

MICROSCALE COMPARISON OF AMF DIVERSITY OF NATIVE AND INVASIVE WOODY PLANTS

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The ca. 230 species of arbuscular mycorrhizal fungi (AMF) are associated with about 80% of land plant species in a mutualistic symbiosis. They are ubiquitous in terrestrial ecosystems and play an important role in nutrient cycling as well as reducing biotic and abiotic stress for plants and modifying interspecies interactions through differentially benefitting distinct plant species. Their importance in arid and semiarid environments - such as the Great Hungarian Plain, our study site - is high as they alleviate the adverse effects of these areas. Considering their omnipresence and the low taxonomic diversity compared to their host partners it is widely accepted that the AMF species are generalists i.e. associate with a broad spectrum of hosts. The question whether there exist specialists among the fungal species, thus seems relevant. This might be answered by comparing the AMF communities found in the roots of native and invasive plant species. In Tatárszentgyörgy, we collected tightly intertwined roots of the native *Juniperus communis* and the introduced *Ailanthus altissima*, both woody species. Partial LSU region of fungal nrDNA was amplified by PCR, using AMF-specific primers. The primers were chosen according to the results of a previous experiment where we tested the efficiency of 4 primer sets on an artificial AMF community. After cloning and sequencing we obtained 622 sequences which formed 69 groups at a 3% similarity threshold. Most of the sequences belonged to groups known only from environmental studies but some sequences could be assigned to described species such as *Glomus macrocarpum*, the type species for Glomeromycota and *Paraglomus majewskii* a recently described basal taxon of the phylum. Some groups were detected either in *Juniperus* or *Ailanthus* while others in both plant species, these were considered as generalist AMF.

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BIOINFORMATICS IN VIROLOGY

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Bioinformatics (nucleic acid and amino acid sequence analyses) dramatically speeded up the understanding the relations among viruses and the finding of novel viruses. Pure biological properties usually can not give enough quantitative data to measure and correctly interpret the exact difference of viruses, and consequently to understand their evolution and establish appropriate taxonomy. PCR can quickly supply sequences of potential viruses in samples, but without homology searches, it would not be possible to identify a virus or a possible contaminant. Excellent and quickly growing databases are available to make homology searches immediately. It is also advisable to build your own confidential database for homology search. Freely available programs can be used to visualize, interpret and compare the electrophoretograms of DNA sequencing, to assemble full viral genomes, to identify possible sequencing mistakes, to predict protein coding regions, to annotate the genomes, to identify genome variants and submit the sequences and their annotation (interpretation) to GenBank. Special programs can be applied to discover and locate homologous recombinations. Without identifying recombinations, phylogenetic calculations may yield incorrect conclusions for newly detected viruses. The results of bootstrap analyses should also be handled cautiously as they highly depend on the number of sequences and can exaggerate similarities. PCR primers can be designed with broad or narrow species specificity as needed for different applications. With available programs, even three dimensional structures can be predicted if homologous proteins had been structurally studied earlier. Besides these promising advantages of using bioinformatics, it is also easy to make big mistakes and draw bad conclusions if not proceeding correctly. An example is the simple pair wise comparison of full genomes of larger viruses instead of comparing the corresponding genes. The correct selection of the right phylogenetic calculations is highly debated, too. Applying “too sophisticated” phylogenetic calculations for very short sequences may cause surprising mistakes. Finally,

compounds. Among these, genomic regions harbouring the genes of the whole operon of these operons contains the genes of the whole operon of these operons which are responsible for the first key step in the pathway of sulfanilic acid induction disclosed proteins likely to be involved in transport. These results might indicate that the elements involved in transport and cleavage require additional iron transporting proteins. These observations. A localization study disclosed that the proteins were membrane associated. This might have a significant impact on the compound should be tightly linked processes. Further studies are required to determine if the interacting with either of these proteins are being involved in the complex is responsible for coupled uptake and conversion.

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MICROBIAL ABUNDANCE D DEGRADATION IN A CO

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In northern airports there is an intensive use of PG. Previous experiments revealed that the degradation of PG occurs at low temperatures when the snow melts, biochemical experiments was to study the role of the microorganisms. The experiments (column volume 170 ml, length 100 cm) were performed at the Airport, Oslo, Norway, from 30 to 70 cm depth in the snow. The flow rate was 0.5 pore volumes (PV) per day (0.5 ml/min). Effluent fractions were collected 3-5 times/day by peristaltic pumps. The effluent contained 27.0 mg/L $\text{CaSO}_4 \cdot 2\text{H}_2\text{O}$, and 1.6 mg/L KHCO_3 . The effluent had the following characteristics. The columns were treated by: S1 (10 mg/L PG). S3 were used as non-contaminated control. The redox potential. To monitor the abundance of total heterotrophic bacteria. have been used, beside the analysis of pH, electrical conductivity, metabolites, main anions, cations, iron and manganese. Microbial growth. microbes against various PG and FO levels. Microbial growth. concentration that can be available during the snow melt. abundance was realised with the enhanced pollution. Significant drop of the redox potential showed a fast adaptation to the changing environment. possible fast adaptation to the changing environment. concentration of 50 mg/L than FO, showing the degradation. degradation was realised in S4, S5 columns. The abundance. is a limit to microbial degradation, the initial dose of PG. abundant bacterial strains are needed in order to maintain the

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[1] B. Libisch, H.K. French, T. Hartnik, A. Anton, B. Biró (2012) Environ

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