

074 Identification of unique DNA regions in Dengue viral strains for targeted genome editing

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The prevalence of Dengue has dramatically increased in the tropics in recent decades. However, the present therapeutic strategies for disease prevention still remains controversial. Therefore, the purpose of this study is to identify a possible molecular target for genome editing which could eradicate the virus. Availability of the genome sequence data and the sophisticated bioinformatics tools are versatile platforms to investigate the novel target for genome editing. The study is based on the genomic sequence data of four dengue virus serotypes obtained from the National Center for Biotechnology Information, sequence similarity search using Basic Local Alignment Tool (BLAST) and the introduction of a novel gene editing technique as a way to eradicate the virus. The nucleotide BLAST search was performed against the nucleotide collection database for different regions of the genomes of all four serotypes. The nucleotide sequences which showed significant similarity with the database sequences were discarded. The nucleotide sequence 3' gaacatcatgtggaagcaaatatcaaatgaattaaaccacatcttacttgaaaatgacatgaaattacagtggtcgtaggagacgttagtggatcttggccaaggaagaaaatgattaggccacaacccatggaacacaataactcgtggaaaagctgggaaaagccaaatcataggagcagatgtacagaataccaccttcat 5' was proposed as the drug target for dengue virus 1, the nucleotide sequence 3' tgtagctccgtcgtggggacgtaaacctgggaggctgcaaacgtggaagctgtacgcacggtgtagcagactagcggtagaggagaccctcccatgacacaacgcagcagcggggcccggagcactgagggaagctgtacctccttgcaggactagaggtagaggagacccccgcaataa aa 5' for dengue virus 3 and the nucleotide sequence 3' aagacattccgcagtggaaccatctaaggatggaaaaactggcaagaggttcttttctcccaccactttcacaagatcttatgaaggatggcgcctcactagtgttccatgtagaaaccaggatgaactgataggagagccagaatctcgcagggagctggatggagcttaagagaaacagcctgcctgggcaaagcttagc 5' for dengue virus 4 respectively. All above sequences code for polyprotein precursors, structural and non-structural proteins and for the translation factors and do not have any sequence similarity to human genomic DNA at expect threshold value of 100. The study also suggests that the sequence specific designer nucleases or the programmed nucleases which functions to precise edition of the above target sequences as a method to eradicate Dengue. Eradication of the virus would have less environmental effects than the present methods of controlling the mosquito, which acts as the vector.

Key words: Dengue, Genome editing, Virus eradication