



An L-system model for root system mycorrhization

Andrea Schnepf (1), Peter Schweiger (2), Jan Jansa (3), and Daniel Leitner (4)

(1) Forschungszentrum Jülich GmbH, IBG-3 Agrosphäre, Germany (a.schnepf@fz-juelich.de), (2) Bio Forschung Austria, Esslinger Hauptstrasse 132-134, 1220 Vienna, Austria, (3) Institute of Microbiology, Academy of Sciences of the Czech Republic, Vídeňská 1083, 14220 Praha, Czech Republic, (4) University of Vienna, Computational Science Center, A-1090 Vienna, Austria

Mineral phosphate fertilisers are a non-renewable resource; rock phosphate reserves are estimated to be depleted in 50 to 100 years. In order to prevent a severe phosphate crisis in the 21st century, there is a need to decrease agricultural inputs such as P fertilisers by making use of plant mechanisms that increase P acquisition efficiency. Most plants establish mycorrhizal symbiosis as an adaptation to increase/economize their P acquisition from the soil. However, there is a great functional diversity in P acquisition mechanisms among different fungal species that colonize the roots (Thonar et al. 2011), and the composition of mycorrhizal community is known to depend strongly on agricultural management practices. Thus, the agroecosystem management may substantially affect the mycorrhizal functioning and also the use of P fertilizers. To date, it is still difficult to quantify the potential input savings for the agricultural crops through manipulation of their symbiotic microbiome, mainly due to lack of mechanistic understanding of P uptake dynamics by the fungal hyphae. In a first attempt, Schnepf et al. (2008b) have used mathematical modelling to show on the single root scale how different fungal growth pattern influence root P uptake.

However, their approach was limited by the fact that it was restricted to the scale of a single root. The goal of this work is to advance the dynamic, three-dimensional root architecture model of Leitner et al. (2010) to include root system infection with arbuscular mycorrhizal fungi and growth of external mycelium.

The root system infection model assumes that there is an average probability of infection (primary infection), that the probability of infection of a new root segment immediately adjacent to an existing infection is much higher than the average (secondary infection), that infected root segments have entry points that are the link between internal and external mycelium, that only uninfected root segments are susceptible (since new infection can only be detected in previously uninfected root) and that there is a maximum percentage of overall root system infection. Growth of external mycelium is based on the model of Schnepf et al. (2008a) but translated into L-system form.

Different hypotheses about the effect of inoculum position (dispersed vs. localized) and about root system infection mechanisms can be tested with this model. This will help to quantify the role of the complex geometric structure of external mycelia in plant P acquisition and to gain mechanistic insights into whole-plant processes affected by mycorrhizal symbiosis.

Literature

Leitner, D., Klepsch, S., Bodner, G., Schnepf, A., 2010a. A dynamic root system growth model based on L-Systems. *Plant Soil* 332, 177-192.

Schnepf, A., Roose, T., Schweiger, P., 2008a. Growth model for arbuscular mycorrhizal fungi. *J R Soc Interface* 5, 773-784.

Schnepf, A., Roose, T., Schweiger, P., 2008b. Impact of growth and uptake patterns of arbuscular mycorrhizal fungi on plant phosphorus uptake - a modelling study. *Plant Soil* 312, 85-99.

Thonar C, Schnepf A, Frossard E, Roose T, Jansa J (2011) Traits related to differences in function among three arbuscular mycorrhizal fungi. *Plant and Soil* 339: 231-245.

Acknowledgements

This research was partly supported by the Austrian Science Fund FWF (Grant No.: V220-N13) and by an APART fellowship of the Austrian Academy of Sciences at the Computational Science Center, University of Vienna (to D.L.).