

FIGURE S1

A phylogenetic hypothesis of the genus *Scleroderma* based on ITS was obtained using sequences from this study and 91 existing GenBank accessions of *Scleroderma* spp., plus three outgroups (*Tremellogaster surinamensis* and two *Astraeus* species). All sequences were aligned with MUSCLE 3.7 (Edgar, 2004) providing 1053 characters in total, with 26.7% variable characters. Alignment refinement/ambiguous sites were eliminated using Gblocks 0.91b (Castresana, 2000) with parameters set to their default values. Maximum likelihood analyses were conducted using PhyML 3.0 (Guindon, 2010) with the SH-like likelihood-approximate ratio test approach, a proportion of variable sites of 0.0, and the substitution model HKY85.

OTUs found in the present study are in red and regions of sampling are indicated by the colour code. *S.*, *Scleroderma*.

REFERENCES

Edgar RC. (2004). MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* 32:1792-1797.

Castresana J. (2000). Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Mol Biol Evol* 17:540-552.

Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O. (2010). New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. *Syst Biol* 59:307-321.

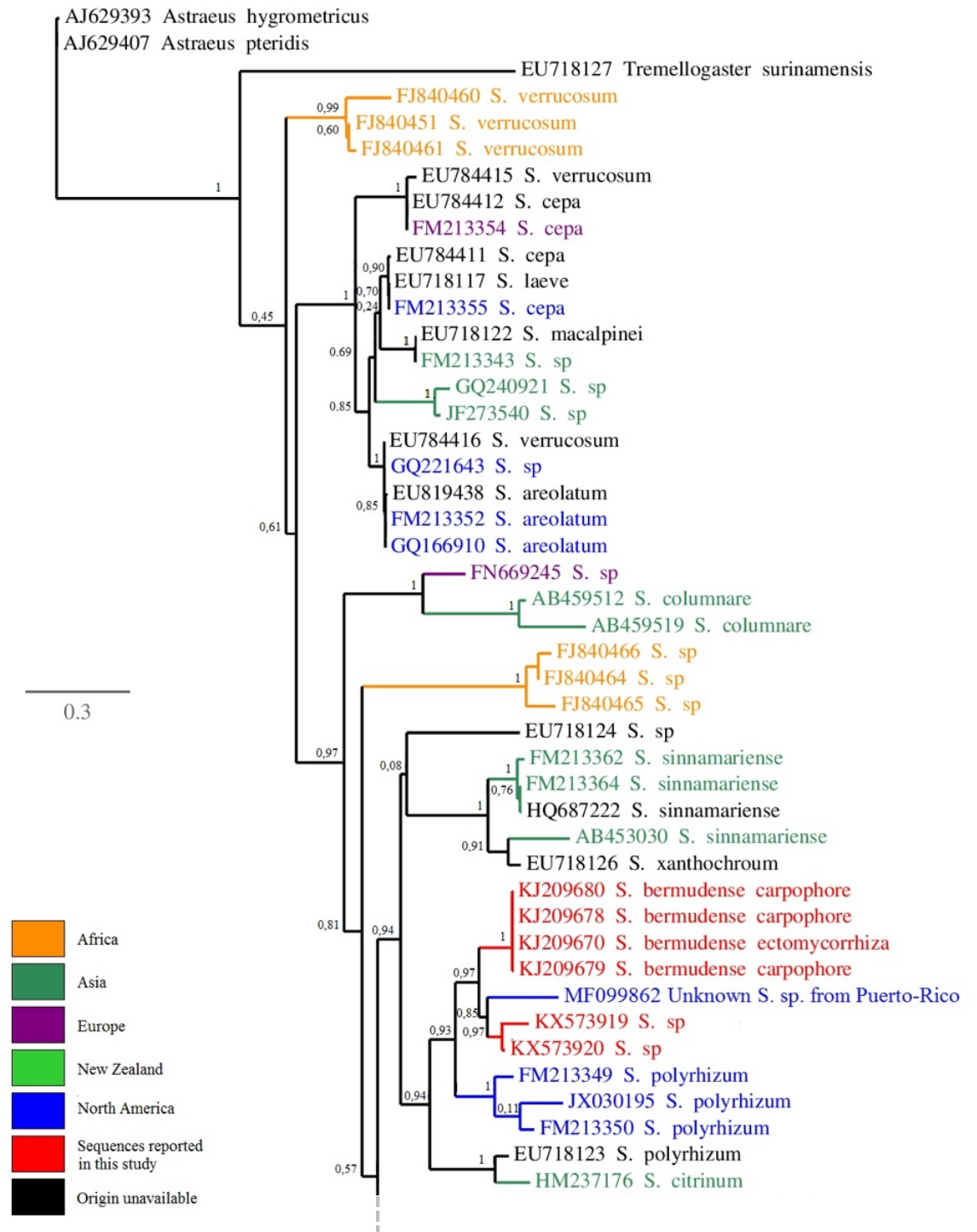


FIGURE S1, continued

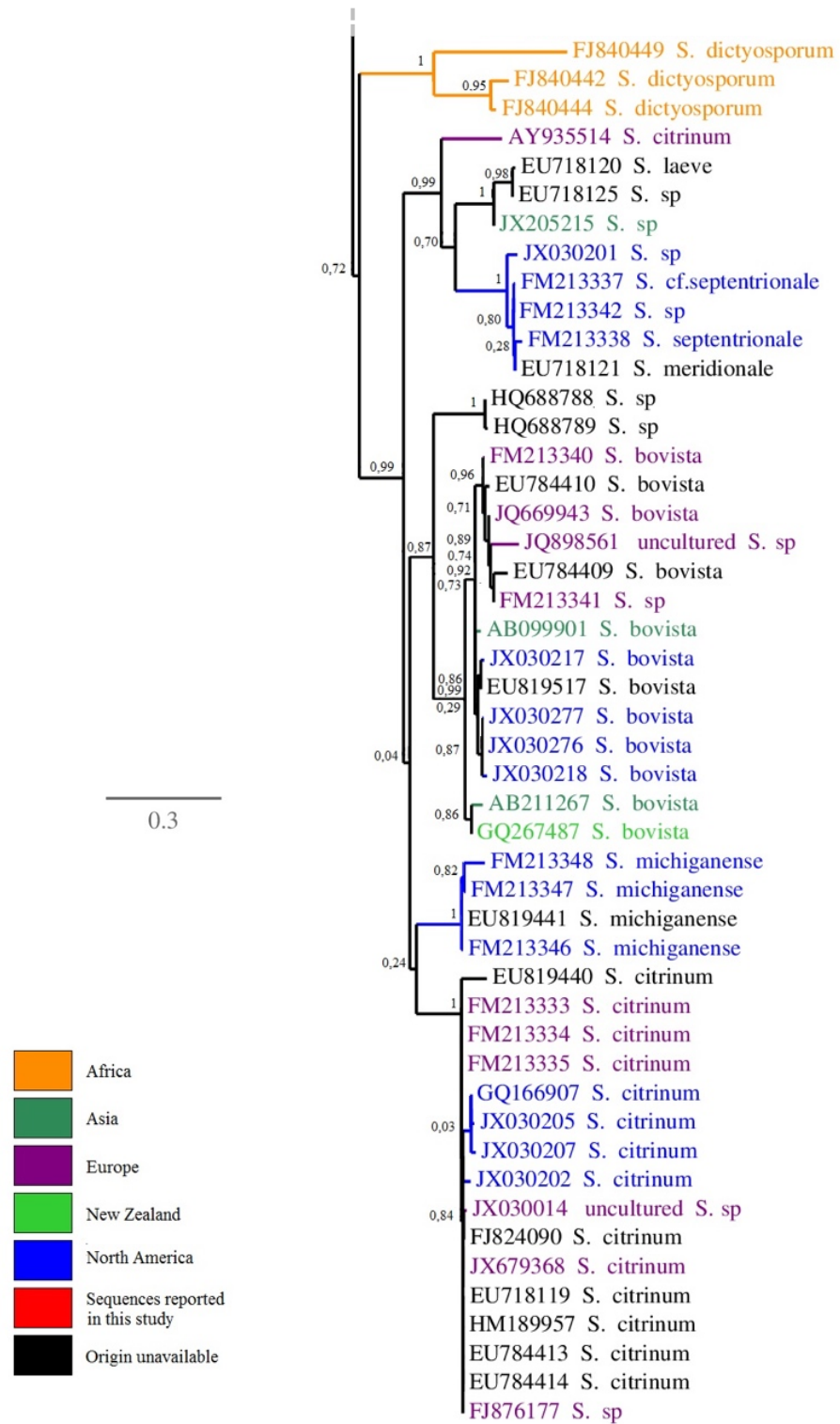


FIGURE S2

Mycorrhizal colonization of 6-months-old seagrape seedlings by *Scleroderma bermudense* (a, grey column) and other fungi (b, black column) after addition of beach soil from three origins, sterilized or not, to sterile seedlings. Numbers in columns are number of repetition showing colonization (out of ten). Bars correspond to standard deviations of total colonization; *, significantly different mycorrhizal colonization by *S. bermudense* according an ANOVA ($P < 0.00001$).

Sterilized seagrape fruits were sown on pots filled with sterilized soil (all sterilizations as in other experiments, see methods in main text) in greenhouse of Laboratoire Commun de Microbiologie in Dakar. After one month of sterile pre-growth, protected from air by aluminium sheets and watered with sterilized water, pots were supplemented with either 10 g of sterilized beach soil (S) or 10 g of non-sterilized soil (NS), added with 250 ml of sterile water. Beach soils and fruits were collected under seagrape from three Guadeloupe sites (Bois Jolan, Cluny and Viard; geocodes in Table S1; $n=10$ seedlings per soil origin and treatment). After 6 months, ectomycorrhizae were analysed as in baiting experiment (five seedlings per treatment; see main text). Contamination occurred in S treatment from Bois Jolan samples.

