

Genetic Variation within Two Sympatric Spotted Gum Eucalypts Exceeds Between Taxa Variation

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Abstract

Population substructure and hybridization, among other factors, have the potential to cause erroneous associations in linkage disequilibrium (LD) mapping. Two closely related spotted gum eucalypts, *Corymbia variegata* and *C. henryi* (Myrtaceae) occur in sympatry in the east coast of Australia and potentially interbreed. They are morphologically similar but are distinguished as separate species based on capsule and foliage size. To determine whether they hybridize in nature and its implications for LD mapping, we investigated the level of molecular divergence between the two species at two sympatric locations separated by 300 kilometres. Very few individuals of intermediate morphology were identified, despite the two species occurring only metres apart. Analysis of genetic structure using 12 microsatellite loci showed that genetic differentiation between populations of the same species at different locations ($F_{ST} = 0.07$ for both species; $p = 0.0001$) was significantly higher than that observed between species at each location (mean $F_{ST} = 0.02$ and 0.04 for Cherry tree and Bunyaville respectively; $p = 0.0001$; all Mann-Whitney U-test $p \leq 0.01$). No species-specific alleles or significant allele frequency differences were detected within a site, suggesting recurrent local gene flow between the two species. The lack of significant allele frequency differences implies no population stratification along taxonomic lines. This suggested that there is little concern for cryptic hybridization when sampling from sites of sympatry for LD mapping.