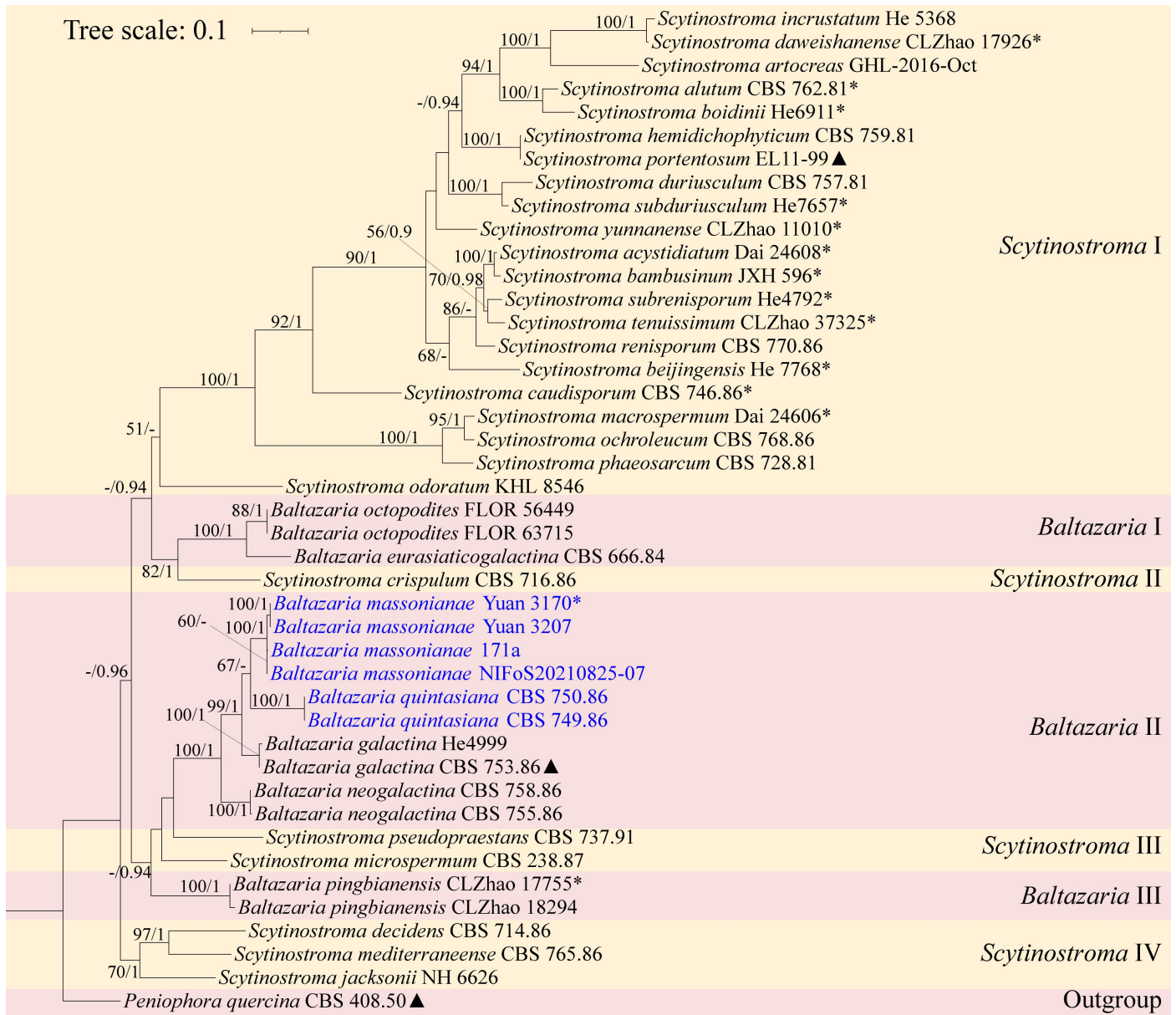




Supplementary Fig. S3 The phylogeny of *Baltazaria* was reconstructed using Maximum Likelihood analysis of combined ITS+nLSU sequences. Bayesian analysis ran for 3.1 million generations (ASDSF < 0.01, ESS > 200). Branch nodes are annotated with Bootstrap support ($\geq 50\%$) and Bayesian posterior probabilities (≥ 0.9). Black triangle (▲) = type species; blue = new species/combinations. Major clades are labelled with Roman numerals.