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Population structure comparisons of three southwest Pacific malaria vectors

There are five major vector species in the southwest Pacific region that come from the dozen or so cryptic species in the *Anopheles punctulatus* group. Population genetic studies into three of these vector species using both mitochondrial and ribosomal DNA markers have shown some interesting and contrasting results. *Anopheles koliensis* from Papua New Guinea shows evidence of a single population expansion throughout its distribution, as well as distinct ribosomal DNA genotypes of no apparent geographic structure. Conversely, *An. farauti* and *An. farauti 2* show strong genetic and geographic population structure with both the mitochondrial and ribosomal markers. One geographic region contained populations of *An. farauti 2* identified as being in mutation-migration-drift equilibrium. Using the mtDNA data and a coalescence-based continuous linear habitat model we derived genetic estimates of lifetime dispersal distance that were in agreement with ecological estimates.