	Čepkelių Nature Reserve	Puszcza Drawska Forest	Puszcza Zielonka Forest	Czerniejewo Forest District	Białowieża Forest		
1 4	South Lithuania	West Poland	Central-West Poland	Central-West Poland	North-East Poland		
location	54°01'50.0" N	52°53'10.0" N	52°33'10.0" N	52°25'20.0" N	52°51'30.0" N		
	24°37'00.0" E	15°44'50.0" E	17°08'35.0" E	17°24'20.0" E	23°53'00.0" E		
climate	humid continental climate (Dfa, Köppen climate classification)						
vegetative cover							
biome	temperate broadleaf forest						
dominant form of vegetation	peatbog/pine forest	decidious forest	decidious forest	decidious forest	corniferous forest		
dominant plant	Scots pine	beech with hornbeam	oak	hornbeam	Norway spruce		
forest management	absent	present	present	present	present		

Table S1. Overview of geographical origin of used fungal material, including the information about vegetative cover.

		-					
	Stage	Temperature (°C)	Time (min)				
1	Initial denaturation	94	3				
2	Denaturation	94	1				
3	Alignment	56	1				
4	Synthesis	72	3				
Repeat steps 2-4, 35 X							
5	Final synthesis	72	10				
6	Hold	4	∞				
	Lid temperature: 105 °C						

Table S2. Used PCR protocol.

Table S3. Results of sequencing the PCR amplification products of the prepared ectomycorrhizal DNA isolates. The "Used sample" column refers to the sample used, with the first letter referring to the used morphotype, and roman numeral and second letter to the isolation and purification method used respectively. The red color marks samples from which sequencing was unsuccessful. The yellow color marks samples from which DNA of contaminating yeast was isolated. Reference sequences and species hypotheses were assigned in reference to the UNITE database.

Used sample		l e	Name	Reference Sequence	Species Hypothesis	BLAST Score	%
Α	IV	B	Debaryomyces hansenii	KY103269	SH190089.07FU	752	100
Α	V	B	Elaphomyces muricatus	EU784198	SH190236.07FU	953	99,62
Α	VI	B	Elaphomyces muricatus	EU784198	SH190236.07FU	968	99,4
Α	V	С	-	-	-	-	-
В	V	B	-	-	-	-	-
B	V	С	Pachyphloeus	UDB032978	SH631019.07FU	361	98,54
С	V	B	Genea hispidula	KJ938839	SH194536.07FU	835	99,78
С	V	С	Genea hispidula	KX168651	SH194536.07FU	344	100
D	V	B	Humaria	EU024888	SH179624.07FU	1011	99,46
E	V	B	Tuber puberulum	HM190013	SH216305.07FU	749	100
Ε	V	С	Tuber puberulum	HM190013	SH216305.07FU	723	99,75
F	IV	B	Amanita rubescens	FJ890031	SH221016.07FU	1061	99,83

F	V	B	Amanita rubescens	KX449422	SH221016.07FU	819	99,12
F	VI	B	Amanita rubescens	FJ890031	SH221016.07FU	1158	99,84
F	V	С	Amanita rubescens	UDB000038	SH221016.07FU	1129	100
G	V	Α	Cortinarius torvus	AJ889977	SH188541.07FU	640	99,71
G	IV	B	Cortinarius torvus	AJ889977	SH188541.07FU	917	99,6
G	V	B	Cortinarius torvus	AJ889977	SH188541.07FU	911	99,4
G	VI	B	Cortinarius torvus	AJ889977	SH188541.07FU	953	99,62
G	v	C	Cortinarius torvus	AJ889977	SH188541.07FU	667	98,16
Н	V	B	Laccaria amethystina	KX449421	SH220959.07FU	1170	100
н	V	С	Laccaria amethystina	KX449421	SH220959.07FU	963	99,81
Ι	III	B	Piloderma sphaerosporum	JQ711966	SH196824.07FU	941	99,81
Ι	IV	B	Piloderma sphaerosporum	JQ711966	SH196824.07FU	942	99,61
Ι	v	B	Piloderma sphaerosporum	JQ711966	SH196824.07FU	941	100
Ι	v	4	Piloderma sphaerosporum	JQ711966	SH196824.07FU	854	100
J	V	Α	Imleria badia	LN877746	SH216653.07FU	516	91,51
J	III	B	Imleria badia	HM190036	SH216653.07FU	1101	99,5
J	V	B	Imleria badia	HM190050	SH216653.07FU	1031	99,47
J	III	С	Imleria badia	HM190036	SH216653.07FU	928	97,78
J	v	С	Imleria badia	HM190036	SH216653.07FU	1092	99,83
К	III	B	Xerocomellus cisalpinus	HM190056	SH221249.07FU	1249	99,71
К	IV	B	Xerocomellus cisalpinus	HM190056	SH221249.07FU	1293	98,9
К	v	B	Xerocomellus cisalpinus	HM190056	SH221249.07FU	1131	98,43
K	V	C	Xerocomellus cisalpinus	HM190056	SH221249.07FU	1175	99,23
L	V	B	Paxillus involutus	UDB015588	SH210482.07FU	1210	98,83
Μ	III	B	Suillus variegatus	L54081	SH176741.07FU	688	100
Μ	IV	B	Suillus variegatus	L54081	SH176741.07FU	715	99
Μ	V	B	Suillus variegatus	L54081	SH176741.07FU	566	99,68
Μ	III	С	Suillus variegatus	L54081	SH176741.07FU	571	98,76
Μ	V	С	-	-	-	-	-
Ν	v	B	Craterellus cornucopioides	KX449405	SH181204.07FU	931	99,22
Ν	VI	B	Craterellus cornucopioides	KX449405	SH181204.07FU	1194	99,83
Ν	V	С	Craterellus cornucopioides	KX449405	SH181204.07FU	959	100
0	III	B	Clavulina coralloides	UDB031967	SH220213.07FU	702	98,26
0	V	B	Clavulina coralloides	AY292292	SH220213.07FU	808	100
0	VI	B	Clavulina coralloides	UDB031967	SH220213.07FU	974	98,9
0	III	С	Clavulina coralloides	EU862223	SH220213.07FU	706	99,23
0	V	С	Clavulina coralloides	AY292292	SH220213.07FU	926	96,92
Р	V	B	Lactarius aurantiacus	KP783446	SH182376.07FU	1092	98,24

Q	III	B	Russula nigricans	KM085390	SH219259.07FU	808	98,68
Q	v	B	Russula nigricans	KM085390	SH219259.07FU	849	99,78
Q	III	С	Russula nigricans	KM085390	SH219259.07FU	833	99,35
R	III	B	Envir: Tomentella	UDB027188	SH217498.07FU	972	99,44
R	v	B	Envir: Tomentella	UDB027188	SH217498.07FU	928	98,85
R	III	С	Envir: Tomentella	UDB027188	SH217498.07FU	952	100
R	v	С	Envir: Thelephoraceae	UDB017056	SH184514.07FU	828	97,72
S	v	Α	Tomentella	UDB014251	SH177961.07FU	1024	99,82
S	III	B	Tomentella	UDB014251	SH177961.07FU	974	99,44
S	IV	B	Tomentella	UDB014251	SH177961.07FU	987	99,81
S	v	B	Tomentella	UDB014251	SH177961.07FU	654	95,42
S	v	С	Tomentella	UDB014251	SH177961.07FU	915	99,4
Т	v	Α	Tomentella terrestris	UDB003315	SH189365.07FU	505	97,95
Τ	III	B	Tomentella	UDB016650	SH189365.07FU	874	98,98
Т	IV	B	Tomentella terrestris	UDB003315	SH189365.07FU	961	98,71
Т	v	B	Tomentella terrestris	UDB003315	SH189365.07FU	869	98,01
Т	VI	B	Tomentella	UDB016650	SH189365.07FU	1201	100
Τ	V	С	Tomentella terrestris	UDB003315	SH189365.07FU	875	98,59
Τ	VI	С	Tomentella terrestris	UDB003315	SH189365.07FU	979	99,08



Figure S1. Electrophoresis results: the columns were loaded with: (L) DNA ladder (peqGOLD 50 bp DNA-Ladder, PEQLAB); and (IA–VIC) PCR products prepared using respective isolation methodproduct as a reaction matrix; the gels (A–T) were prepared with samples from respective fungal taxa, as assigned in the table 1.

Cell lysis protocols:

- I. No lysis
 - 1. ECM root tips were placed in empty Eppendorf tubes; 100 μ L of mili-Q water was added to each

II. Mechanical cell disruption

- 1. ECM root tips were placed in empty Eppendorf tubes; 100 μ L of mili-Q water was added to each
- 2. Samples were homogenized with a sterile disposable micro pestle

III. Chemical lysis

1. ECM root tips were placed in empty Eppendorf tubes; 50 μ L of Extraction buffer (Extract-N-AmpTM Plant PCR Kit, Sigma) was added to each

- 2. Tubes were incubated at 95 $^{\circ}\mathrm{C}$ for 10 min
- 3. 50 μL of Dilution buffer (Extract-N-Amp^{TM} Plant PCR Kit, Sigma) was added to each tube

IV. Enzymatic lysis

- ECM root tips were placed in empty Eppendorf tubes; 100 μL of proteinase buffer (10mM Tris-HCl; 1mM EDTA; 0.5% Tween-20; 1 mg/mL proteinase K; pH 7.5) was added to each tube
- 2. Tubes were incubated at 60 °C overnight

V. Mechanical + chemical lysis

- 1. ECM root tips were placed in empty Eppendorf tubes; 50 μ L of Extraction buffer was added to each tube
- 2. Samples were homogenized with a disposable micro pestle
- 3. Tubes were incubated at 95 °C for 10 min
- 4. $50 \ \mu L$ of Dilution buffer was added to each tube

VI. Enzymatic + chemical lysis

- 1. ECM root tips were placed in empty Eppendorf tubes; 100 μL of proteinase buffer (10mM Tris-HCl; 1mM EDTA; 0.5% Tween-20; 1 mg/mL proteinase K; pH 7.5) was added to each
- 2. Samples were homogenized with a disposable micro pestle
- 3. Tubes were incubated at 60 °C overnight

Lysate purification protocols:

A. No purification

1. Samples were used for further downstream applications

B. Silica columns purification

- 1. 40 μL of the Buffer P was added to the provided isolation mini columns; minicolumns were incubated for 15 min in room temperature (RT)
- 2. 350 μL of the Sol P buffer and 250 μL of 96% ethanol were added to the samples; samples were mixed
- 3. Samples were centrifuged for 1 min at 14000 × g, RT
- 4. From each sample, $600 \ \mu$ L of the supernatant was transferred to the activated mini column placed in a collection tube
- 5. Samples were centrifuged for 1 min at 14000 × g, RT
- 6. The filtrate was discarded from the collection tubes; the remaining supernatant was added to the minicolumns
- 7. Samples were centrifuged for 1 min at 14000 × g, RT
- 8. The filtrate was discarded from the collection tubes; 500 μ L of the Wash PX buffer was added to the minicolumns
- 9. Samples were centrifuged for 1 min at 14000 × g, RT
- 10. The filtrate was discarded from the collection tubes; 500 μ L of the Wash PX buffer was added to the minicolumns
- 11. Samples were centrifuged for 2 min at 14000 × g, RT
- 12. The minicolumns were moved to clean Eppendorf tubes; 100 μ L of the Elution buffer preheated to 70 °C was added to each of the minicolumns
- 13. Samples were incubated for 3 min in RT
- 14. Samples were centrifuged for 1 min at 14000 × g, RT

15. The solution collected in the Eppendorf tubes was used for further downstream applications

C. Chloroform extraction purification

- 1. 25 μL of preparation buffer (1M Tris-HCl; 6M NaCl; 0.5% (w/v) PVP; pH 8) was added to the samples; samples were incubated for 30 min in 60 °C
- 2. $125 \,\mu\text{L}$ of chloroform was added to each sample; samples were vortexed for 2 min
- 3. Samples were centrifuged for 15 min at 10000 × g, RT
- 4. From each sample, 90 µL of aqueous supernatant was transferred to new tube
- 5. $45 \,\mu\text{L}$ of $4 \,\text{M}$ NaCl was added to each sample; samples were incubated on ice for $5 \,\text{min}$
- 6. 270 μL of cold 96% ethanol was added to each sample; samples were incubated for 2 min in RT
- 7. Samples were centrifuged for 8 min at 8000 × g, RT
- 8. The supernatant was discarded; the pellets were washed with 100 μ L 75% ethanol
- 9. The pellets were dried and dissolved in 100 μL mili-Q water
- 10. The final solution was used for further downstream applications