Global AM fungi are dominating mycorrhizal communities in a tropical premontane dry forest in Laipuna, South Ecuador

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Abstract

Tropical dry forests are an intricate ecosystem with special adaptations to periods of drought. Arbuscular mycorrhizal fungi (AMF) are essential for plant survival in all terrestrial ecosystems but might be of even greater importance in dry forests as plant growth is limited due to nutrient and water deficiency during the dry season. Tropical dry forests in Ecuador are highly endangered, but studies about AMF communities are scarce. We investigated the AMF community of a premontane semi-deciduous dry forest in South Ecuador during the dry season. We estimated AMF diversity, distribution, and composition of the study site based on operational taxonomic units (OTUs) and compared the results to those from the tropical montane rainforest and páramo in South Ecuador. OTU delimitation was based on part of the small ribosomal subunit obtained by cloning and Sanger sequencing. Nearly all OTUs were Glomeraceae. The four frequent OTUs were *Glomus*, and comparison with the MaarjAM database revealed these to be globally distributed with a wide range of ecological adaptations. Several OTUs are shared with virtual taxa from dry forests in Africa. Ordination analysis of AMF communities from the tropical dry and montane rainforests in South Ecuador revealed a unique AMF community in the dry forest with only few overlapping OTUs. Most OTUs that were found in both dry and rainforests and on the two continents were globally distributed *Glomus*.

Keywords AMF community · Tropical dry forest · Ecuador · Sanger sequencing

Introduction

Tropical dry forests are a unique biome that can be found in the tropics of South America, Central America, Africa, and Eurasia (Miles et al. 2006). These forests receive less than ~1800 mm rainfall per year and have a dry period from 3 up to 6 months during which most of the vegetation drop their leaves. Tropical dry forests are diverse ecosystems with high levels of endemism and floristic turnover (DRYFLOR et al. 2016). Only 10% of their original extent remains today in

many countries (DRYFLOR et al. 2016), and those remnants are highly endangered due to climate change, habitat fragmentation, and conversion into farmland (Miles et al. 2006).

The Neotropics contain most of all remaining tropical dry forest on Earth with more than half in South America alone (Miles et al. 2006). Neotropical dry forests are distinguished into 12 groups, based on the occurrence and frequency of their woody species (DRYFLOR et al. 2016): (i) Mexico, (ii) Antilles, (iii) Central America–northern South America, (iv) northern inter-Andean valleys, (v) central inter-Andean valleys, (vi) central Andes coast, (vii) Tarapoto-Quillabamba, (viii) Apurímac-Mantaro, (ix) Piedmont, (x) Misiones, (xi) central Brazil, and (xii) Caatinga. For most of the floristic groups, no studies about mycorrhizal communities exist, with the exception of Mexico (i) (Aguilar-Fernández et al. 2009, Carillo-Saucedo et al. 2018, Guadarrama et al. 2014) and Caatinga (xii) in Brazil (Sousa et al. 2018, Marinho et al. 2019, Teixeira-Rios et al. 2018). All of these studies used spores to identify AMF, and based on that, the results show a high level of agreement with dominant representatives of the Glomeraceae and Acaulosporaceae. A better understanding of

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AMF communities is of utter importance to understand ecosystem dynamics and dependencies and to protect the remaining forests (Lugo & Pagano 2019).

We present the first results of AMF community composition for one of the two floristic groups in Ecuador—the Central Andes Coast Forests (vi). To our knowledge, this is the first study about AMF in neotropical dry forests in Ecuador.

The study site is a premontane semi-deciduous dry forest in the Reserva Nacional Laipuna. This forest, also called ceibo forest, is famous for its ceiba trees (*Ceiba trichistandra*), which characterize large areas of the provinces of Manabí, Guayas, El Oro, and Loja (Aguirre et al. 2006). *Tabebuia chrysantha* and species of Bombacaceae are dominating floristic elements in these forests (Aguirre et al. 2006).

The aim of our investigation was to gain knowledge about AMF community composition analyzing root and soil samples with molecular methods and to compare the results to our extensive findings from neotropical rain forests in Southern Ecuador (Haug et al. 2019).

Material and methods

Study area

The study was conducted in the “Reserva Nacional Laipuna” (4° 22' S–79° 90' W) in Southern Ecuador, which belongs to the Tumbesian dry forest ecoregion (Fig. S1). This area is located about 200 km west from our lower and upper rain forest sample sites (for details see Haug et al. 2019). Laipuna is characterized by hilly terrain and altitudes of 600–1450 masl. Precipitation strongly varies from year to year but ranges between 350 and 800 mm (Pucha-Cofrep et al. 2015). Annual precipitation distribution shows a distinctive dry season from June to December and a wet season from January to May. Annual mean temperature is 23.4 °C and shows little variability throughout the year (Pucha-Cofrep et al. 2015).

Vegetation

The ecosystem is classified as a premontane semi-deciduous dry forest (Aguirre et al. 2006). Frequent tree species are *Tabebuia chrysantha*, *Eriotheca ruizii*, *Ceiba trichistandra*, *Erythrina velutina*, *Ipomoea wolcottiana*, *Bursera graveolens*, *Terminalia valverdae*, and *Fulcadea laurifolia* (J. Homeier, unpublished).

Sample collection

Soil and mycorrhizal roots from the topsoil (2–10 cm depth) were sampled during the dry season in October 2016. The

organic layer was loosened with a rake, and sections of several fine-root systems were sampled in plastic bags. Each fine-root system was placed in a separate PCR tube to ensure that each mycorrhizal sample is from a single host plant. Mycorrhizas and soil samples were dried at about 50 °C for 24 h by placing open sample tubes on an electric dryer. After the drying step, silica gel was added, and the tubes were closed for long-term storage.

In total, we collected 95 root and 38 soil samples across sites between 600 and 1250 masl.

DNA isolation

Approximately 5–10 root segments with a length of 2 cm or about 50 mg soil were ground using a carbide ball and a mixer mill (2×1.30 min, frequency 30/s). Total DNA was isolated with either the innuPREP Plant DNA Kit (Analytik Jena, Germany) or the DNeasy Power Soil Kit (Qiagen, Germany) and re-suspended in a final volume of 100 µl elution buffer.

PCR, cloning, and Sanger sequencing

Part of the SSU region of the nuclear ribosomal rDNA repeat was amplified by PCR using a volume of 0.5 µl of the DNA template. A nested PCR approach was applied, amplifying the larger outer fragment with the primer combination NS1/NS4 (White et al. 1990, Lee et al. 2008) and the smaller, inner fragment with the primer pair AML1/AML2 (Lee et al. 2008; for details see Haug et al. 2013). We chose the SSU as the target region because it has been widely used (Öpik et al. 2013, Van Geel et al. 2014); this primer pair is suitable to detect all AMF subgroups (Lee et al. 2008, Van Geel et al. 2014) and provides good comparability with previous studies from other regions (e.g., MaarjAM database: Öpik et al. 2010). It is important to note that AMF species diversity is highly impacted by DNA region, similarity thresholds, and cluster algorithms (Göker et al. 2010), but our main focus is on comparison of AMF composition among different sites and diversity assessment of dry forest AMF.

Amplified PCR products were cloned with the Invitrogen TA Cloning Kit (Life Technologies) following the manufacturer's instructions but using a third of the indicated volumes. Inserts were re-amplified from clones with primers M13F/M13R by picking eight bacterial clones with a separate toothpick and stirring them into one PCR reaction mix per clone. Inserts were digested with restriction enzymes HinfI or AfaI. Digested products were examined on a 0.7% agarose gel. Two clones of the same RFLP pattern were cleaned and sequenced by GATC Biotech (Konstanz, Germany). Whenever the two sequences were not identical, two additional clones of the same RFLP pattern were sequenced. Non-Glomeromycotina sequences (~5% of inserts) were disregarded.

Glomeromycotina sequences were edited with Sequencher (Version 4.9, Gene Codes, Ann Arbor, Michigan), and a BLAST search was performed against the nucleotide sequence database (NCBI) and against the MaarjAM database. When several inserts of a cloned PCR product belonged to the same OTU, only one sequence was included in the final data set.

The final data set (Table S1) consisted of 215 Glomeromycotina sequences: 152 sequences generated from mycorrhizal samples and 63 sequences from soil samples. The sequences were deposited in GenBank (SAMN14381484–SAMN14381698, Table S1).

OTU delimitation

All sequences were ~800 bp long and comprised part of the 18S. Sequences were aligned with MAFFT version 7 (<https://mafft.cbrc.jp/alignment/server/>) (Katoh et al. 2005); MAFFT-L-INS-i, and a distance matrix based on p-distances was created with PAUP for OTU delimitation.

Subsequently, operational taxonomic units (OTUs) were defined as surrogates for species based on sequence similarity with OPTSIL (Göker et al. 2010). We used intermediate linkage clustering and a cut-off value of 99% sequence similarity. This approach splits OTUs if 50% or more of their containing sequences are less than 99% similar to another OTU (for details see Göker et al. 2010). This is the same OTU delimitation approach as in Kottke et al. (2008), Haug et al. (2013), and Haug et al. (2019) to allow a comprehensive comparison with OTUs from the rainforest of Southern Ecuador.

For better comparability, the OTU numbers of the rainforest from the 2019 study (Haug et al. 2019) were retained and marked with an R. The new dry forest OTUs were prefixed with the letter “D” and numbered from 1 to 16.

Singleton sequences (10 in total) were excluded from subsequent analyses.

AMF community analyses

We combined all 152 sequences from mycorrhizal dry forest samples with our existing data set from the mycorrhizal rain forest samples (Haug et al. 2019).

To explore differences in AMF community compositions among sampling sites, we carried out a non-metric multidimensional scaling (NMDS) ordination with metaMDS from the R package VEGAN (Oksanen et al. 2018). The underlying matrix was a Kulczynski dissimilarity matrix derived from OTU abundances of each site. The Kulczynski dissimilarity measure was given the highest rank using R's rankindex test in VEGAN. The metaMDS function in VEGAN allows for calculating the NMDS ordination multiple times with random starts in order to find a stable result (<https://www.rdocumentation.org/packages/vegan/versions/2.4-2/topics/>

Fig. 1 Relative abundance of Glomeromycotina genera in number of sequences. Members of *Glomus* (in light blue) were the dominant mycorrhizal fungi in Laipuna dry forest during the dry season

metaMDS). We used a maximum number of 1000 iterations in a 3-dimensional space.

We performed pairwise PERMANOVA (pairwise.adonis, R) to test for OTU similarity between each site using Holm's correction to control for multiple comparisons.

Results and discussion

AMF community composition of the tropical dry forest in Laipuna

The first results for AMF in a tropical dry forest in Ecuador revealed 27 OTUs from 215 sequences and 133 samples. The rarefaction curve nearly reached the asymptote (Fig. S2) suggesting that few more OTUs are to be found.

Almost all OTUs (93%) belonged to the genus *Glomus* (Figs. 1 and 2) and were found in mycorrhizal samples as well as in the soil (Fig. 3, Table 1). The most abundant OTU was *Glomus* OTU-R31 (= VT69) occurring in 39% of all samples (Fig. 4, Table 1) followed by *Glomus* OTU-R57 (= VT166) found in 23% of the samples. Further frequent OTUs were

Fig. 2 Relative abundance of Glomeromycotina genera in number of OTUs. The number of *Glomus* OTUs was high. Other Glomeromycotina genera and families were almost completely absent

Fig. 3 Venn diagram of OTUs occurring in mycorrhizas and soil. There is a strong overlap of the AMF community in mycorrhizas and in the soil

Glomus OTU-D7 (= VT155) in 13% and OTU-R7 (= VT248) in 11% of the samples (Fig. 4, Table 1). All of these four *Glomus* OTUs are globally distributed, occurring in a variety of biomes (MaarjAM database, <https://maarjam.botany.ut.ee/>). We therefore assume that the dominating *Glomus* OTUs in Laipuna have a range of ecological adaptations and are not specific to dry forest habitats.

In addition to the four dominant *Glomus* OTUs, there were many rare *Glomus* OTUs (Fig. 5, Table 1). Besides the genus *Glomus*, only two more genera, *Claroideoglomus* and *Diversispora*, were found but both in very low numbers. *Diversispora* was represented by only a single sequence (1 OTU) and *Claroideoglomus* by one OTU and four sequences (Figs. 1 and 2, Table 1). The *Claroideoglomus* OTU has a worldwide distribution (VT193 – MaarjAM), and the

Fig. 4 OTU abundance per forest site. Relative abundance of OTUs occurring in > 10% of samples in at least one forest site. The dry forest (orange) and rain forest at 1000 m (green) show an AMF community that is dominated by few frequent OTUs (e.g., OTUR31 from the dry forest and OTUR17 from the 1000 m rain forest occurred in 39% of all samples

each) not found at most other sites. Abundant OTUs from higher elevation forests (≥ 2000 m) show a wide distribution across different altitudes, but even the most frequent OTUs occur only in 16% of all samples

Table 1 OTU numbers and occurrences from the dry and rainforest with corresponding virtual taxa

OTU-No. Rx = numbers from Haug et al. 2019 Dx = new OTUs from the dry forest Laipuna	Number of sequences /percentage in samples	Number of sequences from mycorrhizal samples	Number of sequences from soil samples	Genus of Glomeromy- cotina	Number of sequences at 1000 m (percentage in samples)	Number of sequences at 2000 m (percentage in samples)	Number of sequences at 3000 m (percentage in samples)	Number of sequences at 4000 m (percentage in samples)	Corresponding VT in MaarjAM
D1	4 (3%)	3	1	<i>Glomus</i>					<i>Glomus</i> sp. VT113
R1	4 (3%)	3	1	<i>Glomus</i>	1 (0.5%)	19 (10%)	5 (4%)	4 (3%)	VT113,114,115
D2	8 (6%)	7	1	<i>Glomus</i>					VT113
R2	8 (6%)	8	0	<i>Glomus</i>	22 (10%)	5 (3%)	0	0	VT280
R5	1 (0.75%)	1	0	<i>Glomus</i>	0	5 (3%)	0	1 (0.8%)	VT92
R7	15 (11%)	14	1	<i>Glomus</i>	0	3 (2%)	0	0	VT248
D3	1 (0.75%)	1	0	<i>Glomus</i>					VT99
R29	1 (0.75%)	1	0	<i>Glomus</i>	7 (3%)	7 (4%)	0	0	VT269
R68	7 (5%)	1	6	<i>Glomus</i>	19(9%)	16 (7%)	0	0	VT93
R65	8 (6%)	5	3	<i>Glomus</i>	2 (1%)	1	0	0	VT214
D4	4 (3%)	2	2	<i>Glomus</i>					NEW Laipuna VT93 (98,4%)
D5	4 (3%)	4	0	<i>Glomus</i>					NEW Laipuna VT214 (98,2%)
D6	3 (2%)	2	1	<i>Glomus</i>					NEW Laipuna VT155 (98,1%)
D7	17 (13%)	16	1	<i>Glomus</i>					VT155
D8	3 (2%)	3	0	<i>Glomus</i>					NEW Laipuna VT149 (97,5%)
D9	2 (1.5%)	1	1	<i>Glomus</i>					NEW Laipuna VT342 (98,2%)
D10	4 (3%)	3	1	<i>Glomus</i>					NEW Laipuna VT167 (98,6%)
D11	2 (1.5%)	2	0	<i>Glomus</i>					NEW Laipuna VT167 (97,7%)
D12	11 (8%)	8	3	<i>Glomus</i>					NEW Laipuna VT167 (98,6%)
D13	3 (2%)	2	1	<i>Glomus</i>					NEW Laipuna VT159 (97,5%)
R57	30 (23%)	26	4	<i>Glomus</i>	12 (6%)	0	0	0	VT166
D14	2 (1.5%)	1	1	<i>Glomus</i>					VT414
D15	6 (4.5%)	0	6	<i>Glomus</i>					VT63 <i>Glomus viscosum</i>
D16	10 (7.5%)	1	9	<i>Glomus</i>					NEW Laipuna VT63 (98,6%)
R31	52 (39%)	38	14	<i>Glomus</i>	0	2 (1%)	0	0	VT69 <i>Glomus sinuosum</i> (syn. <i>Sclerocystis sinuosa</i>)
R107	1 (0.75%)	0	1	<i>Diversispora</i>	4 (2%)	0	0	0	NEW Ecuador VT262 98,5%
R115	4 (3%)	1	3	<i>Claroideo- glomus</i>	0	0	4 (3%)	8 (6.5%)	VT193

The colored cells indicate the four frequent OTUs

Diversispora OTU has a close match (98.5% similarity) to VT262 from the MaarjAM database that also occurs in French Polynesia and Micronesia.

The lack of AMF groups other than *Glomus* was unexpected as studies from dry forests in Brazil, yet spore-based and not molecular, showed frequent occurrence of Acaulosporaceae, Gigasporales, and Glomerales (Pagano et al. 2019).

Comparison of AMF from Laipuna with AMF in tropical rain forests of Southern Ecuador

We compared all Laipuna OTUs isolated from mycorrhizal samples at 600–1250 masl with AMF from tropical rain forest sites in Southern Ecuador at 1000–4000 masl (Fig. 6) (Haug et al. 2019). The ordination results show a separate AMF

Fig. 5 Frequency of OTUs based on the number of sequences in the Laipuna Dry Forest. There are few frequent and many rare OTUs

community for the dry forest in Laipuna (Fig. 7). This is supported by the results of pairwise PERMANOVA showing significant differences between the dry forest and the rainforest for all elevation sites above 1000 masl (Table 2). There is some OTU overlap between the dry forest and the lower altitudes of the rainforest (1000 and 2000 masl). Despite the large discrepancies in cloud frequency (Beck et al. 2008), annual rainfall (350–800 mm versus 1950–2230 mm/year), and tree species composition, the AMF community in Laipuna showed similarities with the 1000 masl level by having dominating *Glomus* members and an overlap of seven OTUs (Figs. 4 and 6, Table 1). These overlaps are in agreement with the results of Davison et al. (2021) which found that temperature is one of the most important abiotic drivers for AMF distribution. A distinct AMF community in the dry forest does not necessarily suggest that dry forests AMF are also dry forest specialists as community patterns can be the result of species distribution instead of habitat adaptation (Gai et al. 2006). From studies of AMF in tropical dry and rainforests (Marinho et al. 2018), we know that many species were found in both, dry, and rain forest sites. In addition, many AM fungi seem to be adaptable to different water regimes and thrive in different biomes and ecosystems (Davison et al. 2015). Whether the initial results we are presenting here hold up with more rigorous sampling remains to be seen. The rarefaction

Fig. 6 Shared and unique OTUs of Laipuna Dry Forest with respect to elevation belts of the rain forest. The horizontal bars connecting the same sites indicate the amount of unique OTUs for this site. The thickness of connector lines between different sites represents the percentage of OTUs shared. Laipuna had a high number of unique OTUs and shared several OTUs with the 1000 and 2000 m sites

curve (Fig. S2) shows that sampling was not yet exhaustive. Also, we suggest that in future studies, samples from the wet season should be included as much as possible as frequencies of OTUs, and occurrences might shift between seasons. Differences in AMF species abundance between dry and wet seasons, but no difference in species richness was reported in da Silva et al. (2014) and Maitra et al. (2019). Guadarrama et al. (2014) found differences between the dry and wet season but only for three species—all of them non-*Glomus* AMF: *Gigaspora gigantea* only in the dry season and *Acaulospora foevata* and *Scutellospora erythropus* exclusively in the wet season. On the contrary, Teixeira-Rios et al. (2018) found no statistical difference for AMF communities during dry and wet seasons.

Molecular vs. spore analyses and its influence on the results for *Acaulospora*

The genus *Acaulospora*, which is frequent in the rain forest at high elevations (Haug et al. 2019), was completely absent in samples from the dry forest. This result is in accordance with results from an Afromontane dry forest in Ethiopia (Wubet et al. 2003, 2006, 2009). In the studies conducted by Wubet et al. (2003, 2006, 2009), AMF were extracted from mycorrhizal samples and identified using cloning and Sanger sequencing, revealing a dominance of *Glomus* sequences but no representatives of *Acaulosporaceae*. Furthermore, Rodríguez-Echeverría et al. (2017) studied AMF communities in the Gorongosa National Park (Africa, Mozambique) from soil samples during the dry season using 454 pyrosequencing and found *Acaulosporaceae* only in a negligible amount (0.08% of sequences). The area sampled by Rodríguez-Echeverría et al. (2017) included grasslands, savannas

Table 2 *P*-values of pairwise PERMANOVA for each site

Comparison	Laipuna	1000	2000	3000	4000
Laipuna	—	0.0103	0.0053	0.0017	0.0056
1000	0.0618	—	0.0285	0.0195	0.0285
2000	0.0477*	0.1116	—	0.008	0.0279
3000	0.0170*	0.0975	0.056	—	0.2088
4000	0.0477*	0.1116	0.1116	0.2088	—

P-values after Holm correction are shown in bold. Uncorrected *P*-values are in normal font.

**p*<0.05 significant differences

Fig. 7 **a** NMDS ordination shows turnover of species among sites. Species scores are shown as gray dots and site scores as black labels (see Table S2 for more info). The ellipses around data points show the 95% confidence interval for Laipuna dry forest (pink), the evergreen premontane forest (1000 m, orange), evergreen lower montane forest (2000 m, dark green), upper montane forest (3000 m, light green), and grass paramo/*Polylepis* forest (4000 m, blue) sites. The confidence interval for Laipuna is not overlapping with any of the rainforest sites,

indicating a distinct AMF community. This is supported by PERMANOVA for site comparison Laipuna and upper montane forest ($F=14.285$, $p=0.033$), Laipuna and grass paramo/*Polylepis* ($F=8.937$, $p=0.041$), and Laipuna and evergreen lower montane forest ($F=8.706$, $p=0.041$). Overall stress of the ordination is 0.073 with 3 dimensions ($k=3$). **b** Shepard diagram of the NMDS ordination showing the relationship of the observed dissimilarity with the ordination distance calculated for each run

miombo and dry forests. Due to the high-throughput sequencing method used by Rodríguez-Echeverría et al. (2017), significantly more VTs were found (101 AMF VTs in forests) than in Ecuador, but there is great agreement on the dominance of members of the Glomeraceae family. In contrast, studies from dry forests using spore morphology to identify AMF frequently find Acaulosporaceae and often in high numbers (Aguilar-Fernández et al. 2009, Carillo-Saucedo et al. 2018, Guadarrama et al. 2014, Sousa et al. 2018, Marinho et al. 2019 and Teixeira-Rios et al. 2018).

The reason for the discrepancy of Acaulosporaceae in spore vs. molecular samples remains unknown. Primer sensitivity and molecular methodology seem to be an unlikely reason because the same methods have revealed several Acaulosporaceae in other habitats (e.g., Haug et al. 2019). Furthermore, Wubet et al. (2003, 2006, 2009) and Rodríguez-Echeverría et al. (2017) used a different primer combination and method, and did not find Acaulosporaceae in their samples.

There is evidence that colonization strategies and abundance of extraradical mycelium, spores, and intraradical mycelium differ among AMF groups and between seasons (Hart and Reader 2002, Varela-Cervero et al. 2015). The study of Hart and Reader (2002) compared rate and extent of colonization by measuring percentage root colonization, root fungal biomass, soil hyphal length, and soil fungal biomass of different AMF groups including Acaulosporaceae and Glomeraceae (now

classified as Glomeraceae). Hart and Reader (2002) concluded that “Glomeraceae isolates had high root colonization but low soil colonization, Gigasporaceae isolates showed the opposite trend whereas Acaulosporaceae isolates had low root and soil colonization.” Furthermore, the authors found that Glomeraceae colonized roots faster than Acaulosporaceae and Gigasporaceae and thought this likely to be caused by spore vs. hyphal colonization (Hart and Reader 2002).

We therefore think that it is reasonable to assume that during the dry season, Acaulosporaceae might be readily found in the soil as spores but not in mycorrhizal samples.

Our sampling design included soil samples, so why is it that we still did not detect Acaulosporaceae from soil samples? Hempel et al. (2007) reported that molecular analyses from soil samples have a bias towards hyphal material and might underestimate spore DNA.

In the future, it might be worthwhile to include spore analysis from the soil, in addition to molecular analyses in order to investigate the true AMF potential within an ecosystem. Likewise, to understand which AMF species are actively associated with plants during the dry season, it is necessary to conduct molecular studies on mycorrhizal samples instead of the spores in the soil.

Combining spore analyses with molecular methods would also make the comparison of AMF communities among different dry forests more feasible as many studies from South America are solely based on spore morphology.

AMF community of Laipuna in a global context

Studies of AMF communities in tropical dry forests have only been conducted so far in Mexico (Aguilar-Fernández et al. 2009, Carillo-Saucedo et al. 2018, Guadarrama et al. 2014), Brazil (Sousa et al. 2018, Marinho et al. 2019 and Teixeira-Rios et al. 2018), and Africa (Wubet et al. 2003, 2006, 2009). Albeit the difficulties in comparing spore results vs. molecular results (see paragraph above), all studies conclude a high dominance of Glomeraceae with few abundant species: in Brazil it is *Glomus macrocarpum* (Pagano et al. 2013, Sousa et al. 2018, Marinho et al. 2019); in Mexico it is *Glomus* aff. *fasciculatum* (Aguilar-Fernández et al. 2009, Carillo-Saucedo et al. 2018), *Glomus sinuosum* (Aguilar-Fernández et al. 2009), and *Funneliformis geosporum* (Carillo-Saucedo et al. 2018, Guadarrama et al. 2014). We confirm *Glomus sinuosum* (OTU R31, VT69) and *Glomus* aff. *fasciculatum* (OTU R1, VT113) to occur in Ecuador as well, but only *Glomus sinuosum* was dominant occurring in 39% of the samples. Of the 15 OTUs in the Ecuadorian dry forest that could be assigned to VTs, eleven were also found in the African dry forest of the Gorongosa National Park and eight in an Ethiopian dry forest (Wubet et al. 2009) (Fig. S3). All of the four frequent VTs of the Ecuadorian dry forest also occur in the Ethiopian dry forest (Wubet et al. 2009: *Glomus* NF02 = VT248, *Glomus* NF04 = VT69, *Glomus* NF10 = VT155, *Glomus* NF12 = VT166). An overlap of AMF communities between South America and Africa was also reported by Stürmer et al. (2018) who found many shared species between the South American and African continents (52%) and between the Neotropical and Afrotropic realms (53%). These concordances on two different continents underline the global distribution of AMF. Nevertheless, it should not be neglected that many OTUs/virtual taxa from dry forests of South Ecuador and Africa revealed to be new to science.

This makes the AMF communities of dry forests both in Ecuador and Africa unique and worth preserving.

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Data availability The sequences generated in this study are available in the NCBI Gen Bank (<https://www.ncbi.nlm.nih.gov>) under the accession numbers given in the text.

Code availability Not applicable.

Declarations

Ethics approval Not applicable.

Consent to participate Not applicable.

Consent for publication Not applicable.

Conflict of interest The authors declare no competing interests.

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