



## **Phylogenomics of a megadiverse Australian plant radiation (subtribe Hakeinae, family Proteaceae) reveals entangled gene trees and widespread discordance.**

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Resolving phylogenetic relationships in the presence of conflicting signal across genes is one of the major challenges of the phylogenomic era. Conflicting signal can emerge from biological processes, such as incomplete lineage sorting, or have technical origins, such as from misaligned sequences. As such, decisions made in the process of estimating species trees may result in alternative tree topologies and large variation in branch support values with important systematic consequences. Here we compare alternative alignment cleaning and filtering strategies, and phylogenetic estimation methods (coalescent versus concatenated) in 553 taxa in the plant family Proteaceae, to explore how these methodological choices affect the estimation of relationships in the subtribe Hakeinae. We found that, using concatenated approaches, branch support values were high and the two largest Hakeinae genera, *Hakea* and *Grevillea*, were reciprocally monophyletic. However, using coalescent approaches, we regularly found that *Hakea* was nested within *Grevillea*, branch support values were low, and gene discordance was rampant, regardless of alignment processing decisions. Our results suggest that widespread gene discordance may be the result of rapid radiation and incomplete lineage sorting which demonstrates the importance of assessing the drivers of discordance to understand phylogenetic relationships.

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