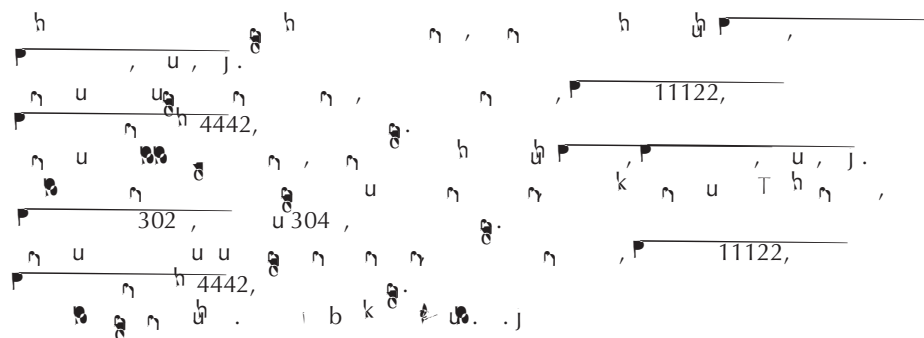


Placing the Fijian Honeyeaters within the meliphagid radiation: implications for origins and conservation

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Abstract. Understanding the evolutionary relationships of threatened species provides an important framework for making decisions about their conservation. However, unrecognised problems with the underlying phylogenetic analyses may bias the decision-making process. Recent phylogenetic studies have improved our understanding of Meliphagidae, but also indicate discordance between molecular datasets. Here, we examine the causes of this discordance using maximum likelihood tree-building and network analyses of identically sampled datasets for four genetic loci. Our results suggest that while we can be reasonably confident of relationships within species groups, discordance within and between molecular datasets tends to obscure relationships towards the base of the meliphagid tree. This ongoing uncertainty likely reflects differences in the sampling of markers and taxa between previously published analyses. To avoid the problems of conflicting data we used divergence time analyses of only the most densely sampled marker, NADH-ubiquinone oxidoreductase chain 2, to investigate the age and origins of the Fijian Meliphagidae. Our analyses suggest two temporally distinct colonisations of the Fijian archipelago. The large-bodied honeyeaters arrived \sim 15.6 million years ago, subsequently diversifying and spreading to Tonga and Samoa. In contrast, Myzomela appears to have arrived within the last 5.0 million years. The phylogenetic results therefore imply that conserving the evolutionary diversity of Meliphagidae in Polynesia requires that effort be spread across both the currently recognised taxa and geographical range.

Additional keywords: Austro-Pacific, conflicting data, divergence time analysis, Meliphagidae, phylogenetic analysis.

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Introduction

The Fijian archipelago is isolated in the Pacific Ocean. Its island neighbours include Tonga and Samoa to the east, but the closest continental landmass is Australia some 3000 km to the west. Fiji comprises over 330 islands ranging from four large volcanic islands with rugged relief (e.g. Viti Levu, Vanua Levu, Taveuni and Kadavu) to smaller low-lying limestone islands (e.g. Kabara, Ogea, Vatulee and Vulaga). The archipelago, which is part of the Polynesia–Micronesia biodiversity hotspot, has a

and New Guinea. Seventeen species are recorded from the islands of Micronesia and Polynesia (Driskell and Christidis 2004; Gardner et al. 2010; Andersen et al. 2014). In Fiji, the family is represented by five phenotypically and ecologically distinctive species (Watling 2001). Three are large-bodied species that primarily occur in forested areas. *Foulehaio carunculatus* and *Gymnozyma viridis* have broadly overlapping geographical distributions, both occurring on the islands of Viti Levu, Vanua Levu, and Taveuni, with *F. carunculatus* also reaching the Lau Archipelago, Tonga and Samoa. The third species, *Xanthotis provocator*, is restricted to the island of Kadavu. Two smaller *Myzomela* species occupy a range of habitats in the Fijian lowlands. *Myzomela jugularis* is relatively common in Fiji whereas *M. chermesina* is restricted to the northern islands of Rotuma.

Over the last 15 years phylogenetic analyses of nuclear and mitochondrial DNA sequences have greatly improved our understanding of the evolutionary relationships and taxonomy of Meliphagidae (e.g. Cracraft and Feinstein 2000; Barker et al. 2004; Driskell and Christidis 2004; Norman et al. 2007

(Table 1

bootstrapping (i.e. <50% BS). The Foulehaio–Xanthotis and Myzomela–*C. niger* lineages also retained the same wider relationships, although both these relationships receive <50% BS (Table 1). The Foulehaio–Xanthotis and Myzomela–*C. niger* clades were also recovered in the 12S and Fib5 trees (Fig. 1e

and 1d, respectively). However, their wider relationships differed from those based on mitochondrial genes. For example, in the optimal Fib5 tree the pairing of Myzomela–*C. niger* was nested within a clade containing *Glycichaera*, *Phylidornis melanops* and *Ptiloprora*; this relationship was strongly supported (Table 1).

NeighbourNet analyses of individual matrices suggested that limited bootstrap support in phyML analyses were, at least in part, due to internal conflict. That is, different positions within the sequences supported contrasting relationships. For ND2 and cytB this conflict was largely restricted to internal relationships; networks were more box-like for these, with distal relationships being more tree-like (not shown). The greater extent of box-like

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