

Research Project

Fungal community assembly and specific mycorrhizal association: Relating fungal and plant invasion in a field experiment

Third-party funded project

Project title Fungal community assembly and specific mycorrhizal association: Relating fungal and plant invasion in a field experiment

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The relations of many organisms to their environment and evolutionary relatives are experiencing unprecedented challenges with potentially far-reaching knock-on effects on the dynamics and functioning of whole ecosystems. This molecular ecological project aims to assess directly in the field the initial stages of community (re-) assembly in natural assemblages of members of the fungal phylum Glomeromycota after disturbance and forced large-scale dispersal. Most members of the Glomeromycota form arbuscular mycorrhizas, which, owing to assistance in mineral nutrient uptake and protection against pathogens, are both important for the ecological performance of individual plants as well as for the dynamics of whole plant communities. The goals of this project are to identify drivers of fungal community assembly and to explore whether controlled and selective association with only a subset of mycorrhizal fungal symbionts may contribute to plant invasiveness. Is it phylogenetic relatedness and thus shared traits that determine whether an immigrant can establish itself among members of an existing fungal assemblage? Do invasive plants selectively choose ruderal or competitive or even alien mycorrhizal fungi?

In a field experiment top soil samples will be reciprocally transferred between eight field sites, four in the North and four in the South of the Swiss Alps, and two each in grasslands with either an alkaline or acidic soil. After mechanical soil preparation and mixing, non-mycorrhized seedlings of a native mycorrhizal generalist host, and such of congeneric non-indigenous plant species, differing in invasive spreading, will be brought to the field. The mycorrhizal fungal assemblages that will colonise the roots of these bioassay plants will be studied after different exposure times by Titanium 454 pyrosequencing of group-specific PCR amplicons of a phylogenetic marker and indicators of specific functional traits. Both, phylogenetic relatedness and relative abundances of assemblage members will be compared statistically and analysed to find evidence for different mechanisms of community assembly, such as neutral assembly, environmental filtering, or complementary functional niche filling.

Management and efforts to manipulate the biodiversity of mycorrhizal fungi will immediately profit from knowing whether chance, abiotic and biotic factors, or the evolutionary history, or any combination of these decide about fungal establishment success among residents. Efforts to combat plant invasions may profit from information about possible specific selective partner choice and

refusal in mycorrhizas.

Keywords Above-belowground interaction, anthropogenic disturbance, invasion, community assembly, dispersal, environmental filtering, functional niche complementarity, limited similarity, phylogenetic & functional community structuring, deep amplicon pyrosequencing

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