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Epidemiology of bluetongue virus in Australasia

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Background: Bluetongue is a vector-borne disease of ruminants caused by bluetongue virus (BTV) belonging to *Reoviridae*. So far, 28 serotypes of BTV have been reported, and distribution of various serotypes is not uniform among different geographical areas. The virus is endemic in tropical areas where vector population is abundant and these areas act as source population for virus spread to the neighbouring temperate sink areas. Australasia is one of the stable source-sink episystems with circulation of different serotypes. During this study, genetic relations of the serotypes circulating in the Australasian region were analysed and the serotypes that are unique to this episystem and those which entered this episystem during recent past were identified.

Methods & Materials: Data about BTV serotypes circulating and genome sequence were collected from public databases. Phylogenetic analysis was done using MEGA and BEAST.

Results: Majority of the BTV serotypes circulating in Australasia are either unique (BTV-20, -21 and -23) to the region or distinct (BTV-1, -2, -3, -4, -9 and 16) from their counterparts in other source-sink episystems and belong to Eastern topotype. Apart from these, serotypes of western origin are also found to be circulating (BTV-2, -5, -7, -10, -12 and -24), and some (BTV-2 and -10) are indistinguishable from the live attenuated vaccines being used in Africa (BTV-2) and USA (BTV-10). However, these two serotypes are not reported outside India.

Conclusion: We could conclude that BTV-20, -21 and -23 are unique to Australasian region and eastern topotype viruses of serotypes BTV-1, -2, -3, -4, -9 and -16 have probably diverged from their western counterparts hundreds of years ago and evolved since then. Among the serotypes of western origin, BTV-5, 7, -12 and -24 seem to have entered this area in the recent past and got established in more than one country whereas vaccine strains of BTV-2 and -10 did not. Identification of circulating serotypes of BTV in this region is important for evaluating virus movement and for vaccine design.

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Dengue seroprevalence in urban dwelling Indonesian children: A nationally-representative study

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Background: Indonesia reports the second highest dengue disease burden in the world. However these passive surveillance data are recognized to be incomplete, to vary widely within the country, and are likely significant underestimates. Age stratified seroprevalence data are relatively unbiased indicators of past exposure and allow understanding of transmission dynamics. These information are valuable for public health planning, control and prevention activities. A nationally representative population-based cross sectional dengue seroprevalence study was conducted in 1 to 18 years old urban Indonesian children.

Methods & Materials: Using a cluster design and a probability proportional to size sampling, 3210 children from 1 to 18 years old in 4 age groups (1 – 4; 5 – 9; 10 – 14 and 15 – 18 years old) were enrolled, following household visits, from 30 clusters distributed from west to east in urban areas of Indonesia. Serum samples were tested for anti-dengue IgG antibodies by indirect ELISA. Using linear and catalytic models the median age of seroconversion and the force of primary infection were estimated.

Results: Data from 3194 children (98.7%) were included in the analysis. Overall, the adjusted national seroprevalence was 69.4% [95%CI: 64.4-74.3] ranging from 33.8% [95%CI: 26.4-41.2] in the 1-4 year old, 65.4% [95%CI:69.1-71.7] in the 5-9 years old, 83.1% [95%CI: 77.1-89.0] in the 10-14 years old, and 89.0% [95%CI: 83.9-94.1] in the 15-18 years old. The median age of seroconversion was 4.8, and considering a constant force of infection we estimated 137 primary infections per 1000 children per year.

Conclusion: This is the first nationally representative dengue seroprevalence study conducted in Indonesia. Dengue seroprevalence is high in Indonesian children: over half of children have been infected by the age of 5. This level of transmission intensity should be associated with increased risk of secondary infection and thus clinically and more severe disease. These data are an additional indicator of national-level burden and will inform implementation of preventive measures, including vaccination.

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