

Deadly mushrooms of the genus *Galerina* found in Antarctica have colonized the continent as early as the Pleistocene

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SUPPLEMENTAL MATERIAL

Original dataset (FULL)

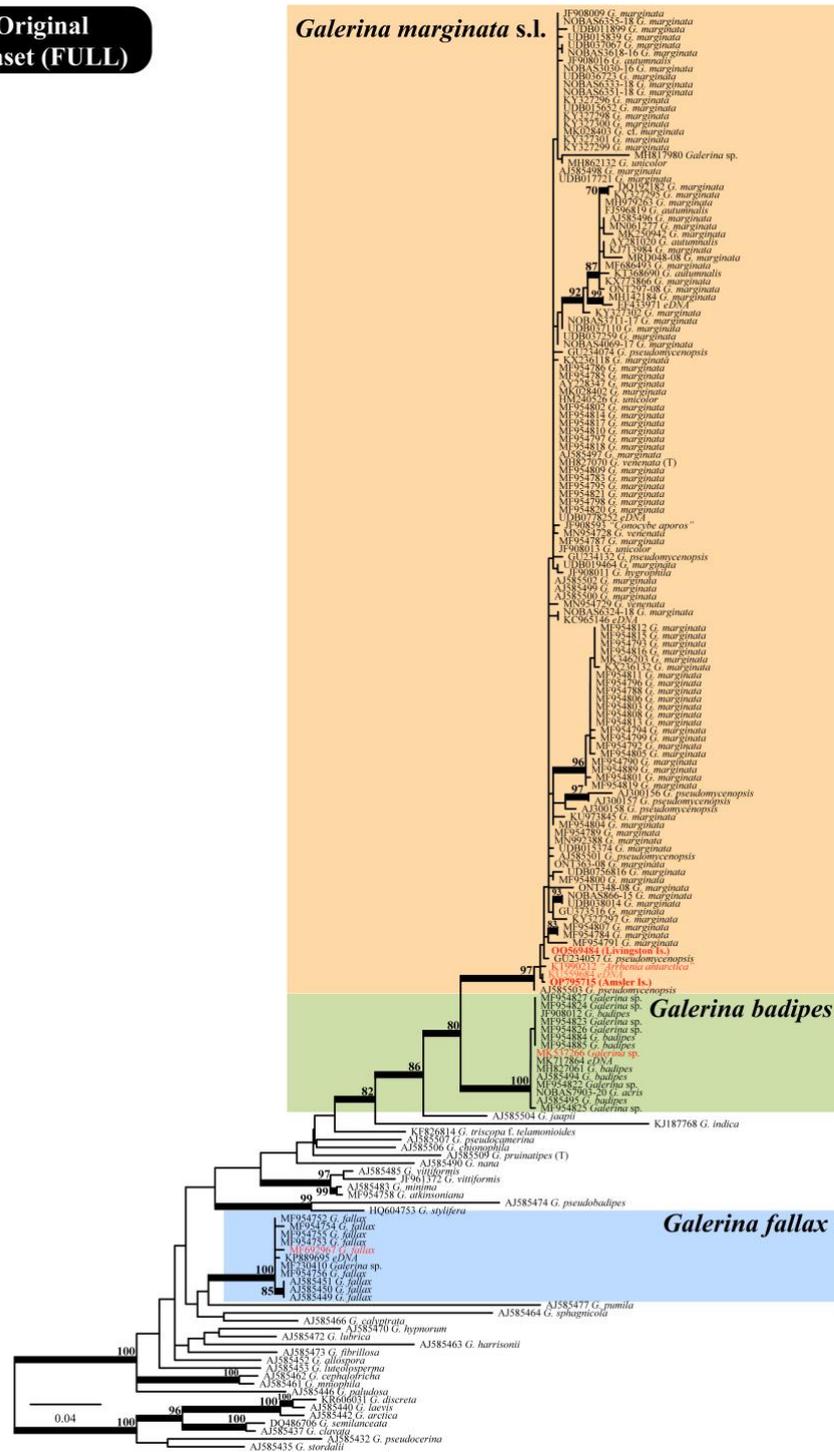


Figure S1. RAxML phylogram obtained with the full, original nrITS alignment (ORG) that depicts relationships among the different *Galerina* species, including the sequences obtained from Antarctic material (terminals in red; newly produced sequences in bold letters). Clades corresponding to species with Antarctic representatives are variously colored. Supported nodes (BS \geq 70%) are indicated with widened branches.

GBlocks-trimmed dataset (GB)

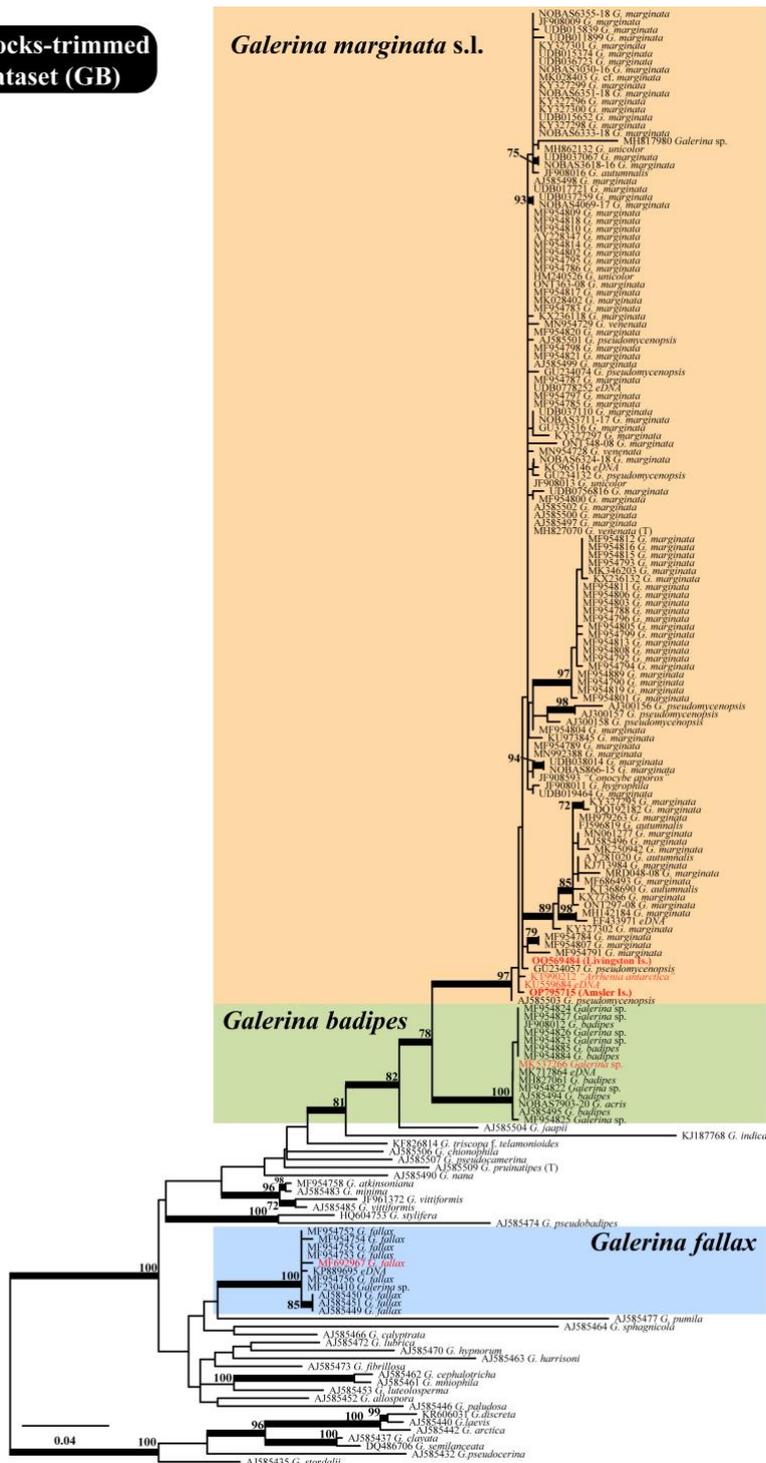


Figure S2. RAxML phylogram obtained with the GBlocks-trimmed nrITS alignment (GB) that depicts relationships among the different *Galerina* species, including the sequences obtained from Antarctic material (terminals in red; newly produced sequences in bold letters). Clades corresponding to species with Antarctic representatives are variously colored. Supported nodes (BS \geq 70%) are indicated with widened branches.

Table SI. Marginal likelihood estimates (MLE) values calculated using Path Sampling and Stepping-Stone to compare BEAST models incorporating alternative clock and tree priors based on the full, original nrITS alignment (ORG). To choose among competing models, we first compared models with different tree priors (Coalescent-Constant Size; Speciation: Yule Process; Speciation: Birth-Death Process), and then models with two possible clocks (Strict clock vs Uncorrelated lognormal relaxed clock). The models used in BEAST runs are highlighted in bold.

	Path Sampling	Stepping-Stone
	Ln (Marginal Likelihood)	Ln (Marginal Likelihood)
Strict clock & Coalescent-Constant size	-6554.1	-6554.8537
Relaxed clock & Coalescent-Constant size	-6517.6	-6518.1713
Strict clock & Yule Process	-6619.0	-6621.2456
Relaxed clock & Yule Process	-6551.5	-6553.7327
Strict clock & Birth-Death Process	-6554.4	-6554.7051
Relaxed clock & Birth-Death Process	-6525.9	-6528.177

Table SII. Marginal likelihood estimates (MLE) values calculated using Path Sampling and Stepping-Stone to compare BEAST models incorporating alternative clock and tree priors based on the GBLOCKS-trimmed nrITS alignment (GB). To choose among competing models, we first compared models with different tree priors (Coalescent-Constant Size; Speciation: Yule Process; Speciation: Birth-Death Process), and then models with two possible clocks (Strict clock vs Uncorrelated lognormal relaxed clock). The models used in BEAST runs are highlighted in bold.

	Path Sampling	Stepping-Stone
	Ln (Marginal Likelihood)	Ln (Marginal Likelihood)
Strict clock & Coalescent-Constant size	-6172.0	-6172.5859

Relaxed clock & Coalescent-Constant size	-6139.7	-6140.4131
Strict clock & Yule Process	-6238.7	-6239.6338
Relaxed clock & Yule Process	-6175.2	-6177.8428
Strict clock & Birth-Death Process	-6178.0	-6178.2071
Relaxed clock & Birth- Death Process	-6146.8	-6148.2925