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Phylogenomics

Jabaily, Rachel Schmidt [1], Gardner, Andy [2], Sessa, Emily Butler [3], Michener, Pryce [4], Johnson, Eden [5], Shepherd, Kelly A. [6].

Molecules, morphology, and monophyly: revising the enigmatic Australian clade *Goodenia* s.l. (Goodeniaceae) using comprehensive sampling and big data.

Previous phylogenetic efforts by our research team have identified the clade *Goodenia* s.l. as the most species rich and taxonomically challenging in the predominantly Australian plant family Goodeniaceae. The largest genus, *Goodenia*, is not supported by consistent morphological characters. Molecular phylogenetics resolve it into three major clades with multiple embedded smaller genera, which are individually variously supported by both molecular and morphological data. We have sought to identify and describe monophyletic clades as genera within *Goodenia* s.l. Our ultimate efforts at fully exploring the phylogeny of *Goodenia* s.l. have included nearly complete sampling of 220+ described species, as well as many undescribed, potentially new species. Sequences of loci *trnL-trnF*, *matK*, and nrITS for all included species were scaffolded onto a strongly supported phylogenetic backbone from next generation genome skimming sequencing of 28 target species. Draft plastome analysis found maximum phylogenetic support for all clades except several key nodes within *Goodenia* Clade C, the most morphologically variable and taxonomically complex clade of *Goodenia* s.l. Mitochondrial exomes yield very high phylogenetic support, and potential phylogenetic conflict between chloroplast, mitochondrial, and nuclear histories was fully explored particularly within Clade C. New genera to be described within *Goodenia* s.l. encompass considerable morphological variability, particularly with convergence in floral form, but now will have strong support from both morphological and molecular data.

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