

Construction of Microsatellite Linkage Maps for *Corymbia*

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Abstract

The genus *Corymbia* is closely related to the genus *Eucalyptus*, and like *Eucalyptus* contains tree species that are important for sub-tropical forestry. *Corymbia*'s close relationship with *Eucalyptus* suggests genetic studies in *Corymbia* should benefit from transfer of genetic information from its more intensively studied relatives. Here we report a genetic map for *Corymbia* spp. based on microsatellite markers identified *de novo* in *Corymbia* sp or transferred from *Eucalyptus*. A framework consensus map was generated from an outbred F2 population (n = 90) created by crossing two unrelated *Corymbia torelliana* x *C. citriodora* subsp. *variegata* F1 trees. The map had a total length of 367 cM (Kosambi) and was composed of 46 microsatellite markers distributed across 13 linkage groups (LOD 3). A high proportion of *Eucalyptus* microsatellites (90%) transferred to *Corymbia*. Comparative analysis between the *Corymbia* map and a published *Eucalyptus* map identified eight homeologous linkage groups in *Corymbia* with 13 markers mapping on one or both maps. Further comparative analysis was limited by low power to detect linkage due to low genome coverage in *Corymbia*, however, there was no convincing evidence for chromosomal structural differences because instances of non-synteny were associated with large distances on the *Eucalyptus* map. Segregation distortion was primarily restricted to a single linkage group and due to a deficit of hybrid genotypes, suggesting that hybrid inviability was one factor shaping the genetic composition of the F2 population in this inter-subgeneric hybrid. The conservation of microsatellite loci and synteny between *Corymbia* and *Eucalyptus* suggests there will be substantial value in exchanging information between the two groups.

Key words: *Corymbia torelliana*; *Corymbia citriodora* subsp. *variegata*; genetic map; hybrid inviability; genetic marker; tree improvement; marker-aided selection.