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Supplementary Material

Genetic diversity and differentiation in south-western Australian bloodwoods (*Corymbia* section *Calophyllae*, Myrtaceae) with different ranges and abundance

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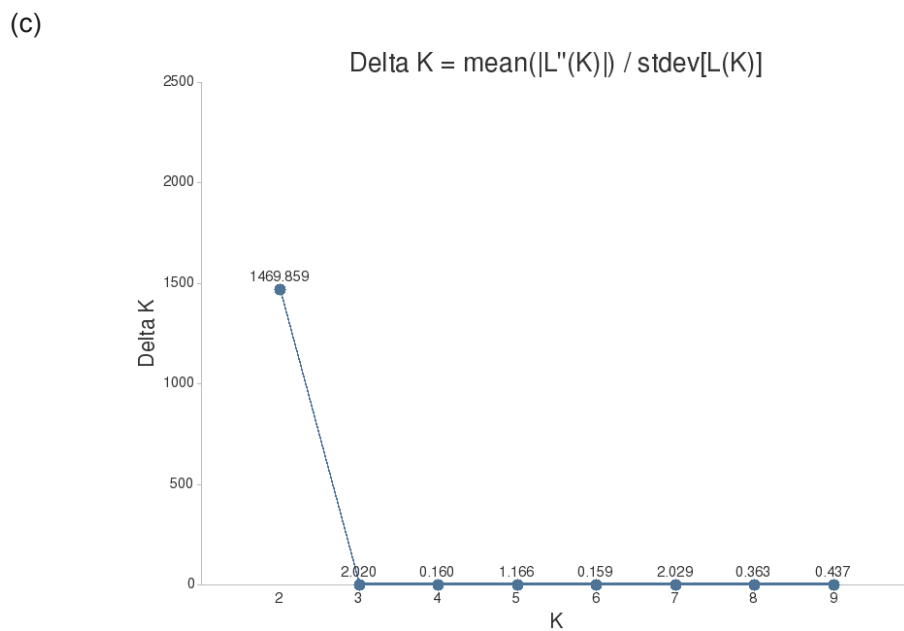
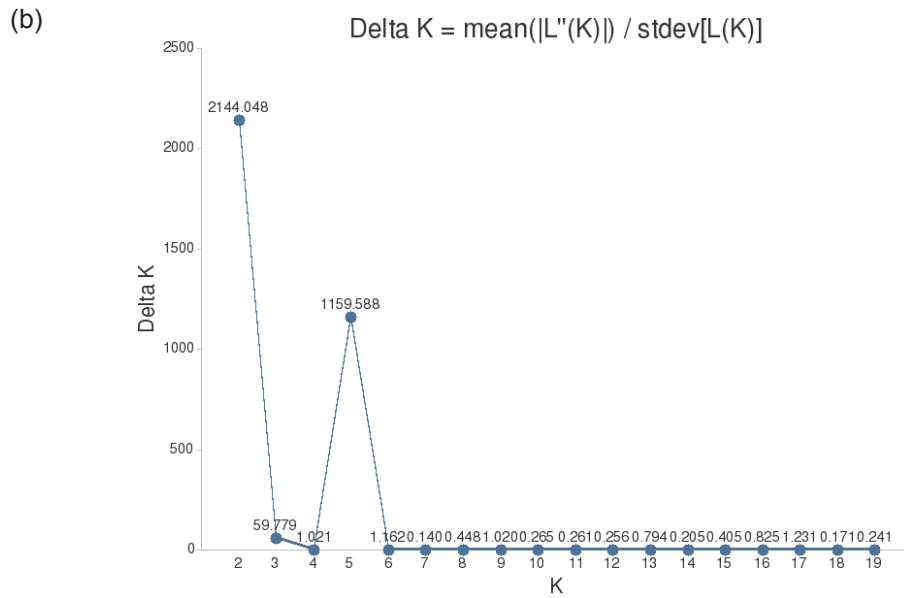
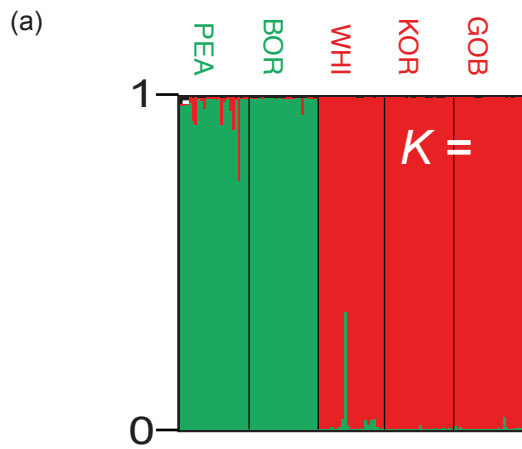


Fig. S1. (a) The genetic structure at $K = 2$ of sampled populations of *Corymbia haematoxylon* and *Corymbia ficifolia* in southwestern Australia inferred using Bayesian assignment of individual nuclear microsatellite genotypes and STRUCTURE (ver. 2.3.4, see <https://web.stanford.edu/group/pritchardlab/structure.html>). (b) and (c) ΔK values used to identify optimum K made using CLUMPAK (see <http://clumpak.tau.ac.il/>; Kopelman *et al.* 2015) for Bayesian inferences of the number of nuclear microsatellite genetic marker clusters made using STRUCTURE (ver. 2.3.4; Pritchard *et al.* 2000) for (b) *Corymbia haematoxylon*, *Corymbia ficifolia* and *Corymbia calophylla*, and (c) *Corymbia ficifolia* and *Corymbia haematoxylon*.

References

- Kopelman NM, Mayzel J, Jakobsson M, Rosenberg NA, Mayrose I (2015) Clumpak: a program for identifying clustering modes and packaging population structure inferences across K. *Molecular Ecology Resources* **15**, 1179–1191. [doi:10.1111/1755-0998.12387](https://doi.org/10.1111/1755-0998.12387)
- Pritchard JK, Stephens M, Donnelly P (2000) Inference of population structure using multilocus genotype data. *Genetics* **155**, 945–959. [doi:10.1093/genetics/155.2.945](https://doi.org/10.1093/genetics/155.2.945)