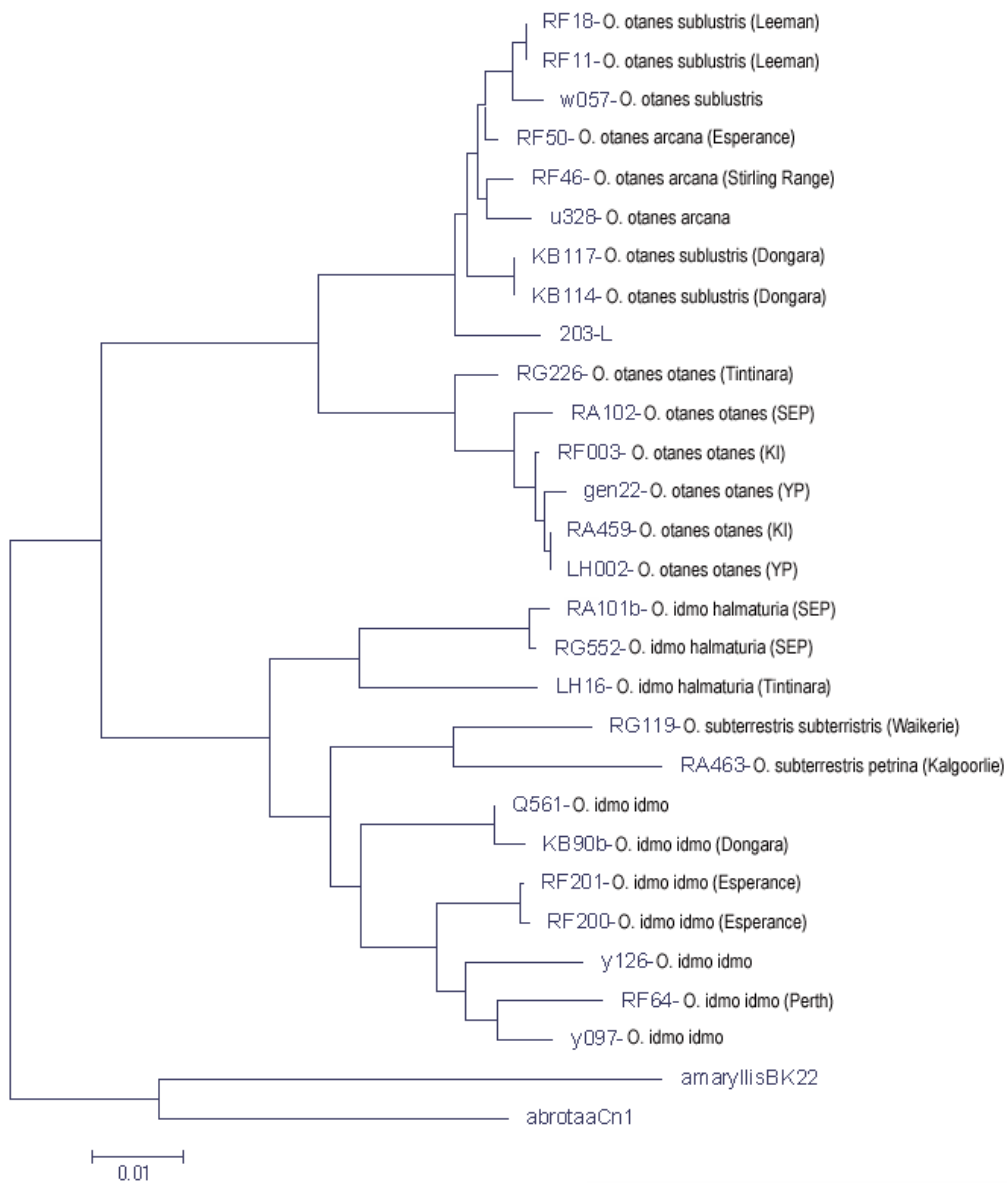


EVOLUTION IN THE PACIFIC

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East-west relationships in Australia revisited: genealogical concordance among three threatened *Ogyris* butterflies restricted to southeastern and southwestern Australia

The division of Australia's temperate (Bassian) flora and fauna into southeastern and southwestern regions is a conspicuous biogeographic feature of the continent. The arid Nullabor plateau has separated these sclerophyll forest biomes for millions of years. Consequently, east-west sister taxon relationships exist in many animal groups that are restricted to sclerophyll communities across the south of the continent. The butterfly genus *Ogyris* (Lycaenidae) includes three closely related species (*idmo*, *otanes* and *subterrestris*), all with tenuous conservation status, and each containing co-distributed subspecies to the east and west of the Nullabor. We use mitochondrial DNA genealogies and coalescent simulations to: a) determine whether these taxa were divided by a contemporaneous event; b) estimate the ancestral population size for each species prior to the split; and c) assess the likelihood of subsequent gene flow during interglacial periods between east and west isolates for each species. We found that the magnitude of divergence (3-4%) was similar for each pair of subspecies; that ancestral population size was probably much greater than it is today for *Ogyris idmo* which has a highly specialised myrmecophilous life history; and that there is no evidence for current or recent gene flow across the Nullabor. We conclude that *Ogyris* taxa restricted to southern temperate biomes are probably relicts from a pre-pleistocene era, when sclerophyll communities were widespread across southern Australia. Our dating of the east-west split for *Ogyris* butterflies (3-4 million years) is compared with available data for mammals and reptiles that share a similarly disjunct distribution. We review the long-standing question of the origin of east-west relationships in Australia's temperate flora and fauna.



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***Ogyris idmo* Species Subgroup.** Single most-parsimonious phylogenetic tree using mitochondrial DNA (COI & cyt B). *O. idmo* subspecies *idmo* and *halmaturia* are paraphyletic.