

infection with foliar pathogenic fungi does not alter the receptivity of Norway spruce seedlings to ectomycorrhizal fungi. Plant and Soil. Velmala¹, Rajala, Smolander, Petäistö, Lilja, Pennanen.

¹ Finnish Forest Research Institute – Metla, PO Box 18, 01301 Vantaa, Finland, sannakajsa.velmala@metla.fi

Electronic supplementary material, online resource 1

Table ESM1 Growth and origin information of Norway spruce (*Picea abies* (L.) Karst.) seed families used in the study Families 612, 298, 1162 represent fast-growing seedlings and families 1183, 394 and 427 slow-growing seedlings. The seed orchard seeds, s1002, are presented only as a reference; therefore, these seedlings are omitted from the mean values calculated for the fast- and slow-growing seedlings. The information of these spruce plus trees is archived in the forest genetic register maintained at the Finnish Forest Research Institute. Growth performance is assessed from 14 yr old trees from 7 to 10 experimental fields. The seedling information overlaps with Velmala *et al.* 2014, New Phytol 201: 610–622.

Growth performance in field	Grouping	Code	Origin and collection year
excellent	Fast	612	Loppi E 5519 x Schielbach ^a E4309, 1998
good	Fast	298	Pöytyä E 239 x Mynämäki E1515, 2000
excellent	Fast	1162	Lammi E 46 x seed orchard Kangasniemi ^b , 1989
poor	Slow	1183	Janakkala E217 x seed orchard Kangasniemi ^b , 1989
poor	Slow	394	Läyliäinen E 7133 x Natural forest ^b , 1983
poor	Slow	427	Loppi E 5514 x seed orchard ^b , 1983
normal	-	s1002	seed orchard Kangasniemi ^b , 1989

a: Germany, b: open pollination, E southern origin (south of the 62nd parallel north)

Table ESM2 Description and ISDN sequence accession numbers of fungal species inhabiting roots and needles of Norway spruce (*Picea abies* (L.) Karst.) seedlings Identification of OTUs is based on BLAST search from the UNITE and INSD databases. OTUs classified as ectomycorrhizal fungi (EMF) included in the NMDS ordination *

Accession number	Classification	Phylum	Potential name UNITE +INSD	Identity	Sequence length bp
KJ909938	Soil fungi	Zygomycota	<i>Mortierella</i> sp.	224 / 225 (99%)	226
KJ909939	Soil fungi	Basidiomycota	<i>Trichosporon porosum</i>	193 / 195 (98%)	200
KJ909940	Soil fungi	Basidiomycota	Uncultured fungus/Cryptococcus	223 / 225 (99%)	224
KJ909941	EMF	Basidiomycota	<i>Amphinema</i> sp.*	221 / 222 (99%)	224
KJ909942	Fungi associated to ECM root tips	Ascomycota	<i>Archaeorhizomyces</i>	170 / 171 (99%)	200
KJ909943	EMF	Basidiomycota	<i>Tylospora asterophora</i> *	241 / 241 (100%)	247
KJ909944	Soil fungi	Ascomycota	<i>Ilyonectria radicola</i>	210 / 210 (100%)	210
KJ909945	EMF	Basidiomycota	<i>Piloderma</i> sp.*	270 / 272 (99%)	272
KJ909946	Fungi associated to ECM root tips	Ascomycota	uncultured fungus	243 / 244 (99%)	246
KJ909947	EMF	Basidiomycota	<i>Piloderma sphaerosporum</i> *	246 / 246 (100%)	247
KJ909948	EMF	Basidiomycota	<i>Amphinema byssoides</i> *	220 / 220 (100%)	220
KJ909949	Fungi associated to ECM root tips	Ascomycota	Uncultured ascomycota	180 / 182 (98%)	244
KJ909950	EMF	Ascomycota	uncultured ascomycotina from <i>Picea abies</i> ECM*	180 / 182 (98%)	200
KJ909951	EMF	Basidiomycota	<i>Thelephora terrestris</i> *	210 / 210 (100%)	269
KJ909952	Fungi associated to ECM root tips	Ascomycota	<i>Phialocephala fortinii</i>	235 / 236 (99%)	236
KJ909953	EMF	Ascomycota	uncultured ascomycotina from <i>Picea abies</i> ECM*	181 / 183 (98%)	201
KJ909954	EMF	Ascomycota	<i>Cenococcum geophilum</i> *	294 / 294 (100%)	294
***	Soil fungi	Basidiomycota	<i>Fomitopsis</i> sp.	61 / 61 (100%)	176**
KJ909955	EMF	Basidiomycota	<i>Lactarius rufus</i> *	198 / 198 (100%)	200
KJ909956	Foliar pathogen	Ascomycota	<i>Gibberella avenacea</i>	213 / 213 (100%)	213
KJ909957	Foliar pathogen	Ascomycota	<i>Botryotinia fuckeliana</i>	243 / 243 (100%)	245

** sequences less than 200 bp, do not gain an ISBN accession number

***CGTAGGTGACCTGCGGAGGATCATTACTGAACACACGAAGGGTTGCTGCTGGCCTCTGGGCATGTGCACACCCGGACTGATCTTCACACACTACAATGTATATGAACGGTATTGCAAGCATTAAATACAACCTTCAGCAACGGATCTCTTGCTCTCGCATCGATGAAGAACGCA

Table ESM3 The effects of foliar treatment and growth performance group on growth, root characteristics and ectomycorrhizal fungal communities of Norway spruce seedlings. Results are based on general and generalised linear mixed models with foliar treatment and growth group and their interaction as explanatory variables and seed origin as a random. Statistically significant *P*-values are bolded.

Trait	Explanatory variable	Df	SS	MS	F	Denom	P
General Mixed Models, <i>lmer</i>							
Shoot (g)	treatment	2	0.370	0.185	4.378	118	0.015
	group	1	0.077	0.077	1.813	3.999	0.249
Root (g)	treatment	2	0.197	0.099	10.34	118	<0.001
	group	1	0.033	0.033	3.419	3.996	0.138
Shoot (mm) autumn	treatment	2	5083	2541	3.118	116.	0.048
	group	1	926	926	1.136	3.99	0.347
	interaction treatment x growth	2	5300	2650	3.251	116	0.042
Shoot (mm) following spring	treatment	2	962	481	0.487	154	0.616
	group	1	1924	1924	1.947	3.999	0.235
Short root density (tips/mm)	treatment	2	0.024	0.012	0.253	118	0.777
	group	1	0.152	0.152	3.219	3.998	0.147
Shoot:Root-ratio	treatment	2	7.523	3.762	9.332	122	<0.001
	group	1	0.139	0.139	0.346	122	0.558
Condensed tannins (mg/g d.w.)	treatment	2	3290	1645	1.404	118	0.250
	group	1	1691	1691	1.444	3.998	0.296
Generalized Mixed Models, <i>glmer</i>							
Root tip number (pcs)	treatment	2			7170		<0.001
	group	1			0.091		0.762
	interaction treatment x growth	2			419		<0.001
EMF OTU richness	treatment	2			1.431		0.489
	group	1			0.483		0.486
Total OTU richness	treatment	2			2.768		0.251
	group	1			3.384		0.066
Col%	treatment	2			0.427		0.808
	group	1			0.029		0.865
Needle damage autumn	treatment	2			75.014		<0.001
	group	1			0.012		0.932
Damage following spring	treatment	2			106.		<0.001
	group	1			4.610		0.032