

Supplementary Materials.

Table S1. Extracellular enzymes, their activities in soil and the two fluorometrically labelled assays (4-methylumbelliferone-MUF and 7-amino-4-methyl coumarin-AMC) containing substrates used in the present analysis.

Enzyme	Target compound	Catalytic activity	Substrates for analysis
Cellobiohydrolase	Cellulose	Hydrolysis of β -1,4 glycosidic bonds in cellulose.	MUF-Cellobioside
β -Glucuronidase	Cellulose	Hydrolysis of β -O-linkages to release D-glucuronic acid	MUF-glucuronide
β -Glucosidase	Cellulose	Hydrolysis of β -D-glucopyranosides at final stage of degradation of cellulose.	MUF-glucoside
β -Xylosidase	Hemicellulose	Hydrolysis of short xylooligomers into single xylose units.	MUF-Xyloside
Laccase	Lignin	Oxidation of phenols in lignin	ABTS
<i>N</i> -acetyl- β -D-glucosaminidase	Chitin	Hydrolysis of chito-oligosacchride into <i>N</i> -acetylglucose amine.	MUF- <i>N</i> -Acetyl-glucosamine
Leucine-aminopeptidase	Proteins and peptides	Release of N-terminal amino acids from polypeptides and proteins.	Leucine-AMC
Acid phosphatase	Phospholipids, inositol phosphate and other organic P compounds	Hydrolysis of ester-phosphate bonds.	MUF-phosphate

Table S2. Identification of ectomycorrhizal taxa associated with *Picea abies* at tree line (1668 to 1791 m). Identification used morphotyping (Agerer 1987–1998) and sequencing of the internal transcribed spacer (ITS) rDNA followed by a BLASTN search in the NCBI and UNITE GenBank DNA database. Taxa identities are based on CodonCode Aligner of the sequences and their first three best matches at the $\geq 95\%$ threshold. Unknown two failed to amplify

Accession	Closest Genbank/Unite Match	Accession	Coverage (%)	Similarity (%)
MF784606	<i>Thelephoraceae</i>	FN669271	99.7%	98%
	<i>Thelephoraceae</i>	UDB025952	99.7%	99%
	<i>Thelephoraceae</i>	UDB005175	99.7%	99%
MF784607	<i>Russula xerampelina</i>	UDB018019	99.7%	99%
	<i>Russula xerampelina</i>	UDB011162	99.9%	99%
	<i>Russula xerampelina</i>	AF418632	99.9%	99%
MF784608	<i>Lactarius aurantiacus</i>	KF432974	99.7%	97%
	<i>Lactarius aurantiacus</i>	AF157412	99.7%	96%
	<i>Lactarius aurantiacus</i>	UDB000312	99.9%	96%
MF784609	<i>Amphinema byssoides</i>	JX907809	99.7%	97%
	<i>Amphinema byssoides</i>	UDB008252	99.7%	97%
	<i>Amphinema byssoides</i>	UDB008257	99.7%	97%
MF784610	Unknown 1	KY522913	99.7%	96%
	fungi	KY522932	99.0%	95%
	fungi	KP889395	98.0%	90%
MF784611	<i>Helotiales</i>	FM992985	99.4%	98%
	<i>Helotiales</i>	HQ211907	99.2%	96%
	<i>Helotiales</i>	HQ211853	99.4%	96%
MF784612	<i>Leotiomyces</i>	FJ152530.1	99.0%	99%
	Uncultured fungus	KP889511	99.0%	99%
	<i>Rhizoscyphus ericae</i>	JQ711893.1	99.0%	99%
MF784613	<i>Tylospora</i> sp	JQ711823.1	100%	99%
	Uncultured fungus	KF618042.1	100%	98%
	<i>Tylospora</i> sp	KM402949.1	98.0%	99%
MF893218	<i>Luellia</i> sp	KC966314	99.7%	99%
	<i>Luellia</i> sp	KF617416	99.7%	99%
	<i>Luellia</i> sp	GU328556	99.6%	98%

Table S3. β -glucosidase, Acid phosphatase, Cellobiohydrolase and β -xylosidase activity on root tips of 10 different ectomycorrhizal taxa of *Picea abies* at tree line (1668 to 1791 m). The activity is calculated on the basis of projected surface area. The roots were collected at Wasserberg in the central Alps, Austria on June 12th, 2016. Values show means \pm SE. Data points within a column not followed by the same letter are significantly different ($P \leq 0.05$) between taxon for each enzyme.

Ectomycorrhizal species	β -glucosidase (pmol mm ⁻² min ⁻¹)	Acid phosphatase (μ mol mm ⁻² min ⁻¹)	Cellobiohydrolase (pmol mm ⁻² min ⁻¹)	β -xylosidase (pmol mm ⁻² min ⁻¹)
<i>Thelephoraceae</i>	81.0 \pm 11.8 bc	77.7 \pm 16.9 c	21.3 \pm 2.9 cd	14.8 \pm 1.3 b
<i>Russula xerampelina</i>	36.6 \pm 3.9 c	347.9 \pm 37.3 a	1.7 \pm 0.1 e	7.4 \pm 1.9 b
<i>Lactarius aurantiacus</i>	85.9 \pm 8.6 abc	87.3 \pm 9.2 c	10.6 \pm 2.6 de	7.1 \pm 0.5 b
<i>Amphinema byssoides</i>	125.0 \pm 12.5 ab	153.6 \pm 23.0 b	54.4 \pm 2.2 a	24.8 \pm 1.5 ab
Unknown 1	77.3 \pm 10.6 bc	87.3 \pm 5.4 c	11.4 \pm 3.4 de	5.1 \pm 0.9 b
Unknown 2	60.6 \pm 4.0 c	113.1 \pm 5.6 bc	24.8 \pm 1.0 bcd	12.2 \pm 0.6 b
<i>Luellia</i> sp	79.4 \pm 12.6 bc	77.3 \pm 10.0 c	17.6 \pm 2.8 cde	9.3 \pm 1.4 b
<i>Helotiales</i>	118.3 \pm 7.3 ab	150.9 \pm 7.4 b	35.4 \pm 3.7 bc	8.7 \pm 1.1 b
<i>Leotiomyces</i>	42.6 \pm 1.5 c	94.8 \pm 2.0 c	14.9 \pm 1.3 de	11.3 \pm 1.3 b
<i>Tylospora</i> sp	138.3 \pm 45.7 a	85.4 \pm 24.6 c	40.8 \pm 16.9 ab	42.9 \pm 21.4 a



Figure S1. Images of the tree line site (1668 to 1791 m) at Wasserberg in the central Alps, Austria.

Left, a view across the site. Right, a typical soil profile.



Figure S2. Profile of ericoid mycorrhizal roots which collected from tree line (1668 to 1791 m) at Wasserberg in the central Alps, Austria in June 2016.

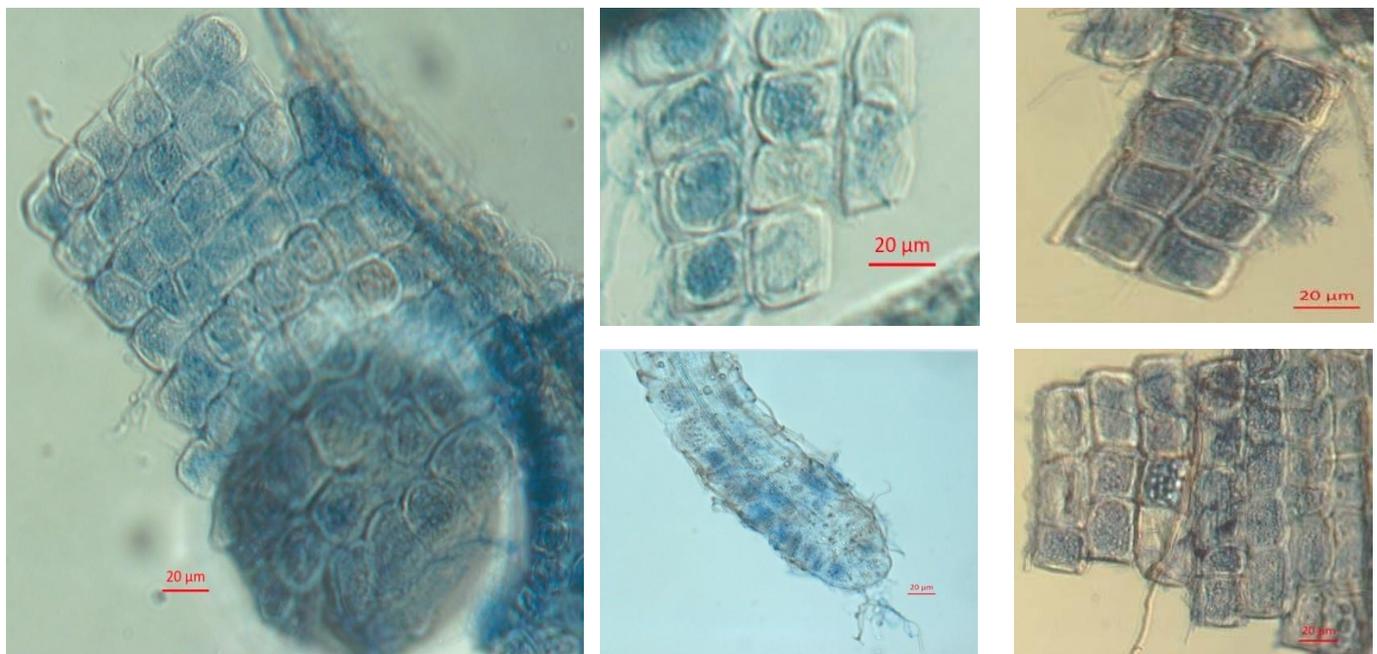


Figure S3. Ericoid mycorrhizal roots structure.