

Quaternary land bridges have not been universal conduits of gene flow

ABSTRACT

Quaternary climate oscillations are a well-known driver of animal diversification, but their effects are most well studied in areas where glaciations lead to habitat fragmentation. In large areas of the planet, however, glaciations have had the opposite effect, but here their impacts are much less well understood. This is especially true in Southeast Asia, where cyclical changes in land distribution have generated enormous land expansions during glacial periods. In this study, we selected a panel of five songbird species complexes covering a range of ecological specificities to investigate the effects Quaternary land bridges have had on the connectivity of Southeast Asian forest biota. Specifically, we combined morphological and bioacoustic analysis with an arsenal of population genomic and modelling approaches applied to thousands of genome-wide DNA markers across a total of more than 100 individuals. Our analyses show that species dependent on forest understorey exhibit deep differentiation between Borneo and western Sundaland, with no evidence of gene flow during the land bridges accompanying the last 1–2 ice ages. In contrast, dispersive canopy species and habitat generalists have experienced more recent gene flow. Our results argue that there remains much cryptic species-level diversity to be discovered in Southeast Asia even in well-known animal groups such as birds, especially in nondispersive forest understorey inhabitants. We also demonstrate that Quaternary land bridges have not been equally suitable conduits of gene flow for all species complexes and that life history is a major factor in predicting relative population divergence time across Quaternary climate fluctuations.