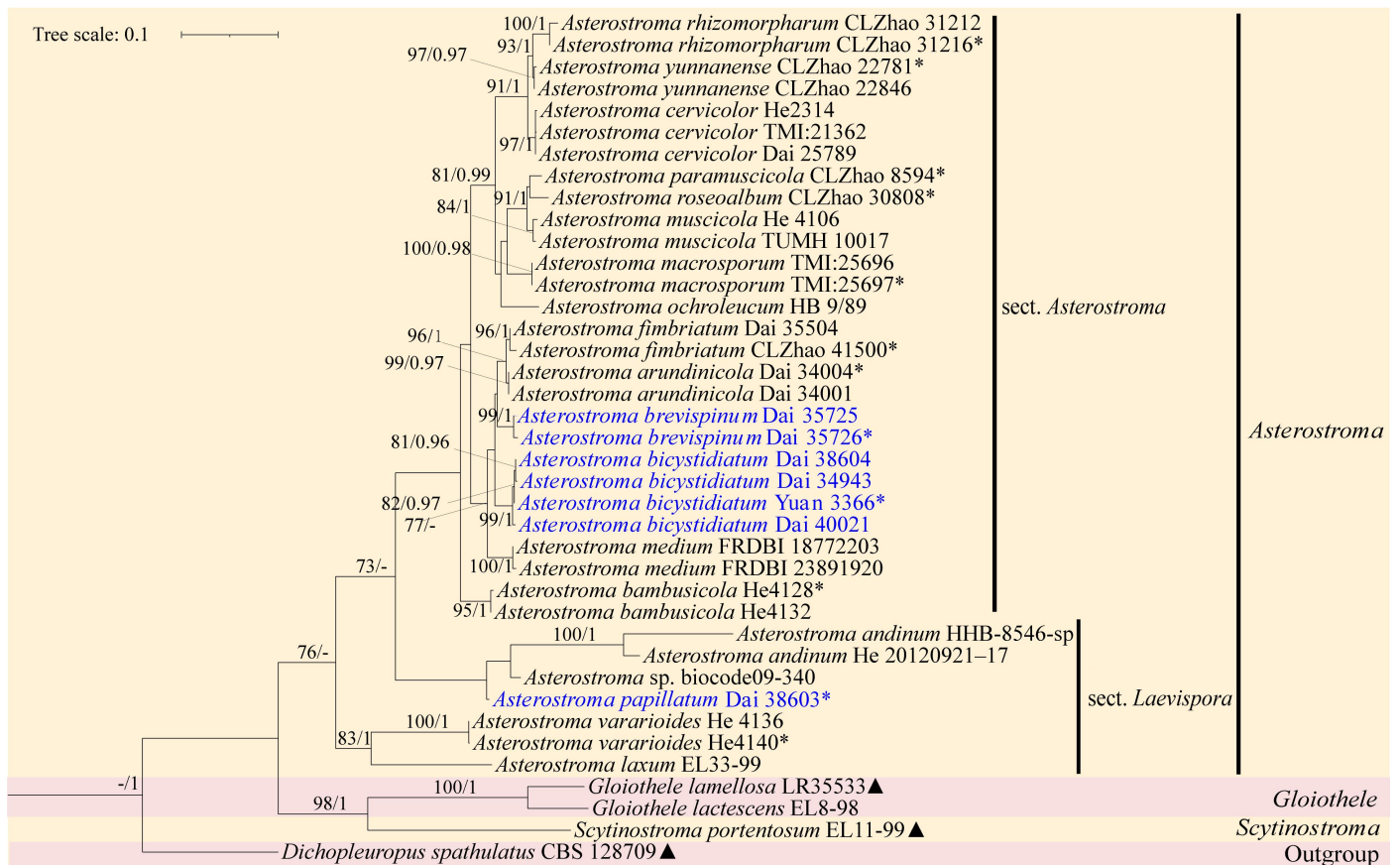




**Supplementary Fig. S2** The phylogeny of *Asterostroma* was reconstructed using Maximum Likelihood analysis of combined ITS+nLSU sequences. Bayesian analysis ran for 45 million generations (ASDSF < 0.01, ESS > 200). Branch nodes are annotated with Bootstrap support ( $\geq 50\%$ ) and Bayesian posterior probabilities ( $\geq 0.9$ ). Black triangle (▲) = type species; blue = new species.