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# *Septoglomus deserticola* emended and new combinations in the emended definition of the family Diversisporaceae

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An updated morphology of spores of *Septoglomus deserticola*, an arbuscular mycorrhizal fungus of the phylum Glomeromycota, is presented based on the original description of the species, only one other its definition recently published and spores produced in pot cultures inoculated with the rhizosphere soil and root fragments of an unrecognized grass colonizing maritime sand dunes of the Hicacos Peninsula, Cuba. Phylogenetic analyses of sequences of the large subunit (LSU) nrDNA region of the Cuban fungus confirmed its affinity with *S. deserticola* deposited in the International Bank for the Glomeromycota (BEG) and indicated that its closest relatives are *S. fuscum* and *S. xanthium*. Phylogenetic analyses of sequences of the small subunit (SSU) nrDNA confirmed the Cuban fungus x *S. fuscum* x *S. xanthium* relationship revealed in analyses of the LSU sequences and thereby suggested the Cuban *Septoglomus* is *S. deserticola*. However, it was impossible to prove directly the identity of the Cuban fungus and *S. deserticola* from BEG based on SSU sequences due to the lack of *S. deserticola* SSU sequences in public databases. In addition, phylogenetic analyses of LSU and SSU sequences confirmed the uniqueness of the recently erected genus *Corymbiglomus* with the type species *C. corymbiforme* (formerly *Glomus corymbiforme*) in the family Diversisporaceae and proved that its LSU sequences group in a clade with LSU sequences of *G. globiferum* and *G. tortuosum*. Consequently, the two latter species were transferred to *Corymbiglomus* and named *C. globiferum* comb. nov. and *C. tortuosum* comb. nov., and the definitions of the family Diversisporaceae and the genus *Diversispora* were emended.

**Key words:** arbuscular mycorrhizal fungi, Glomeromycota, taxonomy

## INTRODUCTION

Arbuscular mycorrhizal fungi (AMF) of the phylum Glomeromycota are associated with ca. 70–90% of land plants (Smith, Read 2008; Brundrett 2009), including those growing in extremely poor maritime sand dunes (Koske 1987; Dalpé 1989; Tadych, Błaszkowski 2000). It is recognized that maritime sand dunes especially favor the development of AMF because of the low content of nutrients and organic matter (Błaszkowski et al. 2009; Błaszkowski 2012). The fungi frequently increase the supply of plants with nutrients and decrease their sensitivity to different abio- and biotic stresses (Schönbeck 1978; Dehn, Schüepp 1989; Griffioen, Ernst 1989; Smith, Read 2008). Although even low colonization of plant roots by AMG can alleviate such stresses (Pongrac et al. 2007), the effect of influence of AMF may differ, because different species or even strains of a given species of AMF may variously affect plants (Abbott, Robson 1981; Kaldorf et al. 1999; Maherali, Klironomos 2007; Sýkorová et al. 2011). Hence numerous unsuccessful attempts of application of AMF probably partly resulted from erroneous species identification and the difficult nature of AM fungal taxonomy (Schüßler et al. 2011; Krüger et al. 2012).

At present the phylum Glomeromycota comprises three classes, five orders, 15 families, 34 genera and ca. 250 species (Oehl et al. 2011a-e; Schüßler, Walker 2010; Błaszkowski 2012). However, results of molecular phylogenetic analyses of sequences of nrDNA extracted from plant roots suggest that less than 5% of the existing species in the world are known to date and that most undescribed species form glomoid spores (Krüger et al. 2009), i.e. spores similar in mode of formation, spore wall structure and in characters of their subtending hypha to those of *Glomus macrocarpum* Tul. & C. Tul., the type species of the genus *Glomus* Tul. & C. Tul. (Schüßler, Walker 2010). Of the described species, ca. 62% produce typical glomoid spores. Glomoid spores form *Pacispora* spp. as well, but they have two spore walls (vs. one in typical glomoid spores), an outer wall, forming the spore surface, and an inner wall, called a germinal wall (Błaszkowski 2012).

Apart from *Glomus* spp., glomoid spores form fungi of 15 other genera, among which the recently erected genus *Septoglomus* Sieverd., G.A. Silva & Oehl is, whose type species is *S. constrictum* (Trappe) Sieverd., G.A. Silva & Oehl. (Oehl et al. 2011c). Currently the genus *Septoglomus* comprises seven species whose spores are dark-coloured and have a 2– to 3–layered spore wall with the innermost layer being laminate (Oehl et al. 2011c; Błaszkowski et al. 2012). None of the layers stains in Melzer's reagent. The spore subtending hyphae of the species usually is cylindrical or constricted, and its pore is closed by a septum.

We established single-species cultures from dark-coloured glomoid spores of the Glomeromycota isolated from a trap culture inoculated with the rhizosphere soil and root fragments of an unrecognized grass colonizing maritime sand dunes of the Hicacos Peninsula, Cuba. Morphological studies of these spores suggested we found an AMF closely related to *S. deserticola* (Trappe, Bloss & J.A. Menge) G.A. Silva, Oehl & Sieverd. Apart from the original description of *S. deserticola* as *G. deserticola* (Trappe et al. 1984), in the literature there is only one other report of morphology of the species prepared from spores obtained from the International Bank for the Glomeromycota (BEG; Błaszkowski 2012). Our doubt of the identity of the two

fungi resulted from differences in colour of their spores; the spores from Cuba were lighter. However, subsequent phylogenetic analyses of sequences of the large subunit (LSU, partial) spore nrDNA region unambiguously placed the Cuban fungus among available LSU sequences of *S. deserticola*. We also obtained sequences of the small subunit (SSU) nrDNA of the fungus from Cuba, but we could not confirm its identity to *S. deserticola* due to the lack of SSU sequences of *S. deserticola* in available databases. However, our phylogenic analyses indicated that the position of the Cuban fungus in a tree with SSU sequences relative to other *Septoglomus* spp. was identical to that in the LSU tree, suggesting the Cuban *Septoglomus* is *S. deserticola*. Thus our SSU sequences significantly widened the range of molecular data on *S. deserticola*.

Phylogenetic analyses of LSU sequences of *G. corymbiforme* Błaszk. recently lead to the erection of a new genus, *Corymbiglomus* Błaszk. et Chwat, with the type species, *C. corymbiglomus* (Błaszk.) Błaszk. et Chwat (Błaszkowski 2012). Subsequent analyses of LSU and SSU sequences of this species confirmed the uniqueness of *Corymbiglomus* and its phylogenetic relationship to *Diversispora* C. Walker et A. Schüssler, emend. G.A. Silva, Oehl et Schüssler and indicated that other species grouping in a clade with LSU sequences of *C. corymbiforme* are *G. globiferum* Koske et C. Walker and *G. tortuosum* N.C. Schenck et G.S. Sm. Thus results of the analyses and morphological similarity of spores of the tree species proved that *G. globiferum* and *G. tortuosum* should became members of the genus *Corymbiglomus*.

The aims of this paper are to update the knowledge on morphology and phylogeny of *S. deserticola*, emend the definitions of the family Diversisporaceae and the genus *Diversispora* and to transfer *G. globiferum* and *G. tortuosum* to the genus *Corymbiglomus*.

## MATERIALS AND METHODS

**Establishment and growth of trap and single-species cultures, extraction of spores, and staining of mycorrhizae.** Spores examined in this study were derived from both pot trap and single-species cultures. Trap cultures were established to obtain living spores and to initiate sporulation of species that may not have sporulated in the field collections (Stutz, Morton 1996). The method used to establish trap cultures, their growing conditions and the methods of spore extraction and staining of mycorrhizae were as those described previously (Błaszkowski et al. 2012b). The growing substrate of trap cultures was the field-collected rhizosphere soil and roots of the plant species sampled mixed with autoclaved coarse grained sand.

Single-species cultures were also established and grown as given in Błaszkowski et al. (2012b). Briefly, the cultures of *S. deserticola* were successfully established from small clusters of spores (5–15) attached by a common mycelium. The growing substrate of the cultures was autoclaved commercially available coarse-grained sand (grains 1.0–10.0 mm diam - 80.50%; grains 0.1–1.0 mm diam - 17.28%; grains < 0.1 mm diam – 2.22%) mixed (5:1, v/v) with clinopthilolite (Zeocem, Bystré, Slovakia) of grains 2.5–5 mm. Clinopthilolite is a crystaline hydrated alumosilicate of alkali metals and alkaline earth metals having, e.g. high ion exchange

capability and selectivity, as well as reversible hydration and dehydration. The sand-clinopthilolite mixture had a pH of 7.3. The cultures were kept in transparent plastic bags, 15 cm wide and 22 cm high as suggested by Walker and Vestberg (1994). The cultures were watered with tap water once or twice a week, harvested after five months when spores were extracted for study. To reveal mycorrhizal root structures, root fragments located ca. 1–5 cm below the upper level of the growing medium were cut off with a scalpel. *Plantago lanceolata* L. was used as host plant in both trap and single-species cultures.

**Microscopy.** Morphological properties of spores and their wall structure were determined after examination of at least 100 spores mounted in water, lactic acid, polyvinyl alcohol/lactic acid/glycerol (PVLG; Omar et al. 1979) and a mixture of PVLG and Melzer's reagent (1:1, v/v). Spores at all developmental stages were crushed to varying degrees by applying pressure to the cover slip and then stored at 65° C for 24 h to clear their contents from oil droplets and examined under an Olympus BX 50 compound microscope equipped with Nomarski differential interference contrast optics. Microphotographs were recorded on a Sony 3CCD color video camera coupled to the microscope.

Terminology of spore structure is that suggested by Stürmer and Morton (1997) and Walker (1983). Spore color was examined under a dissecting microscope on fresh specimens immersed in water. Color names are from Kornerup and Wanscher (1983). Nomenclature of plants is after Mirek et al. (http://info.botany.pl/czek/check.htm), and that of fungi and the authors of fungal names are those presented at the Index Fungorum website http://www.indexfungorum.org/AuthorsOfFungalNames.htm. Voucher specimens were mounted in PVLG and a mixture of PVLG and Melzer's reagent (1:1, v/v) on slides and deposited in the Department of Plant Protection (DPP), West Pomeranian University of Technology, Szczecin, Poland.

**DNA extraction, Polymerase Chain Reaction and DNA sequencing.** Crude DNA was isolated from small spore clusters crushed with a needle in ultra clean water on sterile microscope slides under a dissecting microscope. Amplification, cloning and sequencing were carried out as described in Błaszkowski et al. (2012a). The partial LSU was amplified using the nested PCR with the primer pairs ITS3-28G2 (da Silva et al. 2006; White et al. 1990) and LR1-28G2 (da Silva et al. 2006; van Tuinen et al. 1998), and the partial nrSSU segment was amplified with the primers AML1 and AML2 (Lee et al. 2008). PCR was performed with DreamTag Green PCR Master Mix (2X) (Thermo Scientific, Germany). The PCR conditions for LSU were as those described by Oehl et al. (2011d), and those for SSU were: initial 5 min denaturation at 94° C followed by 30 cycles of 45 s denaturation at 94° C, 45 s annealing at 58° C, 45 s elongation at 72° C and final 5 min elongation at 72° C. The subsequent work with amplicons was carried out as described in Błaszkowski et al. (2012b).

**Sequence alignment and phylogenetic analyses.** Phylogenetic analyses were performed separately with LSU and SSU sequences. To determine the generic affiliation of the Cuban fungus we performed pilot phylogenetic analyses of all its LSU and SSU sequences we obtained with those representing all recognized genera of the Glomeromycota with glomoid spores available in GenBank. The final data sets comprised all our sequences of the putative *S. deserticola*, all published sequences of *S. deserticola* (only LSU sequences), one sequence each of all other described *Septoglomus* spp. (LSU and SSU), except the sequence AF145741 (da Silva et al.

2006), and sequences of other species with glomoid spores mainly deriving from the former *Glomus* group A (Schwarzott et al. 2001). The sequence AF145741 probably represents *Funneliformis coronatus* (Giovann.) C. Walker & A. Schüßler (da Silva, pers. comm.) whose small-spored isolates closely resemble *S. constrictum* spores (Błaszkowski, pers. observ.). The LSU and SSU sequences were aligned with Clustal W (Thompson et al. 1994) with default parameters. Maximum likelihood (ML) and Bayesian (BI) analyses were performed with PHYML (Guindon and Gascuel 2003) and MrBayes 3.1 (Huelsenbeck, Ronquist 2001; Ronquist, Huelsenbeck 2003), respectively. Before the analyses the best-fit substitution models for the alignments were estimated by the Akaike information criterion (AIC) using Topali v. 2.5 (Milne et al. 2004). *Pacispora scintillans* (S.L. Rose & Trappe) Sieverd. & Oehl ex C. Walker, Vestberg & A. Schüßler was outgroup in all analyses. In the ML analyses of LSU and SSU sequences the model employed was TrN + G, and in the BI analyses of both types of sequences we applied GTR+G and HKY+G, respectively. In the ML analysis the transition/transversion ratio for DNA models and the gamma distribution parameter were estimated. Six substitution rate categories were set. Topology and branch lengths and rate parameters were optimized. Support of branches in the ML analysis was estimated in a bootstrap analysis with 1000 replicates. In the BI analyses the Markov chain was run for 5000000 generations, sampling in every 500 steps, and with a burn-in at 3000. The details of the analyses are available on request. Phylogenetic trees were visualized and edited in MEGA5 (Tamura et al. 2011).

## RESULTS

**Molecular analyses.** Maximum likelihood and BI analyses of LSU sequences generated trees of identical topologies. All sequences of the Cuban fungus clustered in a monophyletic group with published sequences of *S. deserticola*, whose a sister clade comprised all the other known *Septoglomus* spp. except for *S. titans* (Fig. 1). The *S. titans* sequence formed a separate branch at the base of the *Septoglomus* clade. Both the clade with S. *deserticola* sequences and the other monophyletic groups of the *Septoglomus* clade were well supported [bootstrap supports (BS) of all clades of > 90%, except for one clade of 69%; posterior probabilities (PP) of all clades of 1, except for one clade of 0.89]. The closest molecular relatives of the Cuban *S. deserticola* were *S. fuscum* Błaszk. et al. and *S. xanthium* Błaszk. et al.

The topologies of trees obtained following ML and BI analyses of SSU sequences also were identical. The SSU sequences of the Cuban fungus grouped in a clade sister to that with sequences of *S. africanum*, *S. constrictum*, *S. fuscum* and *S. xanthium* (Fig. 2). The recently described *S. furcatum* (Blaszkowski et al. 2012) represented a separate linage positioned at the base of the *Septoglomus* clade. The clade with the Cuban *S. deserticola* sequences received very strong supports (BS = 100%, PP = 1), and the supports of the other groups of the *Septoglomus* clade were moderate to high. Similarly as in the LSU tree, the Cuban *S. deserticola* was most closely related to *S. fuscum* and *S. xanthium* (Fig. 2). Unfortunately, we could not determine the similarity of the SSU sequences of the Cuban *S. deserticola* with other SSU sequences of this species because of their unavailability in public databases.

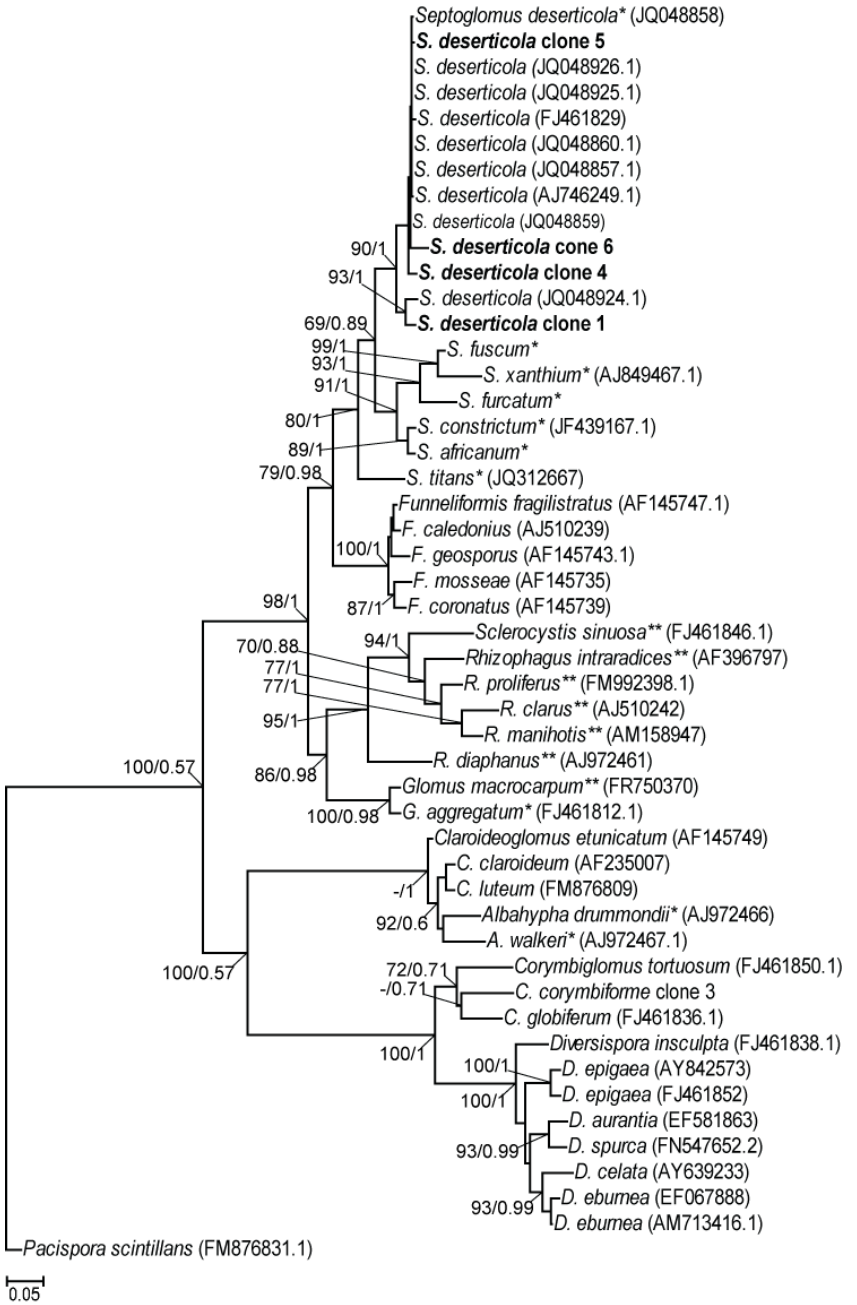



Fig. 1. Maximum likelihood (ML) tree inferred from LSU nrDNA sequences with *Pacispora scintillans* as outgroup. GenBank accession numbers of the sequences are in parentheses. ML bootstrap values ≥50% and the Bayesian posterior probabilities ≥0.50 are shown near the branches, respectively. Sequences of the Cuban *S. deserticola* are in boldface. * = *sensu* Oehl et al. 2011a, ** = *sensu* Schüßler and Walker 2010. Bar indicates 0.05 expected change per site per branch.

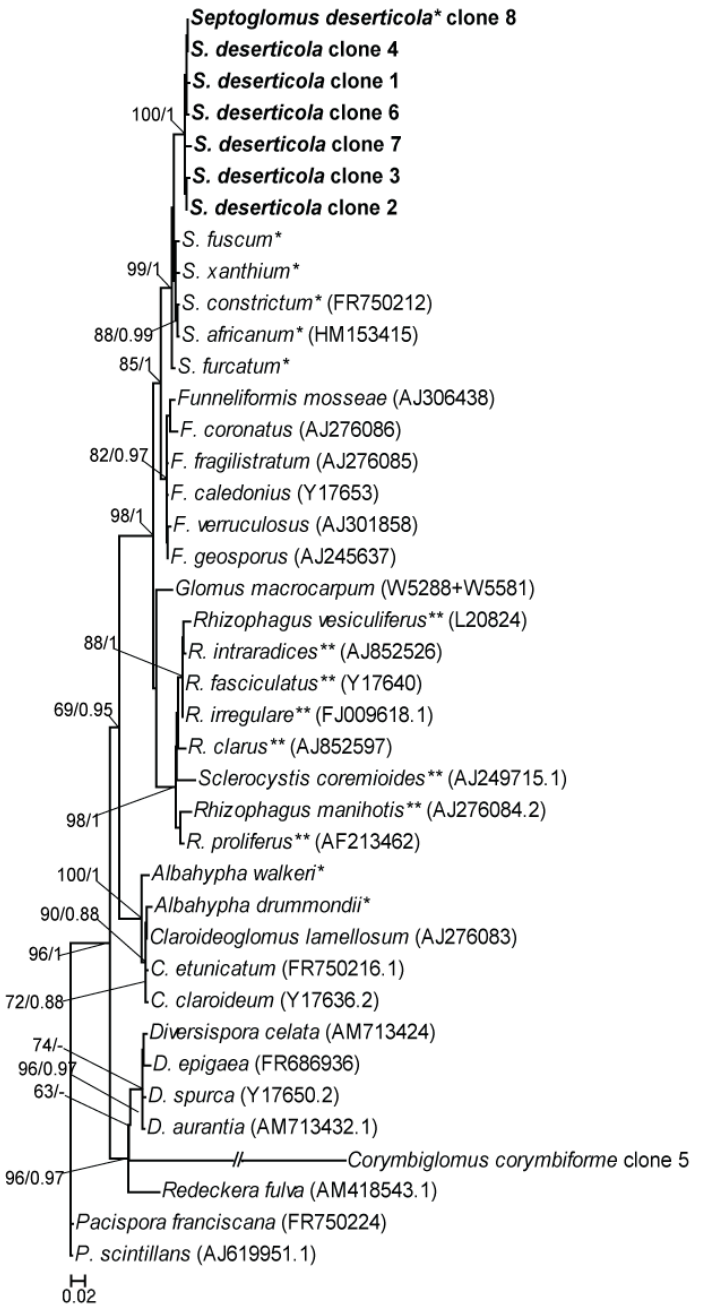



Fig. 2. Maximum likelihood (ML) tree inferred from SSU nrDNA sequences with *Pacispora scintillans* as outgroup. GenBank accession numbers of the sequences are in parentheses. ML bootstrap values ≥50% and the Bayesian posterior probabilities ≥0.50 are shown near the branches, respectively. Sequences of the Cuban *S. deserticola* are in boldface. Branch with the *Corymbiglomus corymbiforme* sequence is shortened by 50%. * = *sensu* Oehl et al. 2011a, ** = *sensu* Schüßler and Walker 2010. Bar indicates 0.02 expected change per site per branch.

## TAXONOMY

***Septoglomus deserticola*** (Trappe, Bloss et J.A. Menge) G.A. Silva, Oehl et Sieverd. Mycotaxon 116: 106. 2011. Figs 3-10
≡*Glomus deserticola* Trappe, Bloss & J.A. Menge. Mycotaxon 20: 123. 1984.

Spores arise in soil singly or in loose clusters lacking a peridium (Figs 3, 7). *Spores* deep yellow (4A8) to light brown (6D8), globose to subglobose, (19–)82(–135) μm diam., sometimes ovoid to pear-shaped, 59–71 × 72–155 μm, with one subtending hypha (Figs 3–9). *Spore wall* composed of two layers (Figs 4, 5, 7–9). Layer 1, forming the spore surface, evanescent, hyaline, (0.5–)1.3(–2.3) μm thick, frequently completely sloughed in mature spores (Figs 4, 5, 7–9). Layer 2 laminate, smooth, deep yellow (4A8) to light brown (6D8), (1.8–)2.5(–3.8) μm thick, frequently thickened at the spore base to form a collar (Figs 4, 5, 7–9). Layers 1 and 2 do not stain in Melzer's reagent. *Subtending hypha* deep yellow (4A8) to light brown (6D8), straight or curved, flared, funnel-shaped, rarely constricted at the spore base, (6.3–)8.1–13.3(–16.8) μm wide at the spore base (Figs 5, 7). *Wall of subtending hypha* deep yellow (4A8) to light brown (6D8), composed of two layers continuous with spore wall layers 1 and 2 (Figs 5, 7). Layer 1 (0.8–)1.0(–1.3) μm thick, layer 2 (2.5–)3.2(–3.8) μm thick; the outer and inner surfaces of layer 2 frequently with side thickenings (Figs 5, 7). *Pore* open, (0.8–)3.1–6.5(–10.8) μm wide at the spore base (Figs 5, 7). *Hyphae of clusters* deep yellow (4A8) to light brown (6D8), straight or branched, (8.0–)11.3(–16.8) μm wide, with a 2-layered wall: a hyaline, evanescent, (0.8–)1.5(–2.5) μm thick, when intact, outer layer and a deep yellow (4A8) to light brown (6D8), permanent, (2.0–)2.6(–2.8) μm thick inner layer (Figs 3, 5, 6, 9, 10). *Germination* unknown.

**Mycorrhizae.** In the field, associated with roots of an unrecognized grass. In addition, lived in symbiosis with *Parthenium argentatum* A. Gray, *P. incanum* Kunth, *Simmondsia chinensis* (Link) C.K. Schneid. (Trappe et al. 1984) and *Uniola paniculata* L. (Sylvia 1986; Sylvia & Will 1988).

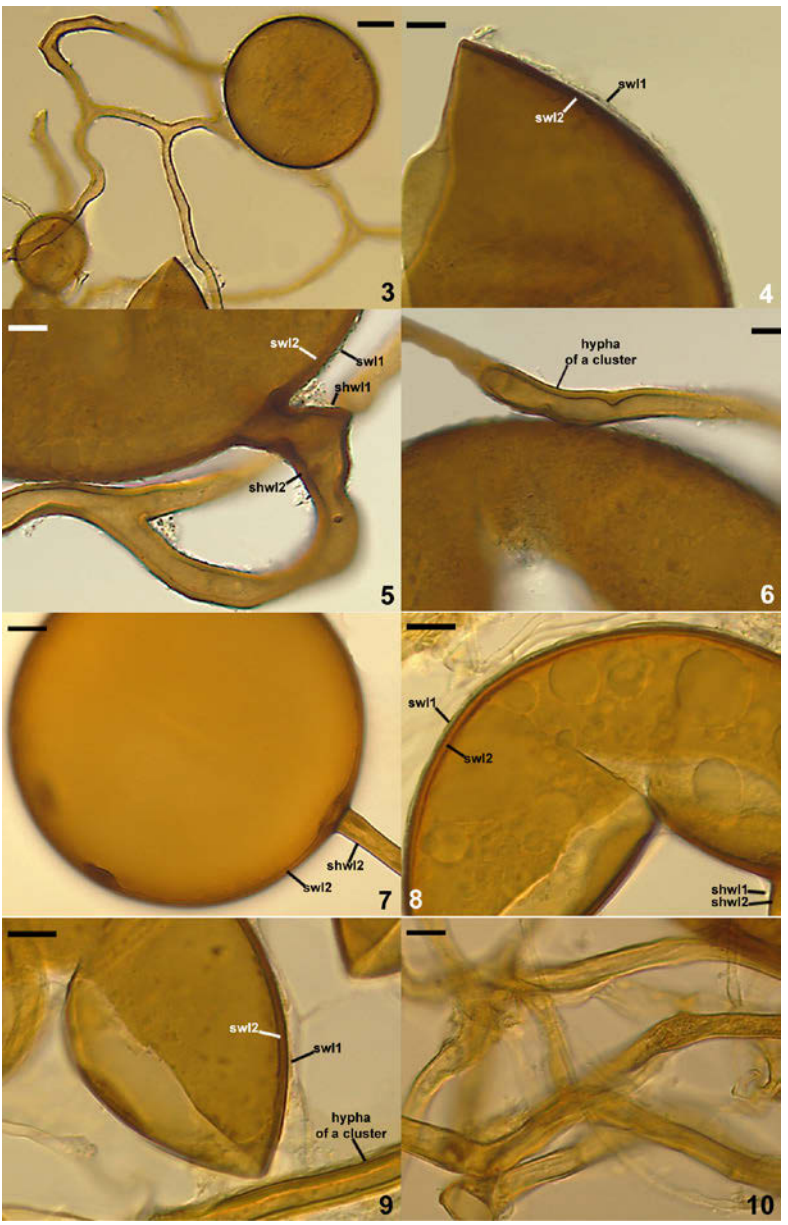
The characters of mycorrhizae from single-species culture of *S. deserticola* remain unknown.

**Etymology.** Latin, *deserticola* (desert dweller), referring to the sandy desert soils in which the fungus was originally found (Trappe et al. 1984).

Specimens examined. Poland. Szczecin, *Błaszkowski J.*, *3144–3146* (DPP), prepared from spores obtained from BEG. Szczecin, under pot-cultured *P. lanceolata*, 18 Dec. 2012, *Błaszkowski J.*, *3353–3357* (DPP), originally coming from the Hicacos Peninsula, Cuba.

**Distribution and habitat**. Found associated with roots of an unrecognized grass colonizing maritime sand dunes of the Hicacos Peninsula, Cuba.

Originally described from spores isolated from sandy desert soils of Arizona, southern California and Texas (U.S.A.; Trappe et al. 1984). Also recorded in maritime dunes of Florida (Sylvia 1986; Sylvia, Will 1988), as well as in other habitats of the U.S.A. (Paulitz, Menge 1986; Bloss, Walker 1987; Augé 1989), Spain (Arines, Vilarino 1991) and India (Ragupathy, Mahadevan 1993). Probably many times mistakenly identified as *Rhizophagus fasciculatus* (Thaxt.) C. Walker & A. Schüssler (formerly *G. fasciculatum* (Thaxter) Gerd. et Trappe (Trappe et al. 1984; Walker, Koske 1987), one of the most frequently reported AMF from




Figs 3–6. *Septoglomus deserticola* from BEG. 3. Intact spores in a loose cluster. 4. Spore wall layers (swl) 1 and 2. 5. Spore wall layers (swl) 1 and 2 and subtending hyphal wall layers (shwl) 1 and 2. 6. Thick-walled hypha of a cluster and a spore. Figs. 7–10. *Septoglomus deserticola* from Cuba. 7. Spore wall layer (swl) 2 and subtending hyphal wall layer (shwl) 2 of intact spore; swl1 and shwl1 are completely sloughed. 8. Spore wall layers (swl) 1 and 2 and subtending hyphal wall layers (shwl) 1 and 2; shwl1 is highly deteriorated. 9. Spore wall layers (swl) 1 and 2 and a 2-layered hypha of a cluster. 10. Loose hyphae of a cluster. Figs. 3, 5–7, 10. Spores in PVLG. Figs. 4, 8, 9. Spores in PVLG + Melzer's reagent. Figs 3–10, differential interference microscopy. Bars: Fig. 3 = 20 µm, Figs. 4–10 = 10 µm.

soil surveys and most often cited as used in studies of plant growth responses (Walker 1985). The fungus reported many times under the epithet *S. deserticola* (Błaszkowski 2012) from different regions of Poland probably is its close undescribed relative. Spores of the fungus are lighter [pale yellow (3A3) to orange (6A6)] and their spore wall layer 1 stains in Melzer's reagent (Błaszkowski 1990; vs. no reaction in *S. deserticola*).

NOTES. Morphologically, *S. deserticola* is most distinguished by its dark-coloured and relatively small spores usually formed in loose clusters (Figs 3–9).

Phylogenetically and morphologically *S. deserticola* is closest to *S. fuscum* (Figs 1, 2), a species recently described from a material coming from maritime sand dunes located near Strand, ca. 50 km southeast of Cape Town, South Africa (Błaszkowski et al. 2012). Both species produce dark-coloured, relatively small spores, usually in loose clusters and have a 2-layered spore wall (Trappe et al. 1984; Błaszkowski 2012; Błaszkowski et al. 2012). However, the mean diameter of globose *S. deserticola* spores is almost 2-fold higher, their spore wall layer 1 is short-lived and usually completely sloughed in mature spores (Fig. 7; vs. semi-persistent, rarely partly deteriorated in mature and older spores in *S. fuscum*) and hyaline (Figs 4, 5, 8, 9); vs. coloured, rarely hyaline), and spore wall layer 2 is much thinner. In addition, the spore subtending hypha of *S. deserticola* is much wider and has much thicker walls and a wider pore.

*Septoglomus xanthium*, another species close in phylogeny to *S. deserticola* (Figs 1, 2), also forms spores almost indistinguishable from those of the latter fungus when they are intact and seen under a dissecting microscope. The two species mainly separate the number of spore wall layers (three vs. two in *S. deserticola*; Figs. 4, 5, 8, 9) and the phenotypic features of spore wall layer 1, forming the spore surface (semi-permanent and coloured in mature spores vs. hyaline and usually completely sloughed at maturity; Figs. 4, 5, 7–0; Trappe et al. 1984; Błaszkowski et al. 2004; Błaszkowski 2012). In addition, *S. xanthium* spores are clearly smaller [(23–)50–70) $\mu$m diam when globose vs. (19–)82(–135) $\mu$m diam when globose], have a much thinner structural laminate spore wall layer and a narrower subtending hypha with thinner walls and a narrower pore.

Of other known species of the Glomeromycota, *S. deserticola* may be confused with small-spored isolates of *Funneliformis coronatus* (Giovann.) C. Walker & A. Schüssler, *S. constrictum* and *S. furcatum* Błaszk., Chwat & Kovács, Ryszka due to their similarly coloured spores (Błaszkowski 2012; Błaszkowski et al. 2012). However, spores of the three latter species usually are much larger and arise only singly (vs. singly and in clusters in *S. deserticola*; Figs 3–9). Other differences between the four species reside in their spore wall structure, phenotypic and histochemical characters of spore wall layers, spore subtending hyphal features and, most importantly, in their phylogenies (Figs 1, 2).

## EMENDATIONS AND NEW COMBINATIONS

**Diversisporaceae** C. Walker & A. Schüßler, emend. Błaszk. et Chwat

Forming spores blastically at the top of a sporogenous hypha (*Glomus*-like spores), laterally on the neck of a sporiferous saccule (*Acaulospora*-like spores) or inside the neck of a sporiferous saccule (*Entrophospora*-like spores). *Acaulospora*-like

spores and *Entrophospora*-like spores as otosporoid and tricisporoid spores, respectively, *sensu* Oehl et al. (2011e). *Glomus*-like spores without a hyphal mantle (diversisporoid spores *sensu* Oehl et al. 2011e) or covered individually with a hyphal mantle consisting of non-branched or branched hyphae. Mantled spores occurring singly or in clusters with two to three spores grouped by interwoven hyphae of their hyphal mantle or in clusters with two to <20 spores formed by spores arisen at the top of sporogenous hyphae dichotomously branched from a parent hypha continuous with an extraradical mycorrhizal hypha. Spores pigmented, with a 1–3-layered spore wall. Subtending hypha straight or recurved, cylindrical to funnel-shaped or constricted. Subtending hyphal wall continuous with and coloured similarly to the spore wall. Pore open or occluded by a septum continuous with the innermost laminae of the structural spore wall, by thickening of the structural spore wall or by spore wall layer 3.
Type genus: *Diversispora* C. Walker et A. Schüssler emend. G.A. Silva, Oehl et Sieverd. Mycotaxon 116: 108. 2011c.

Other genera: *Corymbiglomus* Błaszk. et Chwat. Glomeromycota 272. 2012.
*Otospora* Oehl, Palenz. et N. Ferrol. Mycologia 100: 297. 2008
*Redeckera* C. Walker et A. Schüssler, emend. Oehl, G.A. Silva &Sieverd. Mycotaxon 116: 110. 2011c.
*Tricispora* Oehl, Sieverd., G.A. Silva et Palenz. Mycotaxon 117: 310. 2011e.

***Corymbiglomus*** Błaszk. et Chwat, emend.

Forming *Glomus*-like spores individually covered with a hyphal mantle consisting of non-branched or branched hyphae with or without terminal vesiculate swellings. Spores occurring singly or in clusters. Clusters with two to three spores grouped by interwoven hyphae of their hyphal mantle or with two to <20 spores arisen at the top of sporogenous hyphae dichotomously branched from a parent hypha continuous with an extraradical mycorrhizal hypha. Spores pigmented, with a 1–3-layered spore wall. Subtending hypha straight or recurved, cylindrical to funnel-shaped or constricted. Subtending hyphal wall continuous with and coloured similarly to the spore wall. Pore open or occluded by a septum continuous with the innermost laminae of the structural spore wall, by thickening of the structural spore wall or by spore wall layer 3.

Type species: *Corymbiglomus corymbiforme* (Błaszk.) Błaszk. et Chwat. Glomeromycota 274. 2012.

Other species: *Corymbiglomus globiferum* (Koske et Walker) Błaszk et Chwat, comb. nov.
≡*Glomus globiferum* Koske et Walker. Mycotaxon 26: 133. 1986.

***Corymbiglomus tortuosum*** (N.C. Schenck et G.S. Sm.) Błaszk. et Chwat, comb. nov.
≡*Glomus tortuosum* N.C. Schenck et G.S. Sm. Mycologia 74: 83. 1982.

Notes. The genus *Corymbiglomus* was originally erected based on phylogenetic analyses of LSU sequences of *G. corymbiforme* Błaszk. (Błaszkowski 2012). Results of phylogenetic analyses of LSU and SSU sequences presented here confirmed those

of earlier studies (Błaszkowski 2012) and clearly revealed that species grouping with *C. corymbiforme* in a clade with LSU sequences also are *G. globiferum* and *G. tortuosum* (Figs 1, 2). Similarly as in the phylogenetic analyses of LSU sequences, those of SSU sequences placed *C. corymbiforme* in a position sister to the clade with known *Diversispora* spp. Unfortunately, we could not determine the *C. corymbiglomus* x *C. globiferum* x *C. tortuosum* relationship found in the analyses of LSU sequences, because there are no SSU sequences of the latter two species in available databases. Morphologically, the species link that their spores are covered with a hyphal mantle and they usually occur in clusters.

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## Uzupełnione diagnozy dwóch taksonów – *Septoglomus deserticola* i Diversisporaceae oraz nowe kombinacje w obrębie rodzajów *Glomus* i *Corymbiglomus*

### Streszczenie

Przedstawiono uzupełnioną definicję morfologii zarodników *Septoglomus deserticola*, arbuskularnego grzyba mikoryzowego z gromady Glomeromycota, na podstawie oryginalnego opisu tego gatunku, jego jedynej innej definicji opublikowanej niedawno i zarodników wyhodowanych w kulturach wazonowych zainokulowanych glebą ryzosfrową i fragmentami korzeni nierozpoznanej trawy kolonizującej piaszczyste wydmy nadmorskie Półwyspu Hicacos, Kuba.

Analizy filogenetyczne sekwencji dużej podjednostki (LSU) jądrowego rDNA kubańskiego grzyba potwierdziły jego powinowactwo z *S. deserticola* zdeponowanym w Międzynarodowym Banku Glomeromycota (BEG) i wykazały, że jego najbliższymi krewniakami są *S. fuscum* i *S. xanthium*. Analizy filogenetyczne sekwencji małej podjednostki (SSU) jądrowego rDNA potwierdziły pokrewieństwo trzech taksonów: grzyb kubański x *S. fuscum* x *S. xanthium* ujawnione w analizach sekwencji LSU i przez to zasugerowały, że kubańskie *S. deserticola* jest właściwym *S. deserticola*. Jednak nie było możliwości dowieść bezpośrednio identyczności kubańskiego *S. deserticola* z typowym *S. deserticola* z BEG na podstawie sekwencji SSU z powodu braku sekwencji SSU *S. deserticola* w dostępnych bazach danych. Ponadto analizy filogenetyczne sekwencji LSU i SSU potwierdziły unikatowość niedawno utworzonego rodzaju *Corymbiglomus* z gatunkiem typowym *C. corymbiforme* (wcześniejszym *Glomus corymbiforme*) w rodzinie Diversisporaceae i dowiodły, że jego sekwencje LSU grupują się w kladzie z sekwencjami LSU *Glomus globiferum* i *G. tortuosum*. W konsekwencji dwa ostatnie gatunki zostały przeniesione do rodzaju *Corymbiglomus* i nazwane *C. globiferum* comb. nov. oraz *C. tortuosum* comb. nov., a definicje rodziny Diversisporaceae i rodzaju *Diversispora* zostały uzupełnione.