spain

Phone: +34 957 499261, fax: +34 957 499252, e-mail: jesus.mercado@ias.csic.es

One of our research lines focuses on biological control as a sustainable, environmentally-friendly measure to confront Verticillium wilt of olive (*Olea europaea* L.) (VWO), caused by the soil-borne fungus *Verticillium dahliae*, within an integrated disease management strategy. A number of *Pseudomonas* spp. strains, natural colonizers of olive roots, were shown as efficient biological control agents against VWO. Endophytic lifestyle in olive root tissues was demonstrated under different experimental conditions for one of the most promising strains, *Pseudomonas fluorescens* PICF7. Interestingly, root hairs were shown to play a key role in the endophytic colonization of root tissues by this rhizobacteria. Surface colonization of intact olive roots and endophytic establishment seem to be required for the effective control of VWO by strain PICF7. However, mechanism(s) underlying PICF7-mediated biocontrol of *V. dahliae* and endophytism remain poorly understood. Mutant analysis has revealed that bacterial traits such as siderophore pyoverdine production and swimming motility are involved neither in biocontrol performance nor in endophytic colonization. On the other hand, colonization of olive roots by PICF7 triggers a broad range of transcriptomic changes, mostly related to defense responses to different (a)biotic stresses at both local (roots) and systemic (stems) level. These responses, which seem to be delicately modulated along time, could explain (i) biocontrol effectiveness of strain PICF7 and (ii) how olive tissues recognize and 'tolerate' this bacterium as a non-hostile invader. Another research line is to explore olive roots as the source of culturable (endo)rhizobacteria with potential as biocontrol agents against different soil-borne pathogens.

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(O-11) The effects of afforestation on Collembola density and species number

Edda S. Oddsdottir¹, Arne Fjellberg², Asrun Elmarsdottir³, Gudmundur Halldorsson⁴, Bjarni D. Sigurdsson⁵

¹*Icelandic Forest Research, Mógilsá, IS-116 Reykjavík, Iceland*

²*Entomological Research, Tjømø, Norway*

³*The Icelandic Institute of Natural History, Urridaholtsstraeti 6-8, IS-212 Gardabaer, Iceland*

⁴*Soil Conservation Service of Iceland, Gunnarsholti, IS-851 Hella, Iceland.*

⁵*The Agricultural University of Iceland, Hvanneyri, IS-311 Borgarnesi, Iceland*

E-mail: edda@skogur.is

The effects of afforestation with different tree species on density and species number of Collembola in soil was studied. The study sites were unforested heathland (one site), three Sitka spruce forests (10, 44 and 45 year old), two pine forests (15 and 46 year old) and two old birch forests (grazed and ungrazed). All study sites were located at Skorradalur, West-Iceland. Five plots were selected at each site and 2 soil samples taken from each plot. Soil samples were immediately sealed, placed into plastic bags and transported to the laboratory for extracting soil arthropods. Animals were extracted from the soil samples by using the dry funnel method into 0.6% benzoic acid and Collembola were counted and identified to species.

The results shows that species number of Collembola increases as forests (birch, Sitka spruce or pine) gets older. Furthermore, afforestation increases the density of Collembola in soil in birch and Sitka spruce forests but no changes in density was detected in the pine forests. A Twinspan analysis showed that younger forests and unforested heathland differed in species composition from older forests. Furthermore, a DCA analysis showed that both density and number of species increased as light intensity on the forest floor decreased and ground vegetation cover declined.

There are several factors that influence the distribution of Collembola in soil, for example soil moisture, heat, pH and available nutrition. Fungal hyphae are important nutrition for Collembola and research have shown that fungal fruitbodies are more frequent in older forests, which may explain why density increases as forests grow older.

**(O-12) Ectomycorrhizal communities in managed oak forests in central Poland:
effect of chronosequence and host decline**

Marcin Pietras, Tomasz Leski, Maria Rudawska

Institute of Dendrology Polish Academy of Sciences, Parkowa 5, 62-035 Kórnik, Poland

Phone: +48-618170033, fax: +48-618170166, e-mail: mpietras@man.poznan.pl

Pedunculate oak (*Quercus robur* L.) and sessile oak (*Q. petraea* [Matt.] Liebl.) are a widespread species of ecological and economic importance in Europe. Both species are obligatorily associated with ectomycorrhizal fungi (EMF). Until now several papers describing EMF communities of pedunculate and/or sessile oaks in different ecosystems and site conditions has been published, but none of the previous studies has focused on comprehensive description of EMF communities from one distinctive region. Therefore the aim of this study is to present extensive data describing the fungal species richness and composition of oak forests.

Study sites were located in Krotoszyńskie Forests considered as the largest oak forests in Poland. Altogether 225 soil samples were taken from 19 study sites: stands in different age, various declining tree stage and nursery. Morphological assessment and molecular approach based on PCR and sequencing of the fungal ITS rDNA were performed to identify ectomycorrhizas.

One hundred and ten EMF taxa associated with oaks have been recorded. Generally *Cenococcum geophilum* and *Lactarius quietus* were the most frequent species, excluding nursery and regeneration stage sites. In nursery experiment first mycorrhizas of *Scleroderma verrucosum* were observed 40 days after acorns outplanting. Altogether 8 EMF taxa has been recorded during the first year of seedlings grown. Chronosequence study shown correlation between relative abundance of some group of fungi (*Russula* spp, *Lactarius* spp.) and age of trees. In declining stands lowest number of EMF species richness and highest abundance of *L. quietus* were noted for oaks with high defoliation level.

(O-13) The role of endophytic microbial community in Pine Wilt Disease: diversity and function of microbes

Diogo Neves Proença¹, Paula V. Morais^{1,2}

¹IMAR-CMA, University of Coimbra, Coimbra, Portugal

²Department of Life Sciences, FCTUC, University of Coimbra, Coimbra, Portugal

Phone: +351239824024, e-mail address: diogo.proenca@gmail.com

Pine wilt disease (PWD), a major illness of several *Pinus* species, native to North-America, has spread into Asia and recently into Europe. *Bursaphelenchus xylophilus*, the pinewood nematode (PWN), is considered the only causative agent of PWD. It has been proposed that PWD is a complex disease induced by both PWN and the bacteria it carries. This work aimed to assess the microbial community, within the host-plant and associated with the PWN, in order to elucidate the community structure and to understand roles of several bacteria involved. Cultivation and molecular (DGGE, Illumina) methods were used to assess the endophytic microbial community. Bacteria belonging to the class *Gammaproteobacteria* were the most abundant. DGGE profiles showed that the microbial community was diverse and variable within diseased pine trees. DGGE detected the presence of endophytes belonging to six additional classes when compared to cultivation methods. Furthermore, *Archaea* was found as part of the endophytic community by DGGE and Illumina. Bacteria carried by PWN of Portugal and USA were assessed (Proença et al., 2010;2014) and twenty-one strains showed 100% nematocidal activity towards PWN (Paiva et al., 2013). From these, *Serratia marcescens* A88copa13 produced a serine protease as the nematocidal key factor. The genome of two nematocidal bacterial strains, *Serratia* sp. M24T3 and *Pseudomonas* sp. M47T1, showed both genes involved in nematocidal activity and in plant growth promotion (Proença et al., 2012). In conclusion, considering the diversity of the nematode-associated bacteria and their physiological characteristics, we cannot suggest an active role of the bacteria in PWD.

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(O-14) Quantifying differential impacts of arbuscular and ectomycorrhizae on ecosystem carbon budget

N.A. Soudzilovskaia¹, J.H.C. Cornelissen¹, M.G.A. van der Heijden²; P.M. van Bodegom³

¹*Department of Ecological Sciences, VU University Amsterdam, De Boelelaan 1085, 1081 HV Amsterdam, The Netherlands*

²*Plant-Soil Interactions, Institute for Sustainability Sciences, Agroscope, 8046 Zürich, Switzerland*

³*Institute of Environmental Sciences, Leiden University, Einsteinweg 2, 2333 CC Leiden, The Netherlands*

Phone: +31 643051830, e-mail: n.soudzilovskaia@vu.nl

A significant fraction of soil carbon moves through arbuscular mycorrhizal (AM) and ectomycorrhizal (EM) associations. The impact of AM and EM on the soil carbon budget and carbon transformations is still poorly understood. Absence of global databases on abundance of mycorrhizal fungi in soil and plant roots retards research aimed to understand involvement of AM and EM into soil carbon transformation processes.

Using own data and published studies we have assembled currently world-largest database of plant species-per-site degrees root colonization by mycorrhizal fungi (Soudzilovskaia et al, 2015). The database features records for plant root colonization degrees by AM and EM (above 8000 records in total). Using this database, we quantified global patterns of the relationships between levels of plant root colonization intensity by AM and EM and environmental variables (Soudzilovskaia et al, 2015).

I will show how this data could be used to quantify mycorrhizal contribution to carbon cycling explicitly accounting for plant-associated and extraradical mycorrhizal mycelium abundance, and will discuss the novel method proposed therefore (Soudzilovskaia et al, in revision). Using this method we conducted, for the first time, a quantitative assessment of relative impacts of AM and EM on biomass carbon stocks in tundra ecosystems and showed how biomass carbon stocks and ratios of fungi-to-plant carbon allocation could change due to realistic vegetation shifts from AM to EM dominance via encroachment of the ectomycorrhizal shrub *Betula nana* L. Finally, I will discuss how the proposed method can be applied at various spatial scales from ecosystem to global.

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(O-15) Ectomycorrhizal and soil enzyme activity profiles at the tree line

Lixia Wang¹, Otgonsuren Burenjargal², Douglas Godbold¹

¹ *University of Natural Resources and Life Sciences, Vienna, peter Jordan strasse 82, 1190, Wien*

² *Mongolian University of Life Sciences, Zaisan 17024, mailing box 57, Khan-Uul district Ulaanbaatar*

Pone: 04336764337878, e-mail: lixia.wang@boku.ac.at

At a tree line site (1700m) and a lower elevation site (1100m) in the Austrian Alps, the ectomycorrhizal community structure was determined on *Picea abies* and *Pinus mugo*. The activity of a number of enzymes was determined on two of the dominant ectomycorrhizas for each tree species. In soil, the activity of a range of enzymes was determined from soil under the tree species and under *Rhododendron hirsutum*.

The ectomycorrhizal community structure differed between *Pinus mugo* and *Picea abies* at the higher elevation site, but also between the higher and lower elevation *Picea abies* sites. At the higher altitude *Picea abies* site, the ectomycorrhizal community was dominated by *Cortinarius* sp, whereas at the lower elevation site the community was dominated by *Russula*. In *Pinus mugo* the dominant species were *Amanita muscaria* and *Russula orchroleuca*.

In soil, the activity of the enzymes protease, exoglucanase, phenol oxidase, glucosidase, phosphatase, peroxidase were highest at the lower altitude *Picea abies* site. At the high altitude site, with the exception of phosphatase, the enzyme activities increased in the order *Picea abies* > *Pinus mugo* > *Rhododendron hirsutum*. In roots, the enzyme activities of β -glucosidase, N-acetyl- β -D-glucosaminidase, acid phosphatase, leucine aminopeptidase were higher in mycorrhizal root tips than non-mycorrhizal tips. Between ectomycorrhizal species, the activity of acid phosphatase, averaged for all species of mycorrhizas investigated, was higher in both tree species at the high elevation site, compared to *Picea abies* at the lower elevation. No clear relationship was shown between enzyme activity in the soil and that of the dominant ectomycorrhizal species, and also between the enzyme activity and rate of net nitrogen mineralization.

(O-16) Fungal community structure across treeline ecotone

Martina Vašutová, Magda Edwards-Jonášová, Martin Čermák, Pavel Cudlín

Global Change Research Centre, Academy of Science of the Czech Republic, Na Sádkách 7, 370 05
České Budějovice, Czech Republic

Phone: +420 387 775 631, e-mail: vasutova.m@czechglobe.cz

Treeline is an important ecotone of elevation gradient; it is expected to be significantly affected by climate change. Soil inhabiting fungi have an irreplaceable role in treeline ecosystems as plant symbionts and organic matter decomposers. In Krkonoše Mts., treeline is formed by spruce trees (*Picea abies*) that are gradually replaced by dwarf pine (*Pinus mugo*). Two elevation gradients of 4-5 plots in different vegetation types were established in each of three localities (from 1190-1278 m a.s.l. to 1349-1408 m a.s.l.). Species composition of soil fungi was estimated by 454 pyrosequencing in order to find out a pattern in fungal species diversity and fungal community structure across treeline ecotone.

The number of operational taxonomic units (OTU) per plot, which represent at least 0,5% of sequences, was 22 – 36. We did not find any relation between number of OTU and elevation gradient. *Tylospora fibrillosa*, *Russula ochroleuca* and *T. asterophora* were the dominant mycorrhizal species. *Cryptococcus terricola* and *Mortierella humilis* were the most dominant saprotrophs. Whereas occurrence of mycorrhizal species was mainly determined by elevation and tree height, saprotrophs were influenced by soil properties and vegetation structure (RDA analysis, CANOCO).

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(P-1) Earthworm colonisation of a landfill restored to woodland in East London

F.E. Ashwood^{1*}, K.R. Butt¹, K.J. Doick², E.I. Vanguelova²

¹*Earthworm Research Group, University of Central Lancashire, Preston, PR1 2HE, UK*

²*Forest Research, Alice Holt Lodge, Farnham, Surrey, GU10 4LH, UK*

^{1*}*E-mail: feashwood@uclan.ac.uk*

Earthworms play a crucial role in soil development and the cycling of essential plant nutrients and organic carbon, however much is still unknown about their community dynamics and potential for improving the delivery of soil ecosystem services on restored land. To promote soil development on restored sites, it is beneficial that the soil material provided on these sites is suitable for earthworm colonisation. This work presents the findings of an earthworm colonisation survey of a newly restored woodland on a former landfill site. We investigated the effects of soil physical quality, vegetation cover, and distance from the site boundary on earthworm community composition and population densities across the site. Surprisingly, the results show an even distribution of earthworms from the site boundary to over 20 m into the site within a year of site restoration; a distribution which observed natural colonisation rates cannot explain. Earthworm species richness and abundance is already higher at this site than at an adjoining 5 year old restored landfill site (7 species compared to 5 species, and 207 earthworms m² compared with 48 m²), which had a lower standard of restoration. We discuss the effect of soil compaction on earthworm species richness, abundance and behavioural adaptability in an area of the site which was significantly ($p < 0.05$) more compacted than surrounding areas. These findings indicate that a higher quality of soil material used during the restoration process has had a positive influence on soil biological quality, and likely provided a form of earthworm inoculation.

(P-2) Effect of the species composition of stand on the enzyme activity of forest soils

Ewa Błońska

*Department of Forest Soil, Faculty of Forestry, University of Agriculture in Krakow,
Al. 29-go Listopada 46, 31-425 Kraków*

Email: eblonska@ar.krakow.pl

The aim of the study was to assess how tree species affect the enzyme activity (dehydrogenases and urease) of forest soils. We investigated how the species composition of forest stand by the accumulation of specific substrates in soils for enzymatic reactions affected the catalytic efficiency of enzymes. In order to clarify the obtained results the enzymatic activity was confronted with selected physicochemical properties of the soils. Investigations were carried out in forested areas of Southern Poland. Three paired plots, each 12 m × 12 m, were established in homogeneous, mature (40–80 years) pine (*P. sylvestris*), oak (*Q. robur*), spruce (*P. abies*), beech (*F. sylvatica*) and hornbeam (*C. betulus*) forests. The enzymatic activity showed a variability in soils with different species composition. The highest activity was observed in soils under hornbeam trees. The enzymatic activity of soil was associated with the type of accumulated organic matter and the quality of organic matter expressed as the ratio C/N.

(P-3) Experimental investigation of the effects of forestry treatments on the forest site, regeneration, above- and belowground diversity

Gergely Boros, Bence Kovács, Péter Ódor

*Centre for Ecological Research, Institute of Ecology and Botany
2163 Vácrátót, Alkotmány u. 2-4, Hungary*

E-mail: boros.gergo@okologia.mta.hu

This experiment investigates the effect of different forest management practices on forest site conditions, regeneration and biodiversity. It is a collaborative research between MTA Centre for Ecological Research, Pílisi Parkerdő Company Limited, University of West Hungary and Institute for Soil Sciences and Agricultural Chemistry. The following treatments were carried out in a mature homogenous sessile oak – hornbeam forest using six replicates in a randomized complete block design: preparation cutting, gap creation, micro clear-cut, retention tree group within the clear-cut, control. Light, air temperature and humidity, soil temperature and moisture and topsoil conditions (pH, humus, nutritional constraint) will be measured during the experiment. The processes of natural vegetation (seedlings, herbs and bryophytes) just as above- and belowground invertebrate indicators (carabid beetles and enchytraeid worms) will be monitored in permanent quadrates. Before the treatments the original forest site and vegetation conditions were surveyed for one year (2014). The treatments were carried out in January-February 2015.

Concerning belowground diversity we focused to enchytraeid worms (Annelida, Oligochaeta) as an important decomposer group. We would like to observe the changes in their assemblages: as enchytraeids are determined mainly by soil conditions, the highest turn-over is considered in clear-cut and gap. The retention tree group can buffer the original assemblage for these small size Annelids. 3 quantitative soil samples are taken in every quadrate (90 samples) 2 times per year. Each mature enchytraeid individuals are identified till species level.

(P-4) The experiment of nitrogen addition and artificial drought in Scots pine stand: an effect on soil/litter fungal communities

Rasa Buozytė^{a,c}, Gražina Adamonytė^a, Reda Irėnaitė^a, Jonas Kasparavičius^a, Elena Klyukina^b, Ernestas Kutorga^b, Svetlana Markovskaja^a, Jurga Motiejūnaitė^a

^a *Institute of Botany, Nature Research Centre, Žaliųjų Ežerų str. 49, LT-08406 Vilnius, Lithuania*

^b *Faculty of Natural Sciences, Vilnius University, M.K.Čiurlionio str. 21/27, LT-03101 Vilnius, Lithuania*

^c *Institute of Forestry, Lithuanian Research Centre for Agriculture and Forestry, Liepų 1 str., Girionys, LT-53101 Kaunas distr., Lithuania*

Global climate change along with environment eutrophication may have important implications for coniferous forests, which are considered to be one of the most sensitive ecosystems to different deviations in climate conditions. Fungi are important part of forest ecosystem, and readily respond to the changes of various biotic and abiotic factors. The aim of present study was to investigate the lasting effects of nitrogen addition and of artificial drought on soil/litter fungi community structure and species composition.

The experiments of artificial drought and nitrogen addition were conducted in a 60-year-old Scots pine stand in central part of Lithuania from the spring in 2003 till late autumn in 2005 for drought treatment and till autumn in 2006 for nitrogen addition. Artificial drought was achieved by using the roof construction installed below forest canopy, and held permanently for the whole experimental period. Totally, 2200 kg N/ha was added during the experiment. The investigations of fungi were provided in 2008-2009, following the termination of experimental treatments.

Relationships between fungal community structure and environmental variables (plant species numbers and cover, bryophyte cover, soil and bark pH, tree mortality) were explored. Non-metric multidimension scaling revealed, that both treatments, the nitrogen application and artificial drought, had significant impact on soil/litter fungus species composition, especially on mycorrhizal basidiomycetes: numbers of species (based on fruitbodies) and ectomycorrhizal root tips decreased, and species composition was affected. The effect on soil/litter saprobic fungi was more obvious in species composition than in numbers.

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(P-5) Mineral nutrient turnover in young stands of birch in different forest growing condition and soil types

Mudrite Daugaviete¹, Andis Bardulis¹, Arta Bardule¹, Uldis Daugavietis¹

Latvian State Forest Research Institute „Silava”, Rigas street 111, Salaspils, LV2169, Latvia

Phone (mob.): +371 29154265, fax +371 67901359, e-mail: mudrite.daugaviete@silava.lv

Research data are summarized to understand mineral nutrient turnover in young stands of silver birch (*Betula pendula* Roth) in different forest growing condition and soil types: Aegopodiosa/ alluvial sod-gley soil (ASG); Hylocomiosa/ typical sod calcareous on heavy clay (TSC); Oxalidosa/sod-podzolic soil (SP); Cladinoso-callunosa and Myrtillosa/ typical podzolic sandy soil (TP).

Mineral substance turnover is determined by estimating the tree above- (stemwood, branches, foliage) and below-ground (stumps and roots) biomass volume, the mineral substance content in 0-40 cm deep layer of soil, and evaluating stand vitality. In young stands of birch in fertile soils (ASG, TSC and SP) the biomass components are distributed as follows: stemwood 51.8-59.5%; branches 9.8-12.4%; foliage 5.7-6.8%; stump wood and roots 25-30%. In lean soils (TP) the same indices are 32.3-41.8%, 18.2-24.2%, 13.2-16.1% and 26.8-27.4%, respectively.

The stand performance closely correlates with the basic nutrient (P, N, K, C, Mg) availability in forest soils. In lean TP soils the content of mineral nutrients is no higher than 20-48% of that in more fertile soils (ASG, TSC and SP).

In young stands of birch the uptake of mineral nutrients from 0-40 cm layer of soil for developing the above-ground biomass makes a fairly small proportion of the total: up to 4.8-6.2% for P; 4.9-12.2% for N; 1.1-4.1% for K; 11.6% for Ca; 0.8-7.7% for Mg; in leaner soils the same indices are P 0.1-0.4%, N 1-1.5%, K 0.2-0.6%, Ca 0,1-0.9%, Mg 0.1-0.8%, respectively.

(P-6) **Belowground variation of organic carbon concentrations and stocks in Romanian's forest soils**

Maria Dinca

Forest Research and Management Institute - I.C.A.S. Brasov, Romania

Phone: +040724012688, fax : +0402684133, e-mail: maria.dinca1@gmail.com

10027 soil samples were harvested from forest management plans database (FMP) for the period 2000-2008. The humus percentage was calculated on pedogenetical horizons, and the results were structured on soil types (following Romanian nomenclature, adopted from FAO) and standard depths (ex. 0-10 cm; 10-20 cm; 20-40 cm; >40cm), following European monitoring activity procedure. The organic C stock (t/ha) was also calculated on different depths (especially for depths up to 1 m and up to 30 cm) and soil types. A GIS map regarding the organic C repartition in Romania's forest soils mineral part was also created.

If the content of organic carbon is analyzed on standard depths, the richest soils are: Andosol, Entic podzol, Haplic podzol and Rendzic leptosol. However, based on the quantity of organic carbon stock (t C/ha) across the soil profile, the decreasing hierarchy is the following: Andosol (217 t/ha), Vertisol (187 t/ha), Entic podzol (176 t/ha) and Haplic podzol (167 t/ha). The average total amount of organic carbon (i.e. 137 t/ha) accumulated in Romania's mineral forest soils is comparable with the values obtained in other European areas similar from geographic and climatic point of view. The smallest quantities of organic carbon were accumulated in the following forest soil types: Solonetz, Solonchak and Chernozem, while the largest ones were retained for Andosol, Vertisol and Podzol. Moreover, with regard to geographic distribution, the biggest quantities of organic carbon seem to be accumulated in forest soils from volcanic mountains, whereas the smallest ones are in forest soils from plains.

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(P-7) Decomposition patterns of undisturbed, dead fine roots in temperate tree species in an experimental forest in southwest Poland

Marc Goebel^{1*}, Sarah E. Hobbie², Bartosz Bulaj³, Marcin Zadworny⁴, Joanna Mucha⁴, Lidia Trocha⁴, Kevin E Mueller⁵, Cindy Hall⁶, John Chorover⁷, Jacek Oleksyn^{4,6}, Peter B. Reich⁶, David M. Eissenstat¹

¹Department of Ecosystem Science and Management and Intercollege Graduate Degree Program in Ecology, Pennsylvania State University, University Park, PA, 16802, USA

²Department of Ecology, Evolution & Behavior, University of Minnesota, St. Paul, MN 55108, USA

⁴Polish Academy of Sciences, Institute of Dendrology, Parkowa 5, 62-035 Kórnik, Poland.

³Department of Silviculture, University of Life Sciences in Poznan, Poland

⁵USDA – ARS, 1701 Center Ave., Fort Collins, CO 80526

⁶Department of Forest Resources, University of Minnesota, St. Paul, MN 55108, USA

⁷Department of Soil, Water and Environmental Science, University of Arizona, Tucson, AZ 85721, USA

*Authors current address and for correspondence: Department of Natural Resources, Cornell University, Ithaca, NY, 14850, USA, phone: + 814 574 5035, fax: + 1 607-255-0349; email: mg567@cornell.edu

Through their death and decomposition, plant roots can contribute considerably to biogeochemical cycles. Initial decomposition rates of intact fine root tissues are affected by root anatomy and chemistry, as well as complex interactions with the soil matrix. Here we assessed soil and plant variables that might influence rates of fine root (< 1 mm) decomposition without disturbance of the root-soil matrix, trenching minirhizotron tubes in monoculture plots of 10 temperate tree species at a common garden in southwest Poland to identify for almost 3 years. Minirhizotrons were installed 5 years prior of the treatment. Artifacts common to root decomposition studies such as limited access of soil fauna, disturbance of the rhizosphere and large concentrations of root organic matter were thus avoided.

Severed roots disappeared faster if new root growth had occurred nearby. Persistence of severed roots increased with soil depth, while increasing soil microbial biomass carbon, labile soil carbon content and earthworms decreased severed-root persistence, as did soil porosity and percent clay content. Severed older roots of the two maple tree species had higher root persistence than severed younger roots. Persistence of dead roots was relatively long in this sandy, infertile soil, ranging from 320 to greater than 974 days among four temperate tree family classes. Besides root traits known to influence rates of root decomposition, like root C:N and root Ca, we found that several soil-related factors strongly influenced root persistence which generally remain unconsidered when using traditional root decomposition methods.

(P-8) **Stones create N:P heterogeneity by funnelling rain -
Does this provide nutritional niches for plants and soil microbes?**

Hans Göransson^{1†}, Peter J. Edwards¹, Kristel Perreijn¹, Rienk H. Smittenberg^{2¶},
Harry Olde Venterink^{1#}

¹*Institute of Integrative Biology, ETH Zurich, Universitätstrasse 16, 8092 Zurich, Switzerland.*

²*Geological Institute, ETH Zurich, Sonneggstrasse 5, 8092 Zurich, Switzerland.*

[†]*Present address: Institute of Forest Ecology, University of Natural Resources and Life Sciences (BOKU), Peter-Jordanstrasse 82, 1180, Vienna, Austria.*

[¶]*Present address: Department of Geological Sciences, Stockholm University, 10691 Stockholm, Sweden.*

[#]*Present address: Plant Biology and Nature Management, Vrije Universiteit Brussel, Pleinlaan 2, 1050 Brussels, Belgium.*

Phone: +43 1 476544140, fax: +43 1 476544129, e-mail: hans.goransson@boku.ac.at

Soil nutrient heterogeneity is a key factor affecting species co-existence and therefore the diversity of plant and soil microbial communities. We postulated that such heterogeneity arises not only through physical and biological processes in the soil, but also through aboveground processes when emergent rocks or stones divert precipitation and nutrients in it to their surroundings. To test this idea – which we called the ‘funnelling effect’ of such stones - we placed ion-exchange resin in small boxes beside stones, in open soil and in artificial funnels on a pristine glacial forefield site in Switzerland, and measured the amounts of NH_4^+ , NO_3^- , NO_2^- and PO_4^{3-} that were adsorbed. We obtained strong linear relationships between N adsorbed and rain-collecting area both for stones and funnels. Although the mean rain-collecting area of stones was only 0.02 m^2 , mean N adsorption was around 10 times higher within one cm of stones than further away. These elevated values are equivalent to a local input of $4.6 \text{ g N m}^{-2} \text{ y}^{-1}$, which is 5-10 times the critical N load for alpine grasslands. In contrast, P was not concentrated beside stones, so that N:P stoichiometry varied spatially. *Rumex scutatus* and *Agrostis gigantea* plants that rooted beside stones had significantly higher foliar N concentrations than those growing further away, but the two species showed differing responses in foliar P and N:P. This study clearly demonstrates that aboveground rain-funnelling structures can produce spatial heterogeneity in N supply, thereby creating a diversity of nutritional niches for plants and soil microbes.

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(P-9) Abundance of ectomycorrhizal exploration types of poplars from protected natural habitat to sites with unfavourable environmental conditions

Marina Katanić¹, Saša Orlović¹, Tine Grebenc², Hojka Kraigher²

¹*Institute of Lowland Forestry and Environment, Antona Čehova 13, 21000 Novi Sad, Serbia*

²*Slovenian Forestry Institute, Večna pot 2, 1000 Ljubljana, Slovenia*

Phone: +38121540382, +38121540385, e-mail: marinakatanic44@gmail.com

The aim of our research was to investigate relationship between abundance of ectomycorrhizal exploration types and different site conditions, management systems and environmental conditions (pollution). Four sites with poplars were selected. At „Nursery“ a white poplar clone multiplied *in vitro* was grown, site „Kovilj-Petrovaradin marshes“ is Special Nature Reserve and natural habitat of native white poplar, at site „Timok“, soil was contaminated with pyrite tailings, contained heavy metals and had a low pH, while at the fourth site „Antella“ poplar clone sensitive to ozone was treated with anti-ozonant or irrigated with water (Katanić, 2014; Katanić et al., 2014). Ectomycorrhiza was identified using morpho-anatomical and molecular tools and exploration types of ectomycorrhizae were distinguished based on the amount of emanating hyphae or presence and differentiation of rhizomorphs (Agerer, 2001).

Analysis revealed that on the site „Nursery“ dominated short distance exploration type (with up to 91,5%), while in „Kovilj-Petrovaradin marshes“ the most abundant was short distance exploration type with above 60% then medium distance exploration type with above 30%. On the site „Timok“ medium distance exploration type made up around 90% of all ectomycorrhizal roots. Abundance of exploration types on the site „Antella“ differed in the treatment with antiozonant in comparison with control. In control treated with water the most abundant exploration type was contact (about 50%), while in the treatment with antiozonant short distance exploration type dominated with 60%. Environmental conditions (pollution) could have an significant impact on abundance of ectomycorrhizal exploration types and related functioning of the poplars-related ecosystems.

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(P-10) Root-inhabiting fungi associated with invasive plants of Central Europe

Marta L. Majewska^{1*}, Janusz Błaszowski², Marcin Nobis¹, Agnieszka Nobis¹, Daria Łakomiec¹,
Paweł Czachura¹, Piotr Mleczko¹, Szymon Zubek¹

¹*Institute of Botany, Jagiellonian University, 27 Kopernika St., 31-501 Kraków, Poland*

²*Department of Ecology and Protection Environment, West Pomeranian University of Technology,
17 Słowackiego St., 71-434 Szczecin, Poland*

*E-mail: marta_majewska1@wp.pl

In view of recent reports of possible role of soil fungi in alien plant invasions, we examined 29 invasive plants (tree, shrub and herbaceous species) collected from different habitats (forests, shrubs, meadows and fallows) in southern Poland in respect of their fungal symbiont (arbuscular mycorrhizal fungi – AMF) and endophyte (dark septate endophytes - DSE and *Olpidium* spp.) associations. We determined mycorrhizal status, arbuscular mycorrhizal colonization rate, AM morphology and the presence of fungal endophytes in roots. We also analyzed AMF species composition and chemical properties of soils from under these plants. The arbuscular mycorrhizal (AM) association was recorded in 28 species. Only *Reynoutria japonica* was found to be non-mycorrhizal. The intensity of mycorrhizal colonization varied among species, ranging from 0.4% in *Erechtites hieracifolia* to 89.1% in *Ambrosia artemisiifolia*. The AM colonization pattern in 27 taxa was of the *Arum*-type alone, only *Eragrostis albensis* showed both *Arum* and *Paris* morphotypes. The mycelia of DSE were observed in 26 taxa, while sporangia of *Olpidium* spp. were found in the roots of 7. We found no statistically significant correlations between the fungal root colonization and soil chemical parameters. We also did not find statistically important relationships between AMF, DSE and *Olpidium* spp. colonization. Spores of 12 common and widely distributed around the world AMF (Glomeromycota) species and 3 unidentified species (morphotypes) were isolated from trap cultures established with soils from under the collected plants. The species most frequently found were *Claroideoglossum clariodeum*, *Funneliformis mosseae* and *Septoglossum constrictum*.

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(P-11) Organic matter decomposition in sitka spruce forest under natural soil warming gradient in Iceland

Edda S. Oddsdottir¹, Marja Maljanen², Joonas Maljanen, Bjarni D. Sigurdsson³

¹*Icelandic Forest Research, Mógilsá, IS-116 Reykjavík, Iceland*

²*University of Eastern Finland, FI-70211 Kuopio*

³*The Agricultural University of Iceland, Hvanneyri, IS-311 Borgarnesi, Iceland*

E-mail: edda@skogur.is

Following a major earthquake in 2008, a geothermal gradient was formed under a Sitka spruce (*Picea sitchensis*) plantation established in 1967. The soil temperatures at 10 cm depth increased between 0 and +50°C, causing the death of the trees located at the hottest spots. This area is now one of the three ecosystems in the international research project Forhot.

Three different methods of measuring decomposition rate were used in preliminary studies at the forest site, Litter bags containing dried sitka spruce needles (recalcitrant litter), TBI, or tea bag index were two different sorts of teabags were inserted into the ground. One sort represented easily decomposable litter but the other recalcitrant litter and Birch cellulose paper

The litter bags were incubated for one year period and bags were sampled throughout the year. The other two methods were incubated for 3 or 3.5 months over a growth period (summer time).

After incubation samples were dried and weighted. The weight was compared to the original weight (i.e. before incubated in the field) and the percentage of mass lost during the incubation time calculated.

All three methods showed increased mass loss as the soil temperature went up. However, there was a difference in the mass loss between the methods, with the green tea bags (easily decomposable) and the birch cellulose showing the highest mass loss. The sitka spruce needles in the litter bags decomposed slower than either tea bags or cellulose paper.

These results are only preliminary and further studies with litter bags containing sitka spruce needles and roots (to be incubated above- and belowground in the forest), litter bags containing grass litter (to be incubated in nearby grass-sites within the Forhot project) and tea bags (incubated in all ecosystems) are planned.

(P-12) Challenge in fine root modelling - separation of fine roots into functional compartments to improve ANAFORE forest model output

G. Deckmyn¹, P. Železnik², T. Grebenc², G. Berhongaray¹, J. Cortese², **Yasmine Piñuela Samaniego**^{2,3}, H. Kraigher²

¹ *Plant and Vegetation Ecology, University of Antwerp, Antwerpen, Belgium.*

² *Slovenian Forestry Institute, Večna pot 2, 1000 Ljubljana, Slovenia*

³ *Technical University of Madrid (UPM), Campus Ciudad Universitaria, Avenida de Ramiro de Maeztu s/n, 28040 Madrid, Spain*

Phone: +34 626 25 22 95, e-mail: yasmin.pinuela@hotmail.com

Fine roots and its associated mycorrhizas are major components of the forest carbon balance. The classification of fine roots is not well defined: the roots that are actually taking up the nutrients and water have a fast turnover rate, they are the narrowest and lowest order. The 1-2 mm fine roots have shown significantly turnover rates from mycorrhizae, several studies evidence relatively long life span.

Nevertheless, in many forest-related models, all fine roots are consider to uptake the water and the nutrients in the same way, with comparable short longevity. Besides of this, the difference between mycorrhiza and non-mycorrhiza woody part of fine roots are usually neglected in the models.

Part of forest model ANAFORE was modified: in the simulation of processes in forest soils, non-mycorrhized fine root part and mycorrhizal data was treated separately. To validate the importance of separation the fine root category into functional groups, data was obtained from selected broad leaves forest stand in Slovenia. The contribution to model output was concerning soil carbon and forest growth (GPP & NPP).

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(P-13) Ectomycorrhizal community structure of *Alnus glutinosa* at a saline site in central Poland

Dominika Thiem¹, Agnieszka Piernik², Katarzyna Hrynkiewicz^{1*}

¹*Department of Microbiology, Faculty of Biology and Environmental Protection, Nicolaus Copernicus University, Lwowska 1, PL-89-100 Toruń, Poland, e-mail: hrynk@umk.pl*

²*Chair of Geobotany and Landscape Planning, Faculty of Biology and Environmental Protection, Nicolaus Copernicus University, Lwowska 1, PL-89-100 Toruń, Poland*

High soil salinity is an abiotic factor that may have a negative impact on the growth and development of plants and associated microorganisms. Well-adapted symbiotic fungi can be fundamental for the growth and survival of the host plant in harsh soil conditions (Hrynkiewicz and Baum, 2012). Research into understanding negative impact of high soil salinity influence on ectomycorrhizal associations is on-going.

The main objective of this study was to determine the density and diversity of ectomycorrhizal fungi associated with *Alnus glutinosa* growing in saline soil (central Poland) in relation to changes in salt concentration and other soil parameters.

The EM density varied between 19% and 45% and was not correlated with salinity and pH. Analysis of ectomycorrhizal fungi revealed 3-8 different morphotypes per each test site. Tomentelloid fungi (family Thelephoraceae) were the most numerous group of EM symbionts with the highest levels of ectomycorrhizal colonisation.

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