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Phylogenomics

[Michener, Pryce](#) [1], [Sessa, Emily Butler](#) [2], [Bush, Caroline](#) [3], [Shepherd, Kelly A.](#) [4], [Jabaily, Rachel Schmidt](#) [5].

Grow a backbone: mitochondrial exome sequencing provides a surprisingly rich source of phylogenetically informative characters in the enigmatic Australian clade *Goodenia* s.l.

Relatively ancient, rapid radiations can lead to short and poorly resolved branches deep in a phylogeny. Resolving these relationships can be difficult with Sanger sequences, and even with some of the outputs of next generation sequencing. An under-resolved backbone uniting the clades of *Goodenia* sensu lato (Goodeniaceae) has hampered efforts to identify monophyletic groups ahead of a taxonomic revision of this largest clade (220+ species) in the primarily Australian family. *Goodenia* s.l. is composed of multiple major clades that have consistently received strong support, but the relationships between most of the major clades was underresolved in Sanger sequence based studies. Furthermore, analysis of two nuclear loci revealed relationships conflicting with chloroplast evidence at key nodes, suggesting potential ancient hybridization events. Genome skimming was performed for 28 taxa spanning Core Goodeniaceae, with sampling representing all of the major clades of *Goodenia* s.l. Draft plastomes primarily composed of genic regions generated for these taxa greatly increased confidence in almost all major backbone nodes, except within the most taxonomically complex *Goodenia* Clade C. In addition to the chloroplast and other high-copy nuclear genetic elements, portions of the mitochondrial genome are easy to isolate from genome-skimming data, and readily align to available references because of the highly conserved sequences. Despite relatively low rates of molecular evolution in plants (in contrast to animals), the mitochondrial exomes analyzed across *Goodenia* s.l. have yielded a rich source of phylogenetically informative characters, leading to a fully resolved phylogeny even within Clade C. Rigorous testing of potential incongruences between mitochondrial genes, as well as against chloroplast and nuclear gene histories, was also conducted. While sequencing of individual mitochondrial genes for plant systematics may not yield highly resolved phylogenies, the great amount of mitochondrial gene sequences included from next generation genome skimming is a rich, and underutilized, source of characters to build highly resolved phylogenies, particularly at deep nodes.

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