

RESEARCH ARTICLE

# Dengue in Latin America: Systematic Review of Molecular Epidemiological Trends

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## Abstract

Dengue, the predominant arthropod-borne viral disease affecting humans, is caused by one of four distinct serotypes (DENV-1, -2, -3 or -4). A literature analysis and review was undertaken to describe the molecular epidemiological trends in dengue disease and the knowledge generated in specific molecular topics in Latin America, including the Caribbean islands, from 2000 to 2013 in the context of regional trends in order to identify gaps in molecular epidemiological knowledge and future research needs. Searches of literature published between 1 January 2000 and 30 November 2013 were conducted using specific search strategies for each electronic database that was reviewed. A total of 396 relevant citations were identified, 57 of which fulfilled the inclusion criteria. All four dengue virus serotypes were present and co-circulated in many countries over the review period (with the predominance of individual serotypes varying by country and year). The number of countries in which more than one serotype circulated steadily increased during the period under review. Molecular epidemiology data were found for Argentina, Bolivia, Brazil, the Caribbean region, Colombia, Ecuador, Mexico and Central America, Paraguay, Peru and Venezuela. Distinct lineages with different dynamics were found in each country, with co-existence, extinction and replacement of lineages occurring over the review period. Despite some gaps in the literature limiting the possibility for comparison, our review has described the molecular epidemiological trends of dengue infection. However, several gaps in molecular epidemiological information across Latin America and the Caribbean were identified that provide avenues for future research; in particular, sequence determination of the dengue virus genome is important for more precise phylogenetic classification and correlation with clinical outcome and disease severity.