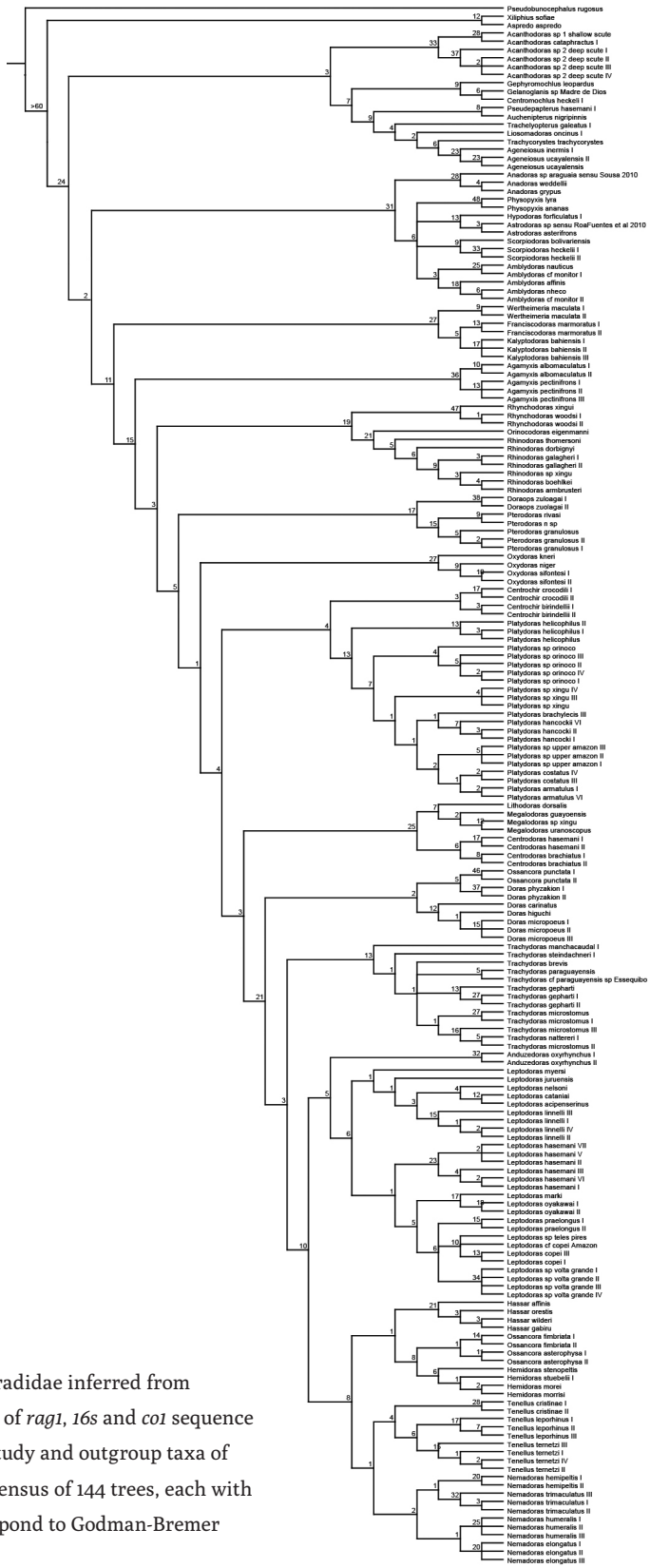

FIGURE S3 | Phylogeny of Doradidae inferred from Maximum Parsimony analysis of *rag1*, *16s* and *co1* sequence data for ingroup taxa of this study and outgroup taxa of Arce H. *et al.* (2013). Strict consensus of 144 trees, each with 6657 steps. Node values correspond to Godman-Bremer support.

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