



Revealing the extent of phylogenomic discordance in the *Eucalyptus* rapid radiation using BUSCO genes.

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The idea that discordance in phylogenomic datasets exists as actual biological signal is being increasingly accepted. Discordance is described as coming from a range of molecular processes such as introgression and incomplete lineage sorting (ILS). The evolutionary history of *Eucalyptus* is particularly rich in a fascinating array of these molecular processes: rapid radiations, hybridization events, ancient and recent introgression, ongoing speciation, ILS, a high recombination rate, and gene duplication events. Amidst this complex web of interconnected factors influencing phylogenetic relationships, we aimed to understand the extent of discordance and its origin by comparing two clades with very contrasting species diversity: the *Exsertaria* (~40 spp.) and *Adnataria* (~120 spp.) sections. We generated genomic sequences and curated a dataset of thousands of single-copy orthologous genes to perform phylogenomic analyses. Our results highlighted extreme levels of discordance due to ILS and introgression. These processes play a pivotal role in the evolutionary dynamics of Eucalyptus species. Understanding the origin and biological meaning of discordance is a necessary step forward in phylogenomics.

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