

Figure S1

Phylogenetic tree inferred using (A) Maximum Likelihood and (B) Bayesian Inference. Bootstrap support values and posterior probabilities are indicated on the branches. The sampled genera are grouped into three main clades, and major topological conflicts are discussed in the text.

Group 1 - *Bifrenaria*, *Hylaeorchis*, *Rudolfiella* and *Scuticaria*. In both analyses, the genus *Bifrenaria* was recovered as comprising three internal groups that broadly correspond to the sections proposed by Meneguzzo & Chase (2024). The first group includes all species assigned to the *Bifrenaria* sect. *Bifrenaria*. However, one individual of *B. leucorrhoda* was placed within this group, although it is expected to belong to sect. *Adipe*. The third group, *Bifrenaria* sect. *Stenocoryne* was also recovered, grouping *B. longicornis* and *B. venezuelana*, the two Amazonian species in the genera. The genus *Scuticaria* exhibited internal rearrangements, likely resulting from polytomies in the phylogenetic reconstruction. In particular, *S. hadwenii* and *S. strictifolia* were recovered within the same clade, without clear phylogenetic separation between the two species. Such result is in agreement to the Catharino & Campacci (2010, Boletim CAOB 80 92-96) which suggested that *S. strictifolia*, described by F. Hoehne in 1947 is just a variation of *S. hadwenii* presenting erect leaves, occurring at high elevations, typically between 1000 and 1200 m, growing in full sun and/or on rocks. This *Scuticaria* clade, suggested by Meneguzzo & Chase (2024) as another clade inside *Bifrenaria*, is sister to *Rudolfiella*, also transferred to *Bifrenaria* by Meneguzzo & Chase (2024), along with *Hylaeorchis*. Both Blanco et al. (2007) and Meneguzzo & Chase (2024) suggestion result in monophyletic genera/genus.

Group 2a - *Brasiliorchis*, *Camaridium*, *Christensonella*, *Cryptocentrum*, *Cyrtidiorchis*, *Inti*, *Mapinguari*, *Maxillaria*, *Maxillariella*, *Mormolyca*, *Pityphyllum*, *Rhetinantha*, *Sauvetrea* and *Trigonidium*. In the ML analysis, *Pityphyllum* was recovered as sister to *Cryptocentrum* + *Inti* + (*Brasiliorchis* + (*Christensonella* + *Mapinguari* + (*Mormolyca* + (*Cyrtidiorchis* + *Sauvetrea*) + (*Rhetinantha* + *Maxillariella*) + (*Trigonidium* + *Maxillaria*) + *Camaridium*))), with high support (Fig. S1). However, in the BI analysis the genus was recovered as sister to the *Inti* + *Cryptocentrum* clade, which in turn was placed as sister to *Christensonella*. *Rhetinantha* was recovered as sister to *Maxillariella*, and this pair was recovered as sister to the clade comprising *Maxillaria* and *Trigonidium* in the ML analysis. In contrast, in the BI analysis these genera were placed in a polytomy together with *Mapinguari*, *Maxillariella*, and

the clade *Mormolyca* + (*Cyrtidiorchis* + *Sauvetrea*). Internal rearrangements were also observed within *Cryptocentrum* and *Camaridium*. Only in BI, one specimen of *Lycaste deppei* was erroneously placed as sister of all remaining genera in group 2a.

Group 2b - *Nitidobulbon*, *Ornithidium*, *Heterotaxis*. These genera were recovered with high support, although the relationships among them were not entirely resolved. The combined matrix recovered *Ornithidium* and *Heterotaxis* as monophyletic genera, but split *Nitidobulbon*, placing *N. cymbidioides* and *N. nasutum* within the *Heterotaxis* clade, while *N. proboscideum* was recovered as the sister lineage to *Heterotaxis*. The close relationship among these three genera is not a novelty, since *Nitidobulbon* and *Heterotaxis* are composed of species removed from *Ornithidium* (Szlachetko *et al.* 2012). Although Schuiteman & Chase (2015) proposed reallocating *Heterotaxis* and *Nitidobulbon* to sections within *Maxillaria* (sects. *Iridofoliae* and *Nitidobulbon*, respectively), the *Heterotaxis*–*Nitidobulbon* clade was not fully resolved in the present study, despite receiving high support. This result suggests potential issues with monophyly and further questions the current circumscription of *Maxillaria*, as even infrageneric ranks such as sections should represent monophyletic groups.

Group 3 - *Anguloa*, *Ida*, *Lycaste* and *Xylobium*. The genus *Xylobium* was recovered as the sister group to *Lycaste*, *Ida*, and *Anguloa*, with strong support in both analyses. All genera within this group exhibited internal rearrangements, likely resulting from polytomies recovered in the phylogenetic reconstruction, particularly in the IB analysis. One specimen of *Lycaste deppei* was placed within Group 2a in the IB analysis, whereas in the maximum likelihood (ML) analysis it was recovered within the genus *Lycaste*. Notably, *Ida*, which is composed of species removed from *Lycaste*, is not sister to *Lycaste*, but to *Anguloa*.

Figure S1A: Maximum Likelihood tree

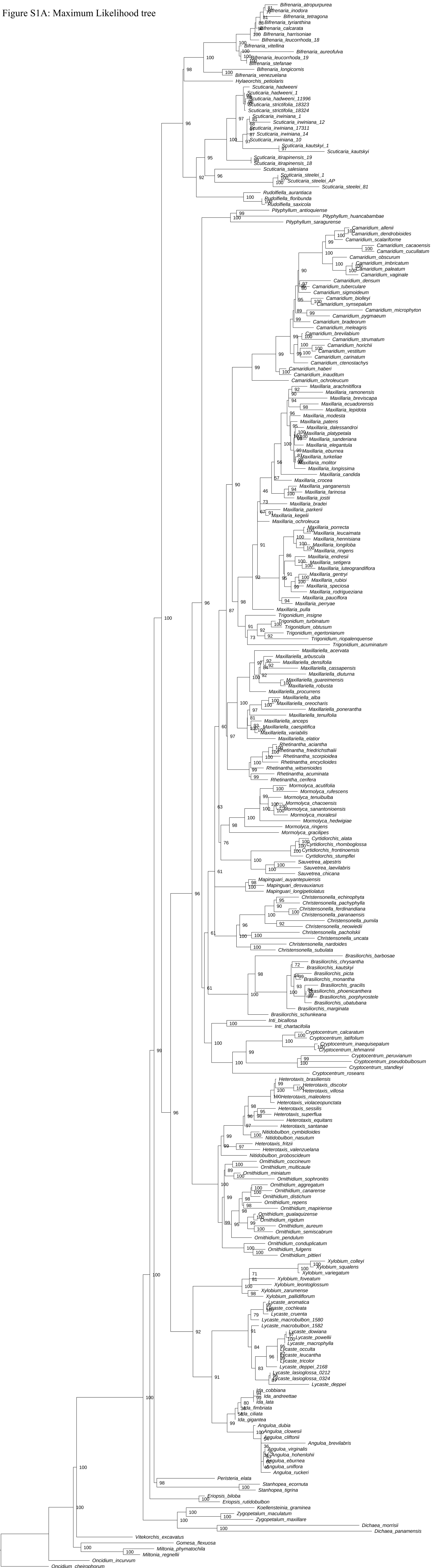


Figure S1B: Bayesian Inference tree

