

Mycorrhiza and drought stress: membrane experiment

Hypothesis:

Mycorrhizal fungi reduce drought stress of regenerating seedlings through a functioning common mycorrhizal network. An interruption of this network increases drought stress.

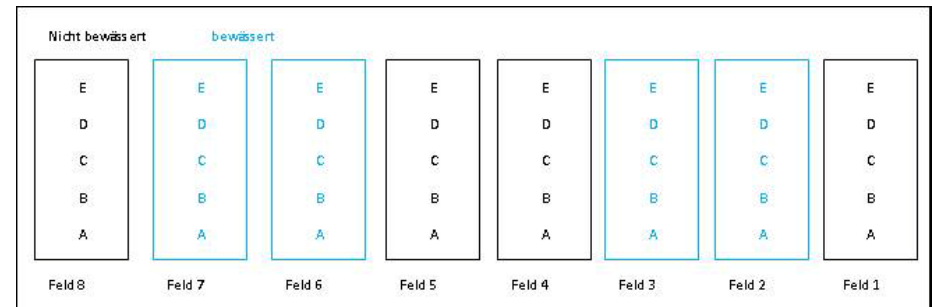
Treatments:

- (1) with 1 μ pore size membranes: impermeable to roots, impermeable to mycelium
- (2) with 51 μ pore size membranes: impermeable to roots, permeable to mycelium
- (3) control: without membrane: permeable to roots, permeable to mycelium

Start: 2011

1. Sampling: Oct 2012: 1 replicate per plot

Final Sampling: end of 2014



Fruitbody productivity and drought stress

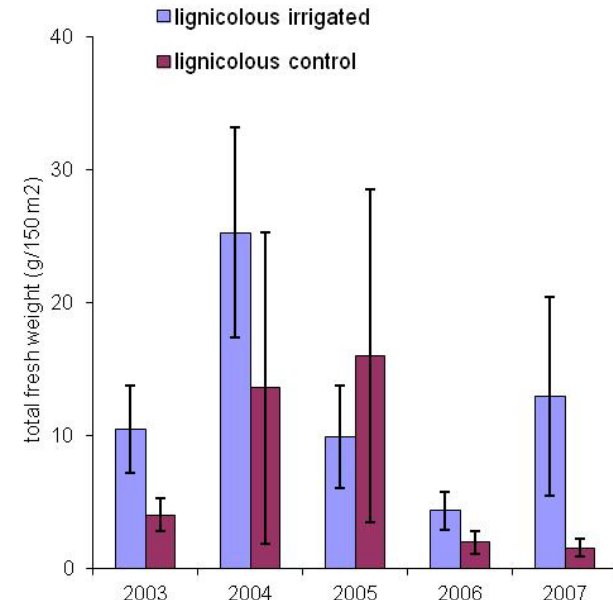
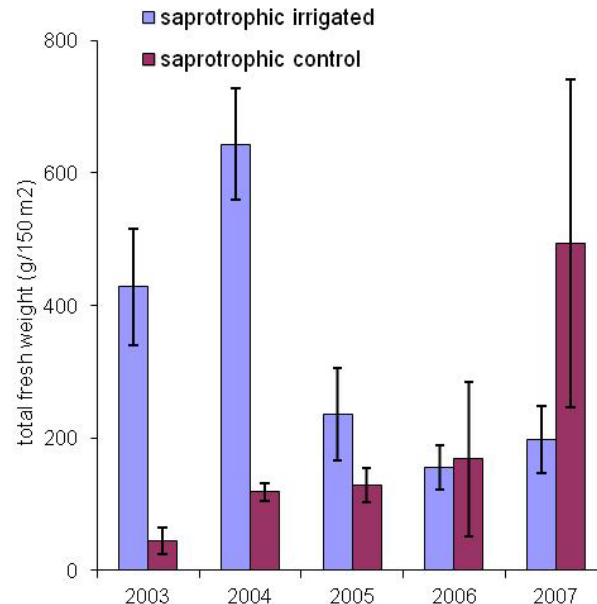
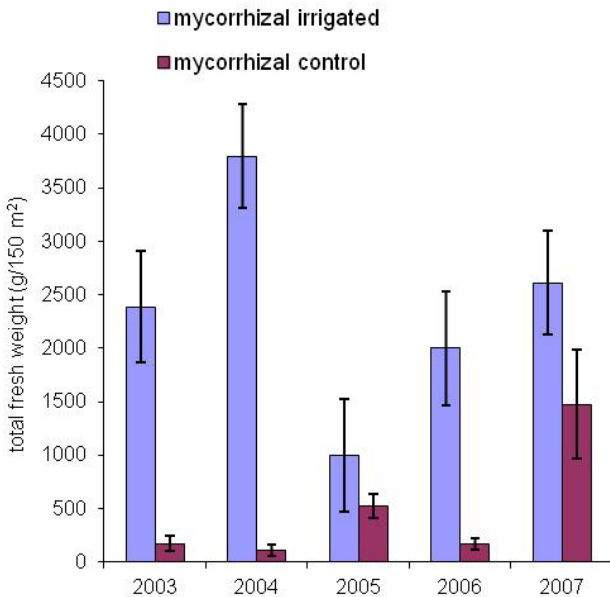
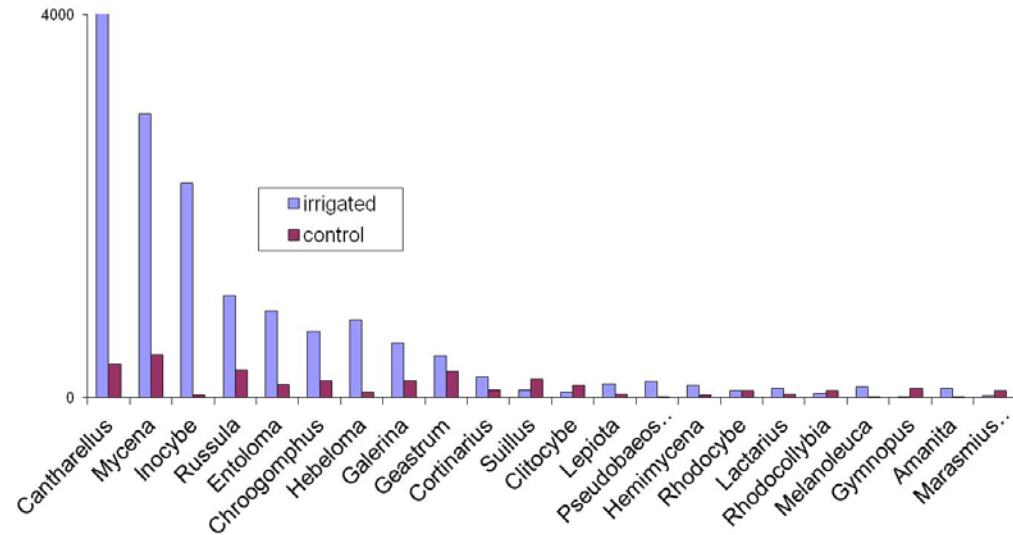
Hypothesis:

Irrigation increases fruitbody productivity and alters community composition

Methods:

All fruitbodies of macromycetes were counted and weighted weekly (weeks 21-52)

Start: 2003 / End: 2007



Mycorrhizal community and - functionality and drought stress

Hypothesis:

Drought stress (and season) changes the ectomycorrhizal (ECM) community and functionality

Methods:

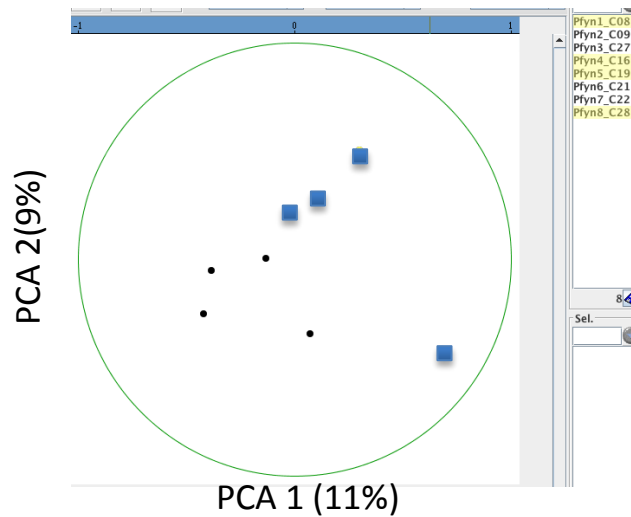
- (1) ECM community assessment at root tips (morphological and molecular)
- (2) ECM root tip counting
- (3) Total fungal community assessment in soil by pyrosequencing
- (4) Functionality: analyses of potential enzyme activities at ECM root tips

Samplings:

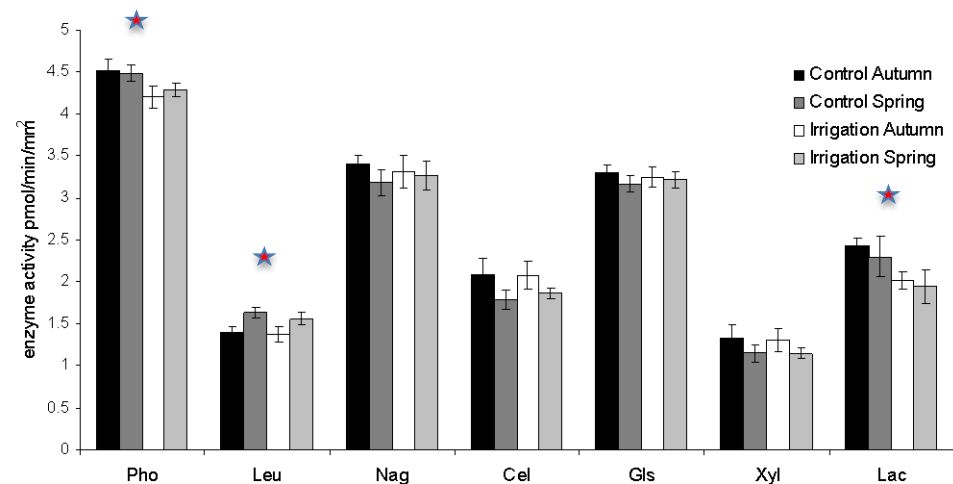
Autumn 2007-spring 2009

(ev repeated in 2014/15 ECM community and SOIL enzyme activities)

Fungal community:



Enzyme activities:



Population structure and gene expression of the ECM *Cenococcum geophilum* and drought stress (Evoltree)

Hypothesis:

Drought stress and tree host genetics changes the genetic and functional structure of *C. geophilum*

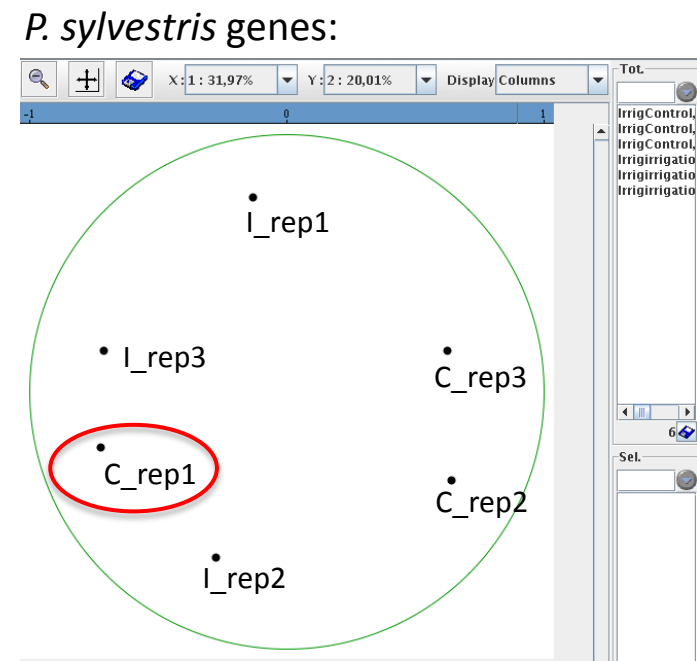
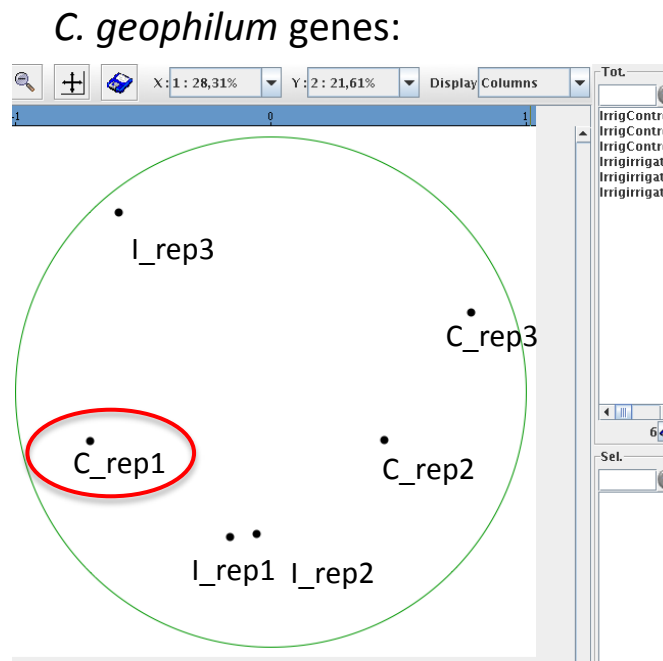
Methods:

- (1) Tree-specific assessment of *C. geophilum* population structure at root-tips (SSRs)
- (2) Analysis of gene expression in *C. geophilum* mycorrhizas (Microarrays)

Samplings:

Autumn 2008

6000 *C. geophilum* genes
7000 Scots pine genes



Future projects / samplings:

- ***Membrane experiment***

Final sampling end of 2014

- ***ECM/Fungal community***

Spring / autumn 2014 or 2015

- ***Fungal/microbial activity: soil enzyme activity analyses***

Spring / autumn 2014 or 2015

- ***Expression of selected genes (e.g., aquaporins) in ECM root tips of *C. geophilum* and other mycorrhizal fungi (qRT-PCR)***

Spring / autumn 2014 or 2015