Australian Systematic Botany, 2016, **29**, 157–166
doi:10.1071/SB16023_AC

Supplementary material

Evolution of Australian *Cryptocarya* (Lauraceae) based on nuclear and plastid phylogenetic trees: evidence of recent landscape-level disjunctions

Marlien van der Merwe[A,D], *Darren M. Crayn*[B], *Andrew J. Ford*[C], *Peter H. Weston*[A] *and Maurizio Rossetto*[A]

[A]National Herbarium of New South Wales, The Royal Botanic Garden Sydney, Mrs Macquaries Road, Sydney, NSW 2000, Australia.

[B]Australian Tropical Herbarium, James Cook University, McGregor Road, Smithfield, Qld 4878, Australia.

[C]CSIRO Land and Water, Tropical Forest Research Centre, Atherton, Qld 4883, Australia.

[D]Corresponding author. Email: marlien.vandermerwe@rbgsyd.nsw.gov.au

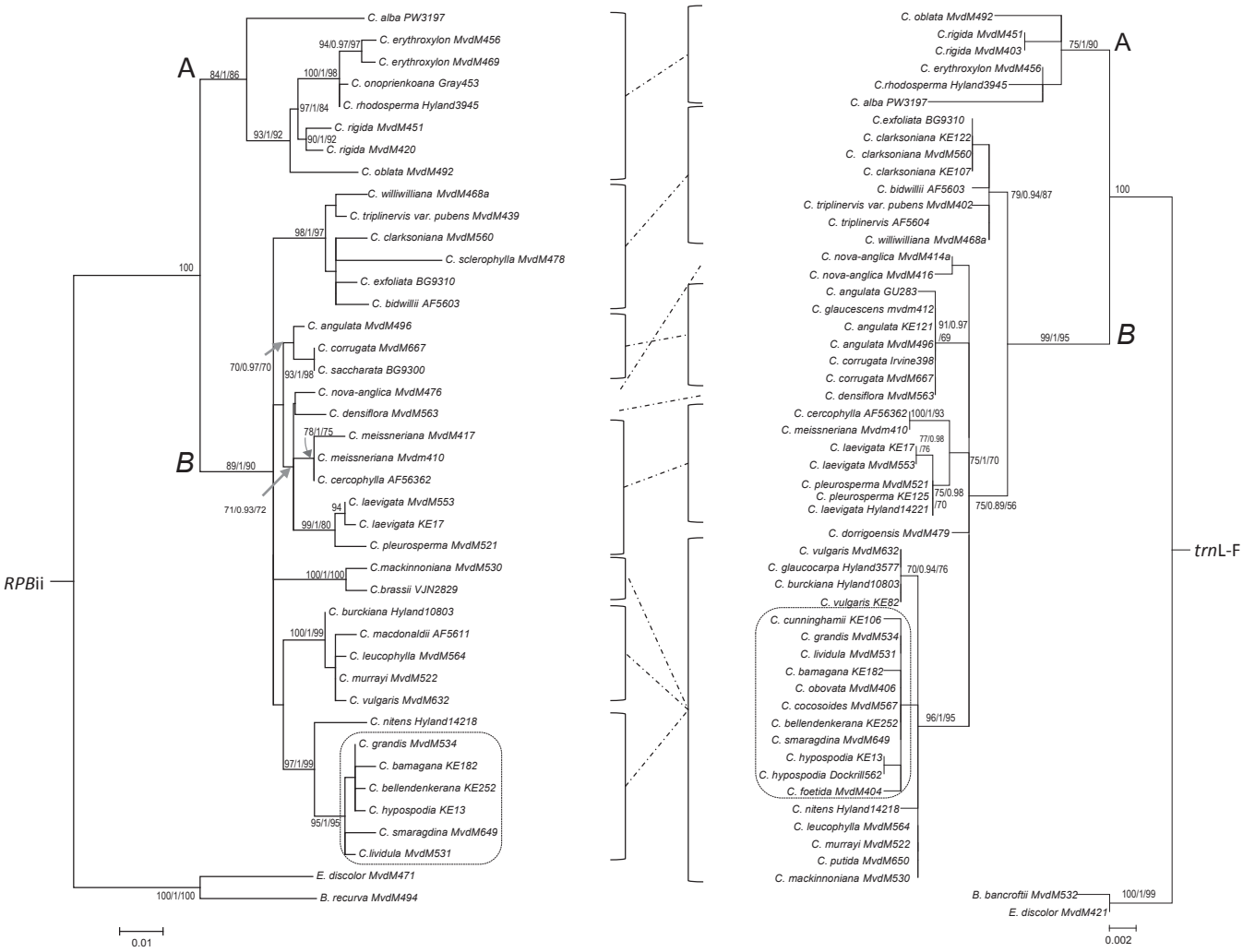

Fig. S1. The nuclear *RPB2* (left) and chloroplast *trn*L–*trn*F (right) gene trees constructed using RAXML. Support values for nodes that received significant support are given in the following order: maximum likelihood (ML) bootstrap, Bayesian posterior probability (BP) and maximum parsimony (MP) bootstrap. Clade names refer to the text. Species with ruminate cotyledons are surrounded by a stippled rectangle. Species names are followed by the details of the collector.

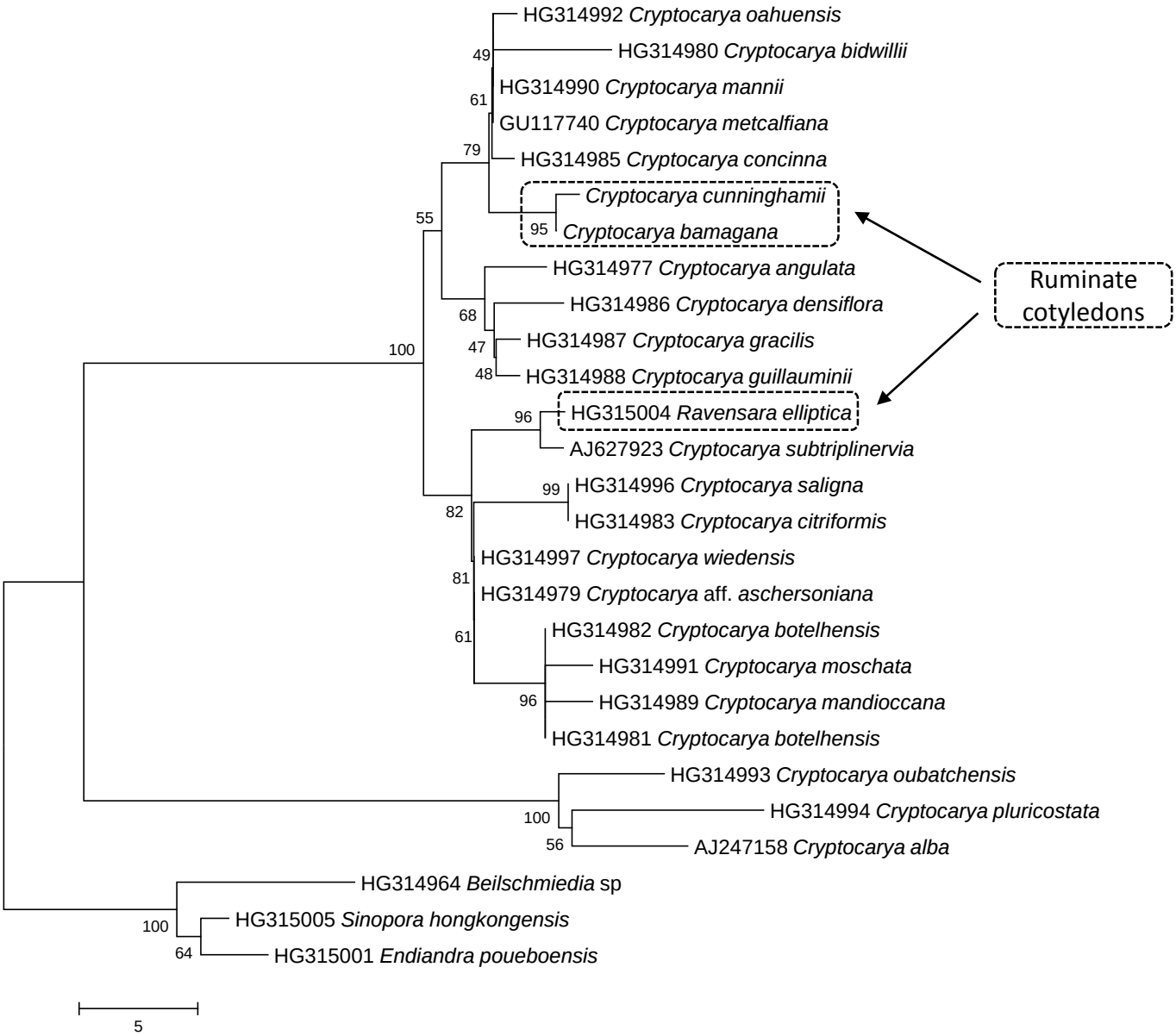

Fig. S2. A phylogenetic tree constructed using a *mat*K sequence alignment of 1618 bp implementing the RAXML method. GenBank accession numbers of sequences obtained from GenBank are provided. The sequence data for the two Australian species with ruminate cotyledons was provided by Mark Harrington.