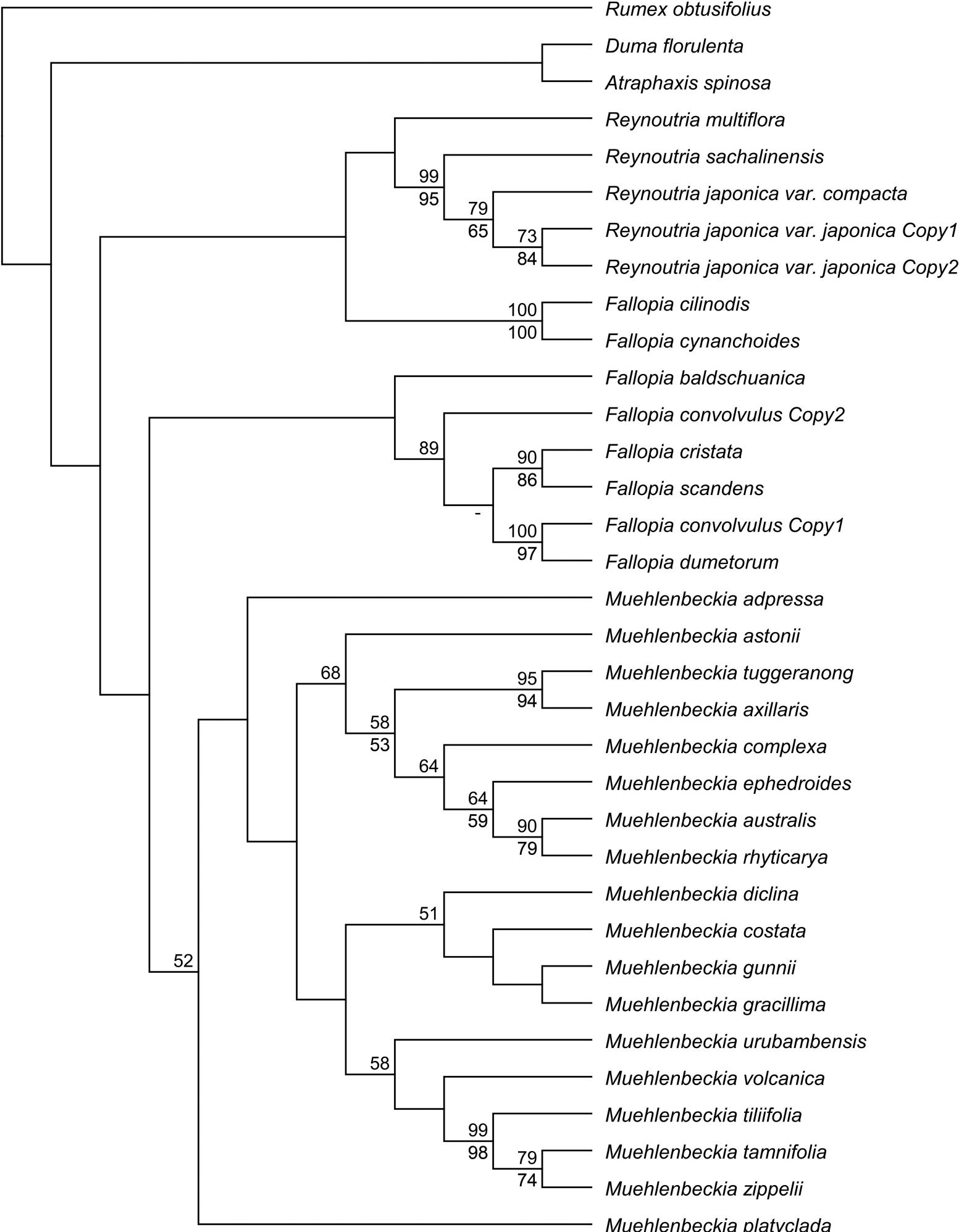
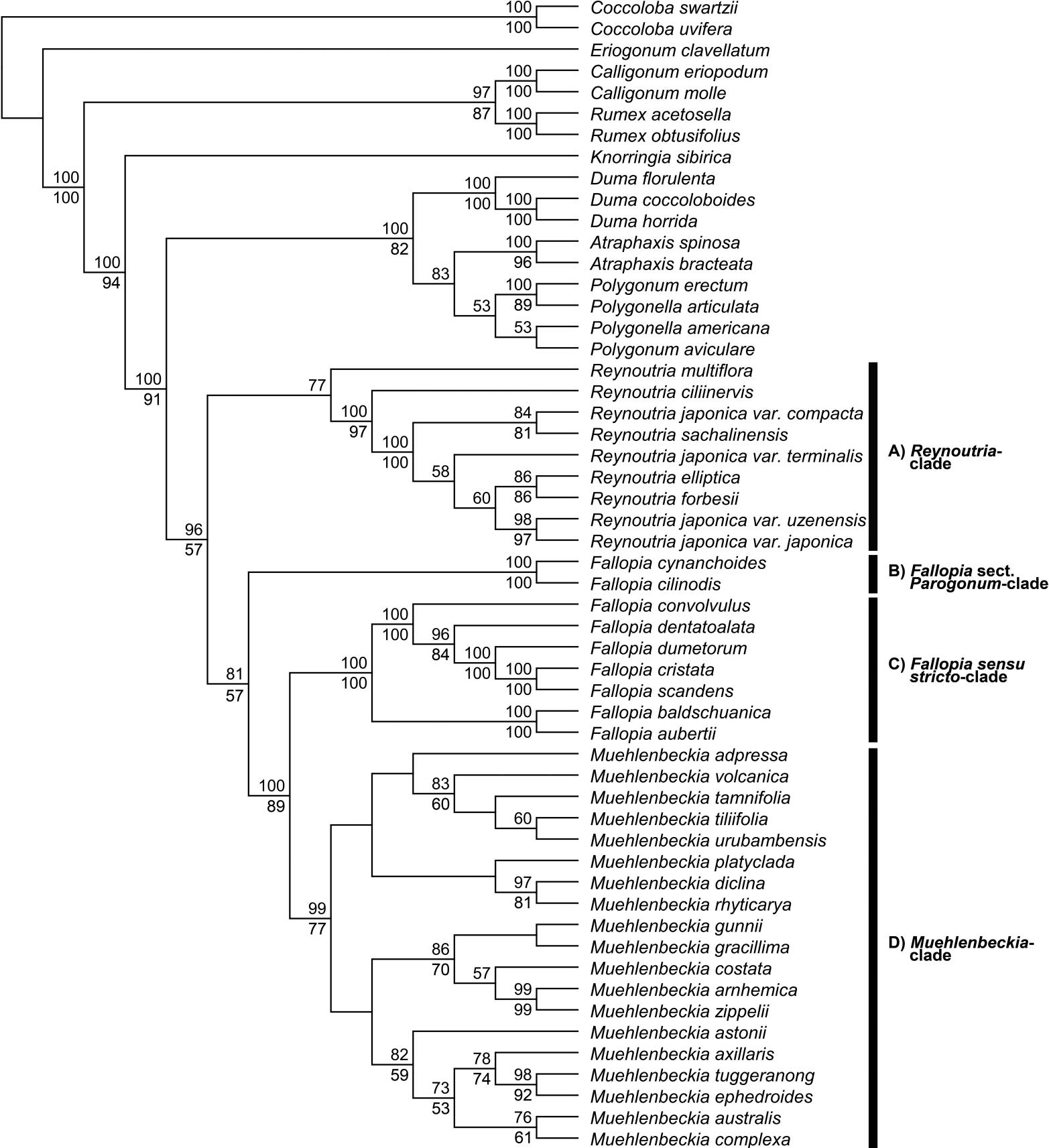


**Figure 1.** A phylogenetic tree generated by a Maximum Likelihood analysis of ITS sequence data. Bootstrap support values ( $\geq 50\%$ ) are displayed above and below the nodes for Maximum Likelihood and Maximum Parsimony analyses, respectively. Maximum Parsimony analysis recovered two equally parsimonious trees (825 steps).



**SFigure 2.** A phylogenetic tree generated by a Maximum Likelihood analysis of *LEAFYi2* sequence data. Bootstrap support values (≥50%) are displayed above and below the nodes for Maximum Likelihood and Maximum Parsimony analyses, respectively. Hyphens (-) indicate nodes where parsimony and likelihood trees differ in branching pattern. Maximum Parsimony analysis recovered three equally parsimonious trees (598 steps).



**Figure 3.** A phylogenetic tree generated by a Maximum Likelihood analysis of concatenated chloroplast sequence data (*matK*, *rbcL*, *trnL-trnF* & *rps16-trnK*). Bootstrap support values ( $\geq 50\%$ ) are displayed above and below the nodes for Maximum Likelihood and Maximum Parsimony analyses, respectively. Maximum Parsimony analysis recovered 191 equally parsimonious trees (1600 steps). The main clades within subtribe *Reynoutriinae* are marked with bars.