Abstract Detail

Systematics Section/ASPT

Gardner, Andrew [1], Sessa, Emily Butler [2], Michener, Pryce [1], Shepherd, Kelly [3], **Jabaily , Rachel Schmidt** [4].

Leveraging the power of next-generation sequencing to resolve the phylogenetic backbone of Core Goodeniaceae.

Uncertain backbone phylogenetic relationships between well-supported major clades are common problems in large-scale plant systematics studies. A nearly comprehensively sampled phylogeny of the Core Goodeniaceae constructed from cpDNA loci *trnL-F* and *matK* resolved the largest genus in the family, *Goodenia*, into three strongly supported clades, with well-supported additional embedded genera. Relationships between the major clades of *Goodenia* s.l. and within sister clade *Scaevola* s.l. were unclear, with low support and short branch lengths. The addition of multiple nuclear loci (nrITS, GAPDH) did not substantially increase phylogenetic support and also suggested alternative topologies. Generic-level taxonomic revisions are clearly necessary within Core Goodeniaceae, but such revisions require a fully-resolved backbone for these major clades. We have taken a whole plastome sequencing approach to reconstruct these relationships, using genome skimming, massively parallel sequencing of 24 taxa that are exemplars of well-supported clades from across Core Goodeniaceae. After performing reference-guided assembly of these plastomes, we explored the effects of excluding non-genic and regions of low coverage on subsequent alignments and tree reconstruction. The ultimate plastome phylogeny is generally congruent with the previous cpDNA topology, but with extensive support for relationships. We have enforced this topology as a constraint for the Sanger-sequenced full Core Goodeniaceae dataset to facilitate placement of all available taxa, and will discuss our resulting recommendations for taxonomic revisions in the group.

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Keywords:
Goodeniaceae
plastome
next-generation sequencing
taxonomy
Asterales.

Presentation Type: Oral Paper:Papers for Sections
Session: 45
Location: River Fork/Grove
Date: Wednesday, July 30th, 2014
Time: 4:15 PM
Number: 45011
Abstract ID:*687*
Candidate for Awards: None