



Combinatorial speciation and ongoing gene flow *Eucalyptus*.

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Eucalypts are hard. It's part of why we love them, and a great stimulus for animated discussions or friendly disagreements. Some of us hope to find the secrets of eucalypts in their genomes, but it is a complex task. Like many speciose genera, incomplete lineage sorting and reticulate evolution are features of *Eucalyptus*. While eucalypts often have somewhat porous species boundaries and shared genetic variation, the evolutionary significance of ancient and ongoing gene flow is not well understood. I will describe our work disentangling the history of introgression in *Eucalyptus* section *Adnataria* at multiple scales using whole-genome short-read sequencing, in conjunction with new long-read-based reference genomes. We are able to identify signatures of ancient and recent introgression, and in some cases can tie them to chromosomal rearrangements. This work has implications for the management of threatened eucalypts, as well as our understanding of diversification and our approaches to classification in *Eucalyptus*.

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