



Museum genomics resolves cryptic species in the Australasian arbovirus vector mosquito *Culex annulirostris* Skuse, 1889 (Diptera: Culicidae).

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The common banded mosquito *Culex (Culex) annulirostris* Skuse, 1889 is the primary vector of Japanese encephalitis virus (JEV) in Australia, among other arboviruses. Although sanger-based molecular studies reported putative cryptic species, taxonomic resolution has been hampered due a lack of employed mosquito taxonomists, destructive sampling techniques and a lack of authoritatively identified reference specimens. By using genome skimming from only one or two legs, we successfully sequenced the complete mitochondrial genome of specimens to identify mosquito species held in Australian museums or reference collections dating back to 1951. We used mitogenome data and morphology to diagnose four cryptic species: *Cx. annulirostris* sensu stricto, *Culex (Culex) somerseti* Taylor, 1912 stat. rev., an undescribed species from Papua New Guinea and north Queensland, and another from the Solomon Islands. Ancestral state reconstruction revealed the recent migration of two independent *Cx. annulirostris* populations from Australia to Papua New Guinea and Timor-Leste, respectively. Adoption of museum genomics will enable improved biosecurity diagnostics, origin tracing of historical incursions using historical collections, and description of the remarkable 170 unnamed mosquito species documented in Australia. Epidemiologists can now complete vector competence testing on each revised species to identify specific roles in disease transmission, including the recent JEV outbreak.

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