Is Angiosperms353 an effective tool for population genomics?

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Targeted sequence capture is a powerful tool for obtaining genomic datasets useful for inferring phylogenetic relationships. The Angiosperms353 (A353) bait kit targets 353 loci shared by most angiosperms and has been successfully used in the Genomics for Australian Plants (GAP) Phylogenomics initiative to reconstruct large-scale relationships among Australian plants. While A353 is a useful tool at the generic and family level, can it be used to tease apart population differentiation for species delimitation and conservation diversity studies? Some have suggested that sequence capture approaches hold promise for population studies while also producing data that can be combined with existing datasets, a feature not usually shared by typical population genomic tools like RADseq. To assess the effectiveness of A353 in comparison to RADseq, we undertook sequence capture for a set of samples previously sequenced with RADseq in the GAP Conservation Genomics initiative. The samples come from species complexes with conservation taxa and unclear taxonomic boundaries, and the original aim was to delimit taxa to inform conservation decisions. This talk will discuss analyses and results from the *Isopogon* dataset, highlight challenges to using the data, and provide a perspective on whether A353 is an effective tool for population-scale analyses.

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