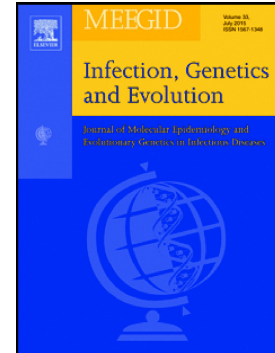


Accepted Manuscript

Genetic diversity and evolution of dengue virus serotype 3: A comparative genomics study

Vaishali P Waman, Mohan M Kale, Urmila Kulkarni-Kale



PII: S1567-1348(17)30022-9
DOI: doi: [10.1016/j.meegid.2017.01.022](https://doi.org/10.1016/j.meegid.2017.01.022)
Reference: MEEGID 3054

To appear in: *Infection, Genetics and Evolution*

Received date: 3 November 2016
Revised date: 14 January 2017
Accepted date: 21 January 2017

Please cite this article as: Vaishali P Waman, Mohan M Kale, Urmila Kulkarni-Kale , Genetic diversity and evolution of dengue virus serotype 3: A comparative genomics study. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. Meegid(2017), doi: [10.1016/j.meegid.2017.01.022](https://doi.org/10.1016/j.meegid.2017.01.022)

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

Genetic diversity and evolution of Dengue virus serotype 3: a comparative genomics study

Vaishali P Waman¹, Mohan M Kale², Urmila Kulkarni-Kale^{1*}

¹Bioinformatics Centre, Savitribai Phule Pune University (formerly University of Pune), Pune-411007, Maharashtra, India

²Department of Statistics, Savitribai Phule Pune University (formerly University of Pune), Pune-411007, Maharashtra, India

* Author for correspondence: Dr. Urmila Kulkarni-Kale, Bioinformatics Centre, Savitribai Phule Pune University (formerly University of Pune), Pune-411007, India. Phone: +91 20 2569 8751/ 2569 0195/ 2569 2039. Fax: +91 20 2569 0087. Email: urmila@bioinfo.net.in, urmila.kulkarni.kale@gmail.com

Abstract

Dengue virus serotype 3 (DENV-3), one of the four serotypes of Dengue viruses, is geographically diverse. There are five distinct genotypes (I-V) of DENV-3. Emerging strains and lineages of DENV-3 are increasingly being reported. Availability of genomic data for DENV-3 strains provides opportunity to study its population structure. Complete genome sequences are available for 860 strains of four genotypes (I, II, III and V) isolated worldwide and were analyzed using population genetics and evolutionary approaches to map landscape of genomic diversity. DENV-3 population is observed to be stratified into five major subpopulations. Genotype I and II formed independent subpopulations while genotype III is subdivided into three subpopulations (GIII-a, GIII-b and GIII-c) and is therefore heterogeneous. Genotypes I, II and GIII-a subpopulations comprise of Asian strains whereas GIII-c comprises of American strains. GIII-b subpopulation includes mainly of American strains along with a few strains from Sri Lanka. Genetic admixture is predominantly observed in Sri Lankan strains of genotype III and all strains of genotype V. Inter-genotype recombination was observed to occur in non-structural region of several Asian strains whereas extent of recombination was limited in American strains. Significant positive selection was found to be operational on all genes and observed to be the main driving force of genetic diversity. Positive selection was strongly operational on the branches leading to Asian genotypes and helped to delineate the genetic differences between Asian and American lineages. Thus, inter-genotype recombination, migration and adaptive evolution are the major determinants of evolution of DENV-3.

Keywords: bioinformatics, complete genome, population structure, molecular phylogeny, positive selection, recombination

Download English Version:

<https://daneshyari.com/en/article/5590629>

Download Persian Version:

<https://daneshyari.com/article/5590629>

[Daneshyari.com](https://daneshyari.com)