Diversity Patterns of Arbuscular Mycorrhizal Fungi in Forest Understorey Plants

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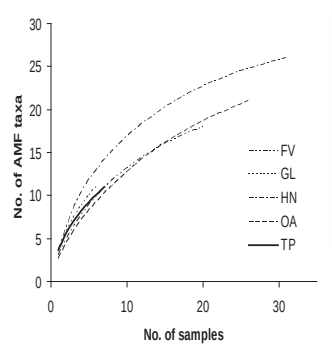
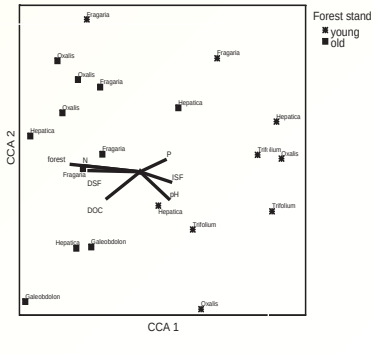
We studied richness and composition of arbuscular mycorrhizal (AM) fungal communities in a boreal herb rich coniferous forest in relation to the local environmental variables.

Roots of five plant species were studied: *Fragaria vesca*, *Galeobdolon luteum*, *Hepatica nobilis*, *Oxalis acetosella*, *Trifolium pratense.* The study site is located in Koeru, Central Estonia. Samples were collected from three sites located in intensively managed young forest stands and in three sites from less intensively managed old forest stands.

We measured the following explanatory variables: plant and moss cover, soil N, P, DOC, and light availability at 30 cm height. Indirect and direct site factors (ISF, DSF) - proportion of diffuse and direct radiation received below the tree canopy as a fraction of total irradiation - were calculated.

On average 3.1 AM fungal taxa were recorded per plant individual among *F. vesca*, *H. nobilis* and *O. acetosella*. The effect of plant species identity on AM fungal taxon richness per plant individual was marginally nonsignificant (GLM analysis, F = 2.832; df = 2, 67; P = 0.066). The average AM fungal taxon richness per *H. nobilis* individual (3.7 taxa) was significantly higher than that per *O. acetosella* individual (2.7 taxa; Tukey HSD test, P < 0.004).

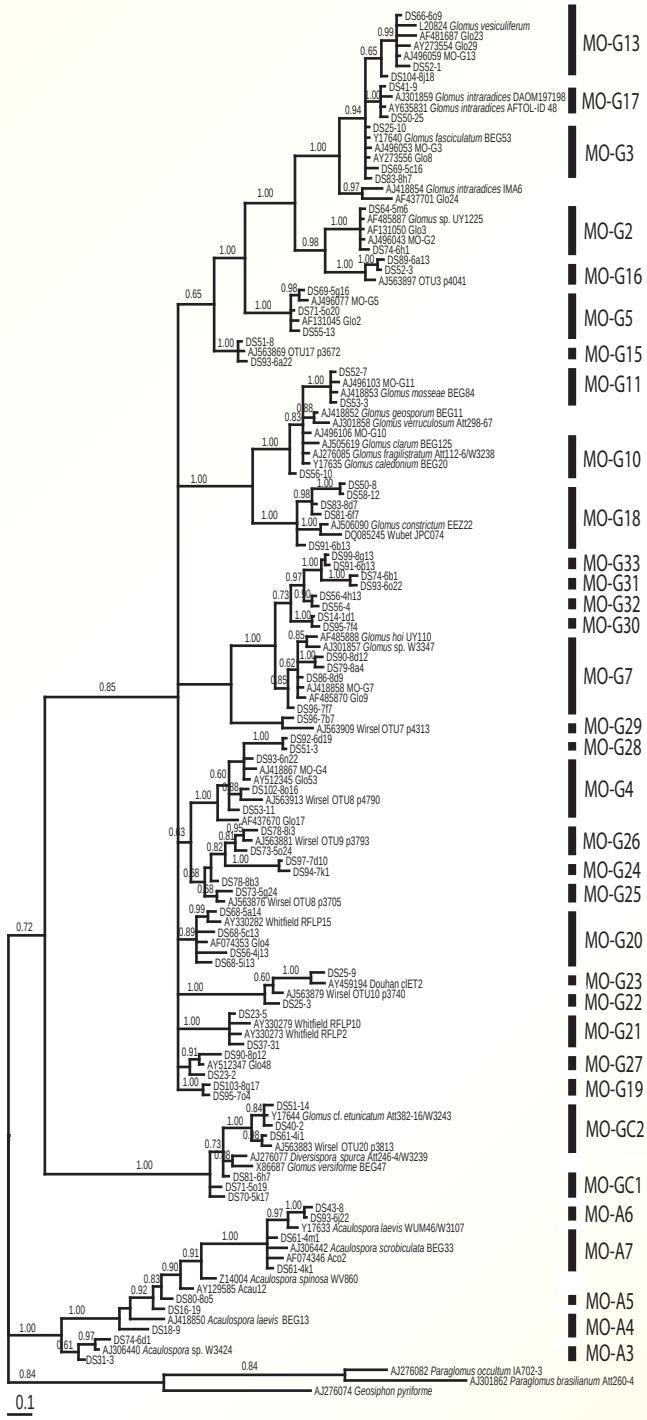




AM fungal taxon richness per 1x1 m subplot was positively dependent on plant species richness of the same subplot (multiple regression, F = 6.28, df = 1, 79, P = 0.014). Neither the measured light and soil parameters, nor the vascular plant and bryophyte cover correlated with the AM fungal richness per subplot.

Forest management type, light and soil conditions explained much of the variation observed in AM fungal taxon composition among samples from one plant species within one stand (Canonical Correspondence Analysis). The first three axes contributed 26.7 % of the total variation. The eigenvalue of CCA1 was significant (Monte Carlo test, P < 0.04). DSF, soil N and forest age explained the majority of the variation in taxon composition (Monte Carlo test, P < 0.01, inter-set correlations 0.62, 0.67 and 0.83). AM fungal community composition did not differ clearly in relation to host plant species.

The observed unexpectedly high richness of Glomeromycota in a temperate coniferous forest indicates the need to obtain descriptive soil fungal community data from a more diverse range of ecosystems. This almost unique richness of Glomeromycota could be speculatively attributed to the relative stability of the ecosystem and/or a rather wide range of host species. Described taxon composition and richness patterns deserve further evaluation in order to establish the role of host plant identity, plant species richness, light availability, and soil conditions as determinants of Glomeromycota taxon distribution at a small scale.



34 Glomeromycota taxa (SSU rDNA sequence groups) were detected in 90 root samples: bayesian analysis with GTR+G+I model implemented in TOPALi including known species and environmental taxa from sequence databases.

Number of clones of AM fungal taxa detected in studied plant species in old and young forest stand types in the order of frequency of occurrence.

Plant sp.	G3	G13	G7	G4	G5	G20	G33	G18	G2	G21	G27	G17	A5	G30	G15	G26	G28	A6	A7	GC1	GC2	G16	A3	G24	G25	G31	G22	G10	G19	G32	A4	G11	G23	G29	total
old stand																																			
FV	57	21	0	6	20	2	0	16	0	7	0	5	0	0	1	0	1	1	0	2	2	0	0	1	0	0	0	0	0	0	0	0	0	0	**142**
GL	19	14	8	4	15	8	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	2	0	2	0	1	0	0	**75**
HN	30	9	36	9	4	8	5	5	1	0	0	0	9	0	3	3	1	0	0	1	0	3	2	0	1	1	0	0	0	0	0	0	0	0	**131**
OA	21	19	12	3	15	6	0	4	20	4	0	0	0	0	2	5	0	0	5	2	1	0	0	0	3	0	0	0	0	0	0	0	0	0	**122**
total	**127**	**63**	**56**	**22**	**54**	**24**	**5**	**25**	**21**	**11**	**0**	**5**	**9**	**0**	**6**	**8**	**3**	**1**	**5**	**5**	**3**	**4**	**2**	**1**	**4**	**1**	**0**	**2**	**0**	**2**	**0**	**1**	**0**	**0**	**470**
young stand																																			
FV	32	28	8	0	0	1	0	0	0	2	0	0	1	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	**77**
HN	31	20	26	20	0	16	18	2	2	1	11	0	2	8	4	0	3	4	0	0	2	1	1	3	0	2	0	0	2	0	0	0	0	1	**180**
OA	59	25	13	9	0	2	1	0	0	1	3	6	0	0	0	0	1	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	1	0	**124**
TP	25	15	5	3	0	2	4	0	1	0	1	2	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	**60**
total	**147**	**88**	**52**	**32**	**0**	**21**	**23**	**2**	**3**	**4**	**15**	**8**	**3**	**12**	**4**	**0**	**4**	**4**	**0**	**0**	**2**	**1**	**2**	**3**	**0**	**3**	**3**	**0**	**2**	**0**	**1**	**0**	**1**	**1**	**441**
total	**274**	**151**	**108**	**54**	**54**	**45**	**28**	**27**	**24**	**15**	**15**	**13**	**12**	**12**	**10**	**8**	**7**	**5**	**5**	**5**	**5**	**5**	**4**	**4**	**4**	**4**	**3**	**2**	**2**	**2**	**1**	**1**	**1**	**1**	**911**