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1 **Ectomycorrhizal fungi in wood-pastures: Communities are**
2 **determined by trees and soil properties, not by grazing**

3

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13 **Keywords:** forest pastures, semi-natural, semi-open, traditional rural biotopes

14 **Abstract**

15 Traditional rural biotopes such as wood-pastures are species-rich environments that
16 have been created by low-intensity agriculture. Their amount has decreased
17 dramatically during the 20th century in whole Europe due to the intensification of
18 agriculture. Wood-pastures host some fungal species that prefer warm areas and are
19 adapted to semi-open conditions, but still very little is known about fungi in these
20 habitats. We studied how management, historical land-use intensity, present grazing
21 intensity, time since abandonment, and stand conditions affect the species richness
22 and community composition of ectomycorrhizal fungi. We surveyed fruit bodies on
23 three 10 m x 10 m study plots in 36 sites and repeated the surveys three times. Half of
24 the sites were currently unmanaged but had a grazing history. We measured soil pH,

25 soil moisture and the basal area of different tree species, and interviewed landowners
26 about grazing history. We found that the proportion of broadleaved trees, soil pH, and
27 soil moisture are the major drivers of the communities of ectomycorrhizal fungi in
28 boreal wood-pastures. Management or grazing intensity did not have significant
29 effects on fungal species richness, whereas historical land-use intensity seemed to
30 have a negative effect on species richness. To conclude, present stand conditions are
31 the most important factors to evaluate when planning the conservation of
32 ectomycorrhizal fungi living in semi-open forest habitats.

33 **1. INTRODUCTION**

34 Traditional rural biotopes are species-rich habitats that have been formed by low-
35 intensity agriculture. Wood-pastures are forested traditional rural biotopes that have
36 been grazed by domestic animals for up to hundreds of years. Long grazing history
37 has notably changed their vegetation structure. Moreover, patchy grazing pressure and
38 commonly performed selective logging have resulted in mosaic-like habitats where
39 open, semi-open and closed patches alternate (Garbarino et al., 2011; Schulman et al.,
40 2008; Vainio et al., 2001; WallisDeVries et al., 1998). In the boreal zone some wood-
41 pastures have quite closed stand structure and they have also been called forest
42 pastures (sensu Takala et al., 2014).

43 The area of traditional rural biotopes has decreased steeply during the 20th
44 century in all European countries (Garbarino et al., 2011; Pykälä and Alanen, 2004).
45 Land abandonment and farming intensification are the main reasons why biodiversity
46 and the amount of these habitats have decreased. In Finland, traditional rural biotopes
47 and many species adapted to these habitats are now threatened. Less than 1 % of

48 wood-pastures remain compared to the area in the 1950's, which was already much
49 lower than in the 1800's (Rassi et al., 2010; Schulman et al., 2008).

50 Traditional rural biotopes host high biodiversity, which is proposed to be caused
51 by management, high habitat heterogeneity, an intermediate disturbance regime, long
52 grazing history, and variable soil properties (e.g. Benton et al., 2003; Cousins and
53 Eriksson, 2002; Oldén et al., 2016; Paltto et al., 2011; Pykälä, 2003, 2001; Saarinen
54 and Jantunen, 2005; Vujnovic et al., 2002). Currently grazed grasslands and wood-
55 pastures have been shown to have higher plant species richness than abandoned ones
56 (e.g. Dullinger et al., 2003; Oldén et al., 2016; Pykälä, 2003). Grazing benefits plant
57 species richness by removing vegetation and breaking the soil surface, and this gives
58 more space to weakly competitive species and thus increases species richness (Olf
59 and Ritchie, 1998; Pykälä, 2001). The amount of light and soil temperature are
60 increased by grazing (Olf and Ritchie, 1998; Pykälä, 2001), which improves the
61 growth conditions for many fungal species (Nitare and Sunhede, 1993). Grazing has
62 been proposed to benefit many fungal species (Jakobsson, 2005; Nauta and Jalink,
63 2001; Nitare and Sunhede, 1993). It has been found that while mowing increases
64 grassland fungal species richness (Griffith et al., 2012), grazing provides a wider
65 range of opportunities to fungal species than mowing (Nauta and Jalink, 2001).
66 Grazing increases heterogeneity by creating a mosaic of vegetation and thus it creates
67 various habitat patches for many species (Nauta and Jalink, 2001; Olf and Ritchie,
68 1998). According to the intermediate disturbance hypothesis it is expected that species
69 richness is highest at intermediate grazing intensity, where habitat heterogeneity is
70 also maximized (Grime, 1973; Milchunas et al., 1988; Mwendera et al., 1997;
71 Vujnovic et al., 2002).

72 Most species-rich traditional rural biotopes have been grazed or mowed with
73 traditional methods for a long time (Cousins and Eriksson, 2002; Myklestad and
74 Saetersdal, 2003; Pykälä, 2003). However, Oldén et al. (2016) did not find clear
75 effects of historical land-use intensity on plant species richness in wood-pastures. In
76 contrast, Lindborg and Eriksson (2004) found that historical landscape connectivity
77 has a strong effect on plant species richness in semi-natural grasslands. Many
78 characteristic grassland fungal species are dependent on continuous management that
79 has lasted for decades (Arnolds, 2001).

80 Soil properties affect species richness and communities in traditional rural
81 biotopes (Oldén et al., 2016; Raatikainen et al., 2007; Roem and Berendse, 2000).
82 Vascular plant and bryophyte species richness has been shown to increase with
83 increasing soil pH (Oldén et al., 2016; Roem and Berendse, 2000). Rousk et al. (2009)
84 found that on arable managed land fungal growth was maximized at pH 4.5 and
85 decreased both above and below that. Also, soil moisture has been shown to affect
86 fungal communities (Kaisermann et al., 2015; McHugh and Schwartz, 2016). It is
87 suggested that fungal populations are sensitive to soil moisture, and water treatments
88 decrease fungal diversity (Kaisermann et al., 2015; McHugh and Schwartz, 2016).

89 Many of the fungal studies are focused on macrofungi species in grasslands
90 (e.g. Arnolds, 2001; Nauta and Jalink, 2001; Öster, 2008). Fungal species from
91 ectomycorrhizal and coprophilous species groups cannot fruit in mowed grasslands,
92 but could have rich communities in grazed wood-pastures (Nauta and Jalink, 2001).
93 Juutilainen et al. (2016) found that the species richness of wood-inhabiting fungi in
94 wood-pastures was lower than in natural herb-rich forests, but wood-pastures hosted
95 some red-listed species and other unique species that were not found in the other
96 studied habitats. Only one study has focused on species of ectomycorrhizal fungi in

97 wooded meadows (Tedersoo et al., 2006). They found that communities of
98 mycorrhizal fungi in managed and forested old wooded meadows differ, but species
99 richness did not differ significantly.

100 The low number of studies on mycorrhizal fungi is alarming because they have
101 an important role in ecosystems (Boddy et al., 2008). It is known that at least 95% of
102 vascular plants have mycorrhizal associations (Moore et al., 2011). There are both
103 specific and non-specific associations between mycorrhizal fungi species and their
104 host trees (Molina et al., 1992; Moore et al., 2011). The reason for low number of
105 fungal studies might be that they are difficult to identify and that there are few
106 specialists who are able to conduct the studies (Boertmann, 1995; Watling, 1995).

107 In order to attain more knowledge on species of ectomycorrhizal fungi
108 inhabiting wood-pastures, we studied the effects of management, grazing history,
109 grazing intensity, time since abandonment and stand conditions on species richness
110 and communities of ectomycorrhizal fungi in wood-pastures dominated by
111 broadleaved, coniferous and mixed trees in the boreal zone. Based on earlier studies
112 we hypothesized that grazing increases fungal species richness and has an effect on
113 community composition, while species richness decreases after abandonment. We
114 also hypothesized that high historical land-use intensity increases species richness,
115 and that present intermediate grazing pressure creates highest species richness. Thus,
116 our main questions were: (1) Do grazed sites have higher species richness than
117 abandoned sites? (2) Does species richness increase with increasing historical land-
118 use intensity? (3) Does the species richness increase with grazing intensity or does it
119 peak with intermediate grazing intensity? (4) Does the species richness increase with
120 time since abandonment or does it peak after abandonment? (5) Is there a difference
121 between fungal communities among grazed and abandoned sites? and (6) How do the

122 present stand conditions affect species richness and community assembly in wood-
123 pastures?

124 **2. MATERIALS AND METHODS**

125 **2.1. Study sites**

126 We confined our study to the province of Central Finland to reduce biological and
127 geographical background variation in the data set. We studied 36 sites. The sites were
128 located in 30 farms so in each farm there were one or two study sites. 32 of the sites
129 were located in the Southern boreal and four in the Middle boreal vegetation zone
130 (Ahti et al., 1968) (Figure 1a).

131 We conducted our study in broadleaved (birch-dominated, *Betula spp.*),
132 coniferous (spruce-dominated, *Picea abies*), and mixed (with a coniferous-
133 broadleaved mixture of *Picea abies*, *Pinus sylvestris*, *Betula spp.*, *Populus tremula*,
134 *Alnus incana*, *Sorbus aucuparia* or a subset of these) wood-pastures, and in each of
135 these three tree classes we included 12 sites. Half of the sites in each class were
136 currently grazed and the other had been abandoned (not grazed currently but had been
137 grazed during the recent history by domestic animals). Because our aim was to study
138 the effects of grazing, we aimed to reduce the variation caused by different stand
139 structure through selecting grazed and abandoned areas with similar tree densities
140 (mature trunks/ha). We could not control the variation in growth site type (which
141 varied from herb-rich to mesic heath) (see Hotanen et al., 2008) or the type of grazing
142 animals because of the small number of potential sites. More information on the study
143 sites is provided in Oldén et al. (2016).

144 Grazed sites were grazed yearly during the summer-autumn period by cattle,
145 horses or sheep. The grazing regime and intensity varies between sites because they

146 are managed by private farmers. In most farms, grazing started in late May or in June
147 and ended in September or when forage was depleted. Most farms use rotational
148 grazing where the animals are moved to a new pasture when forage is depleted. The
149 animals may graze the study site once or more times during the grazing season.

150 **2.2. Data collection**

151 At each study site we established three 10 m x 10 m square study plots based on the
152 dominant tree species and the density of mature trees. Among all study sites, the study
153 plots were at least 17 meters apart from each other. The whole selection procedure
154 was conducted without paying any attention to the ground level vegetation, and
155 during a season with almost no macrofungi producing fruit bodies (June-early July).
156 Thus, other species than trees did not affect the study plot selection.

157 Within the study plots, we recorded fungi growing on the ground and on the
158 surface of dead wood lying on the ground. We surveyed the ground very carefully by
159 pushing plants aside, but did not turn over dead wood pieces to avoid affecting the
160 fungal assemblage on the plots. We counted all the fruit bodies of stipitate
161 ectomycorrhizal macrofungi.

162 We repeated the surveys three times among all the study sites. Ten of the birch-
163 dominated study sites were surveyed three times during September-October in 2010.
164 The remaining two birch-dominated sites as well as all mixed and spruce-dominated
165 study sites were surveyed twice in August-September 2012 and once in September-
166 October 2013. We identified fungi to species level at the site when possible, but
167 collected specimens for microscopic identification if needed (altogether 1100
168 specimens). The abundance of each species in a plot was estimated by counting the
169 number of fruit bodies. With fungi it is difficult to define which fruit bodies belong to
170 one individual (Dahlberg and Mueller, 2011), so the fruit body count does not directly

171 reflect the number of individuals on the plot, but is more like a surrogate of the
172 abundance of the species. While counting the fruit bodies we removed them from the
173 ground to avoid counting the same fruit bodies during the next survey.

174 We separated mycorrhizal species from other species based on the ecological
175 information provided in Knudsen and Vesterholt (2012), Kotiranta et al. (2009), and
176 Kytövuori et al. (2005). Species that were reported in the literature to use both
177 mycorrhizal and saprotrophic strategy (*Hydnum repandum*, *Hydnum rufescens* coll.,
178 etc.) were excluded except for *Paxillus involutus* that was reported to be mainly
179 mycorrhizal. We included only species level data in the analyses. The nomenclature
180 of agarics and boletoids follows Knudsen and Vesterholt (2012) and Aphylloporales
181 Kotiranta et al. (2009). A few exceptions in the nomenclature are indicated by
182 showing the author names in the species list (Table 1 in the Appendix B). These
183 exceptions are situations where Nordic taxonomists currently disagree with the
184 references that we used for nomenclature. The voucher specimens are preserved in the
185 herbarium of the National History Museum of University of Jyväskylä (JYV) and in
186 the personal collection of Kaisa Tervonen.

187 **2.3. Background variables**

188 Measuring historical land-use intensity proved to be complicated in the study area in
189 Central Finland. It was not possible to reliably measure the age of each farm, because
190 historical church records or cadastres do not specify the locations of the farms and
191 properties. Agricultural records have only been collected from the 1920's onwards. In
192 addition, in the 1800's free cattle grazing outside of fenced fields meant that cattle
193 from different farms grazed in the forests surrounding villages (Jäntti, 1945). Thus,
194 we created a surrogate for the historical land-use intensity by counting the number of
195 surrounding farms (within one kilometer buffer zone around each site) in old cadastral

196 maps drawn in the 1850's and 1860's. We assumed that the number of surrounding
197 farms correlates with historical grazing intensity and other traditional agricultural
198 activities.

199 For the abandoned sites the landowners provided information about the year
200 when the site had been abandoned. Time since abandonment varied between 7 and 42
201 years (calculated for year 2012 for all abandoned sites). We don't know the number of
202 animals present in each of the sites but we evaluated grazing intensity at the end of
203 grazing season (September or October 2012). It was evaluated in 2 m x 2 m subplots
204 that were placed inside each corner of each study plot. Thus we had 12 subplots in
205 each site. Grazing intensity was estimated as the proportion of clipped shoots out of
206 all vascular plant shoots that had been at least 5 cm high. This measure was used in
207 analyses as an average value for the whole study site. See more information about the
208 measurements in Oldén et al. (2016). We note that even though the fungal species
209 were surveyed in ten birch-dominated sites in 2010, the grazing intensity was
210 measured also in these sites in 2012. Data on the carrying capacity or stocking rate of
211 the pastures were not available, but based on our visual estimates the grazing intensity
212 was usually at the same level between different years. Examples of vegetation in sites
213 with different grazing intensities are shown in Figure 1b-d.

214 We also collected soil samples from each study plot in June 2013 to measure
215 soil pH and soil moisture. The average value of the three plots was used for each
216 study site in the analyses. See more information on the sampling in Oldén et al.
217 (2016). Within the plots we measured the diameter at breast height (130 cm) of each
218 tree that was at least 130 cm high. The diameters were used to calculate the basal area
219 of trees. For each site, we calculated the proportion of broadleaved trees out of the

220 basal area of all trees. In addition, we calculated the species richness of trees in each
221 site.

222 **2.4. Statistical analyses**

223 We conducted all the statistical analyses on site-level data and built separate models
224 for all sites, grazed sites and abandoned sites. All statistical analyses were performed
225 with R version 3.3.0 (R Core Team, 2016).

226 **2.4.1. Tests among explanatory variables**

227 We tested correlations between the continuous explanatory variables to find out
228 possible collinearity in the statistical models (Spearman's rank correlation). Soil pH
229 correlated significantly with soil moisture, tree species richness, and the proportion of
230 broadleaved trees (Table 1 in the Appendix A). Also, time since abandonment
231 correlated significantly with soil moisture and the proportion of broadleaved trees.
232 Despite these correlations, we included these variables in the statistical models
233 because we wanted to analyze their impacts on fungi simultaneously. However, the
234 results must be interpreted with caution due to the correlations. In addition, the
235 proportion of broadleaved trees correlated significantly and strongly with tree species
236 richness, but we did not include these two variables in the same statistical models.
237 The rest of the variables correlated only moderately or weakly with each other.

238 Moran's test was used to examine possible spatial autocorrelation. The test was
239 done separately for two- and four-nearest-neighbor (2nn and 4nn) structures which
240 were based on the distances between sites. We found that soil moisture and the
241 historical land-use intensity are spatially autocorrelated within 2nn level. Time since
242 abandonment was nearly significant within 4nn level. Results for variables with
243 spatial autocorrelation should be taken with caution. Our sampling setup is probably

244 the main reason for observed autocorrelation. We had two study sites within some
245 farms so those sites share the same farm-specific factors.

246 Wilcoxon tests revealed that the levels of continuous variables did not differ
247 between grazed and abandoned sites.

248 **2.4.2 General Linear Mixed Models**

249 We analyzed the effect of management situation (grazed or abandoned), historical
250 land-use intensity, grazing intensity, time since abandonment, and stand conditions on
251 species richness with General Linear Mixed Models (GLMM). The response variable
252 was the species richness of ectomycorrhizal fungi, explanatory discrete variable was
253 management situation, and explanatory continuous variables were historical land-use
254 intensity, soil moisture, soil pH, tree species richness, grazing intensity, and time
255 since abandonment. We set the inventory time period (either 2010 or 2012+2013)
256 variable as a random effect. The relationships between the response and explanatory
257 variables were expected to be best described by linear and quadratic models. We
258 allowed quadratic effects for soil pH, soil moisture, grazing intensity and time since
259 abandonment.

260 We standardized all continuous variables to zero mean and unit variance to
261 make their effect sizes comparable. We used Negative Binomial GLMM model and
262 chose the best model based on Akaike's Information Criterion values. The first model
263 with all sites was built for management situation, historical land-use intensity, soil
264 pH, soil moisture, and tree species richness. Based on our study questions, we were
265 primarily interested in the effects of management and historical land-use intensity, so
266 we kept these variables in the model and compared all possible models where we
267 varied the presence of soil pH, soil moisture and tree species richness. The second
268 model was built for grazed sites similarly than for all sites, but without management

269 situation and with grazing intensity. In this model we kept historical land-use intensity
270 and grazing intensity, while we found the best model with a subset of soil pH, soil
271 moisture and tree species richness. The third model for abandoned sites always
272 included historical land-use intensity and time since abandonment while we varied the
273 presence of soil pH, soil moisture and tree species richness. The analyses were
274 performed with the function “glmer.nb” from package “lme4” (Bates et al., 2015). See
275 detailed information about GLMM from the Appendix A.

276 **2.4.3. Bioenv-analyses and Nonmetric Multidimensional Scaling**

277 We studied how management situation (grazed or abandoned), inventory time period
278 (2010 or 2012+2013), historical land-use intensity, grazing intensity, time since
279 abandonment, soil pH, soil moisture, and the proportion of broadleaved trees affect
280 the community structure of ectomycorrhizal fungi. Again, we tested the effects
281 separately for all sites, grazed sites, and abandoned sites. We used Chao’s
282 dissimilarity index, which takes into account the number of unseen species (Chao et
283 al., 2005; Oksanen et al., 2015). Our data is based on the observed fruit bodies and
284 several species have probably not been observed on many sites. The different survey
285 years could also have affected the likelihood of observing certain species on different
286 sites. With Chao’s dissimilarities we conducted Bioenv-analysis to reveal the best
287 subset of environmental variables that have the maximum correlation (Spearman)
288 with the community dissimilarities. Because we included also categorical variables,
289 we used Gower distance for calculating distances between the environmental
290 variables. We used function “bioenv” from “vegan” package by Oksanen et al.,
291 (2015). We conducted Nonmetric Multidimensional Scaling (NMDS) to visualize the
292 effects of environmental variables on ectomycorrhizal species composition (function
293 “metaMDS” in “vegan”). We chose three-dimensional solutions. We overlaid the

294 ordination results with environmental factors whose location shows the average
295 location of sites in that category, and with environmental vectors whose length shows
296 the maximum correlations of the continuous environmental variables. In addition, we
297 performed the same Bioenv-analyses and NMDS ordinations with the commonly used
298 Bray-Curtis dissimilarities for comparison. All of the Bray-Curtis analyses are
299 provided in the Appendix A.

300 **3. RESULTS**

301 In this study we recorded 14 831 fruit bodies among all sites, and 11 818 of them
302 were identified to species level and were therefore taken into account in the analyses,
303 including 4843 among grazed and 6975 among abandoned sites. We found 226
304 ectomycorrhizal fungi species out of which 167 species were found from grazed sites
305 and 187 from abandoned sites. On average grazed sites hosted 9.3 species and
306 abandoned sites 10.4 species.

307 The most common species in the data were *Lactarius tabidus* Fr. (28 sites/1296
308 fruit bodies), *Paxillus involutus* (Batsch: Fr.) Fr. (28 sites/333 fruit bodies) and
309 *Laccaria laccata* (Scop.: Fr.) Berk. & Broome (25 sites/1045 fruit bodies). We
310 recorded 16 species of special interest. Two of them are red-listed (NT) in Finland:
311 *Cortinarius rubroviroleipes* Bendiksen & K. Bendiksen (2 sites/14 fruit bodies) and
312 *Inocybe hystrix* (Fr.) P. Karst. (1 site/4 fruit bodies). Three species are not evaluated
313 (NE) in previous IUCN evaluation: *Naucoria submelinoides* (Kühner) Maire (1
314 site/37 fruit bodies), *Russula olivaceoviolascens* Gillet sensu Romagnes (3 sites/12
315 fruit bodies), and *Russula robertii* coll. J. Blum (1 site/4 fruit bodies). 11 species are
316 either quite new to Finland or not yet published. See detailed species list from Table 1
317 in the Appendix B.

318 **3.1 Species richness of ectomycorrhizal fungi**

319 The only variable that had a significant effect on species richness among all as well as
320 among grazed sites was the historical land-use intensity (negative effect) (Table 1,
321 Figure 2e).

322 Among abandoned sites soil moisture (negative effect) and historical land-use
323 intensity (negative effect) affected species richness. Among abandoned sites the
324 species richness increased as time since abandonment increased, and there was also a
325 nearly significant quadratic (humped) effect (Table 1, Figure 2j).

326 Inventory time period (used as a random effect) seems to have a great effect on
327 species richness especially with abandoned sites: More species were observed in sites
328 that were studied in 2012 and 2013 than in the ones that were studied in 2010 (Figure
329 2a-c).

330 **3.2 Community structure of ectomycorrhizal fungi**

331 When all sites were analyzed together, the proportion of broadleaved trees, soil pH,
332 and soil moisture explained the community structure of ectomycorrhizal fungi (Table
333 2 in the Appendix A, Figure 3a with axes 1 and 2).

334 Among grazed sites the community structure was mostly explained by soil
335 moisture and the proportion of broadleaved trees (Table 2 in the Appendix A, Figure
336 3b).

337 Among abandoned sites the community structure was explained by the
338 proportion of broadleaved trees and soil pH (Table 2 in the Appendix A, Figure 3c).
339 Birch-dominated and spruce-dominated wood-pastures were clearly separated in the
340 NMDS ordination, while mixed wood-pastures had intermediate positions and
341 overlapped with the others (Figure 3, symbol size represents the proportion of broad-
342 leaved trees, thus for example spruce dominated sites have small symbol).

343 For the three-dimensional NMDS ordinations the final stress values were 0.150
344 for all sites, 0.126 for grazed sites, and 0.104 for abandoned sites. The results for axes
345 1 and 2 are shown in Figure 3. Results for axis 3 are shown in Figure 1 in the
346 Appendix A and they only emphasize the effect of the proportion of broadleaved
347 trees.

348 **4. DISCUSSION**

349 **4.1. Grazing-related variables did not have clear effects on the fungal** 350 **communities**

351 Historical land-use intensity (historical number of farms surrounding the site within
352 1km) was the most important factor affecting species richness of ectomycorrhizal
353 fungi, but it did not impact community composition. High historical land-use intensity
354 had a significant negative effect on species richness among all sites, grazed sites, and
355 abandoned sites. This is surprising because one could expect that the biodiversity of
356 traditional rural biotopes in general would increase with historical land-use intensity.
357 For example, Lindborg and Eriksson (2004) found that historical landscape
358 connectivity has a strong positive effect on the present species richness of plants in
359 semi-natural grasslands. On the other hand, in our study of these same wood-pastures,
360 we did not find significant impacts of historical land-use intensity on the species
361 richness of either vascular plants or bryophytes (Oldén et al., 2016). One explanation
362 is that many of the species of boreal wood-pastures are primarily forest species
363 instead of grassland species. It seems possible that among ectomycorrhizal fungi there
364 are more species that suffer from human impacts than those that benefit from them. In
365 addition, grazing may not be the most important historical factor determining current
366 fungal assemblages, but instead other practices related to forestry and agriculture may

367 have negative impacts on local fungal diversity. Finally, we assumed that historical
368 land-use intensity correlates with historical grazing intensity, but it may not correlate
369 with the overall length of grazing history or the grazing intensity during the recent
370 decades.

371 Management situation had no effect on fungal species richness, which is in
372 contrast to our hypothesis. Management did not have a clear effect on community
373 composition either. It seems that the communities of ectomycorrhizal fungi are not
374 affected by grazing, although some individual species may respond to it. Instead,
375 vascular plants and bryophytes had higher species richness in the currently grazed
376 sites of this same setup (Oldén et al., 2016), indicating that grazing does have
377 ecological impacts in these boreal wood-pastures.

378 Present grazing intensity did not have any significant effect on species richness.
379 Thus, our result does not support our hypothesis that species richness would be
380 highest at intermediate grazing intensity. With vascular plants there are several studies
381 that show highest species richness with intermediate grazing pressure (Mwendera et
382 al., 1997; Vujnovic et al., 2002), also in these same sites (Oldén et al., 2016).
383 However, data on the stocking rates of grazers in these sites was not available, and
384 our one-time estimation of grazing intensity may not be a comprehensive estimate of
385 all the effects that grazers have on fungi throughout the grazing season and different
386 years. In addition, our results might be affected by the consumption of fruit bodies by
387 the grazers during the study. It is known, and we also noticed ourselves, that the
388 grazers eat fruit bodies (Warren and Mysterud, 1991). It is possible that in sites with
389 high grazing intensity the grazers consumed more fruit bodies, and thus fewer species
390 were observed. However, the grazers may also purposefully seek for some fruit bodies
391 over other food items (Bjugstad and Dalrymple, 1968), and in that case grazing

392 intensity does not correlate with the number of consumed fruit bodies. Grazing
393 intensity had no clear effects on fungal community composition either. Together with
394 the fact that management situation did not affect fungal species richness or
395 community composition, it is clear that trees and soil properties impact fungal
396 communities much more than grazing.

397 Time since abandonment had a positive and also slightly humped effect on
398 species richness, but it had no clear effect on community composition. Thus,
399 according to our results species richness increases slightly with time since
400 abandonment, which is opposite to our hypothesis. Many ectomycorrhizal species
401 may benefit from the increasing number of young trees during the first decades after
402 abandonment, especially if the young trees increase the number of tree species that are
403 available for mycorrhizal symbiosis. In time an abandoned wood-pasture develops
404 towards an old-growth forest, which can offer habitats for species that are dependent
405 on them (Bonsdorff et al., 2014). However, we note that more studies are needed on
406 this topic, especially because the positive effect in our data can be caused by a few
407 long-ago abandoned sites that are biodiversity hotspots due to other properties than
408 grazing.

409 **4.2. Soil moisture affects species richness and community composition**

410 Our result reveals that soil moisture affects the species richness of ectomycorrhizal
411 fungi. It is also one of the main drivers of ectomycorrhizal fungi community
412 composition. We found that high soil moisture in wood-pastures results in low species
413 richness of ectomycorrhizal fungi. However, the effect was significant only among
414 abandoned sites. Our recent study revealed that bryophyte species richness increases
415 with soil moisture in wood-pastures, but vascular plant species richness does not show

416 any clear responses (Oldén et al., 2016). Thus, different species groups respond
417 differently to soil moisture in wood-pastures.

418 It is clear that fungal species need moisture to grow, but one could think that the
419 mycelium of mycorrhizal fungi cannot grow properly if the soil is too moist.
420 However, Kennedy and Peay (2007) found that with increasing soil moisture plant
421 species with ectomycorrhizal associations had greater shoot biomass and
422 photosynthesis than non-mycorrhizal plants. McHugh and Schwartz (2016) instead
423 showed that water treatment decreased fungal diversity. Thus, our result supports the
424 observation of McHugh and Schwartz (2016).

425 **4.3. The proportion of broadleaved trees is the main driver of community** 426 **composition**

427 The proportion of broadleaved trees had the strongest effect on the community
428 composition of ectomycorrhizal fungi. Our result was expected, because it is known
429 that there are specific and non-specific associations between mycorrhizal fungi
430 species and their host trees (Molina et al., 1992; Moore et al., 2011). For example, the
431 fungal communities in spruce-dominated sites differed strongly from other sites,
432 which is reasonable because spruce was often the only tree species present in the
433 plots.

434 Surprisingly, tree species richness did not have a significant effect on species
435 richness of ectomycorrhizal fungi. Since many ectomycorrhizal species are
436 specialized to certain hosts, increasing tree species richness should increase
437 ectomycorrhizal species richness, through the higher number of suitable hosts for
438 different species. One reason why we did not find a significant effect might be that the
439 difference cannot be detected in such a small scale due to high overall beta diversity

440 of fungal communities on small spatial scales (Abrego et al., 2014). The difference
441 might be discovered on a larger scale.

442 **4.4. Soil pH affects community composition**

443 Soil pH had a strong effect on community composition of ectomycorrhizal fungi, but
444 it did not impact species richness. Soil pH correlated strongly with the proportion of
445 broadleaved trees: Most of the sites with high soil pH (max 4.9) are birch-dominated
446 herb-rich forests, while most of the low-pH sites (min 3.1) are heath forests
447 dominated by spruces or mixed trees.

448 Vascular plant and bryophyte species richness has been shown to increase with
449 increasing soil pH (Oldén et al., 2016; Roem and Berendse, 2000). According to
450 Rousk et al. (2009) fungal growth was maximized at pH 4.5 and decreased both above
451 and below that. On the other hand, fungal biomass was highest at pH 6 but decreased
452 with both increasing and decreasing pH (Rousk et al., 2009). Thus it could be
453 assumed that in our quite acidic sites species richness would increase with soil pH,
454 but we did not find significant effects on fungal species richness.

455 **4.5. Survey year affected our results**

456 Fungal surveys were conducted in 10 of the 12 birch-dominated sites on three visits
457 during 2010. Two birch-dominated sites and all mixed and spruce-dominated sites
458 were visited twice during 2012 and once during 2013. Autumn 2010 was quite dry
459 and this could affect our results. In 2010 the numbers of detected fruit bodies were
460 quite similar at the first and second survey visits compared to years 2012-2013, but
461 much lower at the third survey visit. Another source of bias is that many fungal
462 species do not produce fruit bodies every year (Straatsma et al., 2001), and thus a
463 higher species richness can be observed in sites that have been studied during two
464 different years, even though the number of survey visits is the same.

465 These study design problems have somewhat affected our results. Thus, we
466 cannot really be sure how strongly the communities of birch-dominated sites differ
467 from others, and how much the survey years have affected it. However, the effect of
468 the year should be small in the Bioenv-analyses where we used Chao's dissimilarity
469 index, which should take into account the unseen species (Chao et al., 2005; Oksanen
470 et al., 2015). We also corrected for the effect of the survey year in the General Linear
471 Mixed Models by using inventory time period (2010 or 2012+2013) as a random
472 effect.

473 It is also known that studies that are only based on fruit bodies do not reveal the
474 whole fungal community, because of the species that do not produce fruit bodies
475 every year (Abrego et al., 2016; Ovaskainen et al., 2013; van der Linde et al., 2012).
476 However, we argue that even a quite large proportion of undetected species should not
477 mask the potential effects of management situation, for example.

478 **5. CONCLUSIONS**

479 Communities of ectomycorrhizal fungi in wood-pastures are determined by soil
480 properties and tree species composition. Based on our results, grazing-related
481 variables do not impact the communities of ectomycorrhizal fungi in boreal wood-
482 pastures, but (currently grazed and abandoned) wood-pastures may still differ in their
483 species composition from the forests that have no grazing history. Decisions on the
484 management and conservation of wood-pastures should be based on other species
485 groups that respond more clearly to management (such as vascular plants and
486 bryophytes, see Oldén et al. 2016). However, some ectomycorrhizal species or the
487 communities of saprotrophic fungi may still respond to grazing in wood-pastures.
488 More studies are needed to reveal these subjects.

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677 Table 1. Variables from the best models from GLMM analyses (best models chosen based on
678 the lowest AIC values) for ectomycorrhizal species richness for all sites, grazed sites,
679 and abandoned sites. Management is a categorical variable (grazed or abandoned). For
680 the continuous variables grazing intensity, time since abandonment, soil pH, and soil
681 moisture both linear and quadratic (\wedge^2) effects were analyzed, whereas for the historical
682 land-use intensity (the number of farms surrounding the site within 1km in the 1850s-
683 60s) and trees species richness only linear effects were analyzed. Inventory time period
684 was set as a random effect. Variables marked with $^+$ were always kept in the models
685 irrespective of their significance.

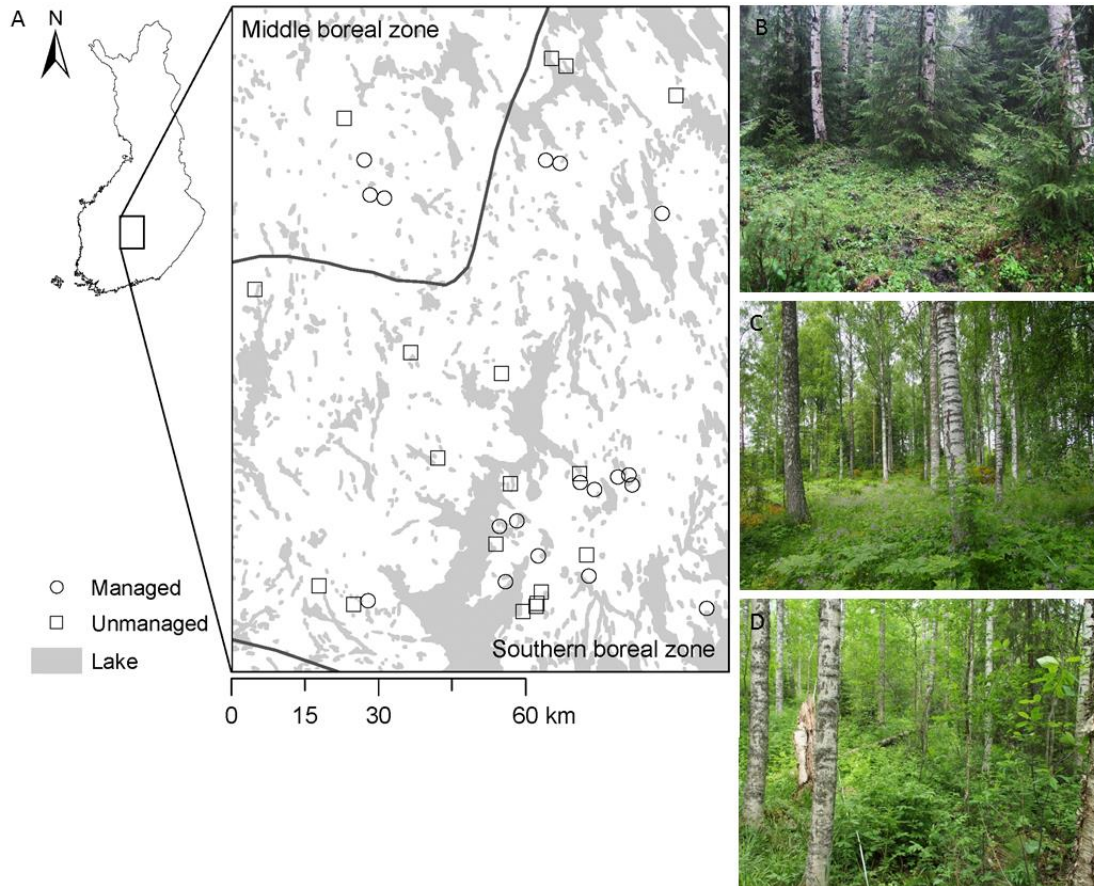
All sites				
	Estimate	Std. Error	z value	P
(Intercept)	3.402	0.127	26.723	<2e-16 ***
*Management: Grazed	-0.123	0.129	-0.958	0.338
*Farms	-0.149	0.065	-2.275	0.0229 *
pH				
pH \wedge^2				
Moisture	-0.100	0.069	-1.458	0.145
Moisture \wedge^2				
TreesSR				
Grazed sites				
	Estimate	Std. Error	z value	P
(Intercept)	3.340	0.089	37.440	<2e-16 ***
+Farms	-0.176	0.077	-2.300	0.0217 *
*Grazing	-0.067	0.077	-0.870	0.386
Grazing \wedge^2				
pH				
pH \wedge^2				
Moisture				
Moisture \wedge^2				
TreesSR				
Abandoned sites				
	Estimate	Std. Error	z value	P
(Intercept)	3.106	0.169	18.412	<2e-16 ***
*Farms	-0.184	0.093	-1.980	0.0477 *
*Abandonment	1.165	0.529	2.200	0.0278 *
Abandonment \wedge^2	-0.497	0.254	-1.958	0.0502 .
pH				
pH \wedge^2				
Moisture	-0.316	0.128	-2.467	0.0136 *

Moisture²

TreesSR

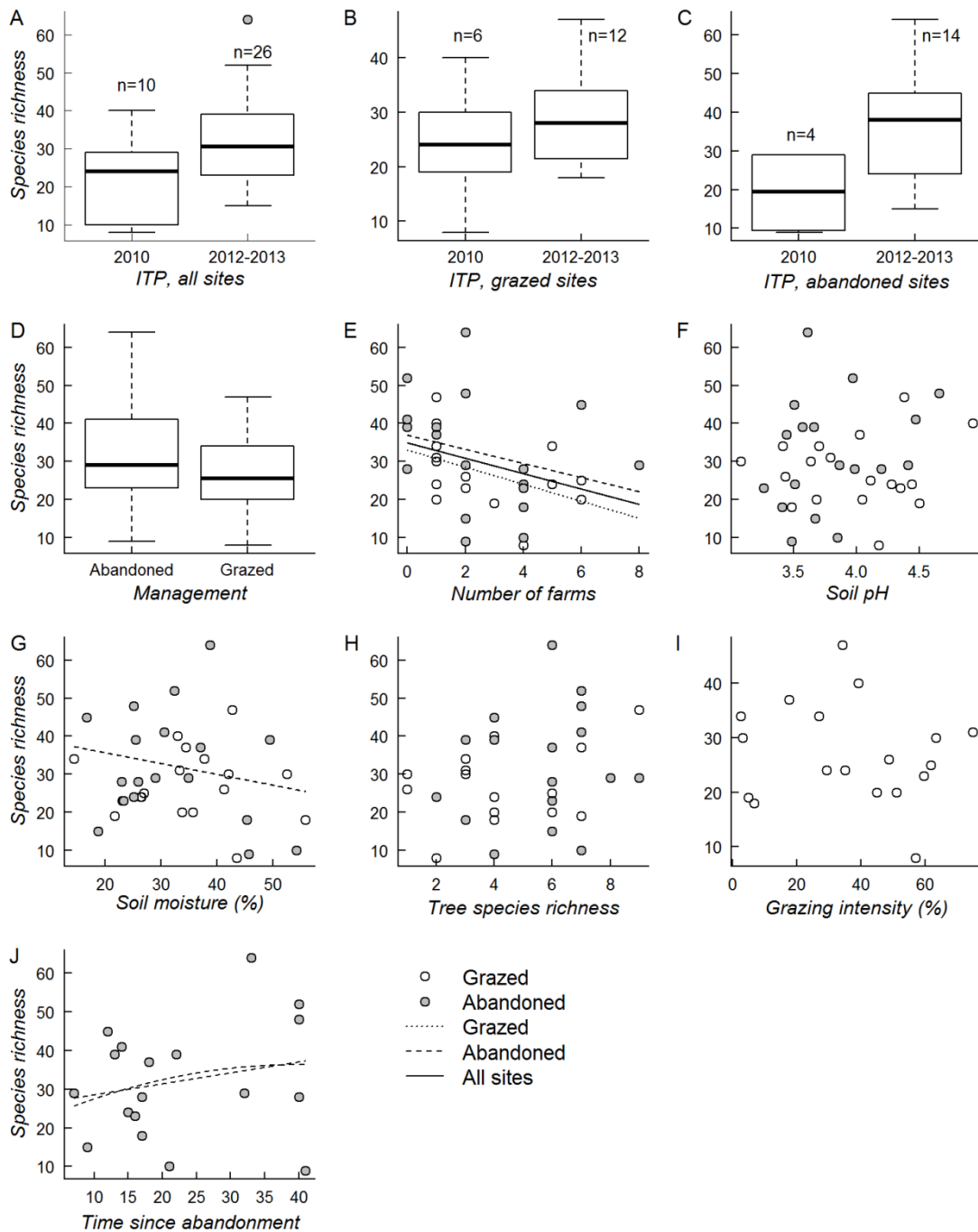
***=p<0.001, **=p<0.01, *=p<0.05, .=p<0.10

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688 Figure 1. a) The 36 study sites located in Central Finland in the southern boreal and the
689 middle boreal vegetation zones. Examples of vegetation in sites of different grazing
690 intensity: b) heavy grazing, c) intermediate grazing, and d) no grazing (abandoned).



692

693 Figure 2. Responses of ectomycorrhizal fungi species richness to inventory time period (ITP)

694 among a) all sites, b) grazed sites, c) abandoned sites, d) management among all sites,

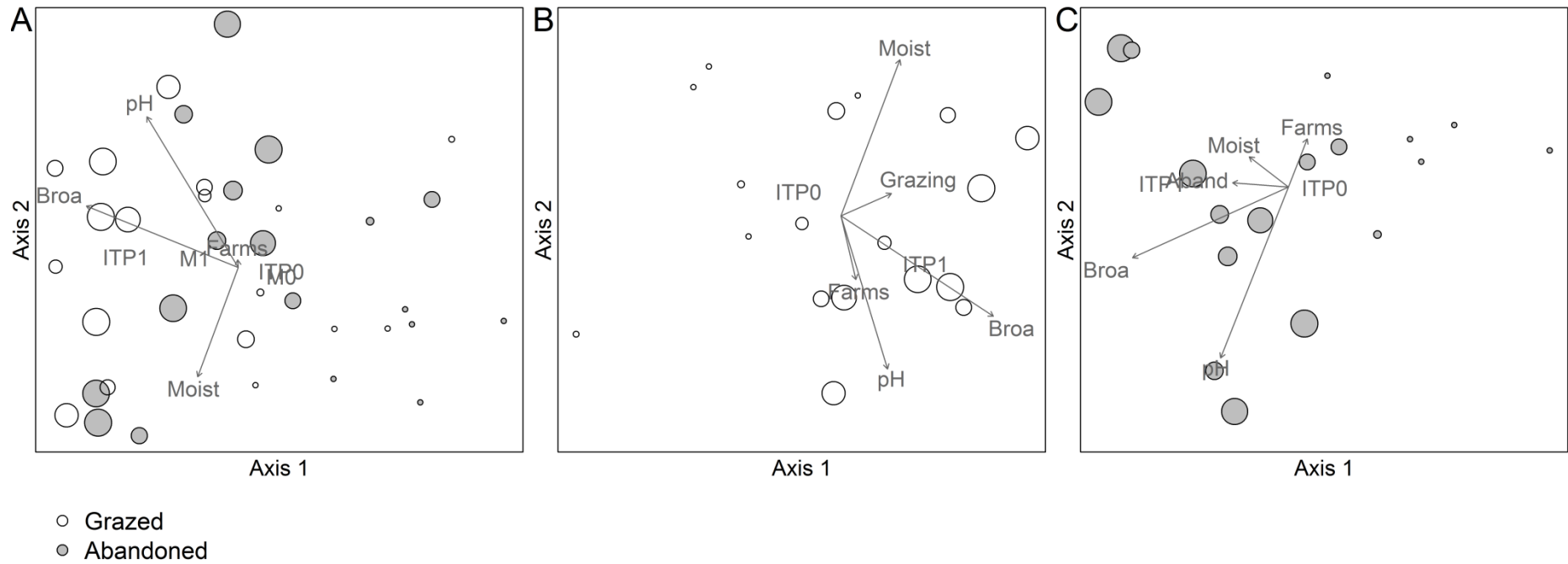
695 e) the number of farms surrounding the site within 1km in the 1850s-60s (historical

696 land-use intensity), f) soil pH, g) soil moisture (% content from the ground), h) tree

697 species richness, i) grazing intensity among grazed sites (% of clipped shoots), and j)

698 time since abandonment (years) for abandoned sites. The fitted linear and quadratic
699 curves represent significant or nearly significant effects from the GLMM analyses.

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Figure 3. Nonmetric Multidimensional Scaling (NMDS) for the community structure of ectomycorrhizal fungi species among a) all sites, b) grazed sites, and c) abandoned sites with axes 1 and 2. Analyses were done with Chao's dissimilarity index. For the categorical variables inventory time period (ITP1 in 2010, ITP0 in 2012-2013) and management (M1 for grazed sites, and M0 for abandoned sites) the location represents the average location of sites in that category. The arrows represent the direction and strength of the a posteriori correlations between the site locations and the continuous environmental variables: the historical land-use intensity (Farms), soil moisture, soil pH, the proportion of broadleaved trees (Broa), grazing intensity on grazed sites, and time since abandonment on abandoned sites. Symbol size represents the proportion of broadleaved trees.

Appendix A for Tervonen et al.: Ectomycorrhizal fungi in wood-pastures:
Communities are determined by trees and soil properties, not by grazing

Authors: Kaisa Tervonen, Anna Oldén, and Panu Halme

1. Detailed information about GLMM
2. NMDS with Bray-Curtis dissimilarity index

Table 1. Correlations between the environmental variables.

Table 2. Results from the Bioenv analyses for mycorrhizal fungi species.

Figure 1. NMDS for the community structure of mycorrhizal fungi species among all, grazed, and abandoned sites with Chao. (Axes 1 and 3)

Figure 2. NMDS for the community structure of mycorrhizal fungi species among all, grazed, and abandoned sites with Bray-Curtis. (Axes 1 and 2)

Figure 3. NMDS for the community structure of mycorrhizal fungi species among all, grazed, and abandoned sites with Bray-Curtis. (Axes 1 and 3)

1. Detailed information about GLMM

In the General Linear Mixed Models (GLMM) we compared models by using as family Poisson or Negative Binomial and decided the best model based on Akaike's Information Criterion values. The selected family was Negative Binomial. We used “bobyqa” as optimizer in the models. We set iteration number to 100 000 with function “glmerControl”. One of the models for grazed site model had “Hessian warning”. We double-checked the results with R’s convergence -help five step instructions to see that with many different optimizers the estimates for the models were similar. Therefore we could trust our results.

2. NMDS with Bray-Curtis dissimilarity index

When analyzing the data with Bray-Curtis dissimilarity index the correlations from Bioenv-analyses were almost the same, but it seems that with Chaos’s index the analysis finds a stronger effect of the proportion of broadleaved trees instead of pH (Table 2 in the Appendix). The NMDS ordinations with Chao’s and Bray-Curtis indexes are somewhat similar (Bray-Curtis NMDS ordinations in the Appendix Figure 2 and 3).

Table 1. Correlations between the environmental variables.

All sites					
	Farms	Moisture	pH	Broadleaved	
Moisture	-0.170				
pH	-0.024	-0.356 *			
Broadleaved	0.024	0.023	0.554 ***		
TreesSR	-0.045	-0.182	0.525 **	0.466 **	
Grazed sites					
	Farms	Moisture	pH	Broadleaved	TreesSR
Moisture	-0.306				
pH	0.183	-0.560 *			
Broadleaved	-0.016	-0.127	0.581 *		
TreesSR	0.010	-0.339	0.592 **	0.287	
Grazing	-0.010	0.034	0.104	0.113	-0.060
Abandoned sites					
	Abandonment	Farms	Moisture	pH	Broadleaved
Farms	-0.176				
Moisture	0.502 *	-0.166			
pH	0.095	-0.288	-0.137		
Broadleaved	0.469 *	0.019	0.152	0.583 *	
TreesSR	0.151	-0.034	0.067	0.682 **	0.717 ***

***=p<0.001, **=p<0.01, *=p<0.05

Table 2. Results from the Bioenv analyses of variables that affect mycorrhizal fungi community. Results are given for both Chao's and Bray-Curtis dissimilarity indexes. Spearman rank correlation was used in the analyses. Inventory time period (DITP: 2010 or 2012 and 2013) and management (Dmana: grazed or abandoned sites) are set as a dummy variables. The proportion of broadleaved trees are represented as "Broadleaved" and the historical land-use intensity as "Farms".

Chao		
All sites		
Size	Variables	Correlation
1	Broadleaved	0.314
2	pH, Broadleaved	0.400
3	pH, Moisture, Broadleaved	0.432
4	DITP, pH, Moisture, Broadleaved	0.365
5	Dmana, DITP, pH, Moisture, Broadleaved	0.338
6	Dmana, DITP, pH, Moisture, Broadleaved, Farms	0.311
Grazed sites		
Size	Variables	Correlation
1	Moisture	0.288
2	Moisture, Broadleaved	0.427
3	pH, Moisture, Broadleaved	0.424
4	pH, Moisture, Broadleaved, Grazing	0.389
5	pH, Moisture, Broadleaved, Farms, Grazing	0.353
6	DITP, pH, Moisture, Broadleaved, Farms, Grazing	0.278
Abandoned sites		
Size	Variables	Correlation
1	Broadleaved	0.417
2	pH, Broadleaved	0.505
3	pH, Moisture, Broadleaved	0.483
4	DITP, pH, Moisture, Broadleaved	0.438
5	DITP, pH, Moisture, Broadleaved, Farms	0.372
6	DITP, pH, Moisture, Broadleaved, Farms, Abandonment	0.318
Bray-Curtis		
All sites		
Size	Variables	Correlation
1	pH	0.313
2	pH, Broadleaved	0.397
3	pH, Moisture, Broadleaved	0.441
4	pH, Moisture, Broadleaved, Farms	0.375
5	Dmana, DITP, pH, Moisture, Broadleaved	0.334
6	Dmana, DITP, pH, Moisture, Broadleaved, Farms	0.309
Grazed sites		
Size	Variables	Correlation
1	Moisture	0.282
2	Moisture, Broadleaved	0.361
3	pH, Moisture, Broadleaved	0.360
4	pH, Moisture, Broadleaved, Grazing	0.344
5	pH, Moisture, Broadleaved, Farms, Grazing	0.311

6	DITP, pH, Moisture, Broadleaved, Farms, Grazing	0.225
Abandoned sites		
Size	Variables	Correlation
1	pH	0.414
2	pH, Broadleaved	0.541
3	pH, Moisture, Broadleaved	0.526
4	DITP, pH, Moisture, Broadleaved	0.473
5	DITP, pH, Moisture, Broadleaved, Farms	0.397
6	DITP, pH, Moisture, Broadleaved, Farms, Abandonment	0.329

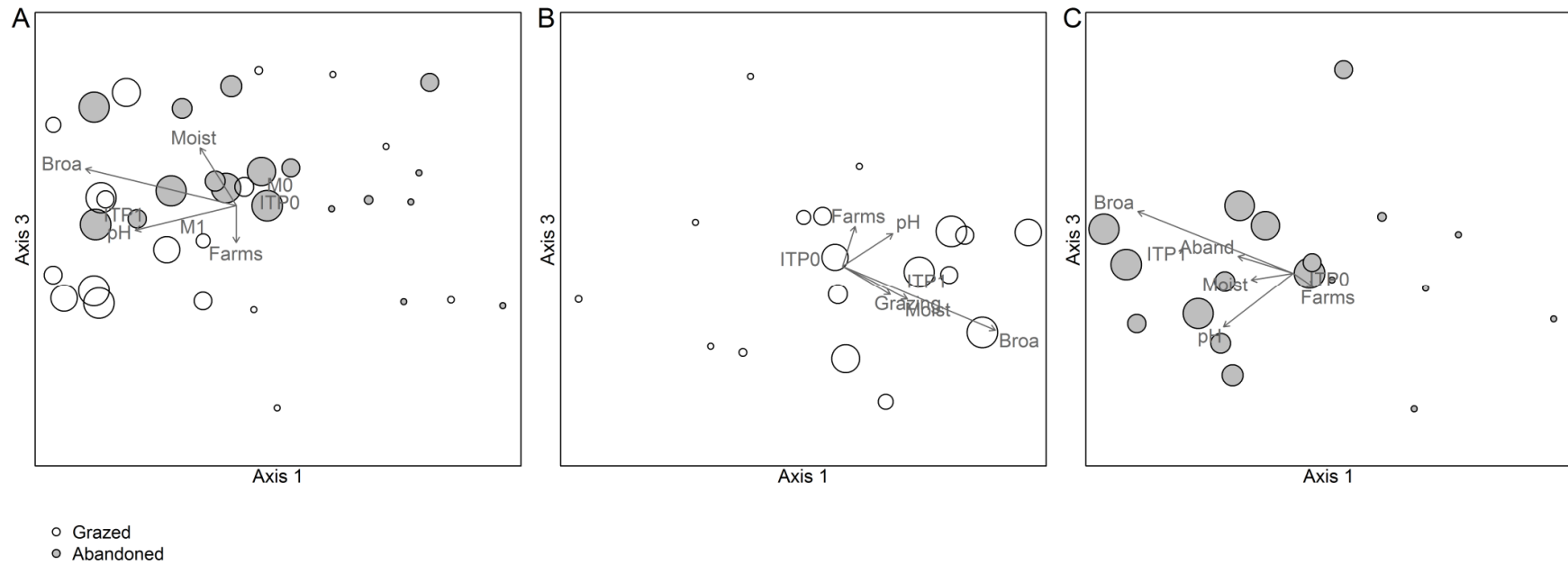


Figure 1. Nonmetric Multidimensional Scaling (NMDS) for the community structure of mycorrhizal fungi species among a) all sites, b) grazed sites, and c) abandoned sites with axes 1 and 3. Analyses were done with Chao's dissimilarity index. For the categorical variables inventory time period (ITP1 in 2010, ITP0 in 2012-2013) and management (M1 for grazed sites, and M0 for abandoned sites) the location represents the average location of sites in that category. The arrows represent the direction and strength of the a posteriori correlations between the site locations and the continuous environmental variables: the historical land-use intensity (Farms), soil moisture, soil pH, the proportion of broadleaved trees (Broa), grazing intensity on grazed sites, and time since abandonment on abandoned sites. Symbol size represents the proportion of broadleaved trees.

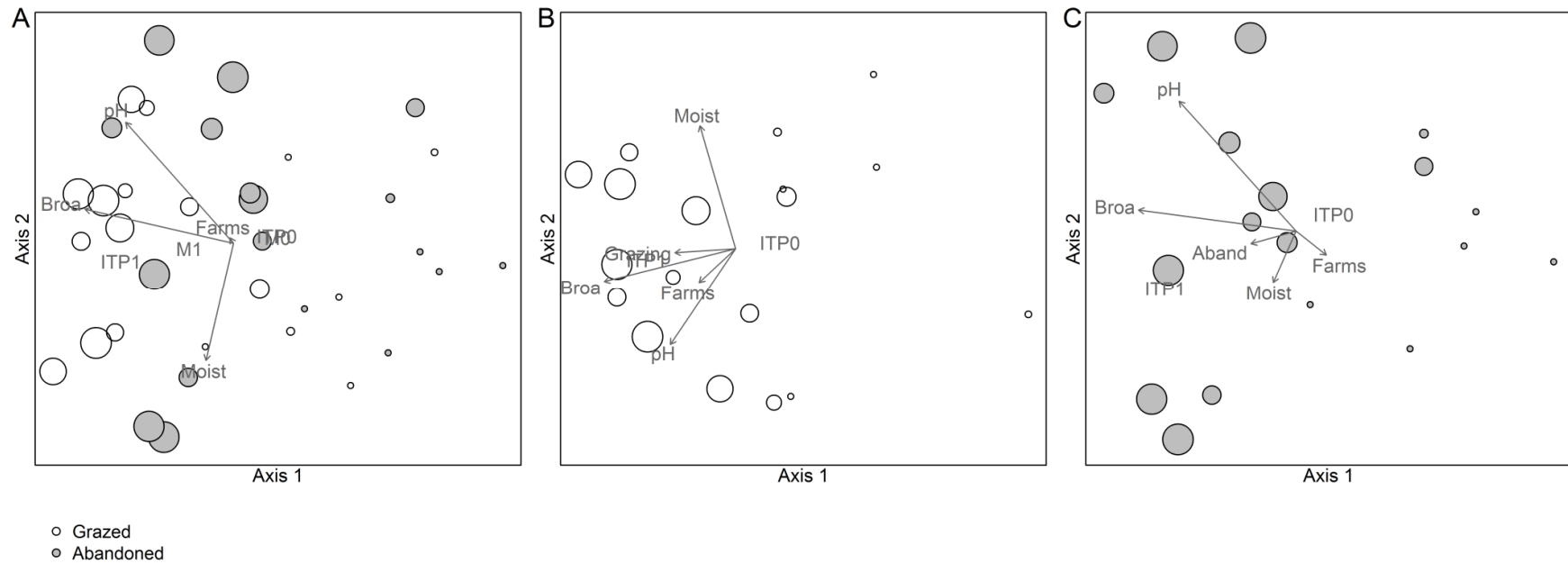


Figure 2. Nonmetric Multidimensional Scaling (NMDS) for the community structure of mycorrhizal fungi species among a) all sites, b) grazed sites, and c) abandoned sites with axes 1 and 2. Analyses were done with Bray-Curtis dissimilarity index. For the categorical variables inventory time period (ITP1 in 2010, ITP0 in 2012-2013) and management (M1 for grazed sites, and M0 for abandoned sites) the location represents the average location of sites in that category. The arrows represent the direction and strength of the a posteriori correlations between the site locations and the continuous environmental variables: the historical land-use intensity (Farms), soil moisture, soil pH, the proportion of broadleaved trees (Broa), grazing intensity on grazed sites, and time since abandonment on abandoned sites. Symbol size represents the proportion of broadleaved trees.

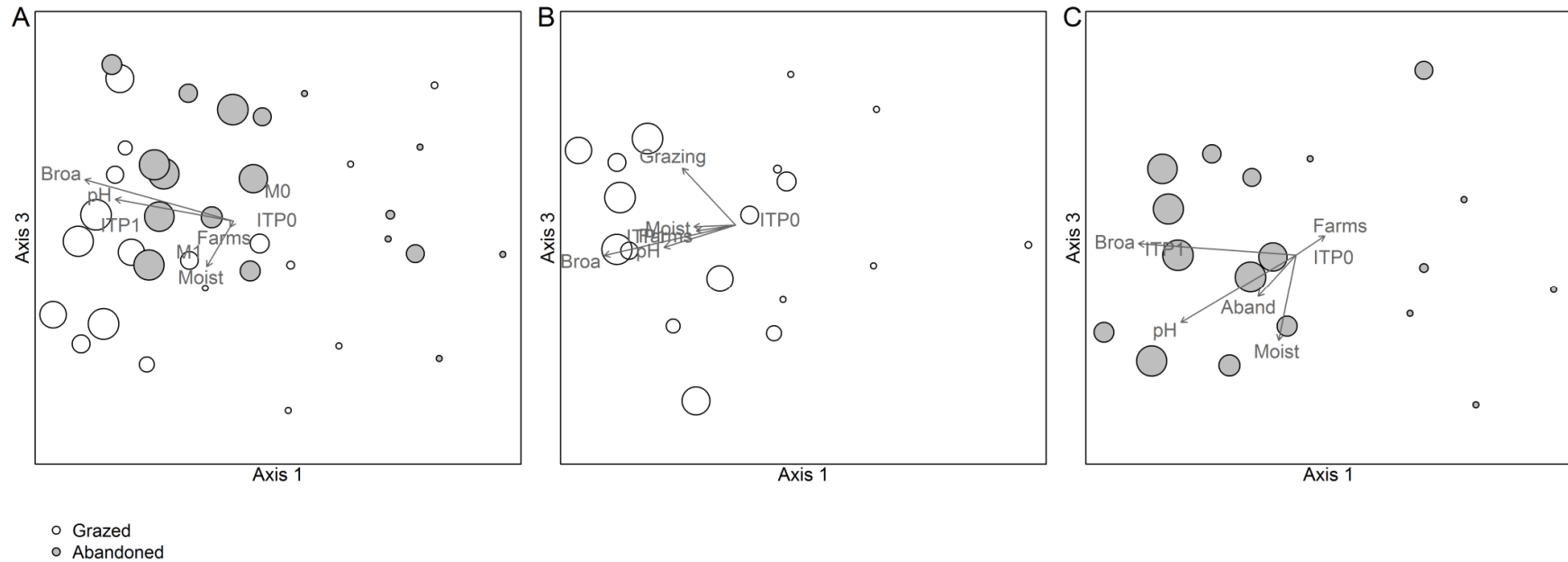


Figure 3. Nonmetric Multidimensional Scaling (NMDS) for the community structure of mycorrhizal fungi species among a) all sites, b) grazed sites, and c) abandoned sites with axes 1 and 3. Analyses were done with Bray-Curtis dissimilarity index. For the categorical variables inventory time period (ITP1 in 2010, ITP0 in 2012-2013) and management (M1 for grazed sites, and M0 for abandoned sites) the location represents the average location of sites in that category. The arrows represent the direction and strength of the a posteriori correlations between the site locations and the continuous environmental variables: the historical land-use intensity (Farms), soil moisture, soil pH, the proportion of broadleaved trees (Broa), grazing intensity on grazed sites, and time since abandonment on abandoned sites. Symbol size represents the proportion of broadleaved trees.

Appendix B for Tervonen et al.: Ectomycorrhizal fungi in wood-pastures:
 Communities are determined by trees and soil properties, not by grazing

Authors: Kaisa Tervonen, Anna Oldén, and Panu Halme

Table 1. List of ectomycorrhizal fungi species found in this study. The nomenclature of agarics and boletoids follows Knudsen and Vesterholt (2012) and Aphylloporales Kotiranta et al. (2009). For a few *Cortinarius* spp., *Inocybe* spp. and *Russula* spp. species the authors have been mentioned. They are species names that specialists want to use or species that are not yet published (ined.) The IUCN status follows Bonsdorff et al. (2010), and not evaluated (NE) species Von Bonsdorff (2012). “NEW” species are species that have not been yet published or are quite new species to Finland. The number of observations among grazed (18), abandoned (18) and all sites (36) are also given.

Species	IUCN	Grazed	Aband	All
<i>Amanita battarrae</i>	LC	0	1	1
<i>Amanita fulva</i>	LC	6	4	10
<i>Amanita muscaria</i> var. <i>muscaria</i>	LC	9	5	14
<i>Amanita muscaria</i> var. <i>regalis</i>	LC	0	2	2
<i>Amanita olivaceogrisea</i>	LC	5	3	8
<i>Amanita porphyria</i>	LC	8	7	15
<i>Amanita rubescens</i> f. <i>rubescens</i>	LC	4	2	6
<i>Amanita virosa</i>	LC	0	1	1
<i>Boletus edulis</i> coll.	LC	6	4	10
<i>Cantharellus cibarius</i>	LC	5	7	12
<i>Chalciporus piperatus</i>	LC	7	8	15
<i>Chroogomphus rutilus</i> var. <i>rutilus</i>	LC	0	2	2
<i>Cortinarius acutus</i>	LC	1	3	4
<i>Cortinarius alboviolaceus</i>	LC	2	3	5
<i>Cortinarius alnetorum</i>	LC	1	1	2
<i>Cortinarius anomalus</i> coll.	LC	4	8	12
<i>Cortinarius anthracinus</i>	LC	3	4	7
<i>Cortinarius armeniacus</i>	LC	1	2	3
<i>Cortinarius armillatus</i>	LC	0	5	5
<i>Cortinarius aurantiomarginatus</i>	LC	0	1	1
<i>Cortinarius balaustinus</i>	LC	0	1	1
<i>Cortinarius biformis</i> coll.	LC	1	3	4
<i>Cortinarius bolaris</i>	LC	0	2	2
<i>Cortinarius borgsjoeënsis</i>	LC	0	1	1
<i>Cortinarius brunneus</i> coll.	LC	2	10	12
<i>Cortinarius bulliardiioides</i>	LC	1	1	2
<i>Cortinarius camphoratus</i>	LC	2	4	6
<i>Cortinarius caperatus</i>	LC	2	4	6
<i>Cortinarius caput-medusae</i> coll.	LC	1	0	1
<i>Cortinarius casimiri</i>	LC	10	12	22

<i>Cortinarius causticus</i>	LC	0	1	1
<i>Cortinarius cf. disjungendus</i>	LC	2	1	3
<i>Cortinarius cf. gossypinus</i>	LC	1	0	1
<i>Cortinarius cf. privignatus</i>	LC	1	0	1
<i>Cortinarius cf. suberi</i>	LC	0	2	2
<i>Cortinarius cinnamomeus</i>	LC	1	4	5
<i>Cortinarius collinitus</i>	LC	2	5	7
<i>Cortinarius colus</i>	LC	0	1	1
<i>Cortinarius colymbadinus</i>	LC	0	2	2
<i>Cortinarius croceus var. croceus</i>	LC	3	4	7
<i>Cortinarius decipiens var. decipiens</i>	LC	1	1	2
<i>Cortinarius delibutus coll.</i>	LC	1	5	6
<i>Cortinarius depressus coll.</i>	LC	1	1	2
<i>Cortinarius duracinus coll.</i>	LC	0	2	2
<i>Cortinarius erubescens</i>	LC	0	2	2
<i>Cortinarius flexipes coll.</i>	LC	7	11	18
<i>Cortinarius gentilis</i>	LC	2	6	8
<i>Cortinarius hedyaromaticus</i> C. Cripps & O.K. Mill.	NEW	1	0	1
<i>Cortinarius hemitrichus</i>	LC	1	2	3
<i>Cortinarius Hinnulei</i>	LC	1	0	1
<i>Cortinarius illuminus</i>	LC	1	0	1
<i>Cortinarius impolitus</i> Kauffman	LC	3	4	7
<i>Cortinarius laniger</i>	LC	0	2	2
<i>Cortinarius lilacinopusillus</i>	LC	0	1	1
<i>Cortinarius limonius</i>	LC	1	0	1
<i>Cortinarius lucorum</i>	LC	1	0	1
<i>Cortinarius malachus</i>	LC	1	0	1
<i>Cortinarius malicorius</i>	LC	1	1	2
<i>Cortinarius mucosus</i>	LC	0	1	1
<i>Cortinarius multiformis coll.</i>	LC	1	3	4
<i>Cortinarius obtusus coll.</i>	LC	1	1	2
<i>Cortinarius pansa</i>	NEW	0	1	1
<i>Cortinarius parvannulatus coll.</i>	LC	2	2	4
<i>Cortinarius pholideus</i>	LC	1	3	4
<i>Cortinarius raphanoides</i>	LC	3	10	13
<i>Cortinarius rubrovioleipes</i>	NT	2	0	2
<i>Cortinarius rusticus</i>	LC	0	1	1
<i>Cortinarius sanguineus var. sanguineus</i>	LC	2	4	6
<i>Cortinarius saniosus</i>	LC	2	4	6
<i>Cortinarius semisanguineus</i>	LC	1	1	2
<i>Cortinarius spilomeus</i>	LC	0	4	4
<i>Cortinarius stillatitius</i>	LC	1	2	3
<i>Cortinarius subtortus</i>	LC	1	1	2
<i>Cortinarius tortuosus</i>	LC	1	0	1
<i>Cortinarius traganus f. traganus</i>	LC	1	5	6
<i>Cortinarius triumphans</i>	LC	6	3	9

<i>Cortinarius trivialis</i>	LC	1	1	2
<i>Cortinarius turmalis</i>	LC	0	1	1
<i>Cortinarius umbrinolens</i>	LC	2	2	4
<i>Cortinarius uraceus</i>	LC	0	1	1
<i>Cortinarius venustus</i>	LC	1	2	3
<i>Cortinarius violilamellatus</i>	LC	1	0	1
<i>Craterellus cornucopioides</i>	LC	1	3	4
<i>Craterellus sinuosus</i>	LC	0	1	1
<i>Gomphidius glutinosus</i>	LC	2	4	6
<i>Hebeloma birrus</i>	LC	12	1	13
<i>Hebeloma mesophaeum</i>	LC	1	2	3
<i>Hebeloma theobrominum</i>	LC	2	0	2
<i>Hygrophorus agathosmus</i>	LC	2	3	5
<i>Hygrophorus erubescens</i>	LC	0	1	1
<i>Hygrophorus hedrychii</i>	LC	0	2	2
<i>Hygrophorus korhonenii</i>	LC	1	2	3
<i>Hygrophorus olivaceoalbus</i>	LC	4	8	12
<i>Hygrophorus pustulatus</i>	LC	4	1	5
<i>Inocybe acuta</i>	LC	1	1	2
<i>Inocybe aff. grammata</i>	NEW	1	0	1
<i>Inocybe aff. napipes</i>	NEW	1	0	1
<i>Inocybe armeniaca Huijsman</i>	LC	0	1	1
<i>Inocybe calamistrata</i>	LC	0	1	1
<i>Inocybe castanea</i>	LC	5	9	14
<i>Inocybe cf. griseoscabrosa</i>	NEW	0	1	1
<i>Inocybe cf. humilis</i> (J. Favre & E. Horak) Estre-Rav. & Vila	LC	2	2	4
<i>Inocybe cf. squarrosa</i>	LC	0	1	1
<i>Inocybe cincinnata var. cincinnata</i>	LC	4	8	12
<i>Inocybe curvipes</i>	LC	1	0	1
<i>Inocybe flavella</i>	LC	1	0	1
<i>Inocybe flocculosa</i>	LC	4	5	9
<i>Inocybe fuscidula var. fuscidula</i>	LC	0	1	1
<i>Inocybe geophylla</i>	LC	11	13	24
<i>Inocybe grammata</i>	LC	0	1	1
<i>Inocybe hystrix</i>	NT	0	1	1
<i>Inocybe lacera coll.</i>	LC	2	1	3
<i>Inocybe leptophylla</i>	LC	1	0	1
<i>Inocybe lilacina</i>	LC	3	6	9
<i>Inocybe lindrothii</i> (P. Karst.) Vauras & E. Larss.	LC	3	2	5
<i>Inocybe maculata</i>	LC	0	1	1
<i>Inocybe mixtilis</i>	LC	5	2	7
<i>Inocybe napipes</i>	LC	3	3	6
<i>Inocybe nitidiuscula</i>	LC	1	3	4
<i>Inocybe proximella</i>	LC	1	1	2
<i>Inocybe rimosa coll.</i>	LC	1	1	2

<i>Inocybe rivularis</i>	LC	1	1	2
<i>Inocybe sindonia</i>	LC	0	1	1
<i>Inocybe soluta</i>	LC	1	0	1
<i>Inocybe sp1.</i>	NEW	1	0	1
<i>Inocybe sp2.</i>	NEW	0	1	1
<i>Inocybe subcarpta</i>	LC	1	0	1
<i>Inocybe subnudipes</i>	LC	0	1	1
<i>Inocybe terrigena</i>	LC	0	1	1
<i>Laccaria laccata</i>	LC	14	11	25
<i>Laccaria tortilis</i>	LC	1	0	1
<i>Lactarius aurantiacus</i>	LC	1	0	1
<i>Lactarius camphoratus</i>	LC	3	10	13
<i>Lactarius deterrimus</i>	LC	2	5	7
<i>Lactarius flexuosus var. flexuosus</i>	LC	3	3	6
<i>Lactarius fuliginosus</i>	LC	1	3	4
<i>Lactarius glyciosmus</i>	LC	11	11	22
<i>Lactarius helvus</i>	LC	0	2	2
<i>Lactarius lacunarum</i>	LC	1	0	1
<i>Lactarius mammosus</i>	LC	1	0	1
<i>Lactarius necator</i>	LC	13	11	24
<i>Lactarius obscuratus</i>	LC	2	2	4
<i>Lactarius rufus</i>	LC	2	3	5
<i>Lactarius sphagneti</i>	LC	0	1	1
<i>Lactarius spinosulus</i>	LC	1	3	4
<i>Lactarius tabidus</i>	LC	13	15	28
<i>Lactarius torminosus</i>	LC	5	6	11
<i>Lactarius trivialis</i>	LC	4	5	9
<i>Lactarius uvidus</i>	LC	0	1	1
<i>Lactarius vietus</i>	LC	5	9	14
<i>Leccinum scabrum</i>	LC	7	2	9
<i>Leccinum variicolor</i>	LC	2	3	5
<i>Leccinum versipelle</i>	LC	0	1	1
<i>Leucocortinarius bulbiger</i>	LC	1	0	1
<i>Naucoria bohémica</i>	LC	3	1	4
<i>Naucoria celluloderma</i>	LC	1	0	1
<i>Naucoria escharioides</i>	LC	1	1	2
<i>Naucoria salicis</i>	LC	1	1	2
<i>Naucoria submelinoides</i>	NE	0	1	1
<i>Paxillus filamentosus</i>	LC	0	1	1
<i>Paxillus involutus</i>	LC	16	12	28
<i>Phaeocollybia arduennensis</i>	LC	1	0	1
<i>Phaeocollybia cf. festiva</i>	LC	1	0	1
<i>Ramaria eosanguinea</i>	LC	0	1	1
<i>Russula adusta coll.</i>	LC	1	2	3
<i>Russula aeruginea coll.</i>	LC	8	2	10
<i>Russula alnetorum</i>	LC	1	0	1

<i>Russula ancillaris</i> Ruots. & Vauras ined.	NEW	2	0	2
<i>Russula aquosa</i>	LC	9	6	15
<i>Russula atrorubens</i>	LC	4	6	10
<i>Russula aurea</i>	LC	0	1	1
<i>Russula betularum</i>	LC	10	11	21
<i>Russula cessans coll.</i>	LC	3	0	3
<i>Russula chloroides coll.</i>	LC	4	2	6
<i>Russula claroflava</i>	LC	5	5	10
<i>Russula consobrina</i>	LC	1	4	5
<i>Russula crassipes</i> Ruots. & Vauras ined.	NEW	3	1	4
<i>Russula decolorans</i>	LC	2	3	5
<i>Russula emetica coll.</i>	LC	0	1	1
<i>Russula fennoscandica</i> Ruots. & Vauras ined.	NEW	0	5	5
<i>Russula foetens</i>	LC	4	2	6
<i>Russula globispora</i>	LC	0	2	2
<i>Russula gracillima</i>	LC	7	3	10
<i>Russula griseascens</i>	LC	2	2	4
<i>Russula integriformis</i>	LC	1	0	1
<i>Russula intermedia</i>	LC	3	6	9
<i>Russula medullata</i>	LC	1	0	1
<i>Russula nana</i>	LC	1	1	2
<i>Russula nauseosa</i>	LC	0	3	3
<i>Russula nitida coll.</i>	LC	5	3	8
<i>Russula olivaceoviolascens</i> Gillet sensu Romagnes	NE	2	1	3
<i>Russula paludosa</i>	LC	2	1	3
<i>Russula pelargonica coll.</i>	LC	4	2	6
<i>Russula pubescens</i>	LC	0	1	1
<i>Russula puellaris</i>	LC	1	2	3
<i>Russula pyrenaica</i> J. Blum	NEW	0	1	1
<i>Russula renidens coll.</i>	LC	1	1	2
<i>Russula rhodopus</i>	LC	2	2	4
<i>Russula risigallina var. risigallina</i>	LC	0	1	1
<i>Russula robertii coll.</i>	NE	0	1	1
<i>Russula roseipes</i>	LC	1	0	1
<i>Russula sanguinea</i>	LC	2	0	2
<i>Russula sapinea</i>	LC	1	0	1
<i>Russula sardonica</i>	LC	1	1	2
<i>Russula turci</i>	LC	1	1	2
<i>Russula velenovskyi coll.</i>	LC	6	7	13
<i>Russula versicolor coll.</i>	LC	0	2	2
<i>Russula vesca</i>	LC	7	5	12
<i>Russula vinosa</i>	LC	3	3	6
<i>Russula vinososordida</i>	LC	1	1	2
<i>Russula violaceoincarnata</i>	LC	3	4	7
<i>Russula vitellina</i>	LC	4	3	7

<i>Russula xerampelina coll.</i>	LC	4	1	5
<i>Suillus luteus</i>	LC	1	1	2
<i>Thelephora palmata</i>	LC	1	1	2
<i>Tricholoma albobrunneum</i>	LC	1	0	1
<i>Tricholoma columbetta</i>	LC	0	1	1
<i>Tricholoma fulvum</i>	LC	7	2	9
<i>Tricholoma inamoenum</i>	LC	2	6	8
<i>Tricholoma saponaceum var. saponaceum</i>	LC	1	1	2
<i>Tricholoma stans</i>	LC	0	1	1
<i>Tricholoma stiparophyllum</i>	LC	4	5	9
<i>Tricholoma vaccinum</i>	LC	0	1	1
<i>Tricholoma virgatum</i>	LC	0	2	2
<i>Xerocomus badius</i>	LC	1	0	1
<i>Xerocomus subtomentosus coll.</i>	LC	4	1	5

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