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**MOLECULAR CHARACTERISATION OF MURRAY VALLEY ENCEPHALITIS VIRUS**

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Murray Valley encephalitis virus (MVEV) is an encephalitogenic mosquito-borne flavivirus endemic to Australia and Papua New Guinea (PNG). The recent re-emergence of this virus in southeast Australia has renewed concerns regarding its potential to spread and cause disease. Four genotypes (GI-IV) of MVEV have been previously recognised: GI and GII circulate in the Australian mainland, while GIII and GIV circulate in PNG. Prior to this study, only one full length genome of MVEV had been reported, that of the prototype strain MVE-1-51 (GI). Here, we report full length genomic sequences of strains representing each of the three other genotypes: OR156 (GII), NG156 (GIII) and MK6684 (GIV). Sequence information was derived using a combination of cDNA subtraction, RT-PCR and 5'- and 3'-RACE. Nucleotide (and amino acid) sequence analysis revealed high levels of similarity between strains, ranging from 90.6% (98.1%) and 94.1% (98.8%); highest levels of identity were found in the non-structural NS5 gene. Phylogenetic analyses were also performed on complete pre-membrane (prM) and envelope (E) genes of geographically and temporally diverse virus strains, including a human isolate from 2008. Phylogeny generated from the E gene was consistent with previous partial E gene analyses and the identification of four distinct genetic types of MVEV. However, analyses with full length genomic and pre-membrane gene sequences revealed a much closer relationship between the PNG strains NG156 and MK6684, and indicated their grouping as a single genotype.

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**DIVERSITY AND SEASONAL SUCCESSION OF COASTAL MOSQUITOES IN THE ADELAIDE REGION OF SOUTH AUSTRALIA**

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Northern coastal suburbs in metropolitan Adelaide, South Australia are often subject to extreme levels of mosquito nuisance biting. The diversity and seasonality of the mosquito community in the coastal area of northern Adelaide was investigated over seven years (2000-7) in the suburb of Globe Derby Park, which is adjacent to both mangrove and samphire swamps. Eight species were identified from adult mosquito collections, with the salt marsh mosquitoes *Aedes camptorhynchus* (Thomson) (55.7%) and *Aedes vigilax* (Skuse) (29.5%) most abundant. These two species display seasonal succession, with the former most abundant in spring and early summer, giving way to the latter in mid-late summer and autumn. The description of such temporal succession in salt marsh mosquitoes in southern Australia is novel and can be explained by the differing local ecology of the two species.