



***Acacia* phylogenomics: an initial assessment using the Angiosperms353 target capture bait set.**

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This study marks the initiation of a Genomics for Australian Plants (GAP)-supported, phylogenomic analysis of the genus *Acacia* – Australia’s largest genus of flowering plants - using the Angiosperms353 target capture bait set. While Sanger amplicon sequencing datasets have previously been compiled for approximately 50% of *Acacia* species, those datasets comprised fewer than 10 markers and lacked phylogenetic resolution in certain parts of the tree, demonstrating the need for a deeper phylogenomic-based sampling of the *Acacia* genome in order to resolve the phylogeny. In this talk, results are presented of an initial phylogenomic analysis of around 10% of *Acacia* species, sequenced for the Angiosperms353 target capture baits and representing all major evolutionary lineages of *Acacia* that had previously been discovered in molecular phylogenies and morphological classifications. Initial phylogenetic analyses, including appropriate outgroups and using several analytical approaches, have revealed clades that are generally congruent when compared to the topologies found in previous molecular phylogenetic studies, and several previously recognised taxa are shown to be monophyletic, although some novel clades and relationships are resolved in our analyses. Topological differences may be due to increased phylogenetic resolution of the markers or differences in the sampling for clades. Due to the level of support for relationships, in combination with the very high success rates for sequencing of silica-dried and older herbarium samples, the Angiosperms353 bait set shows great potential to use as the basis for a larger-scale study of *Acacia* species, with the ultimate aim of generating a new formal classification of the genus.

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