Mushrooms nomenclatural novelties no. 16

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Pycnoporellaceae Audet, fam. nov.
IF554251

Basidiomes resupinate to effused-reflexed, rarely sessile (P. fulgens). Tints of yellow, orange, gray or sometimes olive-colored. Fertile areas smooth or with scattered warts, or poroid.

Hyphal system monomitic, clampless septa in the hyphae or rarely clamped, sometimes branched, with or without crystal, thin or with irregular thick-walled hyphae, hyaline or yellow. Subhymenium dense. Cystidia cylindrical to clavate up to 380 µm long. Basidia narrowly clavate up to 80 µm long reported pedunculate in Crustoderma. Basidiospores hyaline or yellow, smooth, subglobose, ellipsoidal, or cylindrical, IKI-, CB-, binucleated (Pycnoporellus).

Mating system bipolar (Crustoderma) and homothallic? (Pycnoporellus). Nuclear behavior astatocoenocytic (Crustoderma) and holocenocytic (Pycnoporellus). Causing brown-rot decay.

Holotype : *Pycnoporellus* Murrill, Bull. Torrey bot. Club 32(9): 489 (1905).

Other genera accepted in this family: Crustoderma Parmasto, Conspectus Systematis Corticiacearum: 87 (1968).

Comment : Preliminary results with Justo et al. 2017 paper show that Pycnoporellus and Crustoderma are grouped together, in the same clade as Sparassis but without strong support. I verified another sequence KF211281 (RPB1) from Genbank under unverified Sparassis crispa and is very close to the sequence of Sparassis radicata used in the Justo et al. 2017 study. When I used the previous sequence with the sequence from Justo et al. 2017 study I obtained a clearly separate clade 100% supported in bayesian analyses with the same Pycnoporellus, Crustoderma Sparassis and Sarcoporia species from Justo et al. 2017 paper. My unpublished data in bayesian analyses with combined LSU+RPB2 revealed one clade with Pycnoporellus fulgens against 6 species of Sparassis on other clade. Pycnoporellus is grouped with Crustoderma in some papers Ortiz-Santana et al 2013 and Han et al. 2016. See personal phylotrees below about the support of this new family.

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

Table 4 from figure 4

		Genbank	
Taxon	Phylotree	LSU	RPB2
Jahnoporus hirtus	Jhir1606	DQ911606	DQ911608
Oligoporus lacteus	Olact4981	KJ68498	KR610843
Oligoporus rennyi	Orenn7876	AF287876	AY218499
Postia duplicata	Pdupl4976	KJ684976	KR610844
Fomitopsis pinicola	Fpini7858	AF287858	KR610782
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	

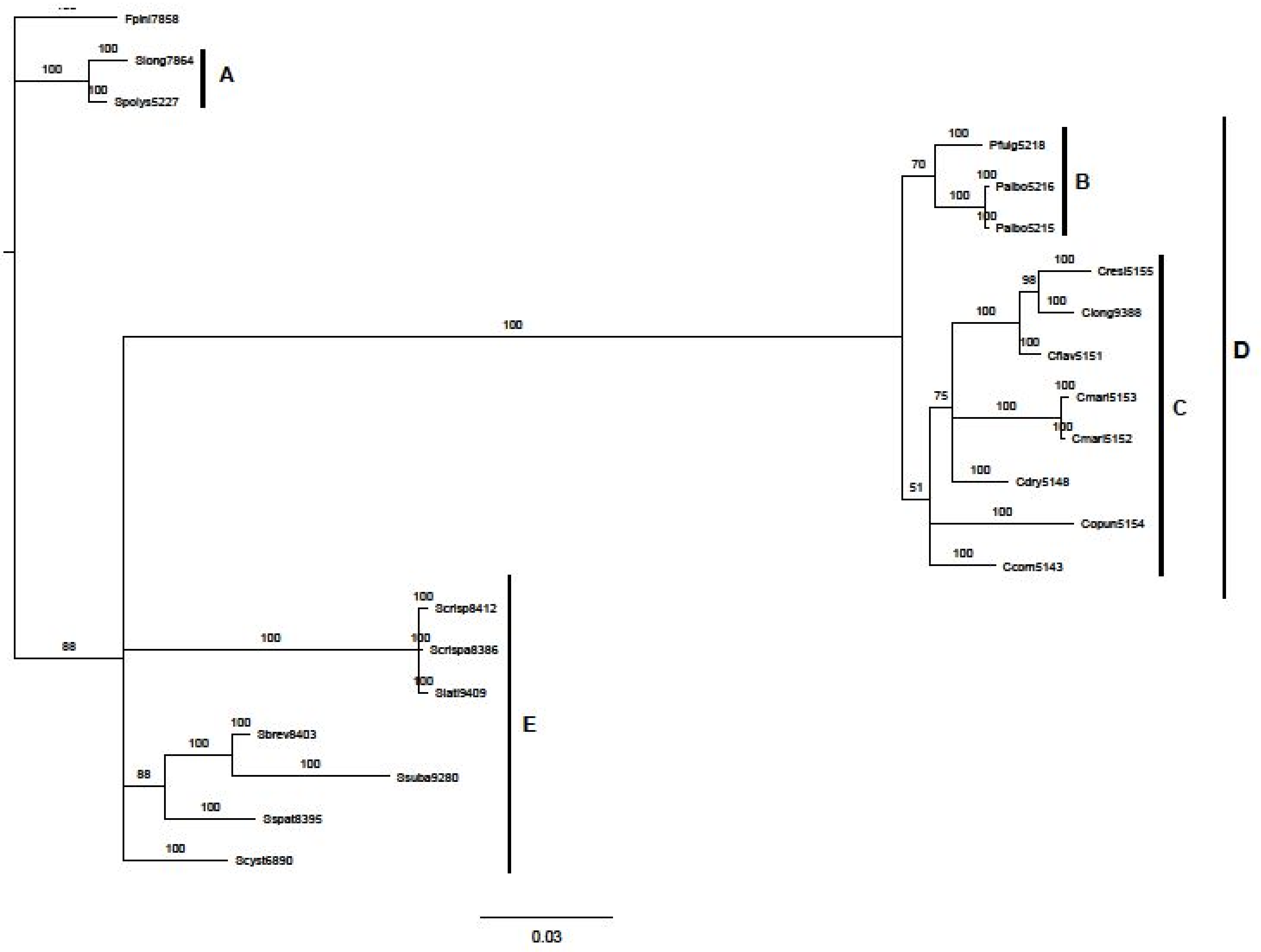

Figure 2: Strict consensus phylotree of large subunit ribosomal RNA gene LSU (partial sequence) calculated by the MrBayes software (Ronquist et al. 2015; 1 000 000 generations). A: *Sarcoporiaceae*; B: *Pycnoporellus*; C: *Crustoderma*; D: *Pycnoporellaceae*; E: *Sparassidaceae;* outgroup: *Fpini7858*

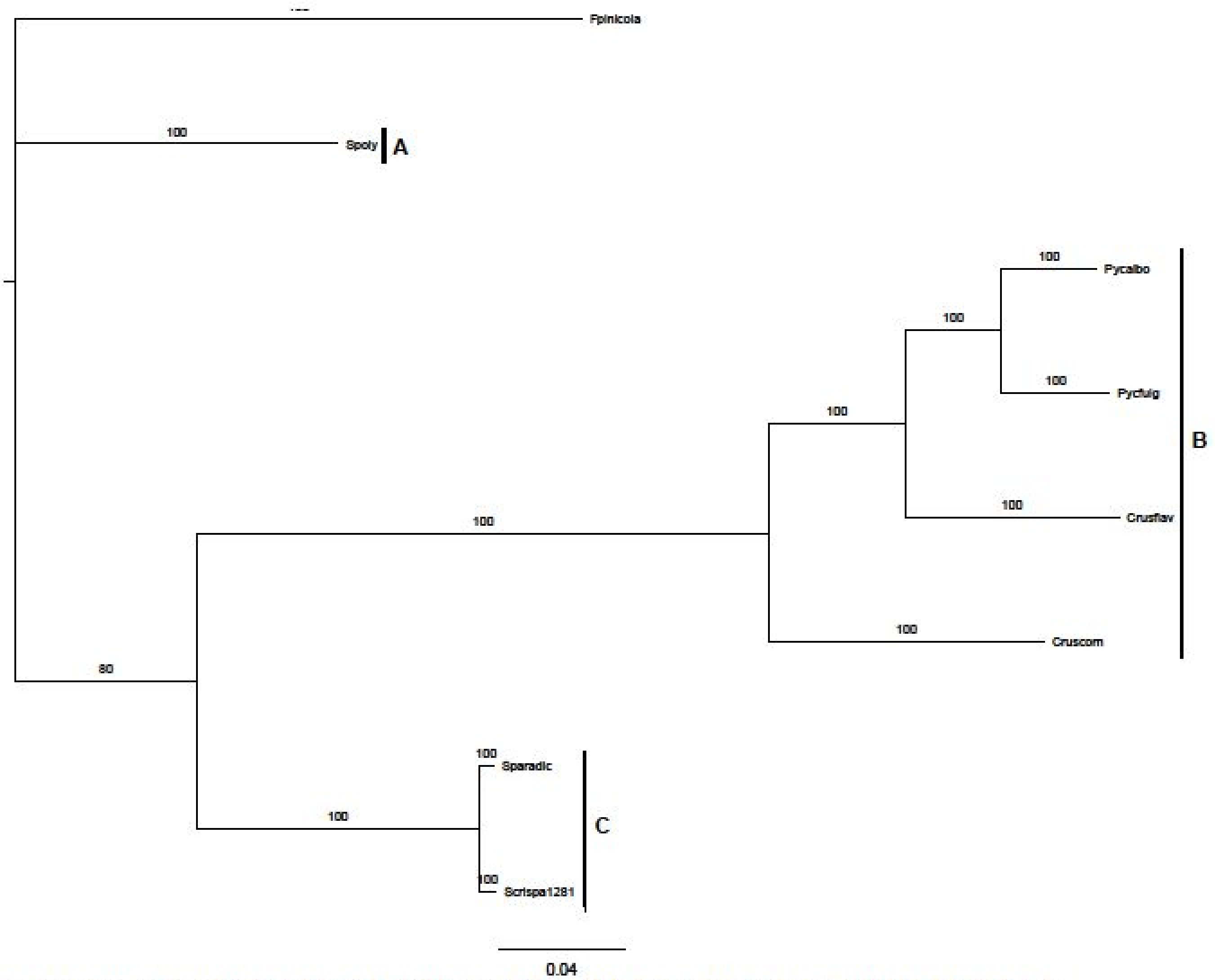

Figure 3: Strict consensus phylotree from multi loci (LSU+RPB1) calculated by the MrBayes software (Ronquist et al. 2015; 1 000 000 generations).
A: *Sarcoporiaceae*; B: *Pycnoporellaceae*; C: *Sparassidaceae;* outgroup: *Fpinicola*

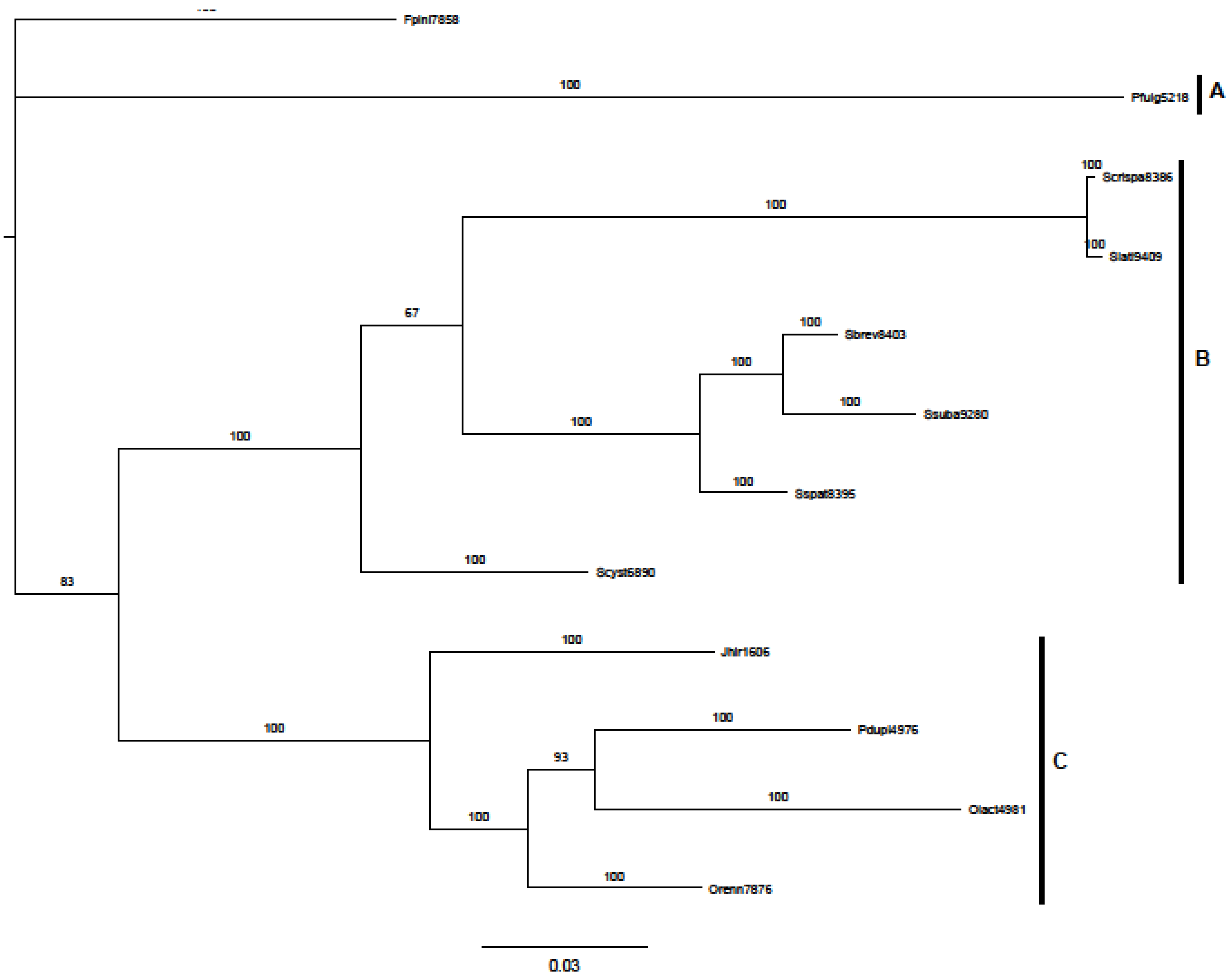

Figure 4: Strict consensus phylotree from multi loci (LSU+RPB2) calculated by the MrBayes software (Ronquist et al. 2015; 1 000 000 generations).
A: *Pycnoporellaceae*; B: *Sparassidaceae; C: Dacryobolaceae;* outgroup: *Fpini*7858