

Gene flow between island populations of the malaria mosquito, *Anopheles hinesorum*, may have contributed to the spread of divergent host preference phenotypes

Luke Ambrose¹, Daniel Ortiz-Barrientos², Robert Cooper³, Neil Lobo⁴, Thomas Burkot⁵, Tanya Russell⁵, and Nigel Beebe¹

¹University of Queensland

²The University of Queensland

³Australian Defence force

⁴University of Notre Dame

⁵James Cook University Division of Tropical Health and Medicine

December 29, 2020

Abstract

Anopheles hinesorum is a mosquito species with variable host preference. Throughout New Guinea and northern Australia, *An. hinesorum* feeds on humans (it is opportunistically anthropophagic) while in the southwest Pacific's Solomon Archipelago, the species is abundant but has rarely been found biting humans (it is exclusively zoophagic in most populations). There are at least two divergent zoophagic (non-human biting) mitochondrial lineages of *An. hinesorum* in the Solomon Archipelago. Since zoophagy is a derived (non-ancestral) trait in this species, this leads to the question: has zoophagy evolved independently in these divergent lineages? Or conversely: has nuclear gene flow or connectivity resulted in the transfer of zoophagy? Although we cannot conclusively answer this, we find close nuclear relationships between Solomon Archipelago populations indicating that recent nuclear gene flow has occurred between zoophagic populations from the divergent mitochondrial lineages. Recent work on isolated islands of the Western Province (Solomon Archipelago) has also revealed an anomalous, anthropophagic island population of *An. hinesorum*. We find a common shared mitochondrial haplotype between this Solomon Island population and another anthropophagic population from New Guinea. This finding suggests that there has been recent migration from New Guinea into the only known anthropophagic population from the Solomon Islands. Although currently localized to a few islands in the Western Province of the Solomon Archipelago, if anthropophagy presents a selective advantage, we may see *An. hinesorum* emerge as a new malaria vector in a region that is now working on malaria elimination.

Hosted file

ME_FINAL.pdf available at <https://authorea.com/users/385895/articles/501137-gene-flow-between-island-populations-of-the-malaria-mosquito-anopheles-hinesorum-may-have-contributed-to-the-spread-of-divergent-host-preference-phenotypes>