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**Phylogenetic systematics of *Baccharis* (Asteraceae: Astereae),
a mega-diverse plant genus in the Americas**

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A comprehensive phylogenetic hypothesis for the predominantly Neotropical American genus *Baccharis* L. is necessary to test its monophyly, clarify the infrageneric relationships within the genus and shed light on its evolutionary and biogeographical history. Given its great morphological diversity and wide geographic distribution, phylogenetic studies based on molecular data to test the monophyly of the genus and investigate the relationships of its infrageneric groups are required, allowing the recognition of clades with evolutionary and biogeographical significance. Therefore, we provide the hitherto most comprehensive phylogenetic hypothesis for *Baccharis*. We performed Bayesian phylogenetic analyses based on four molecular regions from the nuclear and plastid genomes (ETS, ITS, *trnH-psbA*, *trnL-F*; in total 5041 aligned nucleotides) and including 248 species of *Baccharis*, from all previously segregated genera and all subgenera previously recognised, and 44 outgroups belonging to tribe Astereae, totalizing 1080 new sequences. Our results confirm subtribe Baccharidinae to be a monogeneric group, and support a wide circumscription of *Baccharis* as a monophyletic group, including the genera previously segregated from it. Seven main lineages are recognised and treated as subgenera, all of which re-circumscribed as monophyletic lineages. *Baccharis* subgen. *Baccharis*, *B.* subgen. *Molina* and *B.* subgen. *Tarchonanthoides* roughly match previous subgeneric concepts, while *B.* subgen. *Pteronioides* and *B.* subgen. *Stephananthus* are synonyms. Two earlier segregated genera and two formerly existing sections are better placed at subgeneric rank. Four new sections are recognized, and three new statuses at the rank of section will be proposed to accommodate taxa not corresponding to any previously described section, while 22 sections are reduced to synonymy. In total, we propose that *Baccharis* should comprise 433 species divided into 7 subgenera and 47 sections. This study represents a major advance in elucidating the relationships among species in one of the largest plant genera in the Neotropics, which was long considered a taxonomic nightmare. This work constitutes the basis for further exploration of the evolutionary processes that have allowed the genus to attain its wide geographic distribution, morphological variation and complex chemical contents.

Keywords: Baccharidinae, Classification, Compositae, Phylogeny, Taxonomy.