



## Evolutionary and ecological forces influencing population diversification in Bornean montane passerines



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### ABSTRACT

The mountains of Borneo are well known for their high endemism and historical role in preserving Southeast Asian rainforest biodiversity, but the diversification of populations inhabiting these mountains is poorly studied. Here we examine the genetic structure of 12 Bornean montane passerines by comparing complete mtDNA ND2 gene sequences of populations spanning the island. Maximum likelihood and Bayesian phylogenetic trees and haplotype networks are examined for common patterns that might signal important historical events or boundaries to dispersal. Morphological and ecological characteristics of each species are also examined using phylogenetic generalized least-squares (PGLS) for correlation with population structure. Populations in only four of the 12 species are subdivided into distinct clades or haplotype groups. Although this subdivision occurred at about the same time in each species (ca. 0.6–0.7 Ma), the spatial positioning of the genetic break differs among the species. In two species, northeastern populations are genetically divergent from populations elsewhere on the island. In the other two species, populations in the main Bornean mountain chain, including the northeast, are distinct from those on two isolated peaks in northwestern Borneo. We suggest different historical forces played a role in shaping these two distributions, despite commonality in timing. PGLS analysis showed that only a single characteristic—hand-wing index—is correlated with population structure. Birds with longer wings, and hence potentially more dispersal power, have less population structure. To understand historical forces influencing montane population structure on Borneo, future studies must compare populations across the entirety of Sundaland.

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### 1. Introduction

In contrast to the Neotropics and Africa, where comparative phylogeographic investigations of Pleistocene refuges, centers-of-endemism, and dispersal patterns of animals (Cracraft and Prum, 1988; Fjeldså and Bowie, 2008; Haffer, 1987) are common (e.g., Burney and Brumfield, 2009; Ditchfield, 2000; Huhndorf et al., 2007; Smith et al., 2014), such studies in Sundaland—the biogeographic region of Southeast Asia encompassing the Sunda continental shelf and its current land (Malay Peninsula, Sumatra, Java, Borneo, Palawan and small islands)—are rare. Only a handful exist

(Demos et al., 2016; Gorog et al., 2004; Lim et al., 2010; Lim and Sheldon, 2011). This is surprising, not only because studies in Sundaland helped inspire the science of Biogeography (Wallace, 1860), but because the region's potential for comparative phylogeographic study of Pleistocene vicariance, habitat refuges, colonization, community relaxation, and other modes of diversification and extinction is substantial and has been recognized for years (Brandon-Jones, 1996; Cracraft, 1988; Diamond et al., 1987; Heaney, 1991).

Among biogeographic features in Sundaland that merit greater study, the mountains of Borneo are paramount because of the important role they played in preserving and fomenting Southeast Asia's rainforest diversity (de Bruyn et al., 2014; Merckx et al., 2015; Sheldon et al., 2015). Borneo's main mountain chain runs diagonally from Sabah in the northeast, along the Sarawak-

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