Glomeromycota associations with bamboos (Bambusoideae) worldwide, a qualitative systematic review of a promising symbiosis

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Background. Around the world, bamboos are ecologically, economically, and culturally important plants, particularly in tropical regions of Asia, America, and Africa. The association of this plant group with arbuscular mycorrhizal fungi belonging to the phylum Glomeromycota is still a poorly studied field, which limits understanding of the reported ecological and physiological benefits for the plant, fungus, soil, and ecosystems under this symbiosis relationship. **Methods.** Through a qualitative systematic review following the PRISMA framework for the collection, synthesis, and reporting of evidence, this paper presents a compilation of the research conducted on the biology and ecology of the symbiotic relationship between Glomeromycota and Bambusoideae from around the world. This review is based on academic databases enriched with documents retrieved using different online databases and the Google Scholar search engine. **Results.** The literature search yielded over 6000 publications, from which 18 studies were included in the present review after a process of selection and validation. The information gathered from the publications included over 25 bamboo species and nine Glomeromycota genera from eight families, distributed across five countries on two continents. **Conclusion.** This review presents the current state of knowledge regarding the symbiosis between Glomeromycota and Bambusoideae, while reflecting on the challenges and scarcity of research on this promising association found across the world.

Glomeromycota Associations with Bamboos (Bambusoideae) Worldwide: A Qualitative Systematic Review of a Promising Symbiosis

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Abstract

Background. Around the world, bamboos are ecologically, economically, and culturally important plants, particularly in tropical regions of Asia, America, and Africa. The association of this plant group with arbuscular mycorrhizal fungi belonging to the phylum Glomeromycota is still a poorly studied field, which limits understanding of the reported ecological and physiological benefits for the plant, fungus, soil, and ecosystems under this symbiosis relationship.

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Conclusion. This review presents the current state of knowledge regarding the symbiosis between Glomeromycota and Bambusoideae, while reflecting on the challenges and scarcity of research on this promising association found across the world.

Subjects. Mycology, Plant Science

Keywords. Glomeromycota, Arbuscular Mycorrhizal Fungi, Bambusoideae, Bamboo, Symbiosis

Introduction

Bamboos belong to the subfamily Bambusoideae within the Poaceae family (commonly known as grasses) (Clark et al., 2015) and tend to be evergreen plants that flower at prolonged intervals, after which some species die (Banik, 2015). They are a highly versatile group of fast-growing

41   plants for which more than 4000 traditional uses and 1500 commercial applications have been
42   reported (Hsiung, 1988) and are currently used as fuel, building material, raw material for the
43   paper industry, and even as a resource for creating artisanal crafts (Singh et al., 2020). These
44   reasons, along with the resistance properties of their fibers, have earned them the nickname
45   "vegetable steel" (Amada et al., 1997).

46   Furthermore, due to their phenotypic plasticity, bamboo plants are extensively cultivated
47   in numerous regions around the world — in 2007, 36.8 million hectares were counted across
48   temperate, tropical, and subtropical regions (Lobovikov et al., 2007). Most cultivation areas are
49   concentrated in Asia, America, and Africa (Bystriakova et al., 2004), coinciding with the areas of
50   the world that most utilize these plants (de Moura et al., 2019), as well as where their centers of
51   diversity are found. According to Soreng et al. (2022), there are around 136 genera and 1698
52   species of bamboo distributed in the aforementioned zones, with tropical Asia considered the
53   center of bamboo diversity, harboring around 53 genera and 550 species (Bystriakova et al.,
54   2003).

55   Plants do not exist as isolated entities but as complex communities where their organs
56   and tissues constitute diverse niches for microorganisms (Kothe & Turnau, 2018). One of the
57   central themes surrounding the organisms associated with plants are the interactions (not always
58   beneficial) generated with fungi, for which those established with the phylum Glomeromycota
59   stand out (Gehring & Johnson, 2017). This phylum comprises a monophyletic clade of fungi
60   whose members (with the exception of the species *Geosiphon pyriformis* (Kütz). F. West.) are all
61   obligate mutualistic symbionts of plants, better known as arbuscular mycorrhizal fungi or AMF
62   (Smith & Read, 2008).

63   These fungal symbionts, which include over 350 described and accepted morphological
64   species, establish associations with the roots of the vast majority of terrestrial plants around the
65   world. According to recent estimates, this value surpasses 60% or even 80% of plant species on
66   the planet (Heijden et al., 2015; Smith & Read, 2008; Prasad et al., 2017; Brundrett & Tedersoo,
67   2018), with the exceptions being a few plant families that do not exhibit any type of association,
68   such as Amaranthaceae, Brassicaceae, Chenopodiaceae, Caryophyllaceae, Juncaceae,
69   Cyperaceae, and Polygonaceae (Brundrett, 2009).

70   Once they colonize the roots of the host plant, AMF have the ability to develop extensive
71   extraradical networks of mycelium that grow three-dimensionally in the soil matrix and
72   specialize in capturing mineral nutrients and water. These nutrients and water are subsequently
73   transported and translocated to the interior of the plant symbiont in exchange for an energy
74   reward for the AMF in the form of carbohydrates, which are produced through photosynthesis
75   (Smith & Read, 2008).

76   Of all the microorganisms present in soils, Glomeromycota fungi are fundamental to the
77   maintenance and functionality of numerous ecosystem processes. Their symbiotic establishment
78   is related to the development and growth of the plants with which they associate, the
79   maintenance of plant diversity, nutrient cycling, phosphorus solubilization, the facilitation of

80 water and nutrient capture, and soil aggregation, among other ecosystem contributions
81 (Marulanda et al., 2003; Silva-Flores et al., 2019; Heijden et al., 2015).
82   The objective of this systematic review is to provide a summary of the current state of
83 qualitative knowledge reported in the global scientific literature regarding the symbiosis between
84 Glomeromycota fungi and bamboo plants of the Bambusoideae subfamily with which they
85 associate worldwide. This group of plants, once considered the "wood of the poor," is now
86 recognized as "green gold" and presents particularly promising perspectives for environmental
87 issues and a rapidly growing market (Sandhu et al., 2017). Thus, requires the development of
88 strategies to propagate bamboo species quickly and economically, and the stimulation of their
89 growth and development can be achieved through the use of beneficial microorganisms such as
90 AMF (Zamora-Chacón et al., 2019; de Moura et al., 2019).
91

Materials & Methods

93   The present study utilizes a literature search and review process that is summarized in the
94 PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) flowchart,
95 adapted from Page et al. (2021) and Moher et al. (2009). This flowchart follows a clear
96 separation of the stages of identification, screening, eligibility, and inclusion (Fig. 1). An updated
97 PRISMA checklist (Page et al., 2021) with a guide specific to this review is presented in the
98 supplementary material (Table S1).

Search strategies and inclusion criteria

100   To gather relevant literature on the symbiotic association between Glomeromycota and
101 bamboo plants (Bambusoideae) worldwide, academic and bibliographic databases including
102 Scopus, Web of Science, Wiley Online Library, Taylor and Francis Online, Elsevier Science
103 Direct, and Springer Link, as well as the search engine Google Scholar, were utilized.
104 Documents published up until the search date of February 2023 were recovered using the
105 following search equation with keywords and Boolean operators: (Glomeromycota OR
106 "arbuscular mycorrhizal fungi" OR arbuscular OR mycorrhiza OR AMF) AND (Bambusoideae
107 OR Bamboo) AND (Association OR symbiosis).
108   The search was conducted and assessed by both authors using both English and Spanish
109 terms, without imposing language restrictions or applying time restrictions in terms of the date of
110 publication to avoid potential bias. This initial search resulted in over 6300 publications, from
111 which scientific articles published in peer-reviewed and indexed journals were selected, while
112 books, book chapters, and reviews were excluded. The reference lists of the selected literature
113 and articles were used to find additional articles, resulting in a total of 18 scientific articles
114 included in the final review (*Fig. 1*).

Data extraction, compilation, and exclusion criteria

116   The following information related to the focal association was extracted from the
117 compiled selected articles: (1) the country where the study was conducted, (2) the compartment
118 used to perform the taxonomic identification of Glomeromycota specimens, whether it was the
119 soil associated with bamboo plants, bamboo roots, or both; (3) the taxonomic genus of the

120   bamboo host of the AMF, (4) the species (and, if known, variety) of bamboo hosting the AMF;
121   (5) the family, (6) genus, and (7) species (if identified) of the Glomeromycota fungi associated
122   with bamboo, as well as (8) the type of identification used to determine the taxonomic categories
123   of the AMF found, whether it was morphological or molecular (i.e. based on phylogenetic
124   markers).
125   From these documents, secondary information related to the symbiosis established
126   between Glomeromycota and Bambusoideae was also extracted and discussed, particularly
127   information that referred to the effects of the establishment of symbiosis between these groups of
128   fungi and plants. As such, out of the total number of publications found and selected, those that
129   did not explicitly state the taxonomic identity (at any level) of the plant and its associated
130   arbuscular mycorrhizal fungus, beyond the generic classifications of "bamboos" and
131   "Glomeromycota," were excluded from the meta-synthesis, as well as publications classified as
132   "grey literature".
133   Lastly, while the taxonomic information extracted from the mentioned documents was
134   not modified, it was verified according to the latest updates in the mycological databases Index
135   Fungorum (http://www.indexfungorum.org/) and MycoBank (http://www.mycobank.org/) for the
136   Glomeromycota fungi, and according to the freely accessible book "World Checklist of Bamboos
137   and Rattans" for the bamboo plants (Vorontsova et al., 2016).
138
139   **Figure 1. Workflow displaying the search, selection, and eligibility criteria applied to the**
140   **literature, adapted from the PRISMA 2020 guidelines for reporting new systematic reviews**
141   **(Page et al., 2021).**
142

RESULTS
143

Worldwide studies on AMF-bamboo association
144

145   In the field of mycorrhizal symbiosis established between Glomeromycota and
146   Bambusoideae, most studies have been carried out in Asia, particularly in India (Bhattacharya et
147   al., 2002; Debnath et al., 2015; Jamaluddin & Turvedi, 1997; S. Das et al., 2021; P. Das &
148   Kayang, 2010; Jha et al., 2011; Parkash et al., 2019; Babu & Reddy, 2010; Ravikumar et al.,
149   1997; Verma & Arya, 1998; Muthukumar & Udaiyan, 2006; Singh et al., 2020) and China (Guo
150   et al., 2023; Xing et al., 2021; Qin, et al., 2017a; Qin, et al., 2017b; Jin et al., 2022; M. Zhang et
151   al., 2022; X. Zhang et al., 2019; Weixin et al., 2013). There are also some studies from Indonesia
152   (Mansir et al., 2021; Kramadibrata et al., 2007; Kramadibrata, 2011) and one each from Sri
153   Lanka and Japan (Mafaziya et al., 2019; Fukuchi et al., 2011). However, from the Americas,
154   only one report has been published by an indexed journal, a study carried out in Brazil (de Moura
155   et al., 2019), while no studies were reported from other continents or areas where bamboos may
156   establish and develop. Nevertheless, not all the studies mentioned were included in the review
157   for the reasons previously described, leading to a reduced number of publications presented in
158   *Fig. 2*, which summarizes how many publications were carried out in each country. The
159   Bambusoideae taxa reported from each country and where the presence of the association with

160 Glomeromycota has been described are presented in *Table 1*, and the taxonomic groups of
161 Glomeromycota reported in the selected studies from each country are presented in *Table 2*.
162
163 **Figure 2. Map showing the number of studies from each country that include symbiotic**
164 **associations between Glomeromycota and bamboos and identify both symbionts at least to**
165 **the taxonomic level of family.**
166
167 **Table 1. Countries from which bamboo genera and/or species associated with**
168 **Glomeromycota have been reported.** 1 (Jamaluddin & Turvedi, 1997), 2 (Jha et al., 2011), 3
169 (Mafaziya et al., 2019), 4 (Parkash et al., 2019), 5 (Kramadibrata, 2011), 6 (Weixin et al., 2013),
170 7 (P. Das & Kayang, 2010), 8 (deMoura et al., 2019), 9 (Kramadibrata et al., 2007), 10 (Husein
171 et al., 2022), 11 (Verma & Arya, 1998), 12 (Ravikumar et al., 1997), 13 (Muthukumar &
172 Udaiyan, 2006), 14 (Bhattacharya et al., 2002), 15 (Babu & Reddy, 2010), 16 (Mansir et al.,
173 2021), 17 (Qin, et al., 2017a), 18 (Qin, et al., 2017b).
174
175 **Table 2. Countries from which Glomeromycota families and/or genera associated with**
176 **bamboo (Bambusoideae) have been reported, along with the specific reference of the report**
177 **of each fungal taxa.** *Ni* (Not identified)
178
179 **Categorization and description of the general framework of the studies**
180   In the studies, some of the most common approaches involve analyzing rhizospheric and
181 non-rhizospheric soils in search of AMF spores, from which a morphological evaluation is
182 carried out that in most cases results in genus-level resolution, with some being able to identify
183 further to species level. A considerably smaller percentage of studies were found to apply
184 molecular approaches. These use BLAST and specific fungal sequence databases to search for
185 genetic resemblances with previously described and reported species. Other studies that include
186 an analysis of the host bamboo roots often calculate the percentage of mycorrhization or root
187 colonization by AMF and relate it to edaphic or biotic variables of the bamboo. For example,
188 through an analysis of rhizospheric soils from several species of bamboo and their microbial
189 communities, Xing et al. (2021) found that at the phylum level, the relative abundance of
190 Glomeromycota was higher in *Phyllostachys edulis* than in other species of bamboo such as
191 *Phyllostachys sulphurea*, *Phyllostachys bambusoides*, *Sinobambusa tootsik* and *Sasa auricoma*.
192 Meanwhile, Jamaluddin & Turvedi (1997) planted a bambusetum with thirteen different bamboo
193 species corresponding to *Bambusa vulgaris* var. *vittata* and var. *striata*, *Bambusa nutans*,
194 *Bambusa nana*, *Bambusa bambos*, *Bambusa arundinacea*, *Bambusa burmanica*, *Bambusa*
195 *polymorpha*, *Cephalostachyum pergracile*, *Dendrocalamus asper*, *Dendrocalamus strictus*,
196 *Dendrocalamus membranaceus* and *Melocanna baccifera*, and after a subsequent evaluation of
197 their roots, reported that all of them established associations with AMF. Another study included
198 *Bambusa bambos* from three different sampling sites, and all presented the presence of AMF in
199 their rhizospheric soils (Mafaziya et al., 2019). Kramadibrata et al. (2007) studied soil samples

200   from several species of bamboo in Java, Indonesia, and Kramadibrata (2011) described AMF
201   from soils associated with eight species of bamboo on the island of Sumba, Indonesia. More
202   recently, de Moura et al. (2019) characterized the AMF community associated with the bamboo
203   species *Actinocladum verticillatum* and *Bambusa vulgaris* var. *vittata* in Brazil, which showed
204   no significant differences in colonization rates, and Das & Kayang (2010) described that
205   *Bambusa tulda* exhibits an Arum-type AMF colonization, while other bamboo species
206   (*Dendrocalamus hookeri*, *Dendrocalamus hamiltonii*, and *Phyllostachys mannii*) present a Paris-
207   type colonization.
208   Other cases include Fukuchi et al. (2011), who described how the Japanese bamboo
209   species *Sasa senanensis* establishes arbuscular mycorrhizal associations with Glomeromycota;
210   however, they did not report the fungal taxonomy. Debnath et al. (2015) evaluated the presence
211   of AMF in the roots of several bamboo species from two sampling sites in India. The first
212   sampling site included the species *Bambusa balcooa*, *B. tulda*, *B. bambos*, *B. cacherensis*, *B.*
213   *tuldoides*, *Dendrocalamus hamiltonii*, *D. asper*, and *Oxytenanthera nigrociliata*, while the
214   second contained only two species, *Bambusa vulgaris* and *Bambusa polymorpha*. All species
215   from both sites presented roots colonized by AMF. It has also been noted that the bamboo
216   species *Dendrocalamus strictus* is moderately sensitive to AMF colonization, with the presence
217   of such association being restricted to lateral roots, particularly those of the third and second
218   order, respectively, but rarely in the first order roots (Bhattacharya et al., 2002).
219   Based on the aforementioned considerations and information available from each study,
220   the primary factor in categorizing these studies was type of tools used for the identification of
221   Glomeromycota species or taxonomic groups associated with each bamboo species or group,
222   whether through molecular tools, morphological tools, or both (an event that was not observed).
223   The secondary categorization of these studies involved the compartment type used for such
224   taxonomic identification, which could vary depending on the identification technique, since
225   molecular techniques are not restricted by the type of compartment (roots or soil), while
226   morphological techniques can only explore spores extracted from the soil given that exact
227   identification within the roots is practically impossible (Smith & Read, 2008). This
228   categorization allows for an assessment of tools used and compartments analyzed per
229   Bambusoideae species or groups, as shown in *Table 3*, where it is evident that the only
230   compartment studied in all studies, regardless of the AMF identification technique, was soil. It is
231   also apparent that the molecular identification of groups within Glomeromycota was only
232   performed in two studies, both on the same bamboo species, *Phyllostachys edulis*.
233   **AMF composition associated with bamboos**
234   In terms of the Glomeromycota diversity associated with bamboo species, only richness
235   approximations, such as the number of reported species, and composition, such as the assignment
236   of taxonomic identity to the group, were considered in the selected studies. Most studies
237   taxonomically resolved the isolated morphological species from the soils associated with
238   different bamboo species to the genus level, with some cases reaching a finer resolution to
239   species level. In some studies, although the presence of several morphological species within a

240 given genera was recognized, the species was not reported, as in Mafaziya et al. (2019). *Table 3*
241 summarizes the genera and families of Glomeromycota fungi identified in soils associated with
242 every bamboo species reported (grouped by genus), as well as the type of identification and the
243 compartment from which the specimens were obtained. *Figure 3* presents the bamboo genera and
244 species associated with the Glomeromycota genera described in the selected documents, showing
245 that *Glomus* and *Acaulospora* are the AMF genera associated with the most bamboo genera
246 (eight each) and species (25 and 23, respectively). *Gigaspora* followed with associations with six
247 genera and 14 bamboo species, while *Sclerocystis* and *Scutellospora* recorded five genera and 12
248 bamboo species each, and *Ambispora*, *Claroideoglomus*, and *Diversispora* associated with two
249 genera and two bamboo species each. *Entrophospora* and an unidentified Glomeromycota genus
250 were reported to associate with only one bamboo species within a single bamboo genus each.
251
252 **Table 3. Identification method and compartment type from which Glomeromycota have**
253 **been reported in different bamboo species, as well as the fungal groups described for each**
254 **bamboo at the genus and family levels.** Ac (Acaulosporaceae), Am (Ambisporaceae), Ar
255 (Archaeosporaceae), Cl (Claroideoglomeraceae), Di (Diversisporaceae), Gi (Gigasporaceae), Gl
256 (Glomeraceae), Pa (Paraglomeraceae), *Aca* (*Acaulospora*)*, Ent* (*Entrophospora*)*, Ni* (Not
257 identified), *Amb* (*Ambispora*)*, Cla* (*Claroideoglomus*)*, Div* (*Diversispora*)*, Gig* (*Gigaspora*)*, Scu*
258 (*Scutellospora*)*, Glo* (*Glomus*) and *Scl* (*Sclerocystis*); 1 (Jamaluddin & Turvedi, 1997), 2 (Jha et
259 al., 2011), 3 (Mafaziya et al., 2019), 4 (Parkash et al., 2019), 5 (Kramadibrata, 2011), 6 (Weixin
260 et al., 2013), 7 (P. Das & Kayang, 2010), 8 (deMoura et al., 2019), 9 (Kramadibrata et al., 2007),
261 10 (Husein et al., 2022), 11 (Verma & Arya, 1998), 12 (Ravikumar et al., 1997), 13
262 (Muthukumar & Udaiyan, 2006), 14 (Bhattacharya et al., 2002), 15 (Babu & Reddy, 2010), 16
263 (Mansir et al., 2021), 17 (Qin, et al., 2017a), 18 (Qin, et al., 2017b).
264
265 **Figure 3. Chord diagram of the bamboos reported to associate with Glomeromycota.** On
266 the left, the genera of Bambusoideae (on top) and the Glomeromycota genera with which they
267 have been reported to associate. On the right, the genera of Glomeromycota (bottom) and the
268 species of bamboo with which they have been reported to associate (top). Aca (*Acaulospora*)*,*
269 Ent (*Entrophospora*)*, Ni* (Not identified), Amb (*Ambispora*)*, Cla* (*Claroideoglomus*)*, Div*
270 (*Diversispora*)*, Gig* (*Gigaspora*)*, Scu* (*Scutellospora*)*, Glo* (*Glomus*) and Scl (*Sclerocystis*)*.*
271 Bamboo genera: Phyll (*Phyllostachys*), Acti (*Actinocladum*), Bamb (*Bambusa*), Ceph
272 (*Cephalostachyum*), Dend (*Dendrocalamus*), Dino (*Dinochloa*), Giga (*Gigantochloa*), Melo
273 (*Melocanna*), Nast (*Nastus*), Schy (*Schizostachyum*). Bamboo species: A_ve (*Actinocladum*
274 *verticillatum*), B_ar (*Bambusa arundinacea*), B_ba (*Bambusa bambos*), B_bl (*Bambusa*
275 *blumeana*), B_bu (*Bambusa burmanica*), B_gr (*Bambusa grandis*), B_na (*Bambusa nana*), B_nu
276 (*Bambusa nutans*), B_pa (*Bambusa pallida*), B_pe (*Bambusa pervariabilis*), B_po (*Bambusa*
277 *polymorpha*), B_sp (*Bambusa sp.*), B_tu (*Bambusa tulda*), B_vu (*Bambusa vulgaris*), C_pe
278 (*Cephalostachyum pergracile*), D_as (*Dendrocalamus asper*), D_ha (*Dendrocalamus*
279 *hamiltonii*), D_ho (*Dendrocalamus hookeri*), D_me (*Dendrocalamus membranaceus*), D_st

280 (*Dendrocalamus strictus*), D_sp (*Dinochloa sp.*), G_ap (*Gigantochloa apus*), G_at
281 (*Gigantochloa atter*), G_ma (*Gigantochloa manggong*), M_ba (*Melocanna baccifera*), N_re
282 (*Nastus reholttumianus*), P_ed (*Phyllostachys edulis*), P_ma (*Phyllostachys mannii*), S_br
283 (*Schizostachyum brachycladum*), S_li (*Schizostachyum lima*), S_zo (*Schizostachyum zollingeri*).
284

Discussion

286 In addition to the collection and extraction of information related to the symbiotic
287 association between Glomeromycota fungal taxa and Bambusoideae plants (which are described
288 and gathered in the results), discoveries and descriptions of the relationships between symbionts
289 in this association were also identified within the framework of this review from both the
290 selected articles and those that were not necessarily included in the first part of this document.
291 The central results of this review are summarized and discussed below, as well as the reported
292 effects derived from the establishment of such arbuscular mycorrhizal symbiosis between fungi
293 and bamboos from around the world.

AMF assemblages in soils associated with bamboos

295 Based on the information compiled in *Table 3*, there are specific systems, such as those
296 subject to high-impact management, where the composition of the AMF assemblage associated
297 with *Phyllostachys edulis* was dominated by the Glomeraceae family in terms of abundance in
298 sequence numbers (Qin et al., 2017a). However, the same study found that such management did
299 not significantly affect the fungal family, which is consistent with the assertion that Glomeraceae
300 is a disturbance-tolerant group. Acaulosporaceae, on the other hand, is not considered as such,
301 and therefore it can be concluded that under these conditions, *P. edulis* is not an ideal host for
302 Acaulosporaceae (Chagnon et al., 2013; Qin et al., 2017a).

303 Regarding systems derived from plantations, Jamaluddin & Turvedi (1997) reported the
304 presence of five AMF genera (*Glomus*, *Gigaspora*, *Acaulospora*, *Scutellospora*, and
305 *Sclerocystis*) in a bambusetum containing 13 bamboo species; however, despite mentioning some
306 particular morphological species, they did not distinguish which bamboo sample was isolated.
307 They also found that *Bambusa nana* presented the highest AMF colonization, followed by
308 *Bambusa vulgaris* var. *vittata*, while the lowest colonization was obtained by *Bambusa bambos*,
309 generating a gradient ranging from 80% to 33% in terms of mycorrhizal percentage (Jamaluddin
310 & Turvedi, 1997).

311 Similarly, studies such as Parkash et al. (2019) confirmed that *Bambusa tulda*, *Bambusa*
312 *pallida*, *Bambusa nutans*, and *Bambusa bambos* form mycorrhizal associations with AMF after
313 quantifying the percentage of root colonization by these fungal symbionts, with values in all
314 cases exceeding 70%. In specific, within the rhizosphere of *Bambusa bambos*, they identified
315 five morphological species of the genus *Acaulospora* (*A. laevis*, *A. scrobiculata*, *A. lacunosa*, *A.*
316 *mellea*, and *Acaulospora* sp.), seven belonging to *Glomus* (*G. clavisporum*, *G. reticulatum*, *G.*
317 *macrocarpum*, *G. claroideum*, *G. pansihalos*, *G. geosporum*), two in the genus *Gigaspora* (*G.*
318 *gigantea* and *Gigaspora* sp.), and one *Entrophospora* sp. In the rhizosphere of *B. tulda*, they
319 identified a total of four morphological species: *Acaulospora foveata*, *Glomus clavisporum*, *G.*

320 *albidum*, and *Scutellospora* sp. Meanwhile, in *Bambusa pallida*, they reported eight
321 morphological species, two *Acaulospora* (*A. laevis* and *Acaulospora* sp.) and six *Glomus* (*G.*
322 *macrocarpum*, *G. monosporum*, *G. geosporum*, *G. epigaeum*, *G. fasciculatum*, and *Glomus* sp.);
323 and in *Bambusa nutans*, they only recorded one species: *Glomus epigaeum*. Jha et al. (2011)
324 found six species of Glomeromycota (*Acaulospora scrobiculata*, *Glomus aggregatum*, *G.*
325 *arborense*, *G. diaphanum*, *G. intraradices*, and *G. invermayanum*) in the rhizospheric soil of
326 *Dendrocalamus strictus*. Mansir et al. (2021) described the presence of three genera inside the
327 roots of *Gigantochloa atter*, specifically *Glomus*, *Gigaspora*, and *Acaulospora*. In the
328 rhizosphere of *Bambusa* sp., Husein et al. (2022) identified the presence of spores pertaining to
329 the genera *Glomus*, *Gigasporaceae*, and *Acaulospora*, with several morphological species each,
330 but their specific identities were not able to be determined. Additionally, in a study on
331 populations of *Bambusa bambos*, Mafaziya et al. (2019) found 14 AMF morphotypes associated
332 with the rhizospheric soil of the genera *Glomus*, *Scutellospora*, *Gigaspora*, and *Acaulospora*,
333 with *Glomus* being the dominant genus and *Acaulospora* the least represented in terms of
334 abundance.
335   Kramadibrata et al. (2007) found that *Acaulospora foveata* and *A. scrobiculata* associated
336 with *Dendrocalamus asper* and *Gigantochloa apus*, while *Acaulospora tuberculata* established
337 associations with *Bambusa vulgaris*, *Dendrocalamus asper*, *Schizostachyum zollingeri*,
338 *Gigantochloa manggong*, and *Gigantochloa apus*. In addition, *Glomus etunicatum* was
339 associated with *Bambusa vulgaris*, *Dendrocalamus asper*, *Gigantochloa manggong*, and
340 *Gigantochloa apus*; while *Glomus fuegianum* associated with *B. vulgaris*, *D. asper*, and
341 *Schizostachyum zollingeri*. *Glomus* cf. *formosanum* and *Glomus geosporum* were associated with
342 *D. asper* and *G. apus*. *Glomus mosseae* established associations with *S. zollingeri* and *G. apus*,
343 and finally, *Scutellospora calospora* was associated with *G. manggong*. From the island of
344 Sumba, Indonesia, Kramadibrata (2011) reported that *Acaulospora foveata* associated with
345 *Bambusa blumeana*, *Dinochloa* sp., and *Nastus reholttumianus*, while *Acaulospora scrobiculata*
346 associated with *Bambusa blumeana*, *Schizostachyum brachycladum* (green variety), and *Nastus*
347 *reholttumianus*. *Acaulospora tuberculata* was found with *Gigantochloa atter*, *Schizostachyum*
348 *brachycladum* (yellow variety), and *Schizostachyum lima*. Furthermore, *Glomus etunicatum* was
349 associated with *Gigantochloa atter*, and finally, *Glomus rubiforme* with *Gigantochloa atter*.
350   In other studies, inoculants were prepared with isolated AMF identified as *Glomus rosea*,
351 *G. magnicaule*, *G. etunicatum*, *G. heterogama*, *G. maculosum*, *G. multicaule*, *Scutellospora*
352 *nigra*, and *S. heterogama* for application to bamboo. Babu and Reddy (2010) applied the
353 inoculants to *Dendrocalamus strictus* and confirmed fungal colonization. Ravikumar et al.
354 (1997) worked with independent inoculations and all possible combinations of *Glomus*
355 *aggregatum*, *G. fasciculatum*, and *G. mosseae* on *Dendrocalamus strictus*. Under all
356 circumstances, their roots were colonized with a colonization percentage ranging from 30% to
357 60%. This finding is similar to that of Verma and Arya (1998), in which five morphological
358 species were isolated, including *Acaulospora scrobiculata*, *Glomus intraradices*, *G. aggregatum*,
359 *G. mosseae*, and *Scutellospora heterogama*, from the rhizosphere of *Dendrocalamus asper* in

360   order to develop two inoculants: one with the first species (I1) and the other with the remaining
361   four (I2). Furthermore, they tested another inoculant (I3) from isolated teak spores, which
362   contained *Acaulospora scrobiculata*, *A. delicata*, *Gigaspora* sp., *G. ramisporophora*, *Glomus*
363   *intraradices*, *G. geosporum*, *G. mosseae*, *G. etunicatum*, and *Scutellospora pellucida*. These
364   fungi established symbiotic associations with the bamboo species, which was confirmed by
365   quantifying the percentage of colonization within the roots of *D. asper*. The statistical analyses
366   showed that the maximum percentage of colonization was found in I3, followed by I1 and I2,
367   respectively (Verma & Arya, 1998). In 2002, *Dendrocalamus strictus* was inoculated with three
368   species of AMF, namely *Glomus mosseae*, *G. fasciculatum*, and *Gigaspora margarita*
369   (Bhattacharya et al., 2002). Later, in 2011, Jha et al. (2011) inoculated *Bambusa bambos* and
370   *Dendrocalamus strictus* with *Acaulospora scrobiculata*, *A. mellea*, *Glomus aggregatum*, *G.*
371   *cerebriforme*, *G. arborense*, *G. diaphanum*, *G. intraradices*, *G. etunicatum*, *G. fasciculatum*, *G.*
372   *hoi*, *G. occultum*, and *Glomus* sp., and all the fungi established an association with the roots of
373   both bamboo species. Considering that the current veracity of fungal identity of spores present in
374   commercial bio-inoculants is compromised (Vahter et al., 2023), the fact that most of the studies
375   mentioned resorted to the use of trap cultures or direct isolation of Glomeromycota species to be
376   inoculated provides some certainty regarding the accuracy of their results. It was frequently
377   observed that *Acaulospora* and *Glomus* were among the most commonly isolated strains or
378   fungal genera inoculated to different bamboo species, as these AMF genera are commonly found
379   worldwide in a wide range of natural ecosystems including those altered by humans, such as
380   agricultural systems (Davison et al., 2015; Oehl et al., 2017).
381   **Effects of Glomeromycota on host bamboo plants**
382   **On bamboo physiology and morphology**
383   While the effects of symbiosis were not reported for all the bamboo species mentioned,
384   some of them such as *Dendrocalamus strictus* were reported to significantly stabilize the upper
385   layer of the soil due to the nature of their root system and enhance the leaf litter accumulation in
386   response to associations with AMF (Ben-zhi et al., 2005). Furthermore, seedlings of
387   *Dendrocalamus strictus* that were inoculated with *Glomus fasciculatum* and *G. mosseae*
388   (simultaneously) reached the greatest internodal distance of all treatments, followed by bamboo
389   seedlings inoculated only with *G. aggregatum* (Ravikumar et al., 1997). Another study found
390   that *D. strictus* rhizomes reached their maximum length when the inoculation contained only the
391   *G. aggregatum* isolate, followed by the combination of *G. aggregatum* and *G. mosseae*
392   (Ravikumar et al., 1997). Total biomass production in *D. strictus* was also favored by
393   mycorrhizal associations with Glomeromycota fungi, reaching maximum dry matter production
394   when seedlings were inoculated with *G. aggregatum* and *G. fasciculatum* (Ravikumar et al.,
395   1997).
396   In *Bambusa bambos* and *Dendrocalamus strictus*, phosphorus uptake and shoot length
397   increased significantly with all inoculated AMF (8 commercial formulations), except for *Glomus*
398   sp. in *D. strictus* (Jha et al., 2011), indicating that effective AMF utilization can enhance
399   productivity of these bamboo species in the region (Jha et al., 2011). Similarly, Bhattacharya et

al. (2002) found that inoculating some AMF in *D. strictus* seedlings significantly promoted
lateral branching (in number and length) of roots in this species, although no clarifications were
made regarding the status of such fungi in the soil or even the percentage of mycorrhization, only
reports of the morphological response of the seedling root system.

In terms of morphology, as mentioned above for species such as *D. strictus*, AMF
inoculation causes differentiating effects on the structures of inoculated plants. For instance,
inoculating *G. mosseae* and *G. intraradices* in Chenglu bamboo seedlings, a hybrid bamboo
between *Bambusa pervariabilis* (as the female parent) and *B. grandis* (as the male parent),
resulted in a significant increase in the number of shoots, diameter, and total leaf area of the
inoculated plants compared to those not inoculated with AMF (Weixin et al. 2013).

On growth and nutrient uptake

In general, bamboo plants favor the establishment of mycorrhizal symbiosis given their
fast growth which requires high nutrient requirements during the initial growth stages
(Ravikumar et al., 1997). This explains the increase in the rhizosphere of several bamboo species
after establishing a mycorrhizal symbiosis, a phenomenon that has specifically been described in
Bambusa balcooa, *Bambusa vulgaris* var. *vittata* (known as green bamboo) and var. *striata*
(known as yellow bamboo), *Bambusa nutans* and *Dendrocalamus asper* (Singh et al., 2020).

In *Dendrocalamus strictus* (a bamboo species with an extensive root and rhizome
system), inoculation of AMF along with *Aspergillus tubingensis* (an Ascomycota fungus)
showed a synergistic effect on bamboo growth, nutrient uptake (such as P, K, Ca, and Mg), and
reduction in heavy metal translocation to the plant (Babu & Reddy, 2010). Similar effects have
also been observed in other plants that establish associations with AMF (Chen et al., 2007; Chen
et al., 2001). This is consistent with what Muthukumar & Udaiyan (2006) described, who
performed a nursery experiment evaluating the effects of applying a *Glomus aggregatum*
inoculum on promoting the growth of *D. strictus* plants in two different soil types (alfisol and
vertisol). They found that root colonization percentages by *G. aggregatum* (reaching 55% and
confirming the establishment of the association with this AMF species) were positively and
significantly related to the dry weight of bamboo seedlings, and thus to the concentrations of N,
P, and K in their tissues (roots, rhizome, and shoots) (Muthukumar & Udaiyan, 2006). In
addition, Verma & Arya (1998) found that *Dendrocalamus asper* seedlings treated with AMF
inocula extracted from their rhizospheric soil (2) and one associated with Teak were significantly
taller than those that did not receive treatments, and they also presented higher concentrations of
P in their shoots, which they describe as an effect resulting from AMF-mediated improvements
in the efficiency of capturing available P in the soil. Even earlier, Ravikumar et al. (1997) also
reported that AMF association with *Dendrocalamus strictus* seedlings improves their growth
compared to a control not inoculated with AMF, emphasizing that inocula with *G. fasciculatum*
and *G. aggregatum* (alone or in combination) are the best option (among those evaluated) for
achieving the highest rates of growth and total dry matter production.

Another study also described how in *Bambusa bambos* and *Dendrocalamus strictus*, total
dry weight and P uptake (an essential nutrient for plant growth) increased significantly in seven

440 of the eight AMF inoculated plants (Jha et al., 2011). Additionally, the confirmed establishment
441 of symbiotic associations between Chengdu bamboo (a hybrid) and AMF, specifically an
442 inoculum of *Glomus intraradices* and *G. mosseae*, improved the uptake of P and K in inoculated
443 plants, as well as their growth and biomass accumulation, making these AMF good candidates in
444 efforts to increase the production of this hybrid bamboo (Weixin et al., 2013).

445 **Effects of bamboos on AMF assemblages**

446   Host plants are not passive actors during symbiosis, and AMF assemblages are not
447 randomly distributed in patches of host plants but rather tend to associate with particular
448 ecological groups (Davison et al., 2011). Considering this, Guo et al. (2023) described that the
449 rhizospheric soil of bamboo, particularly *Phyllostachys edulis* and four of its forms (*P. edulis* f.
450 *tao kiang*, *P. edulis* f. *luteosulcata*, *P. edulis* f. *pachyloen* and *P. edulis* f. *gracilis*) has more
451 complex, longer, and interconnected fungal networks than those in non-rhizospheric soil, in
452 addition to significant differences in diversity. However, at least for Glomeromycota, abundance
453 appears to be higher in non-rhizospheric soil, suggesting that this is the original pool of species
454 from which the plant root will establish associations with only some of the AMF available in the
455 rhizosphere (Bledsoe et al., 2020, Fiore-Donno et al., 2022). This contrasts with the results of
456 Husein et al. (2022), who showed that the rhizosphere of *Bambusa* sp. has more abundance and
457 diversity of Glomeromycota spores than those of other plants, such as *Cichorium intybus* and
458 *Pinus merkusii*, which, although not compared to the non-rhizospheric soil of these species, gives
459 indications of a possible affinity of *Bambusa* for selecting AMF, or the preference of AMF to
460 associate with this bamboo species.

461   On the other hand, bamboos classified as runners (with leptomorph rhizomes), such as
462 those of the genus *Phyllostachys* that are known for invading and quickly replacing neighboring
463 forest cover, tend to increase the biomass of their associated AMF. This significantly changes the
464 fungal assemblages in the soil, contributing to the formation of aggregates and carbon storage in
465 the system (Xu et al., 2020; Qin et al., 2017). Likewise, when comparing a forest of
466 *Phyllostachys pubescens* with surrounding forests, Quin et al. (2017) found that in the former,
467 both AMF spore density and root colonization rate were significantly higher than in the latter,
468 and that the former favored the presence of the Glomeraceae family but reduced that of the
469 Acaulosporaceae and Archaeosporaceae families.

470   In considering the dominance of some plant species over others, Mafaziya et al. (2019)
471 did not find perceptible changes in the AMF community structure in forest ecosystems after an
472 increase in the dominance of *Bambusa bambos* in these systems. However, when they compared
473 the soil of the forest patches adjacent to the populations of *Bambusa bambos*, these recorded a
474 higher abundance of AMF spores. They therefore conclude that, at least under the conditions of
475 the study, the fungal community shows high resistance to changes in soil surface coverage, as
476 well as resilience to the influence generated by the dominance of a single plant species.

477   Additionally, Jin et al. (2022) found that when extensive management is carried out in
478 bamboo forests, particularly those of *P. edulis* (forests regularly harvested without any
479 management), the abundance of AMF increases substantially leading to an increase in AMF

480 respiration rates and a significant change in carbon cycling within bamboo forest ecosystems
481 produced by AMF.

Challenges ahead

483   Qin et al. (2017 a, b) and Jin et al. (2022) report molecular marker-based approaches to
484 elucidate the composition of AMF assemblages in bamboo forest soils using primers described
485 by Sato et al. (2005) that amplify part of the 18S region (AMV4.5NF and AMDGR). These
486 sequences can then be compared to the MaarjAM database using BLAST (Öpik et al., 2010) to
487 assign taxonomic identities to the Glomeromycota groups in the sample. With similar
488 approaches, Zhang et al. (2022) amplified the ITS region with the ITS1F and ITS2R primers to
489 evaluate the fungal community in the roots, soil, and aerial structures of *Phyllostachys edulis*,
490 and Zhang et al. (2019) amplified the ITS2 region with the ITS3 and ITS4 primers to investigate
491 the rhizospheric community structure of *P. edulis* at the phylum level, identifying sequences
492 using BLAST in the UNITE database. In these studies, they were able to identify groups within
493 the Glomeromycota phylum, but the internal transcribed spacer (ITS) was not proven to be an
494 optimal candidate for barcoding arbuscular mycorrhizal fungi (AMF) because the region alone is
495 exceptionally variable and does not adequately resolve species, especially among closely related
496 taxa. Other primers targeting regions of the small subunit (18S) or large subunit (28S) tend to be
497 biased as the primers only are effective in some taxonomic groups within the Glomeromycota
498 community (Stockinger et al., 2010). In addition, although the specific primers proposed by Sato
499 et al. (2005) are promising in terms of coverage and specificity, Van Geel et al. (2014) highlight
500 that they are biased towards groups within the Glomeraceae family within Glomeromycota, even
501 detecting groups in Basidiomycota and Chytridiomycota, but not detecting any members of the
502 Ambisporaceae family and only a few of the Claroideoglomeraceae and Paraglomeraceae
503 families in Glomeromycota. This situation generates difficulties when comparing the results of
504 studies on AMF diversity and richness or composition, as there is little consistency regarding the
505 target genes and primers used (Van Geel et al., 2014). While there is still no consensus region for
506 AMF barcoding (Kolaříková et al., 2021), recent studies suggest that the ideal approach is to
507 perform nested PCR approaches on different regions of the rRNA gene (Kolaříková et al., 2021).
508 Tedersoo et al. (2022) also recommend that when performing taxonomic identification of a
509 sequence using BLAST that may belong to Glomeromycota (if the selected primers allow it), the
510 searches should preferably be made against the MaarjAM database, not UNITE, as the latter uses
511 reads based on the ITS region, whose disadvantages have been previously mentioned.

512   Bamboo species such as *Phyllostachys edulis* have been described as promising in their
513 roles of carbon sequestration through its mycorrhizal associations. This could lead to increases in
514 planted areas or facilitate their expansion in ecosystems through the application of
515 Glomeromycota bio-inoculants. However, it is imperative to pay attention to the ecological risks
516 this may also entail in terms of negative effects on plant diversity and other soil microorganisms
517 in the colonized areas (Qin et al., 2017). This type of management reduces soil pH, facilitates the
518 hyper accumulation of available N, P, and K, and promotes soil aggregation loss and erosion,
519 which leads to a significant reduction in AMF biomass as well as alterations in soil assemblage

520   diversity (Xu et al., 2008; Shinohara & Otsuki, 2015; Qin et al., 2017a; Liu et al., 2011). This
521   situation can be avoided by promoting responsible and sustainable use and management of the
522   resource such as the intensive management strategies traditionally applied to this bamboo
523   species.
524   As for publications addressing the establishment of these symbiotic associations,
525   although some report evidence of AMF colonization in roots of species such as *Dendrocalamus*
526   *strictus* (Das et al., 2021), they do not include any other evidence in terms of spore identification
527   or genetic material extraction from any of the different compartments where they are found (soil
528   and/or the root of the host plant). As a result, the information conveyed is poor or incomplete, at
529   least within the framework of the objectives of this work.
530   In addition, in some cases the term 'bamboo' is used in a very generic way or even as if
531   constituting a taxonomic rank by itself. This has led to several studies maintaining an ambiguous
532   discourse when discussing the potential of bamboo (in ecological or economic terms) or even of
533   their associated AMF species (i.e. Toh et al., 2018; Patra et al., 2021; Priya et al., 2014;
534   Mafaziya et al., 2019), resulting in a loss of informative value. Additionally, as reported in
535   Debnath et al. (2015), several AMF genera were isolated from different sampling sites
536   (*Acaulospora*, *Ambispora*, *Diversispora*, *Funneliformis*, *Glomus*, *Paraglomus*, *Rhizophagus*, and
537   *Sclerocystis*), but the associated bamboo species was not clarified, nor is it considered that they
538   may be working with other species, which generates noise in the analyses. Rather, studies must
539   clarify which species of bamboo is being referred to, since as evidenced throughout this
540   document, the nature of the symbiosis, its effects, and the potentials of each species of bamboo
541   are, to some degree, specific.
542   This review highlights the need to compile information and build knowledge around a
543   wider range of bamboo species and the symbiotic interactions they form or can potentially form
544   with AMF. It is surprising that in tropical America, a continent where this group of plants is so
545   diverse and where such ecologically, economically, and culturally important groups exist such as
546   the Guadua sub-tribe (specifically *Guadua angustifolia* Kunth in terms of their uses,
547   applications, and distribution range) (Cruz-Armendáriz et al., 2023; Akinlabi et al., 2017; Clark
548   et al., 2015), associations with AMF are so absent in the scientific literature, at least in
549   publications from indexed and/or peer-reviewed journals. This phenomenon may be the result of
550   the ease of producing "gray literature" in terms of speed and low cost, or even to the difficulties
551   involved in submitting and publishing a scientific document, as research often remains in
552   undergraduate and graduate theses, conference proceedings, research reports, memoranda,
553   scientific society documents, bulletins, or websites (Corlett, 2010). This greatly hinders access to
554   information and the construction of knowledge on environmental and social issues such as those
555   exposed in this document. Therefore, the publication of studies focused on this association are
556   the first steps to support efforts aimed to propagate bamboos using AMF in various regions of
557   the world, as proposed by (de Moura et al., 2019). With adequate knowledge of mycorrhizal
558   fungal diversity in the rhizosphere of bamboo species and molecular approaches for analyzing

559 roots and soils, the development of mycorrhizal inoculation programs is guaranteed to make
560 bamboo available as a sustainable resource (Das & Kayang, 2010).
561   Finally, it is important to note that although this document did not modify the names of
562 the taxa assigned to Glomeromycota and Bambusoideae reported in the reviewed documents,
563 taxonomic reorganizations and changes in names or categories have occurred in several cases
564 (i.e. Błaszkowski et al., 2022), with some being assigned as synonyms of a more accepted name,
565 for example. In some cases, even the reported names were fundamentally incorrect, not
566 stemming from any synonymy confusion. Therefore, it is relevant to keep up to date with
567 nomenclatural changes associated with the study groups being investigated to facilitate research
568 and communication both within and outside the academic community. This can be done through
569 specialized databases such as Index Fungorum (http://www.indexfungorum.org/), Species
570 Fungorum (https://www.speciesfungorum.org/), and MycoBank (http://www.mycobank.org/) for
571 Glomeromycota fungi, and literature such as the freely accessible book "World Checklist of
572 Bamboos and Rattans" by (Vorontsova et al., 2016) for bamboos. The current status of the names
573 of Glomeromycota fungi and Bambusoideae bamboos are summarized in *Tables 4* and *5*,
574 respectively.
575
576 **Table 4. Names of the Glomeromycota taxa mentioned in the text, and the current status of**
577 **these names according to Index Fungorum, Species Fungorum, and MycoBank.**
578
579 **Table 5. Names of the Bambusoideae taxa mentioned in the text, and the current status of**
580 **these names according to Vorontsova et al. (2016).**
581

Conclusions

583   This study presents the first systematic review of the current state of knowledge
584 surrounding arbuscular mycorrhizal symbiosis established between plants and fungal taxa within
585 Glomeromycota and Bambusoideae (respectively) worldwide. Asia, specifically India and China,
586 stood out as the continent and countries with the most (and almost all) studies on the topic of
587 review, while no other studies were reported from other continents, except for Brazil with a
588 single publication. This review only considered currently published scientific literature, as the
589 filtering and selection process filtered documents classified as gray literature, a particularly
590 common publication trend in Latin America. As such, although there may be significant interests
591 or efforts to study the symbiosis between AMF groups and bamboo species in Latin America,
592 access to such information is limited.
593   The bamboo species that have been evaluated, described, or evidenced to establish
594 mutualistic associations with arbuscular mycorrhizal fungi (31 species within 10 botanical
595 families) associate with a considerable diversity of Glomeromycota genera and families (17 and
596 eight, respectively, including groups marked as "Ni"). The identification of these groups to
597 species level through the application of molecular markers using samples from the root

598 compartment would contribute to a better understanding of and future perspectives for this
599 symbiotic association.

600   Based on the information compiled here, it is evident that the study of arbuscular
601 mycorrhizal fungi in bamboo species around the world remains incipient and poorly explored,
602 particularly with respect to the biology and ecology of mycorrhizal symbiosis in Bambusoideae.
603 This is surprising considering the growing and robust evidence supporting the role of AMF in the
604 mineral nutrition, water absorption or capture, and protection against biotic and abiotic stress
605 factors in the majority of plants (Fall et al., 2022). As described by de Moura et al. (2019),
606 understanding the dynamics of symbiosis between bamboo and its associated AMF is
607 fundamental for developing management practices aimed at improving plant productivity and
608 reducing production costs for bamboo species of interest. Considering the high ecological,
609 ecosystemic, and cultural value of this plant group, this would expand the spectrum of
610 possibilities in terms of applicability of these species for ecological restoration and the fight
611 against socio-environmental problems.
612

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622 ## ADDITIONAL INFORMATION AND DECLARATIONS
623 ### Competing Interests
624 The authors declare that they have no competing interests.

625 ### Author Contributions
626 - Juan José Sánchez-Matiz performed the search strategy, conceived and designed the
627   experiments, performed the experiments, analyzed the data, prepared the figures, authored or
628   reviewed drafts of the paper, and approved the final draft.
629 - Lucía Ana Díaz-Ariza performed the search strategy, conceived and designed the
630   experiments, performed the experiments, analyzed the data, prepared the figures, authored or
631   reviewed drafts of the paper, and approved the final draft.

632 ### Data Availability
633 The following information is supplied regarding data availability:
634 The PRISMA 2020 Checklist for systematic reviews is available in the Supplemental Files.
635

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Figure 1

Workflow displaying the search, selection, and eligibility criteria applied to the literature, adapted from the PRISMA 2020 guidelines for reporting new systematic reviews (Page et al., 2021).

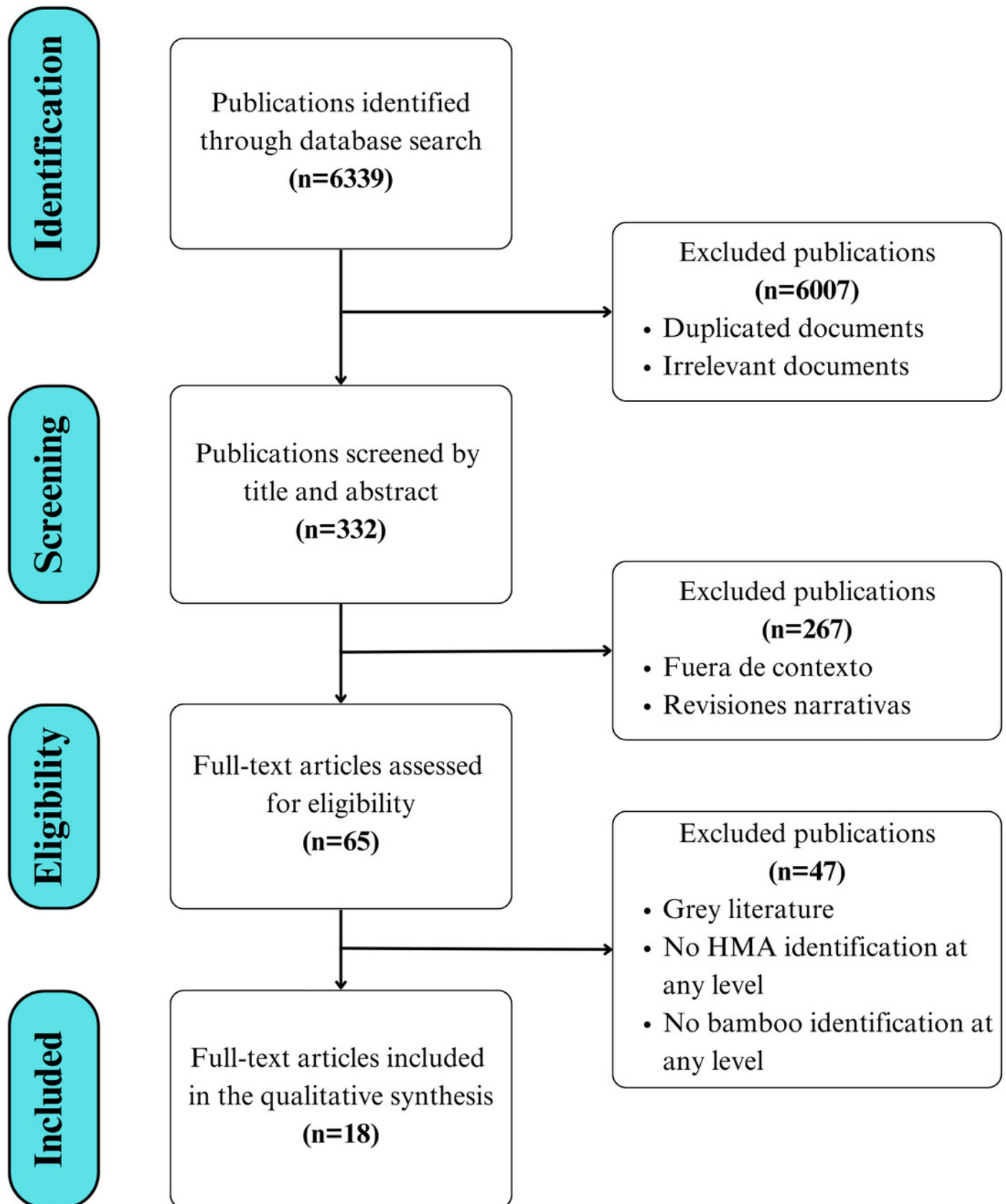



Figure 2

Map showing the number of studies from each country that include symbiotic associations between Glomeromycota and bamboos and identify both symbionts at least to the taxonomic level of family.

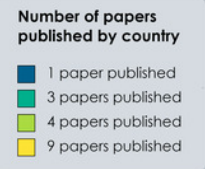
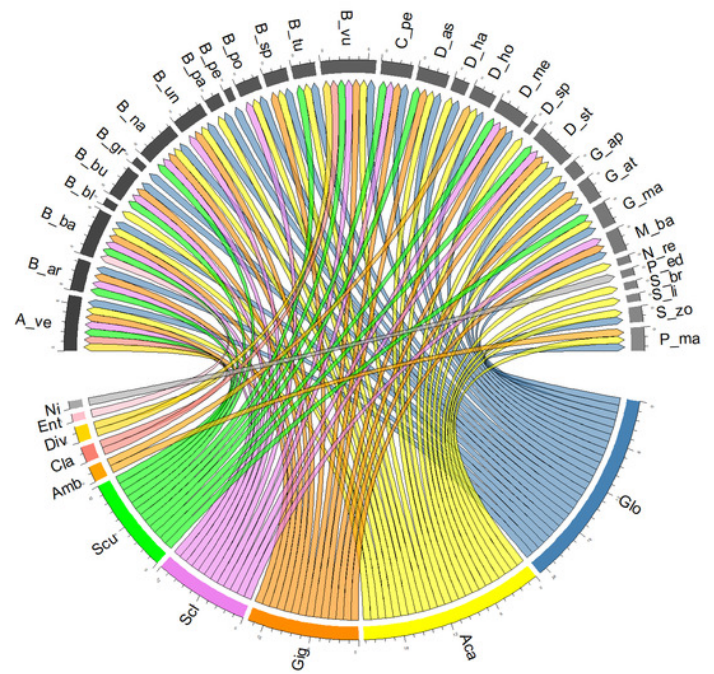
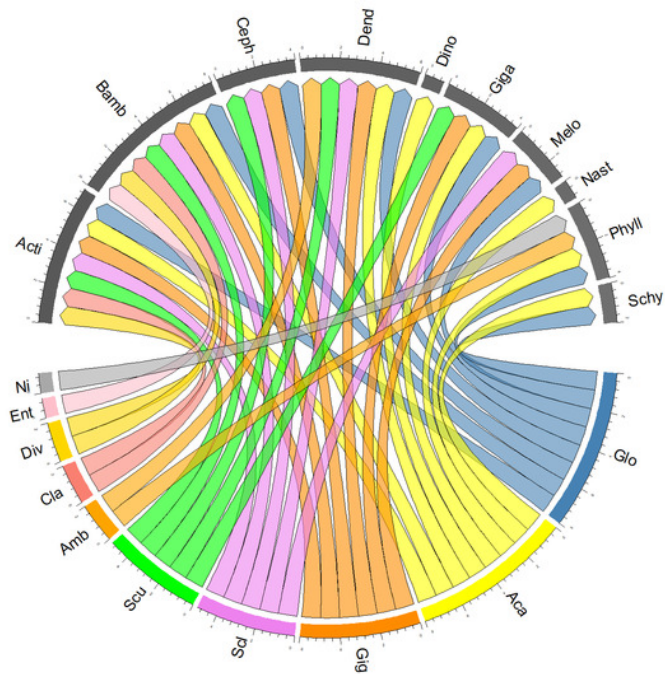



Figure 3

Chord diagram of the bamboos reported to associate with Glomeromycota

On the left, the genera of Bambusoideae (on top) and the Glomeromycota genera with which they have been reported to associate. On the right, the genera of Glomeromycota (bottom) and the species of bamboo with which they have been reported to associate (top). Aca (*Acaulospora*), Ent (*Entrophospora*), Ni (Not identified), Amb (*Ambispora*), Cla (*Claroideoglomus*), Div (*Diversispora*), Gig (*Gigaspora*), Scu (*Scutellospora*), Glo (*Glomus*) and Scl (*Sclerocystis*). Bamboo genera: Phyll (*Phyllostachys*), Acti (*Actinocladum*), Bamb (*Bambusa*), Ceph (*Cephalostachyum*), Dend (*Dendrocalamus*), Dino (*Dinochloa*), Giga (*Gigantochloa*), Melo (*Melocanna*), Nast (*Nastus*), Schy (*Schizostachyum*). Bamboo species: A_ve (*Actinocladum verticillatum*), B_ar (*Bambusa arundinacea*), B_ba (*Bambusa bambos*), B_bl (*Bambusa blumeana*), B_bu (*Bambusa burmanica*), B_gr (*Bambusa grandis*), B_na (*Bambusa nana*), B_nu (*Bambusa nutans*), B_pa (*Bambusa pallida*), B_pe (*Bambusa pervariabilis*), B_po (*Bambusa polymorpha*), B_sp (*Bambusa sp.*), B_tu (*Bambusa tulda*), B_vu (*Bambusa vulgaris*), C_pe (*Cephalostachyum pergracile*), D_as (*Dendrocalamus asper*), D_ha (*Dendrocalamus hamiltonii*), D_ho (*Dendrocalamus hookeri*), D_me (*Dendrocalamus membranaceus*), D_st (*Dendrocalamus strictus*), D_sp (*Dinochloa sp.*), G_ap (*Gigantochloa apus*), G_at (*Gigantochloa atter*), G_ma (*Gigantochloa manggong*), M_ba (*Melocanna baccifera*), N_re (*Nastus reholttumianus*), P_ed (*Phyllostachys edulis*), P_ma (*Phyllostachys mannii*), S_br (*Schizostachyum brachycladum*), S_li (*Schizostachyum lima*), S_zo (*Schizostachyum zollingeri*).

Countries from which bamboo genera and/or species associated with Glomeromycota have been reported.

1 (Jamaluddin & Turvedi, 1997), 2 (Jha et al., 2011), 3 (Mafaziya et al., 2019), 4 (Parkash et al., 2019), 5 (Kramadibrata, 2011), 6 (Weixin et al., 2013), 7 (P. Das & Kayang, 2010), 8 (deMoura et al., 2019), 9 (Kramadibrata et al., 2007), 10 (Husein et al., 2022), 11 (Verma & Arya, 1998), 12 (Ravikumar et al., 1997), 13 (Muthukumar & Udaiyan, 2006), 14 (Bhattacharya et al., 2002), 15 (Babu & Reddy, 2010), 16 (Mansir et al., 2021), 17 (Qin, et al., 2017a), 18 (Qin, et al., 2017b).

1 **Table 1:**

2 **Countries from which bamboo genera and/or species associated with Glomeromycota have**
3 **been reported.**

Bambusoideae taxa	Countries where reported					References
	Brazil	China	India	Indonesia	Sri Lanka	
Actinocladum	+					
A. verticillatum	+					8
Bambusa	+	+	+	+	+	
B. arundinacea			+			1
B. bambos			+		+	2,3,1,4
B. blumeana				+		5
B. burmanica			+			1
B. grandis		+				6
B. nana			+			1
B. nutans			+			2,1
B. pallida			+			2
B. pervariabilis		+				6
B. polymorpha			+			1
B. tulda			+			7,2
B. vulgaris	+		+	+		8,1,9
B. sp.				+		10
Cephalostachyum			+			
C. pergracile			+			1
Dendrocalamus			+	+		
D. asper			+	+		11,5,9,1
D. hamiltonii			+			7
D. hookeri			+			7
D. membranaceus			+			1
D. strictus			+			14,15,4,1,13,12
Dinochloa				+		
D. sp.				+		5
Gigantochloa				+		
G. apus				+		9
G. atter				+		5,16
G. manggong				+		9
Melocanna			+			
M. baccifera			+			1
Nastus				+		
N.				+		5

reholttumianus				
Phyllostachys	+	+		
P. edulis	+			17,18
P. mannii		+		7
Schizostachyum			+	
S. brachycladum			+	5
S. lima			+	5
S. zollingeri			+	9

6 1 (Jamaluddin & Turvedi, 1997), 2 (Jha et al., 2011), 3 (Mafaziya et al., 2019), 4 (Parkash et al.,
7 2019), 5 (Kramadibrata, 2011), 6 (Weixin et al., 2013), 7 (P. Das & Kayang, 2010), 8 (deMoura
8 et al., 2019), 9 (Kramadibrata et al., 2007), 10 (Husein et al., 2022), 11 (Verma & Arya, 1998),
9 12 (Ravikumar et al., 1997), 13 (Muthukumar & Udaiyan, 2006), 14 (Bhattacharya et al., 2002),
10 15 (Babu & Reddy, 2010), 16 (Mansir et al., 2021), 17 (Qin, et al., 2017a), 18 (Qin, et al.,
11 2017b).

Countries from which Glomeromycota families and/or genera associated with bamboo
(Bambusoideae) have been reported, along with the specific reference of the report of
each fungal taxa.

Ni (Unidentified)

1 **Table 2:**

2 **Countries from which Glomeromycota families and/or genera associated with bamboo**
3 **(Bambusoideae) have been reported, along with the specific reference of the report of each**
4 **fungal taxa.**

Glomeromycota taxa and associated reference(s)	Countries where AMF species have been reported with bamboo				
	Brazil	China	India	Indonesia	Sri Lanka
Acaulosporaceae	+	+	+	+	+
Acaulospora	+		+	+	+
(deMoura et al., 2019)	+				
(Husein et al., 2022)				+	
(Jamaluddin & Turvedi, 1997)			+		
(Jha et al., 2011)			+		
(Kramadibrata et al., 2007)				+	
(Kramadibrata, 2011)				+	
(Mafaziya et al., 2019)					+
(Mansir et al., 2021)				+	
(P. Das & Kayang, 2010)			+		
(Parkash et al., 2019)			+		
(Verma & Arya, 1998)			+		
Entrophospora			+		
(Parkash et al., 2019)			+		
Ni		+			
(Qin, et al., 2017a)		+			
(Qin, et al., 2017b)		+			
Ambisporaceae		+	+		
Ambispora			+		
(P. Das & Kayang, 2010)			+		
Ni		+			

(Qin, et al., 2017a)		+			
(Qin, et al., 2017b)		+			
Archaeosporaceae		+			
Ni		+			
(Qin, et al., 2017a)		+			
(Qin, et al., 2017b)		+			
Claroideoglomeraceae	+	+			
Claroideoglomus	+				
(deMoura et al., 2019)	+				
Ni		+			
(Qin, et al., 2017a)		+			
(Qin, et al., 2017b)		+			
Diversisporaceae	+	+			
Diversispora	+				
(deMoura et al., 2019)	+				
Ni		+			
(Qin, et al., 2017a)		+			
(Qin, et al., 2017b)		+			
Gigasporaceae	+	+	+	+	+
Gigaspora	+		+	+	+
(Bhattacharya et al., 2002)			+		
(deMoura et al., 2019)	+				
(Husein et al., 2022)				+	
(Jamaluddin & Turvedi, 1997)			+		
(Mafaziya et al., 2019)					+
(Mansir et al., 2021)				+	
(Parkash et al., 2019)			+		
(Verma & Arya, 1998)			+		

Ni		+			
(Qin, et al., 2017a)		+			
(Qin, et al., 2017b)		+			
Scutellospora	+		+	+	+
(Babu & Reddy, 2010)			+		
(deMoura et al., 2019)	+				
(Jamaluddin & Turvedi, 1997)			+		
(Kramadibrata et al., 2007)				+	
(Mafaziya et al., 2019)					+
(Parkash et al., 2019)			+		
(Verma & Arya, 1998)			+		
Glomeraceae	+	+	+	+	+
Glomus	+	+	+	+	+
(Babu & Reddy, 2010)			+		
(Bhattacharya et al., 2002)			+		
(deMoura et al., 2019)	+				
(Husein et al., 2022)				+	
(Jamaluddin & Turvedi, 1997)			+		
(Jha et al., 2011)			+		
(Kramadibrata et al., 2007)				+	
(Kramadibrata, 2011)				+	
(Mafaziya et al., 2019)					+
(Mansir et al., 2021)				+	
(Muthukumar & Udaiyan, 2006)			+		
(Das & Kayang, 2010)			+		
(Parkash et al.,			+		

2019)			
(Ravikumar et al., 1997)			+
(Verma & Arya, 1998)			+
(Weixin et al., 2013)		+	
Sclerocystis	+		+
(deMoura et al., 2019)		+	
(Jamaluddin & Turvedi, 1997)			+
Ni		+	
(Qin, et al., 2017a)		+	
(Qin, et al., 2017b)		+	
Paraglomeraceae		+	
Ni		+	
(Qin, et al., 2017a)		+	
(Qin, et al., 2017b)		+	

7 *Ni* (Unidentified)

Identification method and compartment type from which Glomeromycota have been reported in different bamboo species, as well as the fungal groups described for each bamboo at the genus and family levels.

Ac (Acaulosporaceae), Am (Ambisporaceae), Ar (Archaeosporaceae), Cl (Claroideoglomeraceae), Di (Diversisporaceae), Gi (Gigasporaceae), Gl (Glomeraceae), Pa (Paraglomeraceae), *Aca (Acaulospora), Ent (Entrophospora),* Ni (Unidentified), *Amb (Ambispora), Cla (Claroideoglomus), Div (Diversispora), Gig (Gigaspora), Scu (Scutellospora), Glo (Glomus)* y *Scl (Sclerocystis);*1 (Jamaluddin & Turvedi, 1997), 2 (Jha et al., 2011), 3 (Mafaziya et al., 2019), 4 (Parkash et al., 2019), 5 (Kramadibrata, 2011), 6 (Weixin et al., 2013), 7 (P. Das & Kayang, 2010), 8 (deMoura et al., 2019), 9 (Kramadibrata et al., 2007), 10 (Husein et al., 2022), 11 (Verma & Arya, 1998), 12 (Ravikumar et al., 1997), 13 (Muthukumar & Udaiyan, 2006), 14 (Bhattacharya et al., 2002), 15 (Babu & Reddy, 2010), 16 (Mansir et al., 2021), 17 (Qin, et al., 2017a), 18 (Qin, et al., 2017b).

1 **Table 3:**

3 **Identification method and compartment type from which Glomeromycota have been**
4 **reported in different bamboo species, as well as the fungal groups described for each**
5 **bamboo at the genus and family levels.**

Compartment and Bambusoideae taxa	Glomeromycota taxa																	Ref.
	Ac			Am		Ar	Cl		Di		Gi			Gl			Pa	
	Aca	*Ent*	*Ni*	*Amb*	*Ni*	*Ni*	*Cla*	*Ni*	*Div*	*Ni*	*Gig*	*Scu*	*Ni*	*Glo*	*Scl*	*Ni*	*Ni*	
Molecular (Soil)			+	+	+		+		+		+					+	+	
Phyllostachys			+	+	+		+		+		+					+	+	
P. edulis			+	+	+		+		+		+					+	+	17.1
Morphological	+	+		+			+		+		+	+		+	+			
Actinocladum	+						+		+		+	+		+	+			
A.	+						+		+		+	+		+	+			8
Bambusa	+	+					+		+		+	+		+	+			
B.											+	+		+	+			1
B.	+	+									+	+		+	+			1.2.3
B.	+																	5
B.											+	+		+	+			1
B.														+				6
B. nana	+										+	+		+	+			1
B. nutans	+										+			+	+			1.4
B. pallida	+													+				4
B.														+				6
B.	+													+	+			1
B. sp.	+										+			+				10
B. tulda	+											+		+				7.4
B.	+					+			+		+	+		+	+			8.1.9
Cephalostachy											+	+		+	+			
C.											+	+		+	+			1
Dendrocalam	+			+							+	+		+	+			
D. asper	+										+	+		+				1.9.5
D.	+													+				7
D.	+			+										+				7
D.											+	+		+	+			1
D. strictus	+										+	+		+	+			15,14,12
Dinochloa	+																	
D. sp.	+																	5
Gigantochloa	+										+	+		+				
G. apus	+													+				9
G. atter	+										+			+				5.16
G.	+											+		+				9
Melocanna											+			+	+			
M.											+			+	+			1
Nastus	+																	
N.	+																	5
Phyllostachys	+			+										+				
P. mannii	+			+										+				7
Schizostachyu	+													+				

S.	+		5
S. lima	+		5
S.	+	+	9

8   Ac (Acaulosporaceae), Am (Ambisporaceae), Ar (Archaeosporaceae), Cl

9   (Claroideoglomeraceae), Di (Diversisporaceae), Gi (Gigasporaceae), Gl (Glomeraceae), Pa

10 (Paraglomeraceae), *Aca (Acaulospora), Ent (Entrophospora),* Ni (Unidentified), *Amb*

11 *(Ambispora), Cla (Claroideoglomus), Div (Diversispora), Gig (Gigaspora), Scu (Scutellospora),*

12 *Glo (Glomus)* y *Scl (Sclerocystis);*1 (Jamaluddin & Turvedi, 1997), 2 (Jha et al., 2011), 3

13 (Mafaziya et al., 2019), 4 (Parkash et al., 2019), 5 (Kramadibrata, 2011), 6 (Weixin et al., 2013),

14 7 (P. Das & Kayang, 2010), 8 (deMoura et al., 2019), 9 (Kramadibrata et al., 2007), 10 (Husein

15 et al., 2022), 11 (Verma & Arya, 1998), 12 (Ravikumar et al., 1997), 13 (Muthukumar &

16 Udaiyan, 2006), 14 (Bhattacharya et al., 2002), 15 (Babu & Reddy, 2010), 16 (Mansir et al.,

17 2021), 17 (Qin, et al., 2017a), 18 (Qin, et al., 2017b).

Names of the Glomeromycota taxa mentioned in the text, and the current status of these names according to Index Fungorum, Species Fungorum, and MycoBank.

1 **Table 4:**

3 **Names of the Glomeromycota taxa mentioned in the text, and the current status of these**

4 **names according to Index Fungorum, Species Fungorum, and MycoBank.**

Name mentioned in text	Current/accepted name (march 2023)
Acaulospora	***Acaulospora* Gerd. & Trappe**
A. scrobiculata	*Acaulospora scrobiculata* Trappe
A. foveata	*Acaulospora foveata* Trappe & Janos
A. laevis	*Acaulospora laevis* Gerd. & Trappe
A. mellea	*Acaulospora mellea* Spain & N.C. Schenck
A. lacunosa	*Acaulospora lacunosa* J.B. Morton
A. tuberculata	*Acaulospora tuberculata* Janos & Trappe
A. delicata	*Acaulospora delicata* C. Walker, C.M. Pfeiff. & Bloss
A. rehmii	*Acaulospora rehmii* Sieverd. & S. Toro
A. cavernata	*Acaulospora cavernata* Blaszk
Ambispora	***Ambispora* C. Walker, Vestberg & A. Schüssler**
A. leptoticha	*Ambispora leptoticha* (N.C. Schenck & G.S. Sm.) C. Walker, Vestberg & A. Schüssler
Claroideoglomus	***Entrophospora* R.N. Ames & R.W. Schneid.**
Diversispora	***Diversispora* C. Walker & A. Schüßler**
Entrophospora	***Entrophospora* R.N. Ames & R.W. Schneid.**
Gigaspora	***Gigaspora* Gerd. & Trappe**
G. margarita	*Gigaspora margarita* W.N. Becker & I.R. Hall
G. gigantea	*Gigaspora gigantea* (T.H. Nicolson & Gerd.) Gerd. & Trappe
Glomus	***Glomus* Tul. & C. Tul.**
G. mosseae	*Funneliformis mosseae* (T.H. Nicolson & Gerd.) C. Walker & A. Schüßler
G. rosea	*Gigaspora rosea* T.H. Nicolson & N.C. Schenck
G. magnicaule	*Glomus magnicaule* I.R. Hall
G. multicaule	*Glomus multicaule* Gerd. & B.K. Bakshi
G. etunicatum	*Entrophospora etunicata* (W.N. Becker & Gerd.) Błaszk., Niezgoda, B.T. Goto & Magurno
G. heterogama	*Dentiscutata heterogama* (T.H. Nicolson & Gerd.) Sieverd., F.A. Souza & Oehl
G. maculosum	*Glomus maculosum* D.D. Mill. & C. Walker
G. aggregatum	*Rhizoglomus aggregatum* (N.C. Schenck & G.S. Sm.) Sieverd., G.A. Silva & Oehl
G. fasciculatum	*Rhizoglomus fasciculatum* (Thaxt.) Sieverd., G.A. Silva & Oehl
G. intraradices	*Rhizoglomus intraradices* (N.C. Schenck & G.S. Sm.) Sieverd., G.A. Silva & Oehl
G.	*Glomus clavisporum* (Trappe) R.T. Almeida & N.C. Schenck

clavisporum	
G. reticulatum	*Glomus reticulatum* Bhattacharjee & Mukerji, Sydowia
G. macrocarpum	*Glomus macrocarpum* Tul. & C. Tul.
G. claroideum	*Entrophospora claroidea* (N.C. Schenck & G.S. Sm.) Błaszk., Niezgoda, B.T. Goto & Magurno
G. pansihalos	*Halonatospora pansihalos* (S.M. Berch & Koske) Błaszk., Niezgoda, B.T. Goto & Kozłowska
G. geosporum	*Funneliformis geosporum* (T.H. Nicolson & Gerd.) C. Walker & A. Schüßler
G. clavisporum	*Glomus clavisporum* (Trappe) R.T. Almeida & N.C. Schenck
G. monosporum	*Funneliformis monosporus* (Gerd. & Trappe) Oehl, G.A. Silva & Sieverd.
G. albidum	*Paraglomus albidum* (C. Walker & L.H. Rhodes) Oehl, F.A. Souza, G.A. Silva & Sieverd.
G. cerebriforme	*Glomus cerebriforme* McGee
G. arborense	*Glomus arborense* McGee
G. hoi	*Simiglomus hoi* (S.M. Berch & Trappe) G.A. Silva, Oehl & Sieverd.
G. diaphanum	*Oehlia diaphana* (J.B. Morton & C. Walker) Błaszk., Kozłowska, Niezgoda, B.T. Goto & Dalpé
G. occultum	*Paraglomus occultum* (C. Walker) J.B. Morton & D. Redecker
G. rubiforme	*Glomus rubiforme* (Gerd. & Trappe) R.T. Almeida & N.C. Schenck
G. epigaeum	*Diversispora epigaea* (B.A. Daniels & Trappe) C. Walker & A. Schüßler
G. tortuosum	*Sieverdingia tortuosa* (N.C. Schenck & G.S. Sm.) Błaszk., Niezgoda & B.T. Goto
G. constrictum	*Septoglomus constrictum* (Trappe) Sieverd., G.A. Silva & Oehl
Sclerocystis	***Sclerocystis* Berk. & Broome**
Scutellospora	***Scutellospora* C. Walker & F.E. Sanders**
S. nigra	*Dentiscutata nigra* (J.F. Redhead) Sieverd., F.A. Souza & Oehl
S. heterogama	*Dentiscutata heterogama* (T.H. Nicolson & Gerd.) Sieverd., F.A. Souza & Oehl
S. calospora	*Scutellospora calospora* (T.H. Nicolson & Gerd.) C. Walker & F.E. Sanders
S. pellucida	*Cetraspora pellucida* (T.H. Nicolson & N.C. Schenck) Oehl, F.A. Souza & Sieverd.

Names of the Bambusoideae taxa mentioned in the text, and the current status of these names according to Vorontsova et al. (2016).

1 **Table 5:**

3 **Names of the Bambusoideae taxa mentioned in the text, and the current status of these**

4 **names according to Vorontsova et al. (2016).**

Name mentioned in text	Current/accepted name (march 2023)
Actinocladum	***Actinocladum* McClure ex Soderstr.**
Actinocladum verticillatum	*Actinocladum verticillatum* (Nees) McClure ex Soderstr.
Bambusa	***Bambusa* Schreb.**
Bambusa arundinacea	*Bambusa bambos* (L.) Voss
Bambusa bambos	*Bambusa bambos* (L.) Voss
Bambusa blumeana	*Bambusa tuldoides* Munro
Bambusa burmanica	*Bambusa burmanica* Gamble
Bambusa grandis	*Bambusa grandis* (Q.H.Dai & X.L.Tao) Ohrnb.
Bambusa nana	*Bambusa multiplex* (Lour.) Raeusch. ex Schult.f.
Bambusa nutans	*Bambusa nutans* Wall. ex Munro
Bambusa pallida	*Bambusa pallida* Munro
Bambusa pervariabilis	*Bambusa pervariabilis* McClure
Bambusa polymorpha	*Bambusa polymorpha* Munro
Bambusa tulda	*Bambusa tulda* Roxb.
Bambusa vulgaris	*Bambusa vulgaris* Schrad. ex J.C.Wendl.
Bambusa sp.	*Bambusa* sp.
Cephalostachyum	***Cephalostachyum* Munro**
Cephalostachyum pergracile	*Schizostachyum pergracile* (Munro) R.B.Majumdar
Dendrocalamus	***Dendrocalamus* Nees**
Dendrocalamus asper	*Dendrocalamus asper* (Schult.f.) Backer
Dendrocalamus hamiltonii	*Dendrocalamus hamiltonii* Nees & Arn. ex Munro
Dendrocalamus hookeri	*Dendrocalamus hookeri* Munro
Dendrocalamus membranaceus	*Dendrocalamus membranaceus* Munro
Dendrocalamus strictus	*Dendrocalamus strictus* (Roxb.) Nees
Dinochloa	***Dinochloa* Buse**
Dinochloa sp.	*Dinochloa* sp.
Gigantochloa	***Gigantochloa* Kurz ex Munro**
Gigantochloa apus	*Gigantochloa apus* (Schult.f.) Kurz
Gigantochloa atter	*Gigantochloa atter* (Hassk.) Kurz
Gigantochloa manggong	*Gigantochloa manggong* Widjaja
Melocanna	***Melocanna* Trin.**
Melocanna baccifera	*Melocanna baccifera* (Roxb.) Kurz

Nastus	***Nastus* Juss.**
Nastus reholttumianus	*Nastus reholttumianus* Soenarko
Phyllostachys	***Phyllostachys* Siebold & Zucc.**
Phyllostachys edulis	*Phyllostachys edulis* (Carrière) J.Houz.
Phyllostachys mannii	*Phyllostachys mannii* Gamble
Schizostachyum	***Schizostachyum* Nees**
Schizostachyum brachycladum	*Schizostachyum brachycladum* (Kurz ex Munro) Kurz
Schizostachyum lima	*Schizostachyum lima* (Blanco) Merr.
Schizostachyum zollingeri	*Schizostachyum zollingeri* Steud.