

# Population structure of an island malaria vector

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We assessed the impact of islands on the population structure of *Anopheles flavirostris*, the primary malaria vector in the Philippines. Islands are possible sites for malaria eradication and for control strategies based on transgenic insects. A phylogenetic analysis of 16 cytochrome oxidase subunit 1 (COI) haplotypes revealed a deep structure of three clades; one basal clade containing genetically disparate haplotypes from Mindanao, and two derived clades, one largely confined to the largest island, Luzon, and a second clade widespread except for Luzon. For the Luzon clade, nested clade analysis revealed an isolation-by-distance effect, and a mismatch distribution analysis diagnosed a recent demographic expansion ( $SDD = 0.0093$ ,  $P = 0.075$ ), which mirrors demographic attributes found in mainland primary malaria vectors and could inflate estimates of gene flow from  $F_{ST}$ . For the widespread clade, evidence of range expansion and past fragmentation and/or long distance colonization from the Visayas or Mindanao to Palawan is suggested. A south to north range expansion of *An. flavirostris* is suggested; estimates of coalescence for the Luzon clade was 214,000 ya, the second clade was 694,000 ya, and for Philippine *An. flavirostris* was 4,856,000 ya, i.e. dating from the Pliocene geological uplift of the archipelago. Present day rather than Pleistocene island association and some, but not all, sea barriers appeared to be important for *An. flavirostris* structure. Our results suggest that both mainland and endemic island malaria vector species need to be considered before any generalizations are made about the population structure of primary and secondary vectors.