Global drivers of obligate mycorrhizal symbionts diversification

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Abstract (200 words):

Arbuscular mycorrhizal fungi (AMF) are widespread microscopic fungi that provide mineral nutrients to most land plants by forming one of the oldest terrestrial symbioses. They have sometimes been referred to as an "evolutionary cul-de-sac" for their limited species diversity and their ecological niches restricted to plant-symbiotic life style. Here we use the largest global database of AMF to analyze their diversification dynamics in the past 500 million years (Myr) based on the small subunit (SSU) rRNA gene. We demonstrate that overall the SSU rRNA gene is variable enough to delineate AMF species and find that AMF have low diversification rates. After a diversification peak around 150 Myr ago, they experienced an important diversification slowdown in the last 100 Myr, likely related to a shrinking of their mycorrhizal niches. Our results identify patterns and drivers of diversification in a group of obligate symbionts of major ecological and evolutionary importance. They also highlight a striking example of a diversification slowdown that, instead of reflecting an adaptive radiation as typically assumed, may result from a limited ability to colonize new niches in an evolutionary cul-de-sac.

Introduction:

Arbuscular mycorrhizal fungi (AMF - subphylum Glomeromycotina) are obligate symbionts sometimes referred to as an "evolutionary cul-de-sac, albeit an enormously successful one" [1, 2]. They have limited morphological and species diversities, yet associate with the roots of >80% of land plants, where they provide mineral resources in exchange for photosynthates [3]. Present in most terrestrial ecosystems, AMF play key roles in plant protection, nutrient cycling, and ecosystem functions [4]. Fossil evidence and molecular phylogenies suggest that AMF contributed to the emergence of land plants [5–8] and coevolved with them for more than 400 million years (Myr)[8–10].

Despite the ecological ubiquity and evolutionary importance of AMF, large-scale patterns of their evolutionary history are poorly known. Studies on the diversification of AMF have been hampered by the difficulty of delineating species, quantifying global scale species richness, and building a robust phylogenetic tree for this group. Indeed, AMF are microscopic soil- and root-dwelling fungi that are poorly differentiated morphologically and difficult to cultivate. Although their classical taxonomy is mostly based on the characters of spores and root colonization [3, 11], AMF species delineation has greatly benefited from molecular data [12]. Experts have defined "virtual taxa" (VT) based on a minimal 97% similarity of a region of the 18S small subunit (SSU) rRNA gene and monophyly criteria [13, 14]. As for many other pragmatic species concepts, VT have rarely been tested for their biological relevance [15], and a consensual system of AMF classification is still lacking [16]. AMF are also poorly known genetically: the full SSU rRNA gene sequence is known in few species [17], other gene sequences in even fewer [10, 18], and complete genomes in very few [19].

The drivers of AMF diversification are unknown. A previous dated phylogenetic tree of VT found that many speciations occurred after the last major continental reconfiguration around 100 Myr ago [20], suggesting that AMF diversification is not linked to vicariant speciation during this geological event. Still, geographical speciation could play an important role in AMF diversification, as these organisms have spores that disperse

63 efficiently [21–23], which could result in frequent founder-event speciation [24]. Other
64 abiotic factors include habitat: tropical grasslands have, for example, been suggested as
65 diversification hotspots for AMF [25]. Besides abiotic factors, AMF are obligate symbionts
66 and, although relatively generalist [4, 26, 27], their evolutionary history could be largely
67 influenced by a diffuse coevolution with their host plants [10, 28, 29]. Over the last 400
68 Myr, land plants have experienced massive extinctions and radiations [29, 30], adaptations
69 to various ecosystems [31, 32], and associations with different soil microorganisms [33, 34].
70 All these factors could have influenced diversification dynamics in AMF.

71 Here, we reconstruct several thoroughly sampled phylogenetic trees of AMF,
72 considering several criteria of species delineations and uncertainty in phylogenetic
73 reconstructions. We combine this phylogenetic data with paleoenvironmental data and
74 data of current AMF geographic distributions, ecological traits, interaction with host
75 plants, and genetic diversity to investigate the global patterns and drivers of AMF
76 diversification in the last 500 Myr.

Material & methods:

Database choice:

We used AMF SSU rRNA gene sequences from MaarjAM database, the largest global database of AMF gene sequences [13]. Ideally, our analyses would be based on several independent genomic regions, however such data has yet to be acquired. In fungi, the usual barcode is the ITS region. However, for several reasons the SSU rRNA gene has been preferred over the ITS in AMF [35], and therefore ITS data on AMF are currently less common. In addition, we confirmed using the dataset of [35] that the ITS are very difficult to align, preventing us from reconstructing a robust phylogeny to investigate AMF evolutionary history (Supplementary Fig. 1).

Virtual taxa phylogenetic reconstruction:

We reconstructed several Bayesian phylogenetic trees of the 384 VT from the corresponding representative sequences available in the MaarjAM database [13] updated in June 2019 (Supplementary Methods 1). We used the full length (1,700 base pairs) SSU rRNA gene sequences from [17] to better align the VT sequences using MAFFT [36]. We selected the 520 base pair central variable region of the VT aligned sequences and performed a Bayesian phylogenetic reconstruction using BEAST2 [37]. We obtained a consensus VT tree and selected 12 trees equally spaced in 4 independent Bayesian chains to account for phylogenetic uncertainty in the subsequent diversification analyses, hereafter referred to as the VT replicate trees. We set the crown root age at 505 Myr [20], which is coherent with fossil data and previous dated molecular phylogenies [8, 10].

Delineation into Evolutionary Units (EUs):

We considered several ways to delineate AMF species based on the SSU rRNA gene. In addition to the VT species proxy, we delineated AMF *de novo* into evolutionary units (EUs) using 5 different thresholds of sequence similarity ranging from 97 to 99% and a monophyly criterion. We gathered 36,411 AMF sequences of the SSU rRNA gene from MaarjAM, mainly amplified by the primer pair NS31–AML2 (variable region) [38, 39] (dataset 1, Supplementary Table 1), corresponding to 27,728 haplotypes. We first built a phylogenetic tree of these haplotypes and then applied to this tree our own algorithm (R-package RPANDA [40, 41]) that traverses the tree from the root to the tips, at every node computes the average similarity of all sequences descending from the node, and collapses the sequences into a single EU if their sequence dissimilarity is lower than a given threshold (Supplementary Methods 2). Finally, we performed Bayesian phylogenetic reconstructions of the EUs using BEAST2, following the procedure described in Supplementary Methods 1.

Coalescent-based species delineation analyses:

Finally, we considered the Generalized Mixed Yule Coalescent method (GMYC) [42, 43], a species delineation approach that does not require specifying an arbitrary similarity threshold. GMYC estimates the time t in a reconstructed calibrated tree that separates species diversification (Yule process – before t) and intraspecific differentiation (coalescent process – after t). GMYC is too computationally intensive to apply on the 36,411 SSU sequences; we used it here on three smaller clades to investigate the ability of the SSU gene to delineate AMF species despite its slow evolution [16], and as a way to evaluate the biological relevance of the VT and various EUs delineations. We selected the following AMF clades: the family Claroideoglomeraceae; the order Diversisporales; and an early-diverging clade composed of the orders Archaeosporales and Paraglomerales. For each clade, we reconstructed Bayesian phylogenetic trees of haplotypes following the procedure described in Supplementary Methods 1. We then ran GMYC analyses (splits R-package [44]) on each of these trees and evaluated the support of the GMYC model compared to a

null model in which all tips are assumed to be different species, using a likelihood ratio test (LRT). If the LRT supports the GMYC model, different SSU haplotypes belong to the same AMF species, *i.e.* the SSU rRNA gene has time to accumulate substitutions between AMF speciation events.

Total diversity estimates:

We evaluated how thoroughly sampled our species-level AMF phylogenetic trees are by estimating the total number of VT and EUs using rarefaction curves and the Bayesian Diversity Estimation Software (BDES [45]) (Supplementary Methods 3).

Diversification analyses:

We estimated lineage-specific diversification rates using ClaDS, a Bayesian diversification model that accounts for rate heterogeneity by modeling small rate shifts at speciation events [46]. At each speciation event, the descending lineages inherit new speciation rates sampled from a log-normal distribution with an expected value $\log[\alpha \times \lambda]$ (where λ represents the parental speciation rate and α is a trend parameter) and a standard deviation σ. We considered the model with constant turnover ε (*i.e.* constant ratio between extinction and speciation rates; *ClaDS2*) and ran a newly developed ClaDS algorithm based on data augmentation techniques which enables us to estimate mean rates through time (https://github.com/OdileMaliet/ClaDS_Julia). We ran ClaDS2 with 3 independent chains, checked their convergence using a Gelman-Rubin diagnostic criterion [47], and recorded lineage-specific speciation rates. We also recorded the estimated hyperparameters (α, σ, ε) and the value $m=\alpha \times \exp(\sigma^2/2)$, which indicates the general trend of the rate through time [46].

In addition, we applied TreePar [48], another diversification approach that does not consider rate variation across lineages, but models temporal shifts in diversification rates

affecting all lineages simultaneously. We searched for up to ten shifts in diversification rates at every 2-million-year interval in each phylogenetic tree. We estimated the number of temporal shifts in AMF diversification rates using maximum likelihood inferences and likelihood ratio tests. We also used CoMET, its equivalent piecewise-constant model in a Bayesian framework (TESS R-package [49, 50]). We chose the Bayesian priors according to maximum likelihood estimates from TreePar, disallowed mass extinction events, and ran the MCMC chains until convergence (minimum effective sample sizes of 500).

We also fitted a series of time-dependent and environment-dependent birth-death diversification models using RPANDA [40, 51] to test the influence of temperature, pCO_2, and land plant fossil diversity on AMF diversification. For the time-dependent models, we considered models with constant or exponential variation of speciation rates through time and null or constant extinction rates (*fit_bd* function). Models with constant rates correspond to the null hypothesis of clock-like speciation, whereas the exponential variation ensures positive rates and are an approximation of diversity dependence, a process often invoked during radiations [52]. For the environment-dependent models, we considered an exponential dependency of the speciation rates with the environmental variable (env), *i.e.* speciation rate=b*exp(a*env), where a and b are two parameters estimated by maximum likelihood (*fit_env* function). The exponential variation corresponds here to a simple linear regression of log-transformed rates. Environment curves were smoothed using the function *smooth.spline* (stats R-package). We used the corrected Akaike information criterion (AICc) to select the best-fit models, considering that a difference of 2 in AICc indicates that the model with the lowest AICc is better.

The influence of temperature was tested on the complete AMF phylogenetic trees, using estimates of past global temperature [53]. As these temporal analyses can be sensitive to the root age calibration, we replicated them using the youngest (437 Myr) and oldest (530 Myr) crown age estimates from [10]. The influence of pCO_2 [54] and of land plant fossil diversity was tested starting from 400 Myr ago, as these environmental data are not available for more ancient times. For these analyses we sliced the phylogenies at 400 and

200 Myr ago, and applied the diversification models to the sliced sub-trees larger than 50 tips. Estimates of land plant diversity were obtained using all available Embryophyta fossils from the Paleobiology database (https://paleobiodb.org) and using the shareholder quorum subsampling method (Supplementary Methods 4; [55]).

All diversification analyses were performed for each delineation on the consensus and on the 12 replicate trees to account for phylogenetic uncertainty. We also considered missing species by imputing sampling fractions, computed as the number of observed VT or EUs divided by the corresponding BDES estimates of global AMF diversity estimated from Sichel distributions (Supplementary Table 2). As such analyses depend on diversity estimates, we replicated all diversification analyses using lower sampling fractions down to 50%.

Testing for potential drivers of AMF diversification:

To further investigate the potential factors driving AMF diversification, we assessed the relationship between lineage-specific estimates of present-day speciation rates and characteristics of each AMF taxonomic unit, *i.e.* VT or EUs.

First, we characterized AMF niche width using a set of 10 abiotic and biotic variables recorded in MaarjAM database for each AMF unit. In short, among a curated dataset containing AMF sequences occurring only in natural ecosystems (dataset 2; [26]), for each AMF unit, we reported the number of continents, ecosystems, climatic zones, biogeographic realms, habitats, and biomes where it was sampled, as well as its number of plant partners, their phylogenetic diversity, and its centrality in the plant-fungus bipartite network, and performed a principal component analysis (PCA; Supplementary Methods 5). For AMF units represented by at least 10 sequences, we tested whether these PCA coordinates reflecting AMF niche widths were correlated with the present-day speciation rates using both linear mixed-models (not accounting for AMF phylogeny) or

MCMCglmm models [56]. For MCMCglmm, we assumed a Gaussian residual distribution, included the fungal phylogenetic tree as a random effect, and ran the MCMC chains for 1,300,000 iterations with a burn-in of 300,000 and a thinning interval of 500.

Next, we tested the relationship between speciation rates and geographic characteristics of AMF units. To test the effect of latitude, we associated each AMF unit with its set of latitudes and used similar MCMCglmm with an additional random effect corresponding to the AMF unit. To account for inhomogeneous sampling along the latitudinal gradient, we re-ran the model on jackknifed datasets (we re-sampled 1,000 interactions per slice of latitude of twenty degrees). Similarly, we tested the effect of climatic zone and habitat on the speciation rates.

Finally, to test the effect of dispersal capacity, we assessed the relationship between spore size and speciation rate for the few (n=32) VT that contain sequences of morphologically characterized AMF isolates [57]. We gathered measures of their average spore length [57] and tested their relationship with speciation rate by using a phylogenetic generalized least square regression (PGLS).

Estimating genetic diversity:

As a first attempt at connecting AMF macroevolutionary diversification to microevolutionary processes, we measured intraspecific genetic diversities across AMF units. For each AMF unit containing at least 10 sequences, we computed genetic diversity using Tajima's estimator [58]($\theta\pi$; Supplementary Methods 6). Using similar statistical tests as above, we investigated the correlation of AMF genetic diversity with speciation rate, niche width, geographic characteristics, and spore size. We tested the robustness of the results to the minimal number of sequences per AMF unit (10, 15 or 20) used to compute genetic diversity and to perform the PCA.

250 These statistical models were replicated on the different phylogenetic trees
251 (consensus or replicates) for each delineation and we reported p-values (*P*) corresponding
252 to two-sided tests.
253

Results:

AMF species delineations & phylogenetic reconstructions:

The EU97.5 and EU98 delineations (obtained using a threshold of 97.5% and 98% respectively) provided a number of AMF units (340 and 641) comparable to the 384 currently recognized VT, while the EU97 delineation had much less (182). Conversely, the EU98.5 and EU99 delineations yielded a much larger number of AMF units (1,190 and 2,647, respectively; Supplementary Tables 3 & 4) that was consistent with the number obtained using GMYC analyses (Supplementary Tables 4 & 5). This supports the idea that some VT might lump together several cryptic species [16](Supplementary Note 1), and that a 98.5 or 99% similarity threshold is more relevant for AMF species delineation. In addition, the GMYC indicated that the actual level of genetic variation within the SSU marker is overall sufficient to separate AMF species-like units among SSU haplotypes (GMYC LRT: $P<0.05$; Supplementary Fig. 2); on average, there are 10 SSU haplotypes for one AMF unit delineated using GMYC (Supplementary Table 5). Rarefaction curves as well as Bayesian and Chao2 estimates of diversity suggested that more than 90% of the total diversity of AMF is represented in our dataset regardless of the delineation threshold (Fig. 1b, Supplementary Tables 2, 5, & 6; Supplementary Note 2), which is consistent with the proportion of new AMF units detected in recent studies [59].

The reconstructed Bayesian phylogenetic trees based on VT and EU species delineations did not yield high support for the nodes separating the main AMF orders; yet, they had similar topologies and branching times of the internal nodes overall (Fig. 2, Supplementary Figs. 3). As expected, finer delineations resulted in an increase in the number of nodes close to the present (Supplementary Figs. 4). However, we observed a slowdown in the accumulation of new lineages close to the present in all lineage through time plots (LTTs), including those with the finest delineations (EU98.5 and EU99; Supplementary Fig. 5).

283

284 **Temporal diversification dynamics:**

285

286 AMF speciation rates ranged from 0.005 to 0.03 events per lineage per Myr (Fig. 2;
287 Supplementary Fig. 6), and varied both within and among AMF orders, with Glomerales
288 and Diversisporales having the highest present-day speciation rates (Supplementary Fig.
289 7). AMF experienced their most rapid diversification between 200 and 100 Myr ago
290 according to estimates of diversification rates through time obtained with ClaDS (Fig. 2;
291 Supplementary Fig. 8), and 150-50 Myr ago according to diversification models with
292 piecewise constant rates (TreePar [48] and CoMET [50], Fig. 2; Supplementary Figs. 9 &
293 10).

294

295 The fast diversification of AMF around 150 Myr ago was followed by a slowdown
296 in the recent past (Fig. 2; Supplementary Fig. 8), as suggested by the plateauing of the LTTs.
297 A global decrease of the speciation rates through time was independently supported by
298 ClaDS, TreePar, and CoMET analyses (Supplementary Figs. 11, 9 & 10), as well as time-
299 dependent models in RPANDA [60](Supplementary Fig. 12). This slowdown was robust
300 to all species delineations (Supplementary Figs. 8, 9, 10, & 12), the branching process prior
301 (analyses not shown), phylogenetic uncertainty, and sampling fractions down to 50%,
302 except in ClaDS analyses where the trend disappeared in some EU99 trees and for
303 sampling fractions lower than 70% (Supplementary Figs. 13, 14, & 15).

304

305 We did not find a strong signal of extinction in our analyses: the turnover rate
306 estimated from ClaDS was generally close to zero (Supplementary Fig. 11b), and models
307 including extinctions were never selected in RPANDA (Supplementary Fig. 12). Similarly,
308 the extinction rates estimated in piecewise-constant models were not significantly different
309 from 0 (Supplementary Fig. 16).

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311

AMF diversification drivers:

When fitting environment-dependent models of diversification, we found high support for temperature-dependent models compared to time-dependent models for all AMF delineations, sampling fractions, and crown ages (Fig. 3; Supplementary Figs. 17, 18, 19, 20, & 21), with the exception of some EU99 trees with a 50% sampling fraction (Supplementary Fig. 21). This signal of temperature dependency was not due to a temporal trend (Supplementary Note 3) nor to an artefact caused by rate heterogeneities (Supplementary Note 4). Evidence for temperature dependency, however, decreased in some clades closer to the present (see Methods), as small trees tend to be best fit by constant rather than environment-dependent models (Supplementary Fig. 22). We detected a significant positive dependency of the diversification rates on CO_2 concentrations in some sub-trees, but rarely found a significant effect of plant fossil diversity (Supplementary Fig. 22).

The PCA of AMF niche width characteristics had a first principal component (PC1) that indicated the propensity of each AMF unit (VT or EUs) to be vastly distributed among continents, ecosystems and/or associated with many plant species and lineages, whereas the second principal component (PC2) indicated the propensity of a given AMF unit to associate with few plant species on many continents (Fig. 4; Supplementary Fig. 23 & 24). Hence, PC1 reflects AMF niche width, whereas PC2 discriminates the width of the abiotic relatively to the biotic niche (Fig. 4a-b; Supplementary Fig. 25). We found a positive correlation between PC1 and lineage-specific speciation rates in the majority of the VT and EU99 trees (Fig. 4c-d; Supplementary Fig. 26a). However, these results were no longer significant when controlling for phylogenetic non-independence between AMF units (Supplementary Fig. 26b), likely because a single *Glomeraceae* clade, including the abundant and widespread morphospecies *Rhizophagus irregularis* and *R. clarus,* had both the highest speciation rates among AMF (Fig. 2a-b) and the largest niche widths (Supplementary Fig. 27).

We found no effect of latitude on speciation rates, regardless of the AMF delineation or the minimum number of sequences per AMF unit (MCMCglmm: $P>0.05$), and no effect of habitat or climatic zone either (Supplementary Fig. 28). Similarly, we recovered no significant correlation between spore size and speciation rate (Supplementary Fig. 29), nor between spore size and level of endemism (Supplementary Fig. 30).

Finally, Tajima's $\theta\pi$ estimator of AMF genetic diversity was significantly and positively correlated with niche width (PC1) for all AMF delineations and minimal number of sequences per AMF unit considered, and in particular with abiotic aspects of the niche (PC2) in many cases (Fig. 4e-h; Supplementary Fig. 26). Genetic diversity was not correlated with speciation rate (Supplementary Fig. 26), latitude, habitat, climatic zone (MCMCglmm: $P>0.05$), or spore size (PGLS: $P>0.05$).

Discussion

AMF species delineations, diversity, and phylogeny:

The species concept is difficult to apply in AMF, which are poorly differentiated morphologically and mainly characterized by environmental sequences [16]. In addition, their reproduction mode is not well known and they have unique nuclear dynamics in their spores and hyphae [61]. Our GMYC analyses suggest that biologically relevant AMF species-like units correspond to SSU rRNA haplotypes with a sequence similarity between 98.5 and 99%. With this criterion of species delineation, we estimate that there are between 1,300 and 2,900 AMF 'species'. These estimates are largely above the number of currently described morphospecies or VT (Supplementary Note 1) but remain low in comparison with other fungal groups, like the Agaricomycetes that include taxa forming ectomycorrhiza [62].

Species delineations and phylogenies constructed from a single gene and short sequences are limited, but in the current state of data acquisition, relatively short metabarcoding sequences provide for most microbial groups, including AMF, the only current possibility to analyze their diversification dynamics [20, 63, 64]. Here, our phylogenies did not resolve the branching of the AMF orders, with node supports similar to those of previous studies [12, 17, 20](Supplementary Note 5), confirming that additional genomic evidence is required to reach consensus. We considered this uncertainty in the phylogenetic reconstruction by repeating our analyses on a set of trees spanning the likely tree space. We hope that our study based on the SSU rRNA region alone will foster efforts to obtain more genetic data, including additional genes and genomic information, with the aim of reconstructing better supported, comprehensive phylogenies.

AMF diversify slowly:

We found speciation rates for AMF an order of magnitude lower than rates typically found for macro-eukaryotes [46, 65], like plants [29], or Agaricomycetes [62]. Low speciation rates in AMF may be linked to their (debated) asexual reproduction [66], to their occasional long-distance dispersal that homogenizes populations globally over evolutionary timescales [67], or to the fact that they are generalist obligate symbionts [68]. Regardless of the proximal cause, and contrary to Agaricomycetes for example, which present a large diversity of species, morphologies, and ecologies, the niche space exploited by AMF is limited to plant roots and the surrounding soil because of their obligate dependence on plants for more than 400 Myr [69, 70]. Thus, although AMF species delineation based on the SSU rRNA gene can be a poor predictor of their functional diversity, our analyses based on this gene has revealed that AMF, despite their ubiquity, have poorly diversified in the last 500 Myr compared with other groups.

We found little evidence for species extinction in AMF, including at mass extinction events. Although AMF are relatively widespread and generalists, and low extinction rates have been predicted before based on their ecology [2], these low extinction rate estimates could also come from the difficulty of estimating extinction from molecular phylogenies [71], one of the limitations of phylogeny-based diversification analyses (Supplementary Note 6).

AMF diversification through time:

The observed peak of AMF diversification detected between 200 and 100 Myr (or 150-50 Myr according to the models) was mainly linked to the fast diversification of the largest family Glomeraceae (Fig. 2). This peak was concomitant with the radiation of flowering plants [28], but also with a major continental reconfiguration, including the breakdown of Pangea and the formation of climatically contrasted landmasses [20]. This period was also

412 characterized by a warm climate potentially favorable to AMF diversification, such that
413 disentangling the impact of these various factors on AMF diversification is not
414 straightforward. Interestingly, a peak of diversification at this period was also found in the
415 Agaricomycetes forming ectomycorrhiza [62].
416
417 This peak of diversification has been followed by a slowdown. Signals of
418 diversification slowdowns sometimes result from methodological artifacts, including
419 incorrect species delineations or under-sampling [72]. We carefully considered uncertainty
420 in species delineations and under-sampling down to 50%. In addition, our GMYC analyses
421 confirmed that the SSU rRNA gene evolves fast enough to delineate AMF species-like
422 units; although some cryptic AMF species can have the same SSU sequence [12], our
423 analyses support the overall existence of several SSU haplotypes per AMF unit.
424 Slowdowns in diversification rates close to the present have often been interpreted as a
425 progressive reduction of the number of available niches as species diversify and
426 accumulate [72, 73]. In AMF, this potential effect of niche saturation could be exacerbated
427 by a reduction of their niches linked to both repetitive breakdowns of their symbiosis with
428 plants and climatic changes. Indeed, in the last 100 Myr, many plant lineages evolved
429 alternative root symbioses or became non-symbiotic [5, 32, 33, 74]: approximately 20% of
430 extant plants do not interact with AMF anymore [4]. Additionally, the cooling of the Earth
431 during the Cenozoic reduced the surface of tropical regions [75, 76], which tend to be a
432 reservoir of ecological niches for AMF [20, 32, 77].
433
434 The difficulty of reconstructing past symbiotic associations prevents direct testing of
435 the hypothesis that the emergence of new root symbioses in plants led to a diversification
436 slowdown in AMF. However, we tested the hypothesis that global temperature changes
437 affected diversification rates and found a strong relationship (Fig. 3). Such associations
438 between temperature and diversification rates have been observed before in eukaryotes
439 and have several potential causes [78]. Two prevailing hypotheses are the evolutionary
440 speed hypothesis, stipulating that high temperatures entail higher mutation rates and

faster speciation [79], and the productivity hypothesis, stating that resources and associated ecological niches are more numerous in warm and productive environments, especially when the tropics are large [80]. The latter hypothesis is particularly relevant for AMF, which have many host plant niches in the tropics and potentially less in temperate regions [81], where a higher proportion of plants are non-mycorrhizal [82] or ectomycorrhizal [32, 62]. Hence, the observed effect of past global temperatures could reflect the shrinkage of tropical areas and the associated decrease of the relative proportion of arbuscular mycorrhizal plants.

A few AMF clades displayed a significant support for diversification models with a positive dependency on CO_2 concentrations, which reinforces the idea that for the corresponding AMF, benefits retrieved from plants could have been amplified by high CO_2 concentrations and fostered diversification [83, 84]. Conversely, we found a limited effect of land plant fossil diversity, which indicates that variations in the tempo of AMF diversification did not systematically follow those of land plants. Still, the possible concordance of the peak of AMF diversification with the radiation of the Angiosperms is noteworthy, in particular in Glomeraceae that frequently interact with present-day Angiosperms [17]. The co-diversification with the plants might have been an important driver from the emergence of land plants until the Mesozoic [2, 10], but less so thereafter, when AMF diversification declined while some flowering plants radiated, including AMF-free groups such as the species-rich Orchidaceae, blurring co-diversification patterns (Supplementary Fig. 31)[30, 85].

AMF recent diversification:

Looking at the correlates of AMF present-day diversification rates, we found no effect of habitat or climatic zone, even though AMF are more frequent and diverse in the tropics (Supplementary Fig. 32)[20, 25, 81] and their speciation rates are positively correlated with global temperature. Further work, including a more thorough sampling of the distribution

of AMF species across latitudes and habitats, would be required to confirm these patterns and to distinguish whether speciation events are indeed no more frequent in the tropics or, if they are, whether long-distance dispersal redistributes the new lineages at different latitudes over evolutionary time scales [25]. Similarly, although the temporal changes in the availability of AMF niches likely influenced the diversification of the group, we found little support for AMF species with larger niche width having higher lineage-specific speciation rates (Fig. 4). We also note that there are important aspects of the niche that we do not (and yet cannot) account for in our characterization of AMF niche width: it is thought that some AMF species may mainly provide mineral nutrients extracted from the soil, whereas others may be more specialized in protecting plants from biotic or abiotic stresses [86] and such (inter- or intra-specific) functional variations may have evolutionary significance. Finally, although spore size is often inversely related to dispersal capacity [87], which can either promote diversification by favoring founder speciation events, or limit diversification by increasing gene flow, we found no significant correlation between spore size and diversification rates, which may be explained either by a weak or absent effect or by the low number of species for which this data is available. In addition, the absence of correlation between spore size and level of endemism suggests that even AMF with large spores experience long-distance dispersal [57, 88]. Thus, if large spores might limit dispersal at smaller (e.g. intra-continental) scales in AMF [22, 89], this does not seem to affect diversification.

In AMF, intraspecific variability is an important source of functional diversity [67, 90] and their genetic diversity may indicate the intraspecific variability on which selection can act, potentially leading to species diversification. Here, geographically widespread AMF species appear to be more genetically diverse, as previously suggested by population genomics [67], but do not necessarily speciate faster. Along with a decoupling between genetic diversity and lineage-specific speciation rate, this suggests that the accumulation of genetic diversity among distant subpopulations is not enough to spur AMF speciation.

Conclusion:

Our findings that AMF have low speciation rates, likely constrained by the availability of suitable niches, reinforce the vision of AMF as an "evolutionary cul-de-sac" [1]. We interpret the significant diversification slowdown in the past 100 Myr as the conjunction of the emergence of plant lineages not associated with AMF and the reduction of tropical areas induced by climate cooling, in the context of obligate dependence of AMF on plants. Diversification slowdowns have often been interpreted as the signal of adaptive radiations [72, 91], that is clades that experienced a rapid accumulation of morphological, ecological, and species diversity [92]. AMF provide a striking example of a clade with slow morphological, ecological and species diversification that features a pattern of diversification slowdown. In AMF, and potentially in many other species groups [78], such a slowdown likely reflects a reduction of the global availability of ecological niches.

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Author contributions:

All the authors designed the study. MÖ gathered the data and BPL performed the analyses. OM and ACAS provided some codes. BPL and HM wrote the first version of the manuscript and all authors contributed substantially to the revisions.

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The authors declare that there is no conflict of interest.

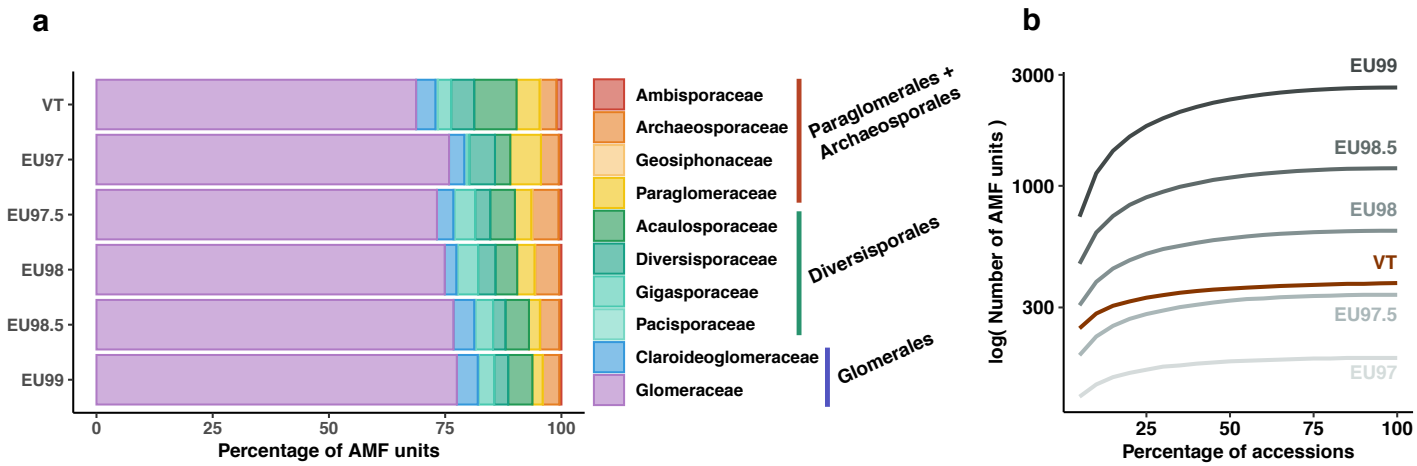
Figures

Figure 1: Molecular-based species delineations of arbuscular mycorrhizal fungi (AMF) give consistent results and indicate a nearly complete sampling.

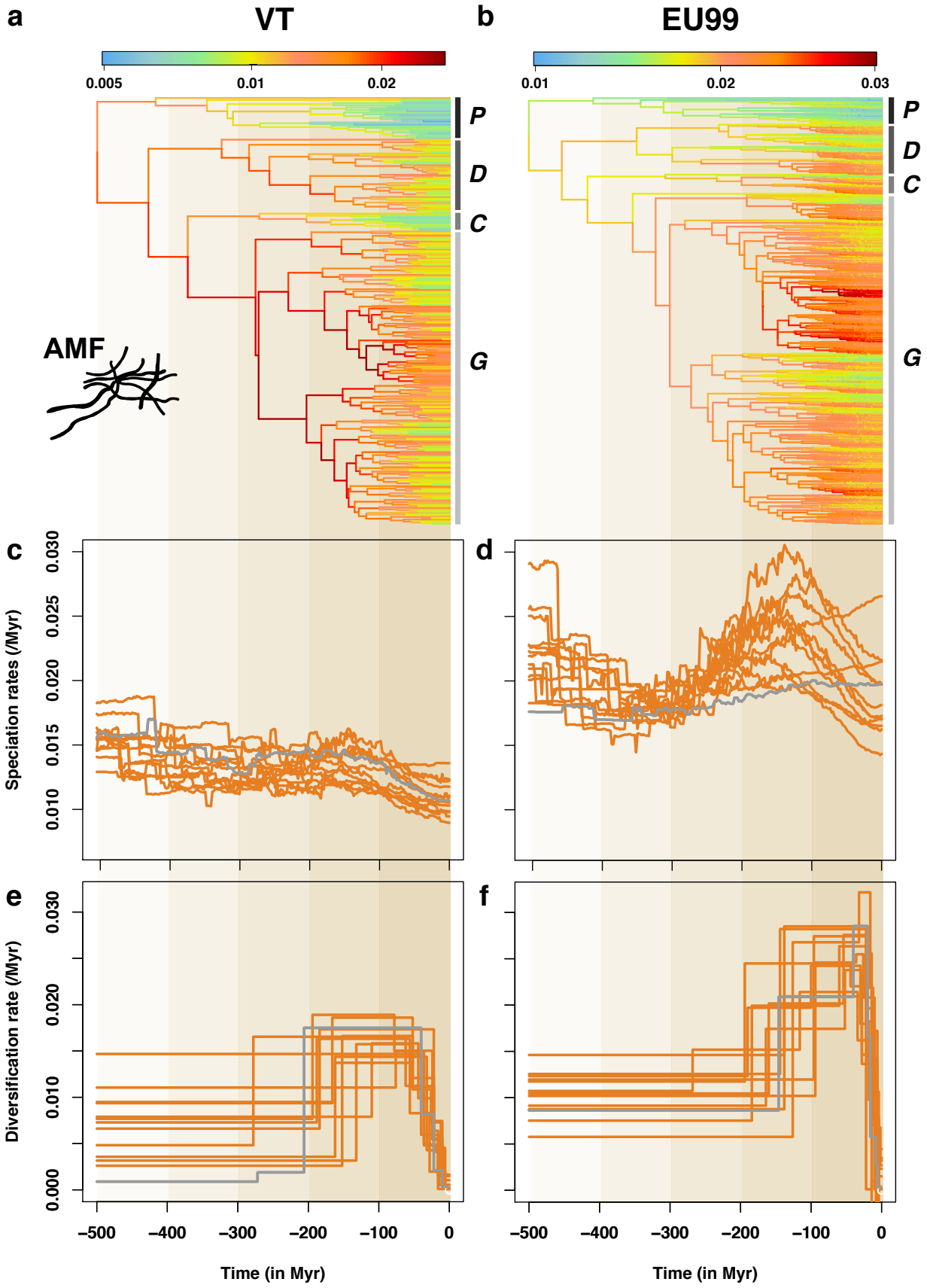
We compared the *virtual taxa* (VT) delineation from [13] with newly-developed automatic delineations into *evolutionary units* (EUs) based on an average threshold of similarity and a criterion of monophyly.

(a) The proportion of AMF units (VT or EUs) in each AMF family reveals constant proportions across delineations, although Glomeraceae tend to be relatively less numerous compared to the other AMF family in the VT delineation. The main AMF orders are indicated on the right of the charts: Paraglomerales + Archaeosporales, Diversisporales, and Glomerales (Glomeraceae + Claroideoglomeraceae).

(b) Rarefaction curves indicating the number of AMF units as a function of the percentage of sampled AMF accession revealed that the AMF sampling in MaarjAM is close to saturation for all delineations (VT or EUs). Rarefactions were performed 100 times every 5 percent and the median of the 100 replicates is represented here.



792 **Figure 2: The diversification dynamic of arbuscular mycorrhizal fungi (AMF) varies**
793 **significantly through time and between lineages.**
794
795 **(a-b):** AMF consensus phylogenetic trees corresponding to the VT (a) and EU99 (b) species
796 delineations. Branches are colored according to the lineage-specific speciation rates
797 estimated by ClaDS using the BDES estimated sampling fraction: lineages with low and
798 high speciation rates are represented in blue and red, respectively.
799 The main AMF clades are indicated with the following letters: *P* = Paraglomerales +
800 Archaeosporales, *D* = Diversisporales, *C* = Claroideoglomeraceae, and *G* = Glomeraceae.
801
802 **(c-d):** Mean speciation rates through time estimated by ClaDS, for the VT (c) and EU99 (d)
803 delineations and using the BDES estimated sampling fraction. The mean speciation rate
804 corresponds to the maximum *a posteriori* (MAP) of the mean speciation rate across all
805 fungal lineages back in time (including extinct and unsampled lineages). Orange and grey
806 lines represent the 12 independent replicate trees and the consensus tree, respectively.
807 Unlike most replicate trees, the EU99 consensus tree tends to present a limited
808 diversification slowdown, which reinforces the idea that consensus trees can be a
809 misleading representation [93].
810
811 **(e-f):** Net diversification rates (speciation rates minus extinction rates) through time
812 estimated by TreePar, for the VT (c) and EU99 (d) delineations and using the BDES
813 estimated sampling fraction. Orange and grey lines represent the 12 independent replicate
814 trees and the consensus tree, respectively.



815

816 **Figure 3: Temperature-dependent diversification models reveal that global temperature**
817 **positively associates with the speciation rates of arbuscular mycorrhizal fungi (AMF) in**
818 **the last 500 million years.**
819
820 **(a):** Average global temperature in the last 500 million years (Myr) relative to the average
821 temperature of the period 1960-1990. The smoothed orange line represents cubic splines
822 with 33 degrees of freedom used to fit temperature-dependent models of AMF
823 diversification with RPANDA. This default smoothing was estimated using the R function
824 *smooth.spline*.
825
826 **(b):** AICc difference between the best-supported time-dependent model and the
827 temperature-dependent model in RPANDA, for the VT (left) and EU99 (right) delineations,
828 using the BDES estimated sampling fraction. An AICc difference greater than 2 indicates
829 that there is significant support for the temperature-dependent model.
830
831 **(c):** Parameter estimations of the temperature-dependent models (speciation rate ~
832 exp(parameter * temperature)). A positive parameter value indicates a positive effect of
833 temperature on speciation rates.
834
835 For both delineations, the boxplots represent the results obtained for the consensus tree
836 and the 12 independent replicate trees. Boxplots indicate the median surrounded by the
837 first and third quartiles, and whiskers extend to the extreme values but no further than 1.5
838 of the inter-quartile range. The horizontal dotted lines highlighted the values estimated for
839 the consensus trees. Compared to the replicate trees, the consensus trees tend to present
840 extreme values (stronger support for temperature-dependent model), which reinforces the
841 idea that consensus trees can be a misleading representation [93].

842

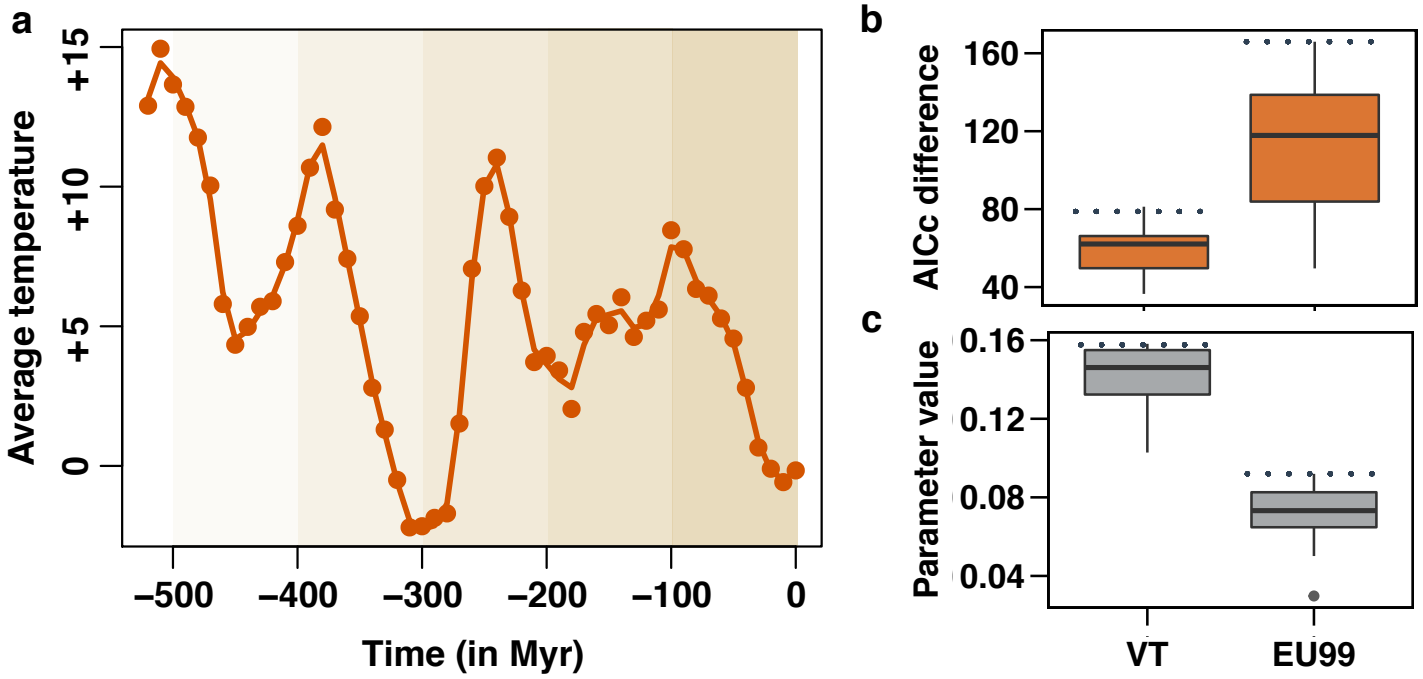


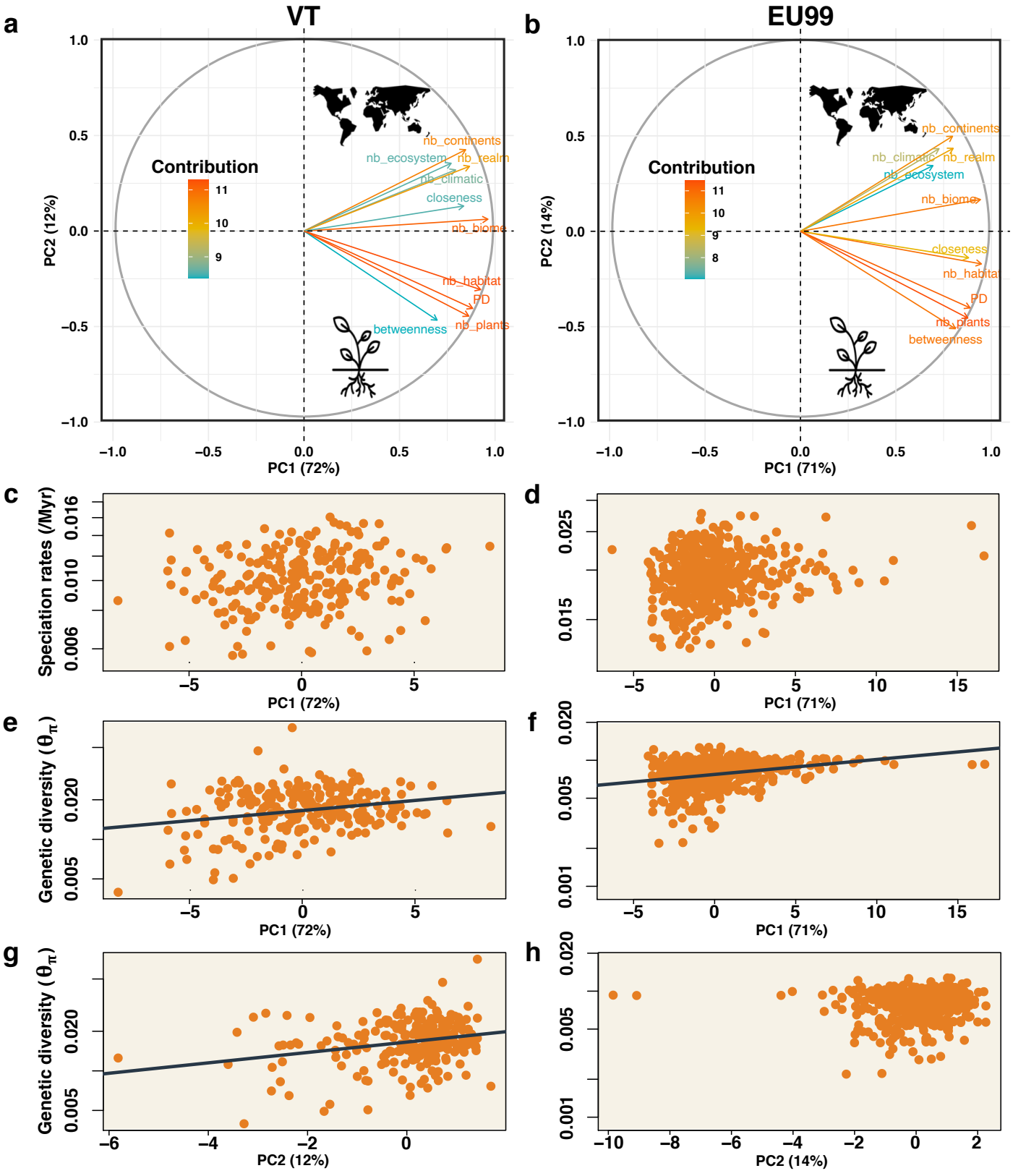
Figure 4: Abiotic and biotic drivers of the species diversification and differentiation of arbuscular mycorrhizal fungi (AMF)

(a-b): Projection of 10 abiotic and biotic variables on the two principal coordinates according to the VT (a) or EU99 (b) delineations. Principal coordinate analysis (PCA) was performed for the AMF units represented by at least 10 sequences. Colors represent the contribution of the variable to the principal coordinates. The percentage for each principal coordinate (PC) indicates its amount of explained variance.

Tested variables were: the numbers of continents on which the AMF unit occurs (nb_continent), of realms (nb_realm), of ecosystems (nb_ecosystems), of habitats (nb_habitats), of biomes (nb_biomes), and climatic zones (nb_climatic) [13], as well as information about the associated plant species of each unit, such as the number of plant partners (nb_plants), the phylogenetic diversity of these plants (PD), and the betweenness and closeness measurement of each fungal unit in the plant-fungus interaction network (see Methods).

(c-d): Speciation rates as a function of the PC1 coordinates for each VT (c) or EU99 (d) unit. Only the AMF consensus tree is represented here (other replicate trees are presented in Supplementary Fig. 26).

(e-h): Genetic diversity (Tajima's $\theta\pi$ estimator) as a function of the PC1 (e-f) or PC2 (g-h) coordinates for each VT (e-g) or EU99 (f-h) unit. Only the AMF consensus tree is represented here (other replicate trees are presented in Supplementary Fig. 26). The grey lines indicate the statistically significant linear regression between the two variables inferred using MCMCglmm.



867