

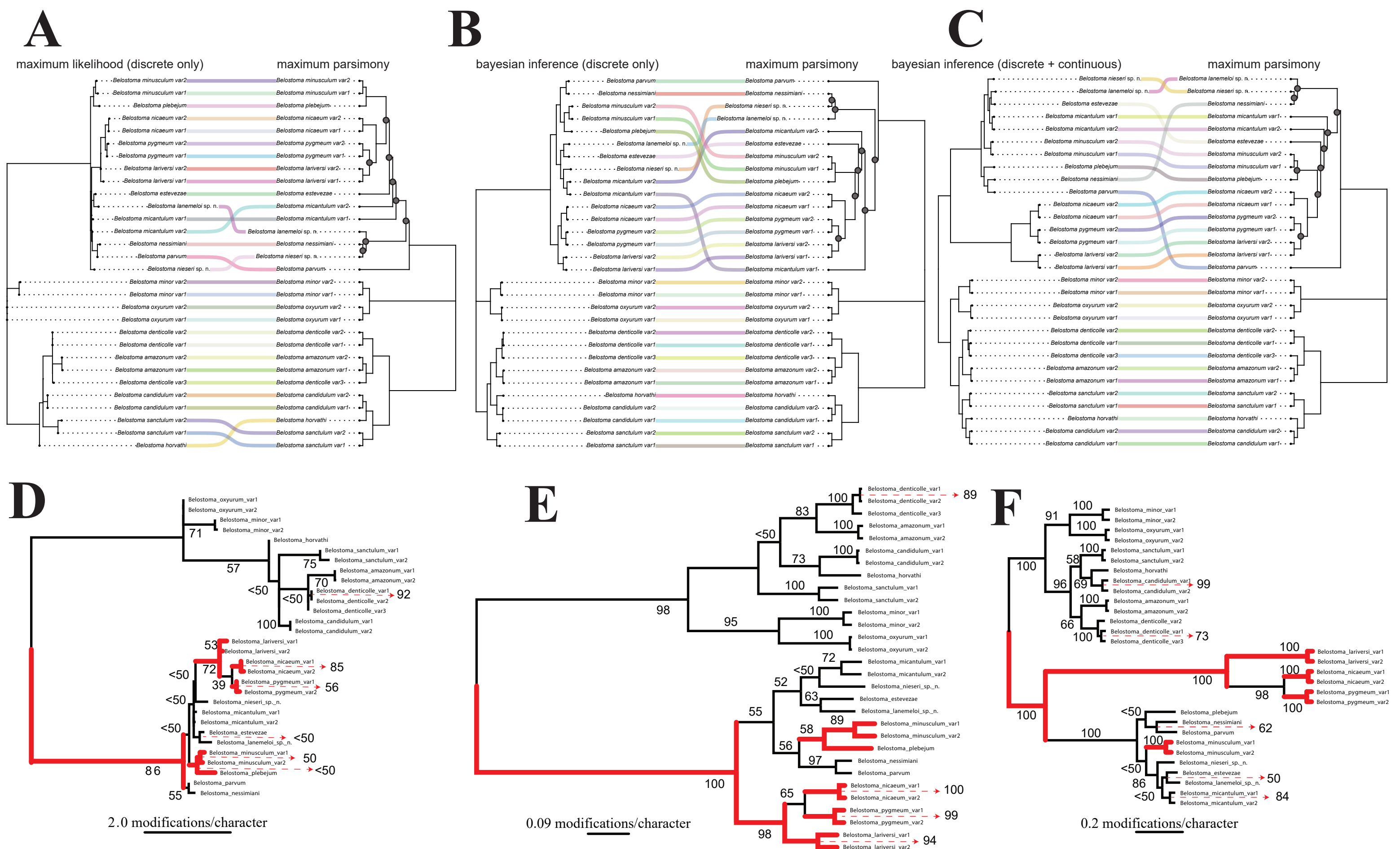


Figure S1. Phylogenetic trees based on maximum parsimony, maximum likelihood, and Bayesian inferences. **A-C** Co-phylogenies for the *Belostoma plebejum* group. Lines connect the same tip labels. **D** Maximum likelihood inference performed on the matrix with discrete characters. Numbers above or below branches refer to bootstrap (if > 50%). **E** Bayesian inference performed on the matrix with discrete characters. Numbers above or below branches refer to posterior probabilities (if > 50%). **F** Bayesian inference performed on the matrix with all datasets combined. Numbers above or below branches refer to posterior probabilities (if > 50%). Thicker clades refer to those also found by maximum parsimony analyses.