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Title: Phylogenomic reconstruction of Australian carnivorous *Drosera* L. (Droseraceae) using a hybrid capture approach

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Abstract

Drosera L. are a cosmopolitan genus of carnivorous plants that are most diverse in the southern hemisphere. Approximately half of the global species diversity occurs in Australia, however the evolutionary relationships between Australian taxa remain poorly resolved.

Previous studies show conflict between phylogenetic tree topologies and traditional morphological classifications; however, these earlier studies were limited to two genetic marker loci (*rbcL* and 18S) and include comparatively few Australian *Drosera*. To fill this knowledge gap, we partnered with the Genomics for Australian Plants Initiative (GAP), aiming to sequence representatives of all *Drosera* clades occurring in Australia. Additional samples were included from species occurring outside of Australia, to place our results in a global context.

Using a targeted sequence capture approach with the OzBaits and Angiosperms353 bait sets, we recovered genomic data from hundreds of nuclear loci for 96 *Drosera* samples, representing approximately half of the *Drosera* species diversity in Australia. As higher classification concepts differ among authors, we aimed to include sequence data from the type species for each subgenus and section, where possible.

While the broad tree topology is congruent with other molecular studies, novel relationships are found between taxa within multiple clades. Particularly novel relationships are found among the tuberous *Drosera* (subg. *Ergaleium* sect. *Ergaleium*), including multiple suspected instances of convergent evolution. This robust, broad scale phylogenetic framework provides the most comprehensive view of the evolution of Australian *Drosera* to date and is the first of several ongoing molecular studies into the genus.

Key words

Australian flora, carnivorous plants, *Drosera*, Droseraceae, phylogenomics, systematics