

Supplementary Material 2:

Additional results

Associated paper: Assessing a Bayesian approach for detecting exotic hybrids between
plantation and native eucalypts

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Table 1. Genetic diversity parameters for six *Eucalyptus* species genotyped at 10 microsatellite loci. Parameters: n = number of individuals genotyped; N_a = average number of alleles per locus; P_a = total number of private alleles; H_e = expected heterozygosity; H_o = observed heterozygosity.

Species	n	N_a	P_a	H_e	H_o
<i>E. camaldulensis</i>	97	25.2	28	0.89	0.78
<i>E. cypellocarpa</i>	97	22.8	13	0.91	0.82
<i>E. globulus</i>	87	19.3	6	0.87	0.78
<i>E. nitens</i>	88	17.2	4	0.83	0.68
<i>E. ovata</i>	100	20.9	5	0.82	0.68
<i>E. viminalis</i>	87	23.2	8	0.89	0.82
Hybrids combined	50	18.3	3	- ^a	0.91
Total	606	21.0	66	0.87	0.78

^a it is inappropriate to calculate H_e across multiple species

Table 2. Comparison of the accuracy of two- and six-way Bayesian cluster analysis for indentifying hybrids. Comparisons are the average across 50 simulated parental and 50 simulated F₁ generations for each combination between *Eucalyptus globulus* and five other species.

Combination	Accuracy (%)	
	Two-way analysis	Six-way analysis
<i>E. camaldulensis</i> x <i>globulus</i>	99	85
<i>E. cypellocarpa</i> x <i>globulus</i>	84	65
<i>E. nitens</i> x <i>globulus</i>	99	92
<i>E. ovata</i> x <i>globulus</i>	97	83
<i>E. viminalis</i> x <i>globulus</i>	94	69

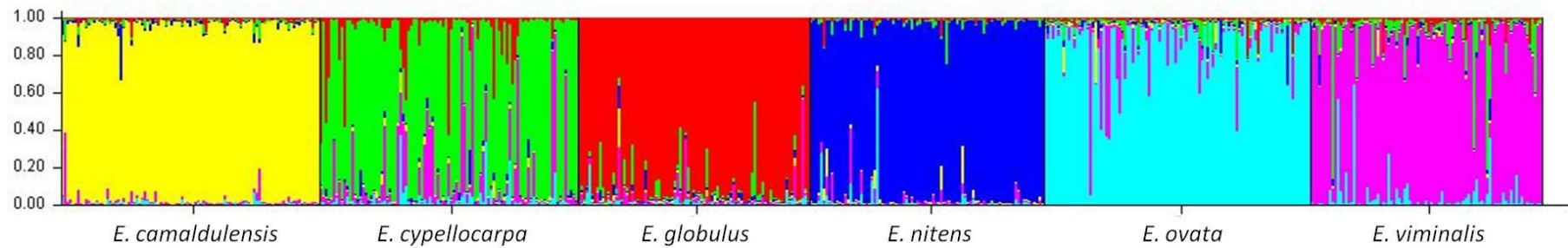


Figure 1. Proportion of genotype membership of 556 individuals from six eucalyptus species based on Bayesian cluster analysis (in STRUCTURE) at $K = 6$, using no *a priori* species information. All individuals were genotyped at 10 microsatellite loci. Each individual is represented by a single vertical line that is partitioned based on its genotype affinities to one of six genetic clusters (represented by the six colours), and samples are ordered based on their morphological species classification. The genotype affinities of the samples clearly correspond to the species classifications indicating that STRUCTURE differentiates the six species at $K = 6$.