

# GENETIC DIVERSITY AND CROSS-COMPATIBILITY OF CADAGI (*Corymbia torelliana*): IMPLICATIONS FOR HYBRID BREEDING

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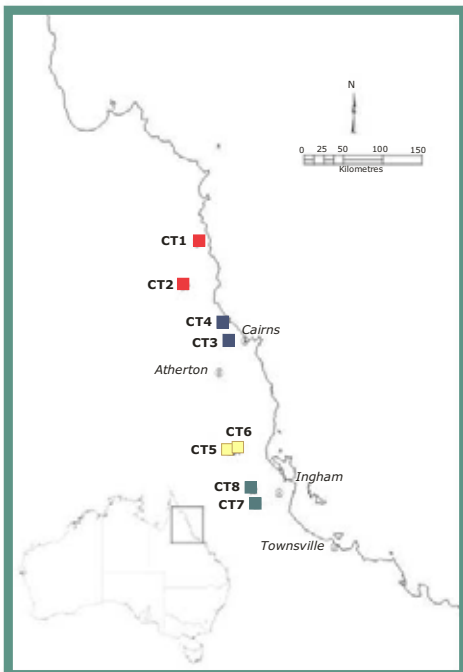
## BACKGROUND

Cadagi's (*Corymbia torelliana*) natural distribution is restricted to the rainforest margins in North Queensland between Ingham and Cooktown, however, it has been widely planted as an ornamental and in amenity plantings, particularly in southeast Queensland. Hybrids with spotted gum taxa show great potential for hardwood plantation forestry in northern Australia, particularly in marginal rainfall areas.

## GENETIC DIVERSITY

To assess the level of genetic diversity within and between the populations, leaf material from sixteen individuals from each of eight populations of *C. torelliana* were sampled from across the species' geographic range (Figure 1). In addition, 37 *C. torelliana* individuals from amenity plantings around southeast Queensland, that have been used in controlled pollinations with spotted gum taxa, were sampled in order to identify the most likely origin of this material and the level of genetic diversity captured in the breeding program.

Genomic DNA was extracted from all individuals using Qiagen's Plant DNeasy Mini Kit. Six microsatellite markers developed in *C. citriodora* subsp. *variegata* (Jones *et al.* 2001) and a chloroplast DNA locus (JL<sub>A</sub><sup>+</sup>; Freeman *et al.* 2001) were utilised in order to understand both contemporary and historical relationships between populations of *C. torelliana*.

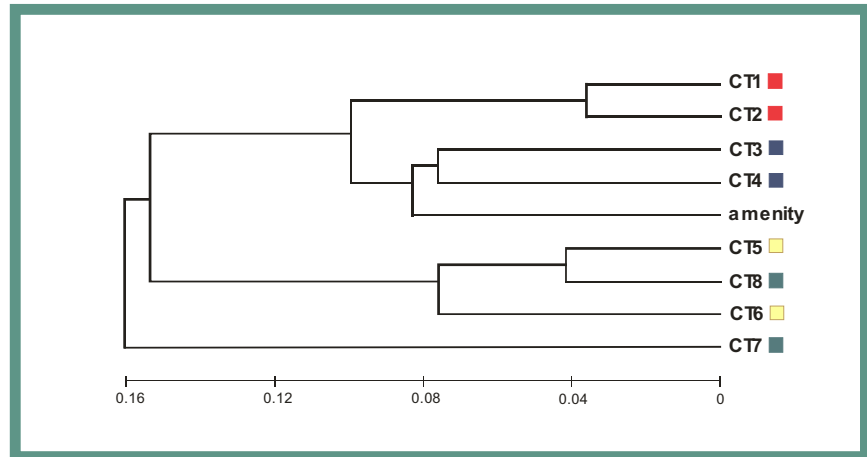


**Figure 1:** Location of sampled *C. torelliana* populations

The microsatellite data revealed a high level of genetic diversity within the natural *C. torelliana* populations, with overall expected and observed heterozygosity being 0.808 and 0.766 respectively. The amenity trees also had high levels of heterozygosity ( $H_E=0.832$  and  $H_O=0.788$ ). Inbreeding levels (overall  $F=0.058$ ) were not significant in *C. torelliana* except for the two northern populations (CT1&2).

Although only 5.5% of total genetic variation found using microsatellites was between the natural *C. torelliana* populations, it was geographically structured (Figure 2). A similar pattern of variation was also found using chloroplast DNA (data not shown). The amenity trees were more closely related to *C. torelliana* populations, CT3 & 4, however, individual assignment tests are required to confirm this.

**Figure 2:** UPGMA phenogram of Nei's 1978 genetic distance between *C. torelliana* populations and amenity trees



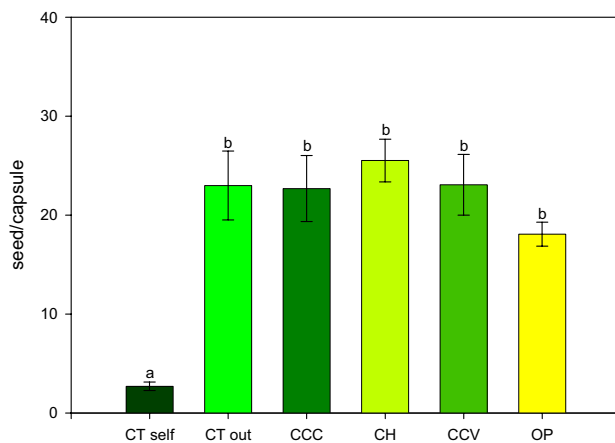
### CROSS-COMPATIBILITY

To examine the cross-compatibility of *C. torelliana* (CT) with spotted gum taxa, controlled pollinations were undertaken using a replicated block design over two flowering seasons. In 2002, eight CT amenity trees were chosen and five pollen treatments (CT self, CT outcross, CCC, CCV, CH) were applied in three replicates of 50 flowers to each tree. Open-pollinated capsules were also collected from the CT trees in the 2002 season. In 2003, nine CT amenity trees were pollinated with three replicates of 35 flowers using five pollen treatments (CT self, CT outcross, CCC, CCV and CX). For each pollen treatment and flowering season, capsule retention, seed weight, total seed yield and seed/capsules were calculated (eg. Figure 3). Preliminary results suggest that pollinations with the spotted gum taxa examined were comparable to those pollinated with outcross CT pollen. Seed from four CT trees per season was tested for germination and the height of seedlings measured prior to planting.

### IMPLICATIONS FOR HYBRID BREEDING

The majority of the genetic variation in *C. torelliana* has been captured in the amenity trees used in creating hybrids with spotted gums. The origin of the amenity trees is most likely to be the Kuranda region. Broadening the genetic base of the breeding population should be targeted towards collection from populations at the southern extremity of *C. torelliana*'s natural range.

Further analysis will provide greater insight into the attrition rates inherent in creating F<sub>1</sub> hybrids. The controlled pollinations undertaken will also allow selection of parents with good breeding values and provide outstanding families and individuals to target for deployment.



**Figure 3:** Average seed produced per capsule in 2002 crosses on CT trees (n=8) with different pollen parents.

### REFERENCES

- Jones *et al.* (2001) *Molecular Ecology Notes* 1: 276-278.
- Freeman *et al.* (2001) *Australian Journal of Botany* 49: 585-596.

### ACKNOWLEDGEMENTS

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