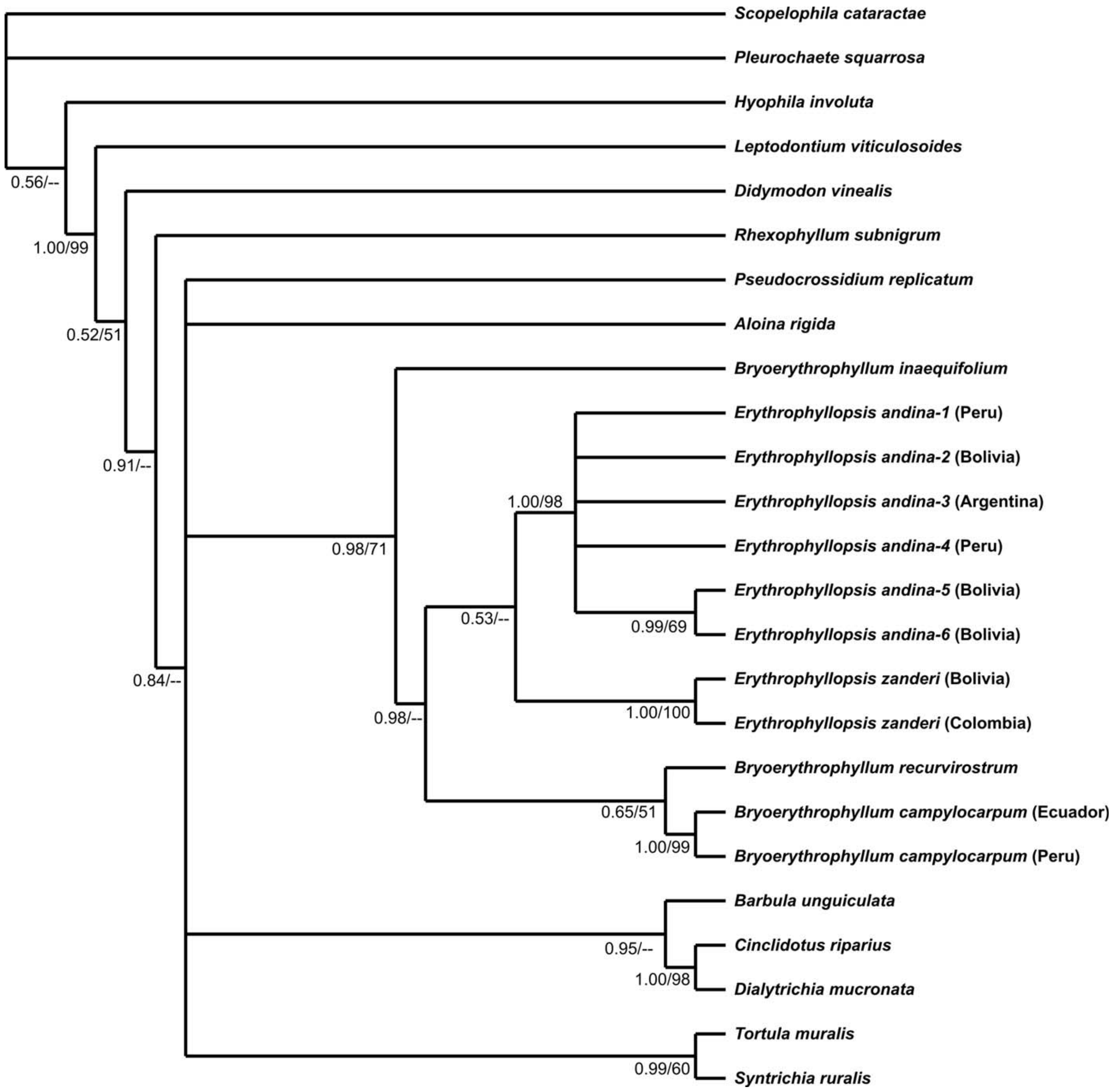

FIG. 1. Majority-rule (50%) consensus tree resulting from Bayesian analysis of a combined 2-gene data set, *trnL-F* and *trnG*. Numbers at nodes indicate Bayesian posterior probabilities and MP bootstrap values.

Zander (1993) proposed. Werner et al. (2004), in their molecular phylogeny of Pottiaceae, found that *Erythrophyllopsis* and *Erythrophyllastrum* formed a clade that was supported in all their analyses (68% BS by MP, 82% by Neighbor-Joining, and 98% by MrBayes). However, it is worth mentioning that only one marker and one sample of each taxon was used in that study. Zander (2006), based on that molecular analysis and the morphological similarities of both genera, synonymyzed *Erythrophyllastrum* with *Erythrophyllopsis.* In the current state of knowledge of the Pottiaceae, we think it is more reasonable to maintain both species in one genus, *Erythrophyllopsis*. In this way, we avoid the proliferation of monotypic genera that are poorly defined based on a vague combination of morphological characters. Further investigations based on additional informative DNA markers can also help to clarify this question.

The phylogenetic analyses also show that *Erythrophyllopsis* is nested in *Bryoerythrophyllum*. It is important to point out that only three species of *Bryoerythrophyllum* have been sampled and this is a cosmopolitan genus represented by 24 more species (Zander 1993). The genus *Bryoerythrophyllum* is a taxonomically complex genus, and a more detailed study, focused in resolving its phylogenetic relationships, could reveal the existence of different subgroups. One possible alternative would be to merge *Bryoerythrophyllum* with *Erythrophyllopsis* (since the latter is the older at generic rank). Both genera share morphological characters such as hyaline axillary hairs, red KOH coloration of the lamina, and ventral and dorsal stereid