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**Use of morphological and molecular methods in identification of Asian bush mosquito, *Aedes japonicus* (Theobald, 1901), in Sri Lanka**

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Conducting routine entomological surveillance to identify new vectors and changes in the distribution patterns of vectors is important for the management of mosquito borne diseases in Sri Lanka. A recent preliminary entomological survey reported the presence of *Aedes japonicus* in Sri Lanka in March 2021. Therefore, the current study was conducted to validate the presence of *Ae. japonicus* in Sri Lanka, based on morphological and molecular evidence. The search for *Ae. japonicus* breeding sites and developmental stages using standard siphoning methods were conducted in Kosgama and Palleanugala areas located in the Districts of Colombo and Kegalle, respectively, from May to December 2021. Collected immature stages were reared up to the fourth instar stage or adult, and specimens were identified to species level using standard morphological keys. Further, DNA was extracted from the head, and thoracic regions of the reared mosquitoes and Polymerase Chain Reaction (PCR) was performed. The amplified products were sequenced at a commercial facility (Macrogen Inc. co. Ltd., Seoul, Korea). Subsequently, the sequences were analysed for sequence identity using NCBI BLAST analysis and Geneious Trial (version 7.1.3). Based on the morphological characteristics, larvae of *Ae. japonicus* were identified from both study areas. *Ae. japonicus* was reported only from natural breeding containers such as bamboo plants and tree holes in both study areas. The molecular analysis further confirmed the morphological identification. Further, newly reported *Ae. japonicus* population denoted a close relationship to the Austrian/Slovenian population. *Ae. japonicus* is well adapted to temperate climates and has been reported to possess a strong tendency to expand and colonies into new territories, which is facilitated by human-mediated, passive transportation. According to Unweighted Pair Group Method with Arithmetic Mean (UPGMA) based hierarchical cluster analysis, newly discovered *Ae. japonicus* denoted strong affinity to a previously detected *Ae. japonicus* strain in Eastern Austria/Slovenia. The dispersal and population dynamics of *Ae. japonicus* should be thoroughly surveyed in Sri Lanka, as this species is a potential vector of Japanese Encephalitis.

**Keywords:** *Aedes japonicus*, Mosquito, Sri Lanka

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