Eco-virological survey of Aedes mosquito larvae in selected dengue outbreak areas in Malaysia

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ABSTRACT

Background & objectives: Transovarial transmission of dengue virus in the Aedes vectors is now a well-documented phenomenon reported from many parts of the endemic areas in the world, which played an important role in initiating and maintaining the outbreak in human populations. This study investigated the factors affecting breeding habitats and the relationship with transovarial dengue virus in larvae of Aedes aegypti and Ae. albopictus.

Methods: Larval surveillance was conducted in dengue outbreak areas in Malaysia from 2008 until 2009. Sampling was carried out based on habitat type, water condition (substrate type), canopy coverage, temperature and pH at breeding habitats. RT-PCR was performed to detect presence of transovarial dengue virus in larvae collected in the study areas.

Results: A total of 789 breeding habitats were identified during this study and the majority of these breeding sites were plastic containers (57.46%). Aedes albopictus dominated most of the water condition surveyed, while Ae. aegypti indicated preference toward habitats with clear water. Aedes aegypti was selective in selecting ovipositional sites compared to Ae. albopictus where shaded areas were shown to be the most preferred. From a total of 363 mosquito larvae pools, 23 (6.3%) pools were positive for dengue virus where 18 of them were from Ae. albopictus and five were from Ae. aegypti mosquito larvae pools.

Interpretation & conclusion: This study indicated the presence of transovarial transmission of dengue virus in immature Ae. aegypti and Ae. albopictus in the field. This study also showed that combination of water conditions, canopy coverage, temperature and pH of breeding habitats were the factors affecting the larval population. The study suggested that larval survey programme could serve as a tool not only to monitor the local dengue vector distribution but also to provide objective information for taking appropriate action by the community against dengue vectors.

Key words Aedes aegypti; Aedes albopictus; dengue; larval surveillance; virus infection rate

INTRODUCTION

Dengue is a disease caused by four antigenically distinct single-stranded RNA viruses, denoted as dengue type 1, 2, 3 and 4 of the genus Flavivirus, family Flaviviridae¹-². The infection can be manifested in a range of symptoms from relatively mild flu-like syndrome with rash, commonly known as dengue fever (DF), to severe and potentially fatal disease known as dengue hemorrhagic fever (DHF) or dengue shock syndrome (DSS) which is characterized by capillary leakage, thrombocytopenia and hypovolemic shock. In Malaysia, classical dengue fever was first documented in 1901-02, while the first reported outbreak of DHF occurred in 1962. Since then dengue has remained endemic, with one or more of the four dengue serotypes co-circulating in the country and outbreaks of DHF being reported periodically.

During the first quarter of 2012, the State of Selangor recorded the highest dengue cases in Malaysia with 1271 cases reported from January 2012 onwards. This figure was almost half of the number of cases (2854) reported nationwide³. At present, neither an effective vaccine nor a specific drug is available for DF/DHF. Management of patient is via intravenous fluid therapy which helps to maintain patient’s body fluid. It is for these reasons that control of dengue is currently focusing on controlling the vectors, Aedes aegypti and Ae. albopictus (Diptera: Culicidae) that transmit dengue.

Vector surveillance allows timely implementation of emergency mosquito control measures such as space application of chemical insecticides against adult mosquitoes and destruction of their breeding places to contain an outbreak. Unfortunately, when the adult mosquito density is low, direct entomological monitoring is not sensitive anymore as an indicator to serve as an early warning surveillance system for outbreak prevention. It is in this