



Appendix S11: Biogeographic ancestral range estimation using BioGeoBEARS including range probability scores

Ancestral range estimation for the Cryptocarya group using BioGeoBEARS based on the DEC+TS+*j* model, with ancestral ranges, and [dispersal rate scalars](#) between regions for each time slice (TS1, TS2, TS3). Roman numerals on the nodes represent crown nodes of important colonisation events, discussed in the text and shown in [Table 4](#). Pies on the nodes and branches show the probability of each range being the 'true' ancestral range. These ranges can comprise one to three combined regions, as indicated by single letters or a combination of these (e.g., FG = Northern Australia and Malesia). Regions are abbreviated as follows: A = Andean-Argentinian, B = Neotropical, C = Southern Africa, D = African, E = Madagascan, F = Northern Australia, G = Malesian, H = Indian-Indochinese, I = Neozealandic-Patagonian and J = Eurasiatic (see [Carta et al., 2022](#)). Three modes of range inheritance (range expansion, local extinction, and narrow vicariance) are indicated as symbols on branches in the phylogeny.