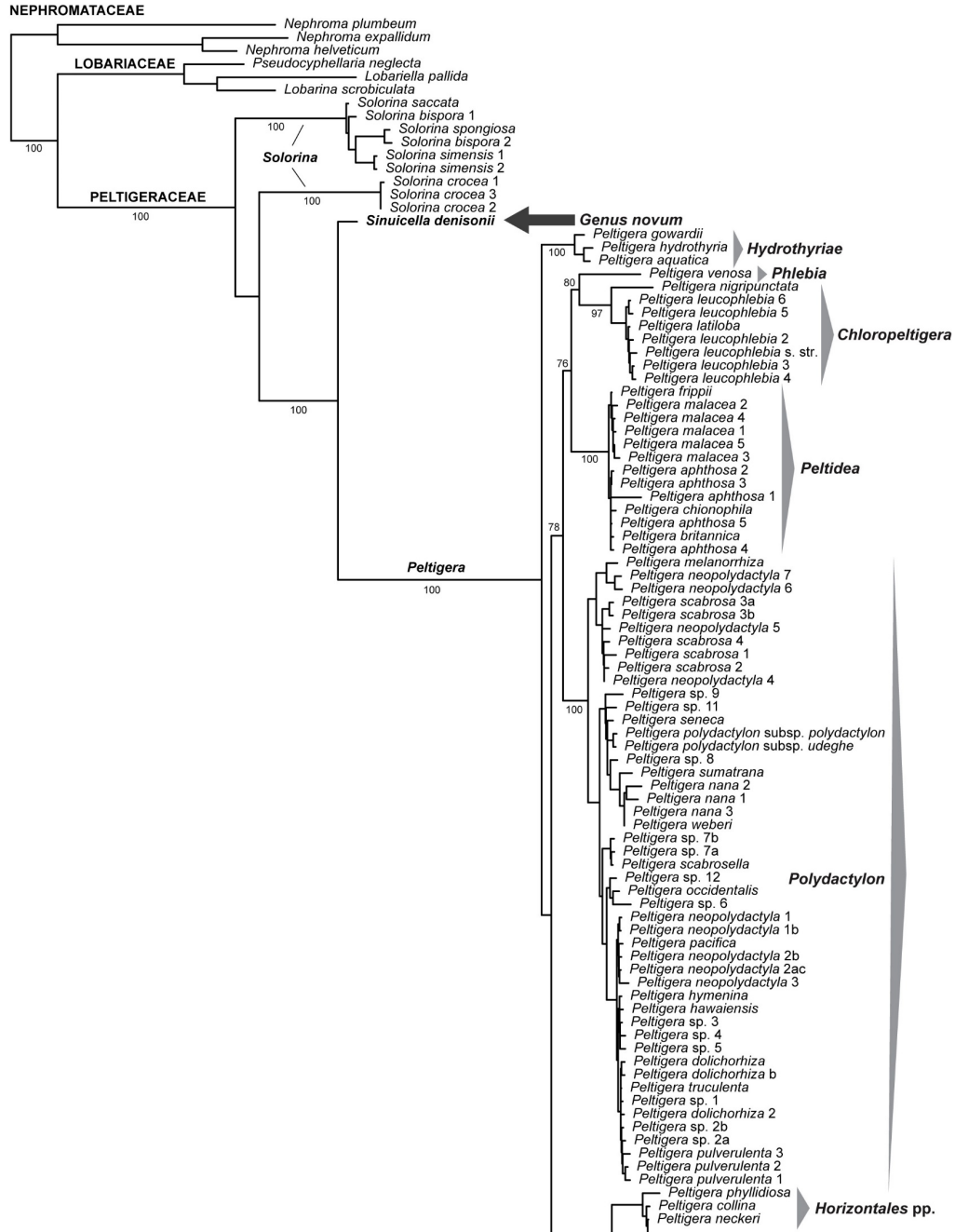
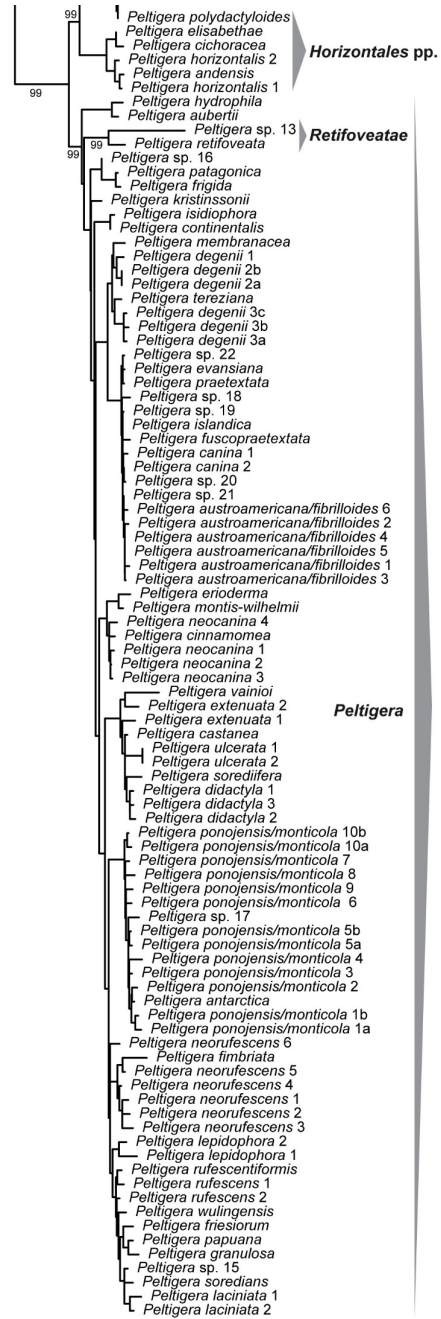


Supplementary Material Figure 1. Phylogenetic relationships inferred from maximum likelihood (ML) analyses based on a 4-locus data set (ITS+nuLSU+ β -tubulin+ *RPB1*) for 185 taxa representing *Peltigeraceae* and six outgroup species from the closely related families *Lobariaceae* and *Nephromataceae* (Supplementary Material Table 2). *Nephroma* was used to root the tree (following Miadlikowska *et al.* 2014a). Bootstrap support values >70% are provided for the main clades (i.e., sections, genera and families). The scale bar represents number of nucleotide substitutions per site. This phylogeny is based on modified a 7-locus data set from Chagnon *et al.* (2019). Classification follows Lücking *et al.* (2016) and Miadlikowska & Lutzoni (2000).





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