

# Rescuing the ectomycorrhizal biodiversity associated with South American *Nothofagaceae* forest, from the 19th century naturalists up to molecular biogeography

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The southernmost portion of the Andes in South America hosts *Nothofagaceae* forests that form ectomycorrhizal (EcM) associations. We compiled all the published reports of EcM taxa from these woodlands, based on fruit-body collections and molecularly identified root tips. This resulted in 87 peer-reviewed research papers dealing with EcM associations from *Nothofagaceae* forests published over the past 62 years. Based on these papers the EcM richness and its association with *Nothofagaceae* species was analyzed. Represented by 45 genera (34 Basidiomycetes and 11 Ascomycetes), 479 EcM taxa have been recorded, plus an additional 46 EcM taxa which are potentially EcM. *Cortinarius* was the most frequent and diverse genus, with 64.9% of total species. *Nothofagus dombeyi* had the highest number of unique EcM species, followed by *N. pumilio*, *N. antarctica* and *Lophozonia obliqua*. The EcM community associated with *Nothofagus* species, except *N. nitida*, showed higher similarities among themselves, than with *Lophozonia* and *Fuscospora* species. Beta diversity indexes showed EcM *Nothofagus* species have 29–42% niche overlap, while *Nothofagus*—*Lophozonia* only had 1–16%. The assessment of the accuracy of the EcM diversity, host specificity and community structure deserve further studies combining phylogenetic analysis based on broad ecological surveys. On the basis of pre-selected criteria *Austropaxillus statuum*, *Cortinarius fragilis*, *Cortinarius xiphidipus* and *Hallingea purpurea* are proposed as candidates for nursery spore inoculations, and should be subject to scientific evaluation to determine costs and benefits.

## Introduction

The Andean-Patagonian region, along the southernmost portion of the Andes Mountains in South America, nourishes forests dominated by *Nothofagaceae* Kuprian species (Cabrerá, 1976), distributed between 30 to 56° S on both sides of the Andes mountains. The region comprises 11 species of *Nothofagaceae* from three genera: *Nothofagus*, *Lophozonia* and *Fuscospora*, forming extensive monospecific and mixed forests (Dimitri and Orfila, 1985; Donoso Zegers, 2006; Heenan and Smissen, 2013). Ectomycorrhizal (EcM) associations play a key role in the functioning of all these forests (Singer and Morello, 1960; Valenzuela Flores, 1993; Fontenla *et al.*, 1998).

*Nothofagaceae* forests are characterized by low atmospheric pollution (Perakis and Hedin, 2002), poorly developed volcanic soils (Satti *et al.*, 2007) with low availability of phosphorous (P) and a high capacity to store water and buffer pH changes (Diehl *et al.*, 2003). *Nothofagus pumilio* (Poepp. & Endl.) Krasser is distributed from 35 to 56° S on both sides of the Andes, and occupies

the upper limit of the mountain forest. *Nothofagus antarctica* (G. Forst.) Oerst. shares the *N. pumilio* distribution, but due to its drought resistance, it is mostly present in the forest-steppe ecotone area. *Lophozonia obliqua* (Mirb.) Heenan & Smissen and *L. alpina* (Poepp. & Endl.) Heenan & Smissen, both with very high wood quality, have more restricted distributions, growing from 30 to 41° S and 35 to 40.5° S respectively in both Chile and Argentina. Evergreen *N. dombeyi* (Mirb.) Oerst. grows from 30 to 47° S in Argentina and Chile, forming the main type of forest in areas with high humidity, close to lakes and river margins, in pure stands as well as associated with all the other *Nothofagaceae* species except *N. betuloides* (Mirb.) Oerst.; the latter is distributed from 40 to 56° S (Dimitri and Orfila, 1985; Donoso Zegers, 2006). Chile has five other species restricted to the west side of the Andes: *Fuscospora alessandri* (Espinosa) Heenan & Smissen, *L. glauca* (Phil.) Heenan & Smissen, *L. macrocarpa* (A. DC.) Heenan & Smissen and the hybrid *L. x leonii* Espinosa, all with very narrow distributions (from 35 to 36.5° S), and *N. nitida* (Phil.) Krasser

forming oceanic forests distributed from 40 to 49° S (Dimitri and Orfila, 1985; Donoso Zegers, 2006).

Studies have shown that the establishment of *Nothofagaceae* forests in Argentina and Chile depends on EcM associations (Singer and Morello, 1960; Singer and Moser, 1965; Garrido 1988; Carrillo *et al.*, 1992; Valenzuela Flores, 1993), reporting EcM colonization rates higher than 70% (Diehl *et al.*, 2008; Longo *et al.*, 2011). High colonization rates together with the fact that *Nothofagaceae* species do not show a P deficit, suggests that EcM constitute an effective adaptation mechanism of *Nothofagaceae* to P-deficient soils (Diehl *et al.*, 2003, 2008; Agüero *et al.*, 2014), making trees more aggressive and resistant to adverse conditions, well adapted to disturbances and also have the ability to act as pioneers (Garrido, 1988; Valenzuela Flores, 1993).

The EcM fungal species richness associated with a tree species over its natural distribution provides important information needed for ecological studies, management decisions and selection of appropriate EcM fungal species for inoculation programs. The assessment of the EcM biota associated to South American *Nothofagaceae* started with the exploration campaigns and first taxa descriptions from C. Spegazzini (1887a, b) at the end of the 19th century. These pioneering studies were followed by diverse taxonomical reports and ecological studies up to until the modern era, including molecular tools for EcM detection and identification. However, all of this information is scattered and has not yet been compiled, organized and published.

Species of *Nothofagaceae* forests in South America, particularly *N. pumilio*, exhibit extensive degraded areas as it has been widely exploited for its timber. Herbivory by both cervids and cattle (Veblen *et al.*, 1996; Vázquez, 2002), and the increased frequency of forest fires during recent decades are preventing regeneration of these valuable forests. Sustainable silvicultural management, conservation decisions and restoration actions promoted by state institutions and land-owners/private investors have been initiated recently, as has the mass production of seedlings to support regeneration and the establishment of new forests (Barroetaveña *et al.*, 2009). Knowledge about EcM richness, which species are shared, and which are specific to each *Nothofagaceae*, is necessary to build distribution models that support conservation decision making, together with defining suitable species to incorporate EcM inoculation programs in nurseries producing *Nothofagaceae*.

This aims of this review were to: (1) compile the reported EcM taxa associated with *Nothofagaceae* species growing in South America, based on fruiting body collections and molecularly identified root tips, from published accounts; (2) to examine the EcM species richness by fungal genera, along with their associations with *Nothofagaceae*; (3) propose EcM species to be scientifically and technically evaluated as candidates in inoculations (via spores) of *Nothofagaceae* species.

## Material and methods

A total of 87 research articles on EcM from *Nothofagaceae* forests, published in Spanish, German and English language from peer-reviewed research journals and books over the past 62 years, was located using online database searches using the keyword phrases 'ectomycorrhizal fungi', '*Nothofagus*

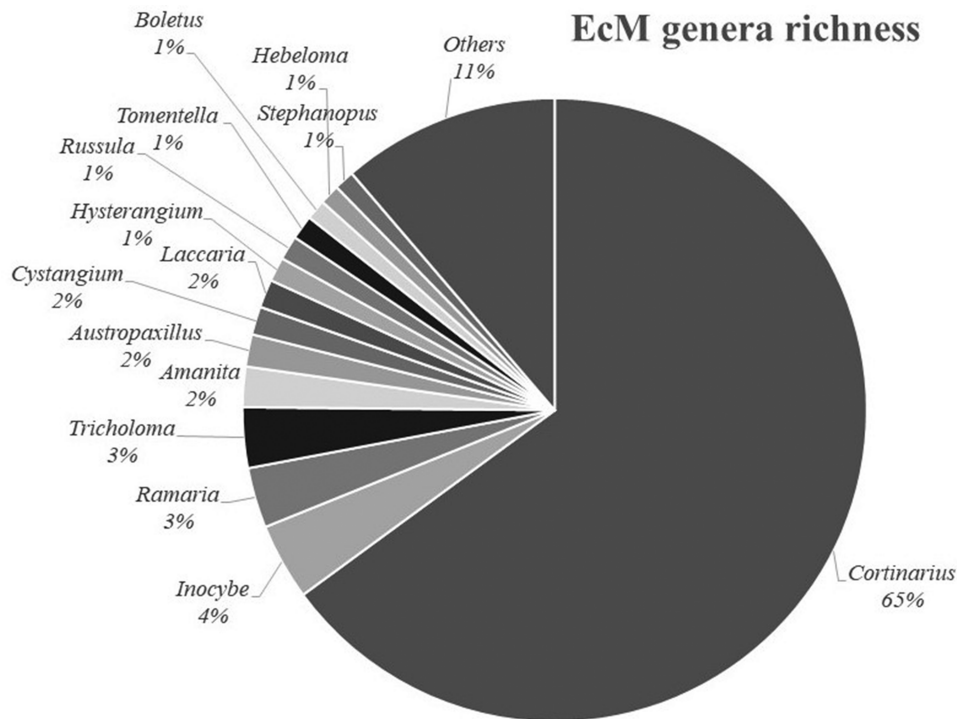
mycorrhizas', '*Nothofagus* forest', 'Ectomycorrhizae Patagonia'. Publications that compiled EcM records but did not provide novel citations were not included in the database and the subsequent analysis.

The EcM fungal species and their references were listed for each *Nothofagaceae* species in South American forests (Supplementary Table S1). Records were obtained from all the published information about EcM fungal taxa, both from fruiting bodies records or molecularly identified EcM root tips. Molecular identifications were included at species level only with BLAST >98% and at genus level with BLAST >90% (Schoch *et al.*, 2014). The complete lists of taxa include infrageneric records; varieties are included separately. All EcM fungal species reported were from forests clearly dominated by the reported species. When records came from mixed forests, all species present were recorded in the analysis. Potential Basidiomycetes and Ascomycetes EcM taxa that belong to a genus whose EcM condition is still under discussion (Rinaldi *et al.*, 2008; Tedersoo and Smith, 2013, 2017; Ágüeda-Hernández, 2014; Kõljalg *et al.*, 2013) were also compiled and highlighted in Supplementary Table S1.

The EcM status of all taxa, at least at genus level, are included in the concept of lineages by Tedersoo and Smith (2013, 2017), and checked with Rinaldi *et al.* (2008), Ágüeda-Hernández (2014) and UNITE (Kõljalg *et al.*, 2013). Taxa currently known to be saprophytic were excluded. Names and authors of each taxon follow the Index Fungorum database (<http://www.indexfungorum.org/Index.htm>); if the name had changed, the currently accepted name was underlined (Supplementary Table S1). The sporocarp habit of each taxon was classified as: epigeous, hypogeous, corticioid (C, fruitbodies resupinated), or subhypogeous.

The total number of citations of each EcM species by tree species, summarized in Supplementary Table S2 was used as a preliminary indicator of frequency to estimate EcM richness, shared species, beta diversity indices, cluster analysis and niche overlap by host tree. Ambiguous species (when associated tree species was not specified by the author) and potential EcM registers were not included. Alpha diversity was estimated by Richness and Chao richness. Differences in these indices between tree species were analyzed by non-parametric ANOVAs with Kruskal Wallis test at 0.05 significance level. All the analyses were performed with the statistical package InfoStat for Windows 10 (Di Rienzo *et al.*, 2017). Niche overlap by tree species and beta diversity were estimated by Jaccard, Sorensen, Morisita-Horn and Bray-Curtis indices using EstimateS (Colwell, 2013).

To examine similarities between tree species considering their associated EcM communities, a Cluster analysis was performed using InfoStat for Windows 10 (Di Rienzo *et al.*, 2017). The outcome of these results was used to consider integrating the biogeographical district classification proposed by Cabrera and Willink (1980) for South American *Nothofagaceae* forests: *Maulino district* from coastal and humid Chilean zones (from 34.9 to 37.3° S latitude) including *F. alessandri*, *L. x leonii*, *L. glauca*, *L. macrocarpa*, *L. obliqua* and *N. dombeyi*; *Maguellan district* from Argentina and Chile (from 47 to 56° S latitude) including *N. betuloides*, *N. antarctica*, *N. pumilio*, *N. nitida*; *Deciduous forest district* from east xeric Argentina and Chile (from 37 to 44° S latitude) including *N. antarctica*, *N. pumilio*; *Pehuen district* from Argentina and Chile (from 37.5 to 40.2° S latitude) including *N. antarctica*, *N. pumilio* and *L. obliqua* associated with *Araucaria*



**Figure 1** Ectomycorrhizal fungi genera richness.

*araucana* and *Valdivian district* from Argentina and Chile humid zones (from 37.3 to 47° S latitude) including *N. dombeyi*, *N. nitida*, *L. alpina* and *L. obliqua*.

The selection of EcM candidate species for spore inoculations was based in Barroetaveña (2004) and Bassani *et al.* (2013), considering the following characteristics: (a) ease of harvesting fruiting bodies, determined by size and fruiting habit (epigeous and/or sub-hypogeous considered easy to find; hypogeous considered difficult to find); (b) fruiting abundance, determined by frequency of observations in the field, citations in the present review, and size of fruiting bodies; (c) fruiting period throughout the year; (d) spore density (spores per unit of fruiting body weight, considering complete fruit bodies for hypogeous species, and only the pileus for epigeous or sub-hypogeous species); (e) tree species reported as hosts; (f) previous reports in seedlings.

## Results

### EcM taxa associated with *Nothofagaceae* in Patagonia: species richness, frequency, specific and shared species

The overall analysis showed that 479 taxa were recorded for *Nothofagaceae* distributed in South American forest (Supplementary Table S1), represented by 45 genera, 34 of them Basidiomycetes and 11 Ascomycetes (Figure 1). There are 17 Basidiomycetes species from 5 genera and 29 Ascomycetes from 9 genera that are potentially EcM (Supplementary Table S1). *Cortinarius* represents the most diverse genus, with 311 species and another 11 registered from root tips at generic level (BLAST between 89–97%) (Nouhra *et al.*, 2013). *Inocybe* presented 19

species, followed by *Tricholoma* and *Ramaria* with 15 species each, *Amanita* with 10 species, *Austropaxillus* with 8 species, *Cystangium* and *Laccaria* with 7 species, *Russula*, *Tomentella* and *Hysterangium* with 6 species, *Boletus*, *Hebeloma* and *Stephanopus* with 5 species each, while the remaining 31 genera had less than 5 species (Figure 1). Of all the taxa reported, 89.8% are epigeous, 6.3% are hypogeous, 1.9% are sub-hypogeous and 2.1% are corticioid (Supplementary Table S1).

The total number of EcM species by *Nothofagaceae* ranged between 22 for *L. x leonii* and 320 for *N. dombeyi* (Table 1). *Nothofagus dombeyi* and *N. pumilio* yielded a high number of exclusive EcM species (115 and 44 respectively) representing 36 and 18% of their total EcM species, while *L. x leonii* and *F. alessandri* showed no unique species (Table 1). *Austropaxillus boletinoides* Singer and *A. statuum* (Speg.) Bresinsky & Jarosch were the most reported ones (20 records), followed by *Cortinarius austrolimonius* Moser & Horak, *C. flammuloides* Moser & Horak and *C. magellanicus* Speg. with 17 records (Figure 2; Supplementary Table S2). Of the EcM compiled species, 37.6% had only one record (Supplementary Table S2).

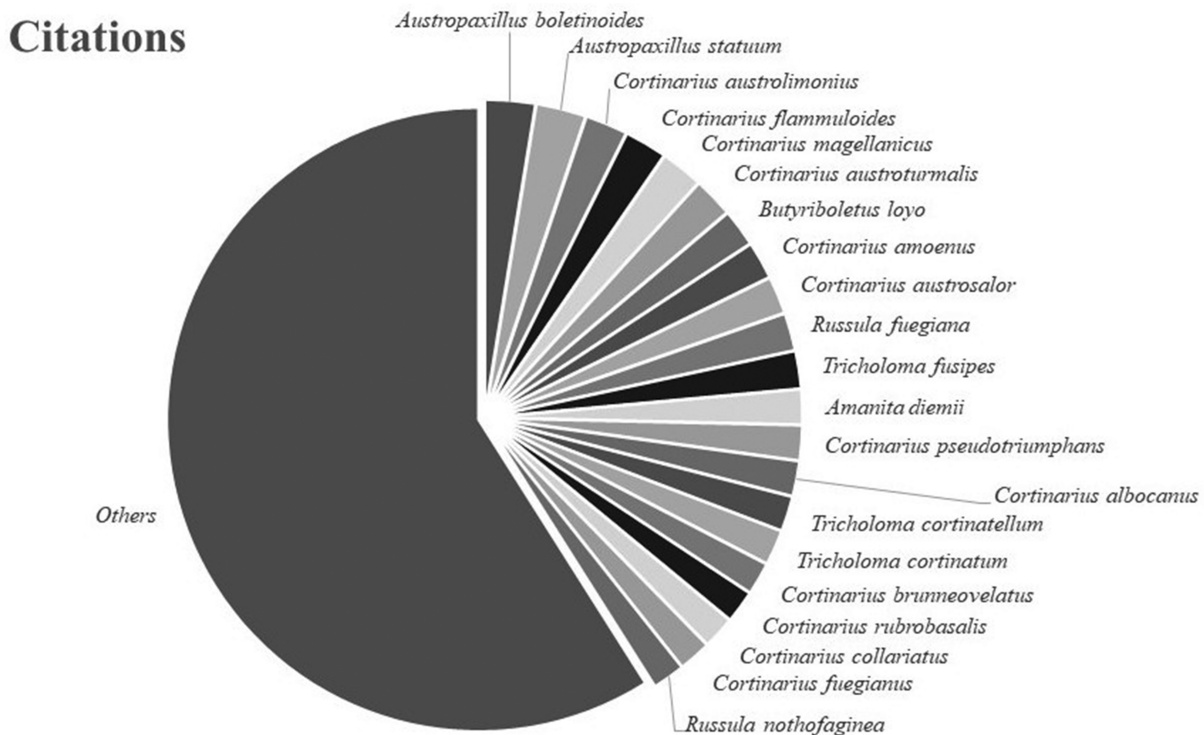
The EcM richness (S) was significantly different among tree species (Kruskal Wallis,  $H = 1079.33$ ;  $P < 0.0001$ , Table 1), *N. dombeyi* being the richest (307 species) and *L. x leonii* the least rich (7 species) (S index, Table 1). Similar results were found for the Chao richness index (Kruskal Wallis,  $H = 1011$ ;  $P < 0.0001$ , Table 1).

The EcM community associated with *Nothofagus*, except *N. nitida*, showed higher similarities among themselves compared with *Lophozonia* and *Fuscospora* species (Figure 3). *Lophozonia alpina* and *L. obliqua* clustered together close to the unique

**Table 1** Number of EcM cited, exclusive species, potential EcM species and alpha diversity by *Nothofagaceae* species.

Tree species	Cited species	Exclusive EcM species	Exclusive EcM %	Potential species	S	S Chao	Biogeographical district
<i>F. alessandri</i>	43	0	0.00	8	29 <sup>a</sup>	33.31 <sup>a</sup>	Maulino
<i>L. alpina</i>	58	2	3.45	17	43 <sup>b</sup>	42.31 <sup>b</sup>	Valdivian
<i>L. glauca</i>	57	3	5.26	8	43 <sup>b</sup>	47.82 <sup>b</sup>	Maulino
<i>L. macrocarpa</i>	26	2	7.69	8	11 <sup>a,c</sup>	12.82 <sup>c</sup>	Maulino
<i>L. obliqua</i>	84	13	15.48	23	69 <sup>d</sup>	73.08 <sup>d</sup>	Maulino, Pehuen, Valdivian
<i>L. x leonii</i>	22	0	0.00	8	7 <sup>c</sup>	7.05 <sup>c</sup>	Maulino
<i>N. antarctica</i>	165	16	9.70	16	150 <sup>e,f</sup>	147.11 <sup>e,f</sup>	Maguellanic, Desiduous, Pehuen
<i>N. betuloides</i>	128	1	0.78	20	113 <sup>d,e</sup>	111.18 <sup>d,e</sup>	Maguellanic
<i>N. dombeyi</i>	320	115	35.94	16	307 <sup>g</sup>	295.45 <sup>g</sup>	Maulino, Valdivian
<i>N. nitida</i>	54	7	12.96	8	39 <sup>b</sup>	41.11 <sup>a,b</sup>	Maguellanic, Valdivian
<i>N. pumilio</i>	248	44	17.74	31	233 <sup>f,g</sup>	227.54 <sup>f,g</sup>	Maguellanic, Desiduous, Pehuen

\*Different letter means significant differences at  $P < 0.05$  (Kruskall Wallis).

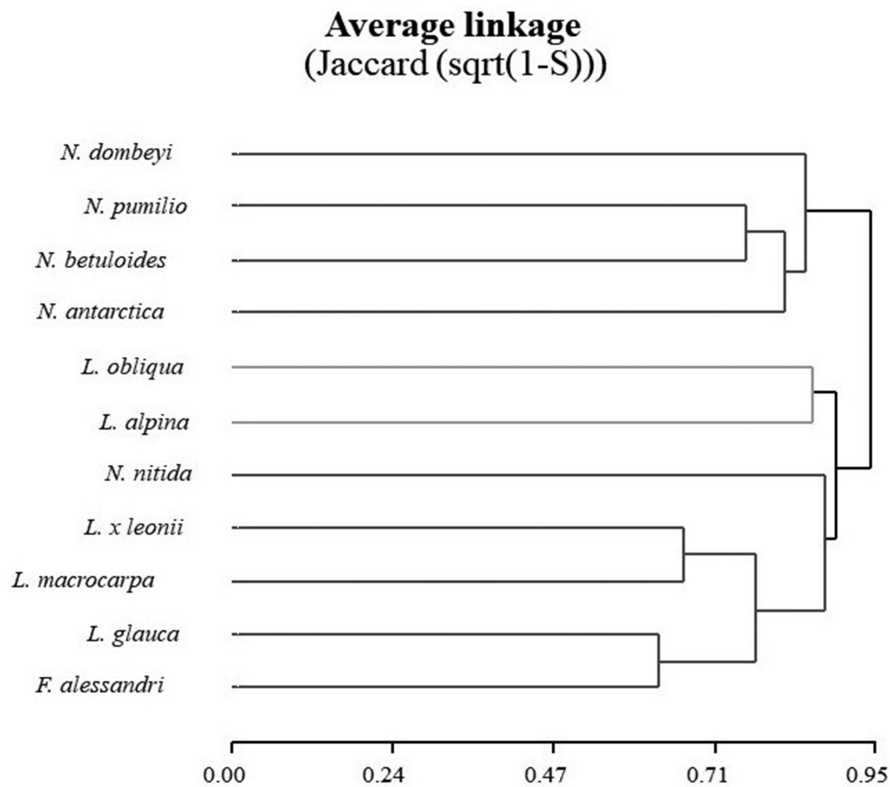
**Figure 2** Ectomycorrhizal genera representativeness (%).

Chilean *Nothofagaceae* species (Figure 3). In the same sense, the beta diversity indexes of the EcM *Nothofagus* species had 29 to 42% niche overlap, while *Nothofagus*—*Lophozonia* only had 1 to 16% (Jaccard index, Table 2), confirmed by the other beta diversity indices.

### Selection of fungal candidate species for EcM spore inoculations

Applying the selected assessment criteria based on reviewed publications, the following species are proposed as potential candidates for nursery inoculations:

***Austropaxillus statuum*** : harvest of fruiting bodies is easy given that it is an epigeous species, with pileus diameter between 5 and 10 cm. Fruiting abundance is high (Bassani *et al.*, 2013), with 20 citations in the database (Table 1, S1). Fruiting occurs from March to April, more abundantly early in the season. Spore density is intermediate, with good viability conservation (Bassani *et al.*, 2013). Hosts are *Nothofagus pumilio*, *N. dombeyi*, *N. antarctica*, *N. nitida*, *L. glauca*, *F. alessandri*. *Austropaxillus* mycorrhizas have been reported by Godoy and Palfner, (1997) from nursery *L. alpina* seedlings and from successful axenical synthesis with all Patagonian *Nothofagaceae* with colonization rates between 51–100% (Garrido, 1988). Edibility: not edible (Gamundí and Horak, 1993).



**Figure 3** Cluster analysis showing similarities between *Nothofagaceae* considering their associated EcM communities.

***Cortinarius fragilis*** : harvest of fruiting bodies is easy given that it is a sub-hypogeous species, with pileus diameter up to 4 cm. Fruiting abundance is intermediate (Bassani *et al.*, 2013), with 8 citations in the database (Table 1, S1). Fruiting occurs from March to May. Spores density is intermediate, with good viability conservation (Bassani *et al.*, 2013). Hosts are *N. pumilio*, *N. dombeyi*, *N. antarctica*, *L. alpina* and *L. obliqua*. *Cortinarius* has been reported from *L. alpina* seedlings (Fernández *et al.*, 2015) and from *N. antarctica* seedlings (Salgado Salomón *et al.*, 2018a). Edibility: unknown.

***Cortinarius xiphidipus*** : harvest of fruiting bodies is easy given that it is an epigeous species, with pileus diameter between 5 and 10 cm. Fruiting abundance is low (Bassani *et al.*, 2013), with 6 citations in the database (Table 1, S1). Fruiting occurs from March to May. Spores density is low, with medium viability conservation (Bassani *et al.*, 2013). Hosts are *N. antarctica*, *N. dombeyi*, *N. pumilio*. *Cortinarius* has been reported from *L. alpina* seedlings (Fernández *et al.*, 2015) and from *N. antarctica* seedlings (Salgado Salomón *et al.*, 2018a). The species is reported as edible (Toledo *et al.*, 2014; Gamundí and Horak, 1993).

***Hallingea purpurea*** : harvest of fruiting bodies is hard, given that it is an hypogeous species with fruiting diameter less than 1.5 cm, although forming nests with several bright violet fruit bodies, which are easy to observe and locate. Fruiting abundance is medium to low (Bassani *et al.*, 2013), with 8 citations in the database (Table 1, S1). Fruiting occurs from March to May. Spore

density is high although with low viability conservation (Bassani *et al.*, 2013). Hosts are *N. dombeyi*, *N. pumilio* and *N. betuloides*. No records from *Nothofagaceae* seedlings have been found. Edibility: unknown.

## Discussion

The 45 EcM genera detected for South American *Nothofagaceae* represent 17.6% of 256 EcM genera worldwide revised by Tedersoo and Smith (2013), Rinaldi *et al.* (2008) and Tedersoo *et al.* (2010). Although our records of Ascomycetes genera correspond to 17.2% of worldwide reported genera, we have listed another 29 Ascomycetes species from 9 genera that could be EcM.

*Nothofagus dombeyi* showed the highest number of EcM species, probably because of its wide distribution (Donoso Zegers, 2006) mostly in areas with high humidity, close to lakes and river margins with temperatures favorable for fungal fruiting. Moreover, its accessibility has made it one of the most studied species, followed by *N. pumilio*, also widely distributed in Patagonian forests (Donoso Zegers, 2006).

The analyses of similarities between the EcM biota associated to each *Nothofagaceae*, with the biogeographical distribution of each tree and their associations in the territory, using the district classification, showed correspondence with trees biogeographical distributions. The highest niche overlapping occurs in the Magellanic district, where *N. pumilio* forms mixed forests with *N. betuloides*, a species restricted to this district. *Lophozonia obliqua* form a single cluster with *L. alpina*, but their niche overlapping

**Table 2** Beta diversity indices by *Nothofagaceae* species.

First sample	Second sample	Shared species observed	Jaccard classic	Jaccard %	Sorensen classic	Morisita-Horn	Bray-Curtis
<i>L. alpina</i>	<i>L. glauca</i>	8	0.105	10.5	0.19	0.191	0.159
<i>L. alpina</i>	<i>L. macrocarpa</i>	2	0.041	4.1	0.078	0.065	0.056
<i>L. alpina</i>	<i>L. obliqua</i>	18	0.196	19.6	0.327	0.367	0.305
<i>L. alpina</i>	<i>L. x leonii</i>	0	0	0	0	0	0
<i>L. alpina</i>	<i>N. antarctica</i>	20	0.118	11.8	0.211	0.196	0.164
<i>L. alpina</i>	<i>N. betuloides</i>	14	0.1	10	0.182	0.225	0.169
<i>L. alpina</i>	<i>N. dombeyi</i>	34	0.109	10.9	0.196	0.272	0.19
<i>L. alpina</i>	<i>N. nitida</i>	6	0.082	8.2	0.152	0.168	0.122
<i>L. alpina</i>	<i>N. pumilio</i>	23	0.092	9.2	0.168	0.193	0.139
<i>L. glauca</i>	<i>L. macrocarpa</i>	2	0.041	4.1	0.078	0.106	0.066
<i>L. glauca</i>	<i>L. obliqua</i>	16	0.17	17	0.291	0.386	0.286
<i>L. glauca</i>	<i>L. x leonii</i>	5	0.119	11.9	0.213	0.207	0.179
<i>L. glauca</i>	<i>N. antarctica</i>	16	0.092	9.2	0.168	0.22	0.134
<i>L. glauca</i>	<i>N. betuloides</i>	16	0.116	11.6	0.208	0.262	0.178
<i>L. glauca</i>	<i>N. dombeyi</i>	35	0.112	11.2	0.202	0.315	0.162
<i>L. glauca</i>	<i>N. nitida</i>	6	0.082	8.2	0.152	0.149	0.115
<i>L. glauca</i>	<i>N. pumilio</i>	21	0.083	8.3	0.154	0.232	0.101
<i>L. macrocarpa</i>	<i>L. obliqua</i>	4	0.055	5.5	0.104	0.114	0.081
<i>L. macrocarpa</i>	<i>L. x leonii</i>	0	0	0	0	0	0
<i>L. macrocarpa</i>	<i>N. antarctica</i>	3	0.019	1.9	0.038	0.057	0.035
<i>L. macrocarpa</i>	<i>N. betuloides</i>	2	0.017	1.7	0.033	0.103	0.035
<i>L. macrocarpa</i>	<i>N. dombeyi</i>	4	0.013	1.3	0.025	0.021	0.017
<i>L. macrocarpa</i>	<i>N. nitida</i>	0	0	0	0	0	0
<i>L. macrocarpa</i>	<i>N. pumilio</i>	3	0.013	1.3	0.025	0.039	0.018
<i>L. obliqua</i>	<i>L. x leonii</i>	1	0.014	1.4	0.027	0.041	0.021
<i>L. obliqua</i>	<i>N. antarctica</i>	29	0.155	15.5	0.269	0.241	0.221
<i>L. obliqua</i>	<i>N. betuloides</i>	16	0.098	9.8	0.178	0.214	0.167
<i>L. obliqua</i>	<i>N. dombeyi</i>	44	0.134	13.4	0.236	0.362	0.225
<i>L. obliqua</i>	<i>N. nitida</i>	6	0.061	6.1	0.114	0.142	0.113
<i>L. obliqua</i>	<i>N. pumilio</i>	29	0.107	10.7	0.194	0.226	0.143
<i>L. x leonii</i>	<i>N. antarctica</i>	1	0.007	0.7	0.013	0.009	0.009
<i>L. x leonii</i>	<i>N. betuloides</i>	1	0.009	0.9	0.017	0.012	0.012
<i>L. x leonii</i>	<i>N. dombeyi</i>	3	0.01	1	0.019	0.026	0.013
<i>L. x leonii</i>	<i>N. nitida</i>	0	0	0	0	0	0
<i>L. x leonii</i>	<i>N. pumilio</i>	1	0.004	0.4	0.008	0.022	0.004
<i>N. antarctica</i>	<i>N. betuloides</i>	51	0.244	24.4	0.392	0.428	0.362
<i>N. antarctica</i>	<i>N. dombeyi</i>	96	0.269	26.9	0.424	0.513	0.414
<i>N. antarctica</i>	<i>N. nitida</i>	8	0.045	4.5	0.086	0.143	0.089
<i>N. antarctica</i>	<i>N. pumilio</i>	104	0.378	37.8	0.549	0.617	0.493
<i>N. betuloides</i>	<i>N. dombeyi</i>	74	0.216	21.6	0.355	0.428	0.324
<i>N. betuloides</i>	<i>N. nitida</i>	20	0.155	15.5	0.268	0.323	0.259
<i>N. betuloides</i>	<i>N. pumilio</i>	101	0.417	41.7	0.589	0.564	0.452
<i>N. dombeyi</i>	<i>N. nitida</i>	18	0.056	5.6	0.105	0.151	0.095
<i>N. dombeyi</i>	<i>N. pumilio</i>	134	0.333	33.3	0.5	0.598	0.491
<i>N. nitida</i>	<i>N. pumilio</i>	14	0.055	5.5	0.104	0.138	0.085

was low. The fact that *L. obliqua* is distributed in 3 districts, growing together with *L. alpina* only in the Valdivian district, could explain why the former has more citations and exclusive EcM species, determining their differences in diversity. *Lophozonia* and *Fuscospora* species restricted to the Maulino district appear clustered together along with *N. nitida*. This fact suggests that the

observed EcM community similarity is associated more with the biogeographical distribution of the tree than with *Nothofagaceae* speciation. On the other hand, 42.4% of the total EcM compiled are exclusive to one tree species, with 78.3% associated to the most studied *N. dombeyi* and *N. pumilio*. This evidence suggests that more surveys are needed for the other *Nothofagaceae* and

also that most of the species reported in this review need combined population genetics analyses and wide-ranging studies of phylogeography, as the increased reproductive isolation with longer distances can lead to lineage divergence, or even hide cryptic speciation (Vincenot and Selosse, 2017).

It is currently accepted that dispersal limitation, host dependency and specificity, plant-soil feedback, and effects of EcM common mycelium networks could drive EcM fungal succession (Dickie *et al.*, 2013; Teste and Dickie, 2017). The shift in EcM community associated with growth stages for South American *Nothofagaceae* forests has not yet been elucidated, nor the effects of site conditions or anthropogenic impacts. It has been reported that seedlings could present a reduced diversity of EcM communities compared to mature stands (Ważny and Kowalski, 2017), that some EcM species can be present at any stage of ecosystem development (Matsuda and Hijii, 2004; Twieg *et al.*, 2007), while others has high association with seedling stages (Cline *et al.*, 2005; Ważny and Kowalski, 2017). All these considerations should be taken in account to select candidate species for inoculation programs. We reviewed a group of species proposed as spore inoculum from a practical perspective, underlining that they are easy to apply, do not require expensive infrastructure nor qualified personnel for their production, are very abundant, low volume, easy to handle and tolerate long storage periods (Rincón *et al.*, 2007; Bassani *et al.*, 2013). Moreover, given the importance of edible fruiting bodies as a highly profitable non-timber forest product for Patagonian native forests, profuse fruiting is a desirable characteristic to prioritize edible mycorrhizal species. We consider spore inoculation is the most realistic option for local nurseries that probably cannot afford the cost of mycelium production or purchase. Nonetheless, EcM taxa other than those proposed here have been reported from nurseries and naturally established *Nothofagaceae* seedlings as *Descolea* (Palfner *et al.*, 2008; Valenzuela Flores *et al.*, 2008; Álvarez *et al.*, 2009; Fernández *et al.*, 2015; Salgado Salomón *et al.*, 2018a), *Hebeloma* (Fernández *et al.*, 2015; Salgado Salomón *et al.*, 2018a), *Sebacina*, *Inocybe*, *Laccaria*, *Genea* (Fernández *et al.*, 2015; Marín *et al.*, 2018), *Tomentella* (Kuhar *et al.*, 2016; Fernández *et al.*, 2013, 2015; Salgado Salomón *et al.*, 2017, 2018a), *Clavulinaceae* (Fernández *et al.*, 2015), *Thelephorales* (Fernández *et al.*, 2015), *Pyrenomataceae* (Fernández *et al.*, 2013; Salgado Salomón *et al.*, 2018a). To broaden the perspective of EcM species best suited to inoculate nursery plants, especially for those with low fruiting frequency, small spores production or corticioid habit, mycelium inoculum production, mycorrhizal infection and field performance tests will be required. Furthermore, vegetative inoculum has been reported as more convenient for certain species (Kuek, 1994; Brundrett *et al.*, 2005). Other edible EcM species not suitable for spores inoculation, such as those from the *Cortinarius magellanicus* complex and *Ramaria patagonica* (Toledo *et al.*, 2014; Barroetaveña and Toledo, 2016; Salgado Salomón *et al.*, 2018b) could be tested with this technology.

Subsequent to the important work reported by Moser and Horak (1975; 278 taxa) from Patagonia, comparatively few species have been described from Australia and New Zealand *Nothofagaceae* species (Gasparini and Soop, 2008). Only 61 species (including the genus *Dermocybe*) were reported in Fungi of Australia (May and Wood, 1997), with at least 16 taxa doubtfully determined (Gasparini and Soop, 2008). According

to Segedin and Pennycook (2001), 98 species have been reported from New Zealand (including the genera *Dermocybe*, *Cuphocybe*, *Rapacea*, *Rozites* and *Thaxterogaster*, now considered as *Cortinarius*) (McKenzie *et al.*, 2000). Since these checklists were available, 32 *Cortinarius* taxa have been published from Australia (Gasparini, 2001, 2004, 2007) and 98 from New Zealand (Soop, 2001, 2002, 2003, 2005, 2013, 2014, 2016; soop *et al.*, 2018), and many more EcM taxa are likely to be found in unexplored ecosystems from southern temperate forest (Tedersoo and Smith, 2013). Shared species with New Zealand *Nothofagaceae* forests includes *Cenococcum geophilum*, *Cortinarius melleomitis* and *Laccaria tetraspora* (McKenzie *et al.*, 2000), while *Laccaria laccata*, *Cenococcum geophilum*, *Cortinarius teraturgus* and *C. amoenus* are shared with Australian *Nothofagaceae* forests (Tedersoo *et al.*, 2009, Horton *et al.*, 2017).

The dominant and rich genus *Cortinarius* associated with *Nothofagaceae* species included in this review, is a large and complex genus within the Agaricales, with synonymized genera present in Patagonia previously classified as *Thaxterogaster*, *Rozites* and *Dermocybe* (Peintner *et al.*, 2001, 2002). It is the most diverse EcM genus of *Nothofagaceae* forests in all its distribution (Moser and Horak, 1975; Garrido, 1986; Dickie *et al.*, 2009; Nouhra *et al.*, 2013). Horton *et al.* (2017) have proposed that Cortinariaceae dominate temperate *Eucalyptus* forests irrespective of forest type, and that the lack of host specificity may partly account for their diversity and abundance, which seems similar to what happens in *Nothofagaceae* forests in Patagonia, with a high number of shared species. On the other hand, recent studies show that *C. magellanicus*, previously reported as widely distributed and shared between *Nothofagaceae* in the Southern Hemisphere (Horak, 1967; Moser and Horak, 1975; Horak and Wood, 1990; Palfner, 2001; Segedin and Pennycook, 2001; Garnica *et al.*, 2003; Toledo *et al.*, 2014), is a complex of species composed of at least four phylogenetic lineages, each with strong regionalism and distinct host associations (Salgado Salomón *et al.*, 2018b). Vouchers morphologically identified as *C. magellanicus* from N. Zealand are now *C. vitreopileatus* var. *similissimus* Peintner & Horak (Salgado Salomón *et al.*, 2018b) questioning the specific taxonomy of others *Cortinarius* species reported as Gondwanically distributed. The fact that BLAST searches of South America *Cortinarius* sequences from type material in UNITE and NCBI do not give any results with similarities higher than 95% for most of them (Frøslev *et al.*, 2007; Nouhra *et al.*, 2013), highlights again a huge gap concerning South American reference data.

Corticioid fungi commonly produce their flat, sheet-like fruiting bodies on the underside of dead wood, twigs and similar plant litter on the forest floor. The mycorrhizal nature of a few of those hundred corticioid species in the Northern Hemisphere has been known for a long time, but in most cases the mycorrhizal evidence was discovered in the late 1900s. Confirmed ectomycorrhizal genera include *Amphinema*, *Byssocorticium*, *Byssosporia*, *Piloderma*, *Pseudotomentella*, *Tomentella*, *Tylospora* (Tedersoo and Smith, 2013). Corticioid genera suspected to contain ectomycorrhizal species are *Sistotrema*, and *Trechispora* (Erland and Taylor, 1999; Rinaldi *et al.*, 2008; Tedersoo *et al.*, 2010; Tedersoo and Smith, 2013). In boreal forests, *Tomentella subilacina* (Ellis & Holw.) Wakef., *Amphinema byssoides* complex and *Tylospora fibrillosa* Donk. are promiscuous species among the most abundant

members of EcM fungal communities (Iwanski and Rudawska, 2007; Tedersoo *et al.*, 2008). In Australia, *Tomentella-Thelephora* (Thelephorales) prevailed on isolated seedlings of *Lophozonia cunninghamii* (Hook.f.) Heenan & Smissen. Studies in Patagonia (Argentina) also showed that the *tomentella-thelephora* (5 spp.), *tullasnella* (2 spp.) and *sebacina* (3 spp.) lineages were present in the fungal community of *Nothofagus dombeyi*, *L. obliqua* and *L. alpina* forests (Fernández *et al.*, 2013, 2015; Kuhar *et al.*, 2016; Nouhra *et al.*, 2013, Salgado Salomón *et al.*, 2018a).

Numerous unpublished sequences from *Nothofagaceae* environmental samples have been uploaded to UNITE, belonging to EcM lineages as *cortinarius* (103), *linocybe* (66 seq.), *pyrenomataceae* (49 seq., including the *pulvinula*, *Ootidea*, *Itarsetta*, *genea-humaria*, and *wilcoxina* lineages), *tomentella-thelephora* (46 seq.), *tullasnella* (19 seq.), *tuber-helvella* (19 seq.), *Idescolea* (17 seq.), *pachyphloeus-amylascus* (14 seq.), *terfezia-peziza depressa* (14 seq in UNITE)/*clavulina* (10 seq in UNITE), *sebacina* (7 seq in UNITE), *tremellodendropsis* (6 seq.), *hebeloma-ainicola* (6 seq.), *tricholoma* (5 seq.) and *hysterangium* (2 seq.), although identified at genus or family level. The genus *Tremellodendropsis* has been reported by Truong *et al.* (2017a) for *N. dombeyi* roots with low similarity and therefore deserves further analysis. Also, several species groups of the Pezizales could not be matched with any of the known ectomycorrhizal or non-mycorrhizal taxa (Tedersoo *et al.*, 2010, 2013).

Considering the gaps in South American reference data about EcM diversity, it is necessary to move forward incorporating sequences from type materials or from accurately determined vouchers to confirm the richness of fungal species in mutualism. Future research combining phylogenetic analysis based on wide ecological surveys would allow revising the real diversity, host specificity and community structure of the EcM biota associated to *Nothofagaceae* forests in South America.

## Supplementary data

Supplementary data are available at *Forestry* online.

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## Conflict of interest statement

None declared.

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