

# UNRAVELING THE TAXONOMIC COMPLEXITY OF *ERYNGIUM* L (APIACEAE)

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*Eryngium* is the largest and arguably the most taxonomically complex genus in the family Apiaceae. Infrageneric relationships within *Eryngium* were inferred using sequence data from the chloroplast DNA *trnQ-trnK* 5'-exon and nuclear ribosomal DNA ITS regions to test previous hypotheses of subgeneric relationships, explain distribution patterns, reconstruct ancestral morphological features, and elucidate the evolutionary processes that gave rise to this speciose genus. In total, 157 accessions representing 118 species of *Eryngium*, 15 species of *Sanicula* (including the genus *Hacquetia* that was recently reduced to synonymy) and the monotypic *Petagnaea* were analyzed using maximum parsimony and Bayesian methods. Both separate and simultaneous analyses of plastid and nuclear data sets were carried out because of the prevalence of polyploids and hybrids within the genus. *Eryngium* is confirmed as monophyletic and is divided into two redefined subgenera: *Eryngium* subgenus *Eryngium* and *E.* subgenus *Monocotyloidea*. The first subgenus includes all examined species from the Old World (Africa, Europe, and Asia), except *Eryngium tenue*, *E. viviparum*, *E. galioides*, and *E. corniculatum*. *Eryngium* subgenus *Monocotyloidea* includes all examined species from the New World (North, Central and South America, and Australia; herein called the “New World sensu stricto” clade) plus the aforementioned Old World species that fall at the base of this clade. Most sectional and subgeneric divisions previously erected on the basis of morphology are not monophyletic. Within the “New World sensu stricto” group, six clades are well supported in analyses of plastid and combined plastid and nuclear data sets; the relationships among these clades, however, are unresolved. These clades are designated as “Mexican”, “Eastern USA”, “South American”, “North American monocotyledonous”, “South American monocotyledonous”, and “Pacific”. Members of each clade share similar geographical distributions and/or morphological or ecological traits. Evidence from branch lengths and low sequence divergence estimates suggests a rapid radiation at the base of each of these lineages. Conflict between chloroplast and nuclear data sets is weak, but the disagreements found are suggestive that hybrid speciation in *Eryngium* might have been a cause, but also a consequence, of the different rapid radiations observed. Dispersal-vicariance analysis indicates that *Eryngium* and its two subgenera originated from western Mediterranean ancestors and that the present-day distribution of the genus is explained by several dispersal events, including one trans-Atlantic dispersal. In general, these dispersals coincide with the polytomies observed, suggesting that they played key roles in the diversification of the genus. The evolution of *Eryngium* combines a history of long distance dispersals, rapid radiations, and hybridization, culminating in the taxonomic complexity observed today in the genus.