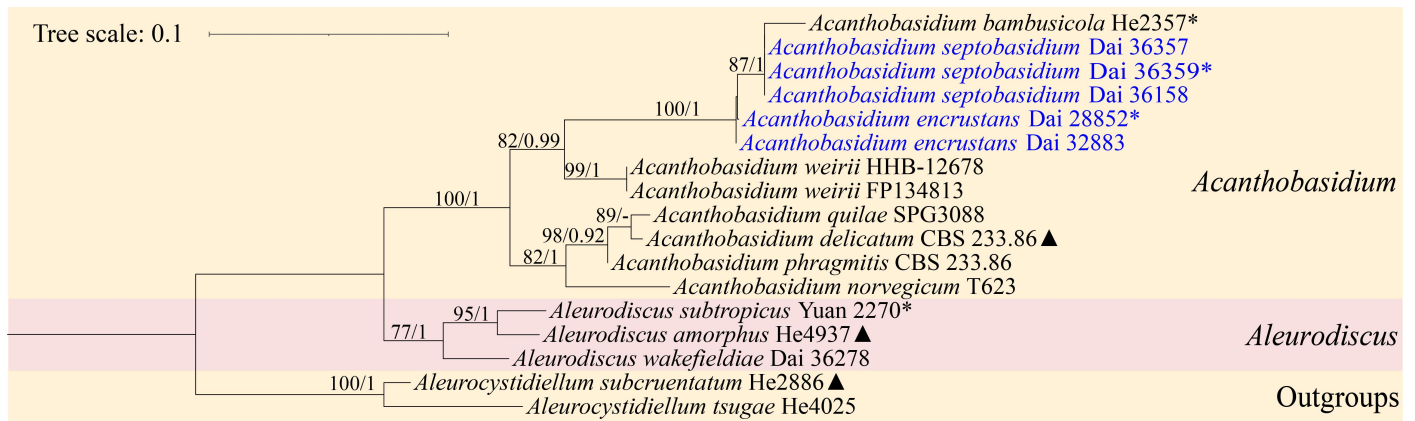




Supplementary Fig. S1 The phylogeny of *Acanthobasidium* was reconstructed using Maximum Likelihood analysis of combined ITS+nLSU sequences. Bayesian analysis ran for 1.5 million generations; convergence achieved (ASDSF < 0.01, ESS > 200). Branch nodes are annotated with Bootstrap support ($\geq 50\%$) and Bayesian posterior probabilities (≥ 0.9). Black triangle (▲) = type species; blue = new species.