First complete genome sequence of circulating dengue virus serotype 3 in Jeddah, Saudi Arabia

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Abstract

Here we report the first full-length genome sequence of dengue virus serotype 3 (DENV-3) from a strain isolated from a patient in Jeddah, Saudi Arabia, in 2014. The genome consists of 10 635 bp and shows close similarity to circulating genotype III isolates from Singapore, suggesting possible importation, most probably during religious pilgrimages to Saudi Arabia.

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Keywords: Dengue virus, DENV, full genome, genotypes, Saudi Arabia

Original Submission: 7 August 2017; Revised Submission: 11 September 2017; Accepted: 19 September 2017

Article published online: 23 September 2017

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Dengue virus (DENV) is an arbovirus transmitted primarily by Aedes aegypti and Ae. albopictus mosquitoes. It causes a disease ranging from acute dengue fever (DF) to severe dengue haemorrhagic fever (DHF) or dengue shock syndrome [1]. Dengue is endemic in ~100 countries in tropical and subtropical regions of the world; current estimates suggest that ~40% of the world’s population are at high risk of dengue infection, and there are 50–100 million annual DF cases, resulting in 500 000 DHF and 22 000 deaths [https://www.cdc.gov/dengue/epidemiology/index.html]. There are four antigenically and genetically distinct DENV serotypes (DENV-1 to -4) which are further classified into different genotypes genetically.

DENV-3 has been classified into five different genotypes [2–4]. DENV-3 has been circulating and causing several outbreaks in the western region of Saudi Arabia (the cities of Jeddah and Makkah) since its first isolation, in 1997 in Jeddah, until now, although with lower prevalence compared to DENV-1 and DENV-2 [5–10]. However, there has been no report of any DENV-3 full genome sequence from Saudi Arabia. Therefore, in this study, we report the first full genome of DENV-3 strain isolated from Jeddah, Saudi Arabia.

Serum and plasma samples were obtained from a patient suspected to have DF at King Abdulaziz University Hospital in 2014, with ethical approval obtained from the Unit of Biomedical Ethics (approval 19-14). The serum sample was found positive for anti-dengue IgM but not IgG antibodies, suggesting an acute primary DENV infection, which was confirmed by real-time RT-PCR using the plasma sample as previously described [11]. The full genome sequence of the DENV-3-Jeddah-2014 isolate was then obtained as previously described [12]. The sequenced length of this isolate was 10 635 bp with an open reading frame coding for 3390 aa.

Phylogenetic analyses based on full genome and complete envelope gene of this strain and isolates representing diverse geographical locations were conducted using the maximum
Full genome analysis showed close clustering of the DENV-3-Jeddah-2014 isolate with genotype III isolates collected between 2004 and 2007 from Sri Lanka and Singapore, with highest similarity to strain GU370053, which was isolated in 2007 from Singapore (Fig. 1(a)). However, because of the temporal difference between the DENV-3-Jeddah-2014 isolate and closely related strains, as well as the limited number of available full genome sequences, a phylogenetic tree based on the envelope (E) gene was constructed using all available E gene sequences in the GenBank database within the clade of interest (Fig. 1(b)). These results suggest that the DENV-3-Jeddah-2014 strain might have been introduced from Singapore to Jeddah, most probably during religious pilgrimages (Hajj and Umrah).

To our knowledge this is the first report of the DENV-3 full genome from Saudi Arabia. It should help in the study of the evolution of DENV-3 in the region. However, more studies and sequences are required to clearly monitor dengue importation into Saudi Arabia.

**Nucleotide sequence accession number**

The virus genome sequence described here has been deposited in the GenBank database as accession number KJ830751.
Acknowledgements

Supported in part by grants from the Deanship of Scientific Research (DSR), King Abdulaziz University, Jeddah, Saudi Arabia (grants RG/34/2 and 543/141/1432). The authors thank DSR for technical and financial support.

Conflict of Interest

None declared.

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