

## Mushrooms nomenclatural novelties no. 18

Effectively published 2018-02-09 06:37:55 (ISSN 2560-9548)

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**Sarcoporiaceae** Audet, fam. nov.

**IF554252**

Basidiomes annual, resupinate to effused-reflexed, soft, white to cream at first with reddish tints but distinctly reddish-brown after bruising, brown and brittle on drying.

Hyphal system monomitic with clamp connections, thin to thick-walled, KOH-, IKI-.

Basidiospores slightly to strongly cyanophilous, dextrinoid, thick-walled, often guttulate, uninucleated.

Nuclear behavior heterocytic and mating system tetrapolar heterothallic. Causing brown-rot decay on conifers and hardwoods.

Holotype : *Sarcoporia* P. Karst., Hedwigia 33: 15 (1894).

Comment: In the Antrodia clade *Sarcoporia* is exceptionally tetrapolar in mating system, whilst mostly brown rotters are bipolar (Hibbett & Donoghue 2001).

This genus is in the same clade with *Sparassis* in Justo & al. 2017 paper but without strong support. My unpublished result with SSU rRNA in Bayesian analyses show that *Sarcoporia* under *Parmastomyces transmutans* Genbank AY293143 is in clade different from the genera *Sparassis*, *Pycnoporellus* and *Crustoderma*.

Table 1 from figure 1

		Genbank
Taxon	Phylotree	18S
Daedalea quercina	Dquerc9067	U59067
Parmastomyces transmutans	Ptrans3143	AY293143
Sparassis brevipes	Sbrev8381	AY218381
Sparassis crispa	Scrispa8379	AY218379
Sparassis crispa	Scris8376	AY218376
Sparassis spathulata	Sspat9096	U59096

Table 2 from figure 2

		Genbank
Taxon	Phylotree	LSU
Crustoderma corneum	Ccorn5143	KC585143
Crustoderma dryinum	Cdry5148	KC585148
Crustoderma flavescens	Cflav5151	KC585151
Crustoderma longicystidia	Clong9388	AY219388
Crustoderma marianum	Cmari5152	KC585152
Crustoderma marianum	Cmari5153	KC585153
Crustoderma opuntiae	Copun5154	KC585154
Crustoderma resinosum	Cresi5155	KC585155
Fomitopsis pinicola	Fpini7858	AF287858
Pycnoporellus fulgens	Pfulg5218	KC585218
Pycnoporellus alboluteus	Palbo5215	KC585215

Pycnoporellus alboluteus	Palbo5216	KC585216
Sarcoporia longitubulata	Slong7864	KM207864
Sarcoporia polyspora	Spolys5227	KC585227
Sparassis brevipes	Sbrev8403	AY218403
Sparassis crispa	Scrispa8386	AY218386
Sparassis crispa	Scrisp8412	AY218412
Sparassis cystidiosa	Scyst6890	AY256890
Sparassis latifolia	Slati9409	LC159409
Sparassis spathulata	Sspat8395	AY218395
Sparassis subalpina	Ssuba9280	KY039280

Table 3 from figure 3

		Genbank	
Taxon	Phylotree	LSU	RPB1
Crustoderma corneum	Cruscorn	KC585143	KY949037
Crustoderma flavescens	Crusflav	KC585150	KY949038
Fomitopsis pinicola	Fpinicola	EU23229	KY949004
Pycnoporellus alboluteus	Pycalbo	KC585214	KY949039
Pycnoporellus fulgens	Pycfulg	KC585218	KY949040
Sarcoporia polyspora	Spoly	KC585226	KY949022
Sparassis crispa	Scrispa1281	KF053384	KF211281
Sparassis radicata	Sparadic	KF053407	KY949023

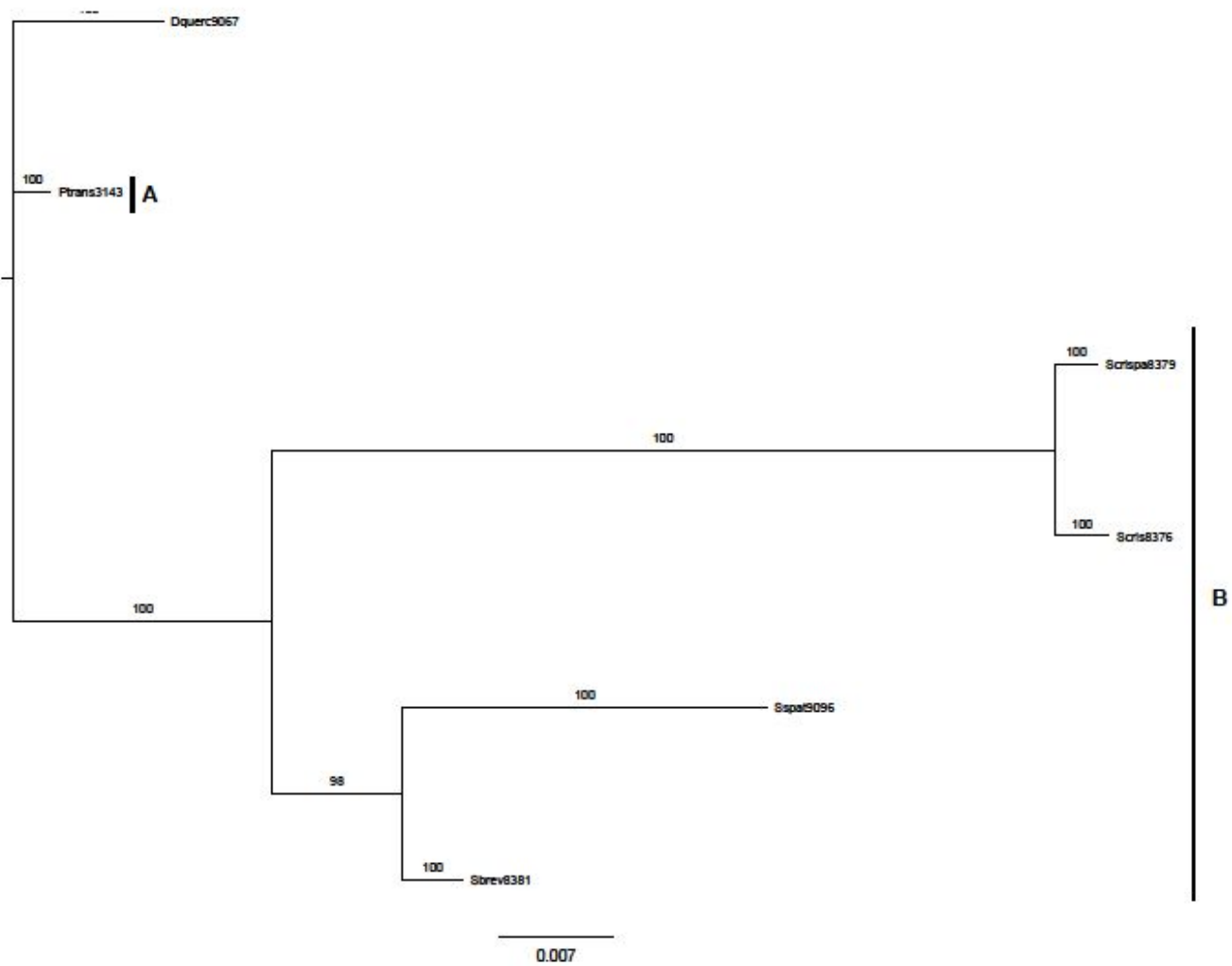


Figure 1: Strict consensus phylogree of small subunit ribosomal RNA gene 18S (partial sequence) calculated by the MrBayes software (Ronquist et al. 2015; 1 000 000 generations). A: Sarcoporiaceae; B: Sparassidaceae; outgroup: *Dquerc9067*

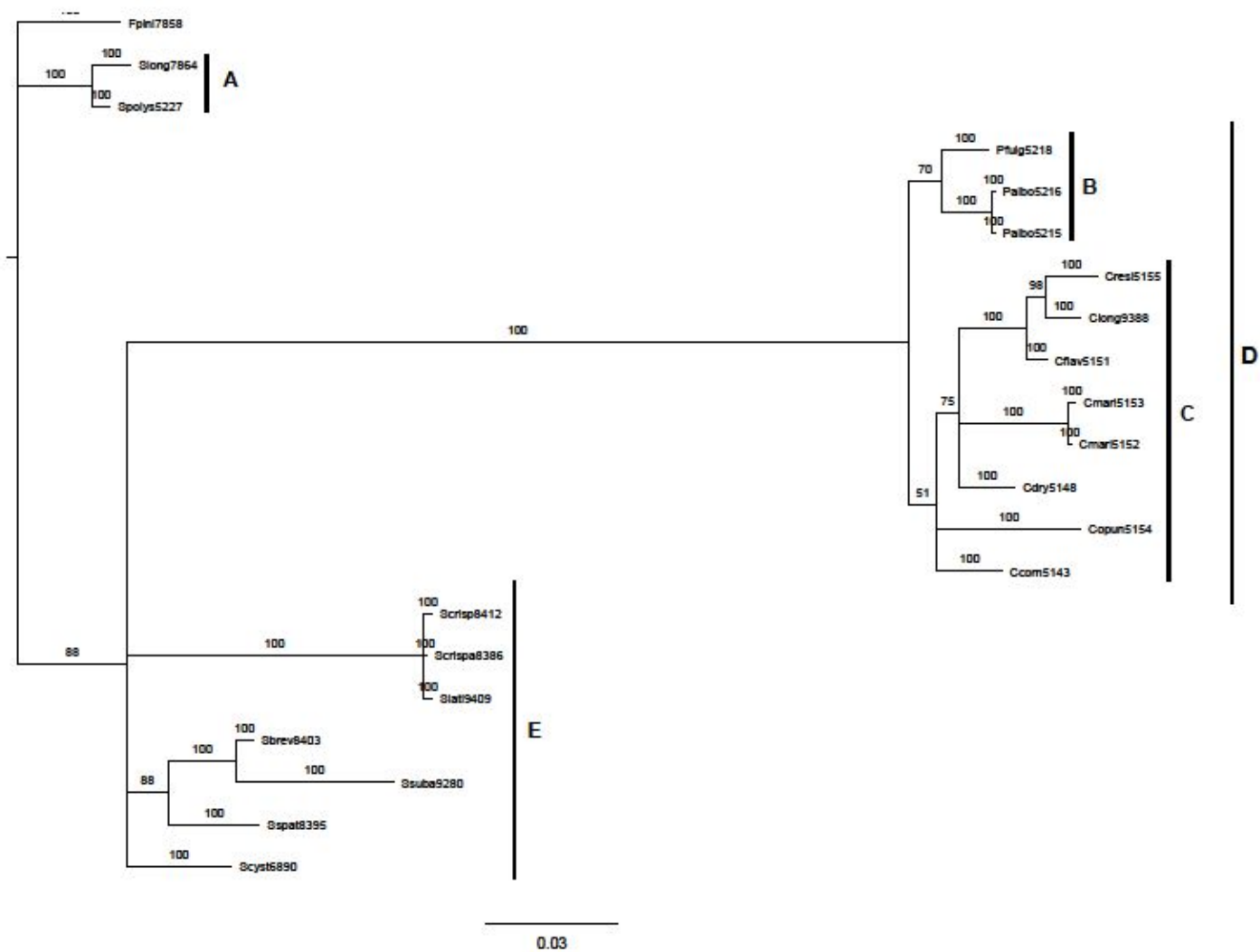


Figure 2: Strict consensus phylogenetic tree of large subunit ribosomal RNA gene LSU (partial sequence) calculated by the MrBayes software (Ronquist et al. 2015; 1 000 000 generations). A: Sarcoporiaceae; B: Pycnoporellus; C: Crustoderma; D: Pycnoporellaceae; E: Sparassidaceae; outgroup: *Fpini7858*

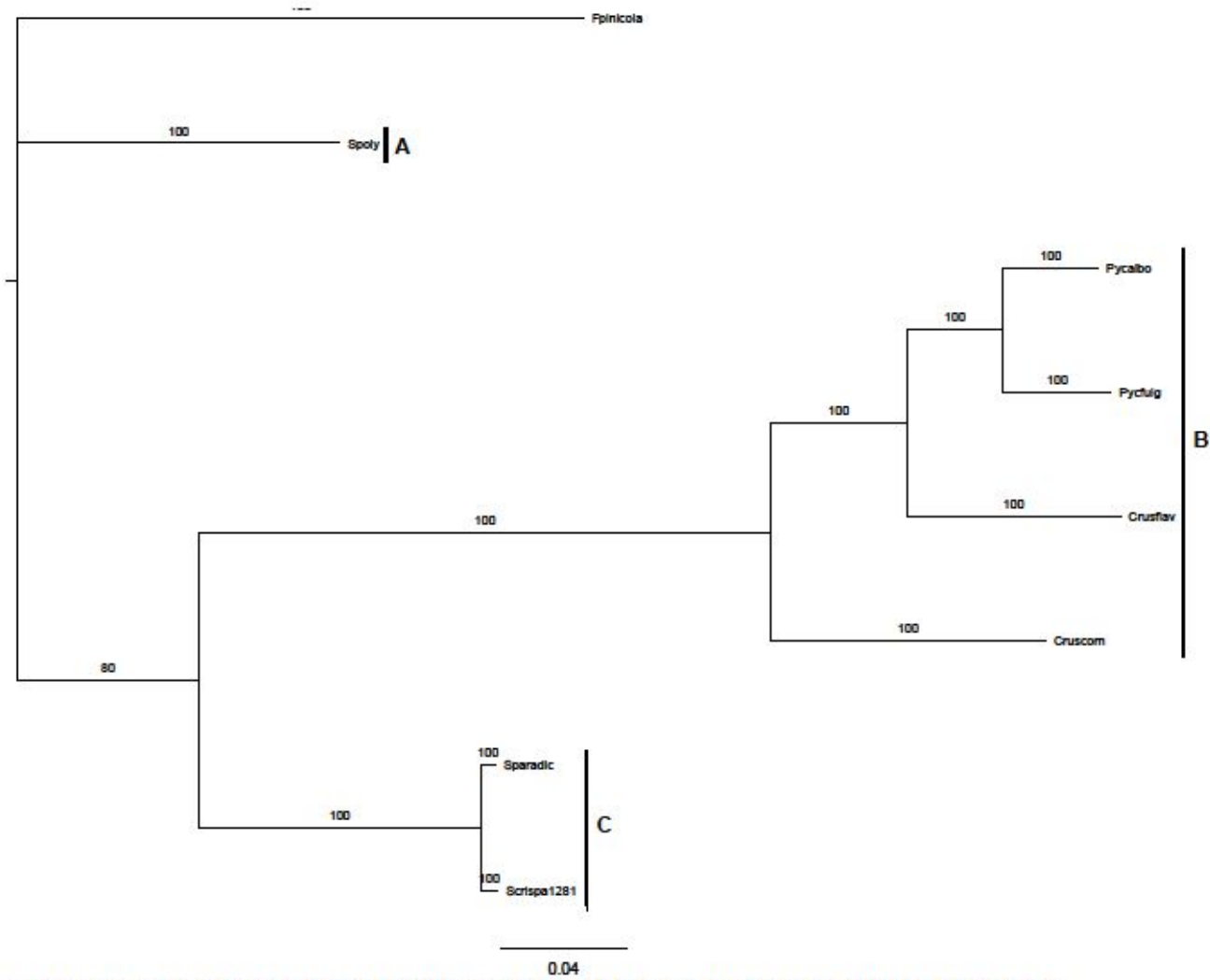


Figure 3: Strict consensus phylogeny from multi loci (LSU+RPB1) calculated by the MrBayes software (Ronquist et al. 2015; 1 000 000 generations).  
 A: Sarcoporiaceae; B: Pycnoporellaceae; C: Sparassidaceae; outgroup: *Fpnicola*