

## Immunomics: It's Role in Zika Virus Infection

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### Editorial

Zika virus infection is a new problematic arbovirus infection. The infection is a dengue like illness but can result in unwanted neurological complication and abnormal child born to infected mother [1]. The infection occurs worldwide at present and it is still the global public health issue. To manage this infection, there is still no specific antiviral drug. Searching for new effective drug is widely performed. For prevention of the disease, the prevention of mosquito bite and safe sex is the main recommendation. As a new infection, the expected most effective preventive measure against Zika virus infection is the vaccination [2]. Nevertheless, there is still no specific vaccine against Zika virus at present [2].

Drug and vaccine search is the present focused research issue worldwide. Several new advanced biomedical technologies are used. Of several techniques, the use of bioinformatics is very interesting. The new branch of bioinformatics namely immunomics is interesting and can be applied in management of several diseases including to infections. For the Zika virus infection, the application of immunomics is an interesting issue that should be mentioned. At first, the immunomics technique can be applied for searching of new vaccine candidate. Finding epitope is the first step of vaccine development and it can be done based on immunomics. Of interest, there are many new publications on epitopes of Zika virus derived from immunomics [3-5]. The first world report is by Wiwanitkit and Wiwanitkit [4]. According to tat study, "784YIMDEAHFTDPSSIAARGYI1803" is the best epitope. In another report, Dey et al. reported finding on some epitopes of Zika virus and noted that "These peptides can be expected to form the basis for a nascent peptide vaccine which, enhanced by incorporation of suitable adjuvants, can elicit immune response against the Zika virus infections [5]". Usman Mirza et al. noted that the detected epitopes can be further tested using immunomics investigation and

mentioned that the stability of the resulting peptide-MHC I complexes could be further studied by molecular dynamics simulations [6].

It is no doubt that immunomics is useful for Zika virus research and it is the hope for finding the way to manage the disease. At present, the specific resource of immunomics for Zika virus is also easily available via ZikaVR [7]. ZikaVR "comprises of whole genome sequences, their respective functional information regarding proteins, genes, and structural content. Additionally, it also delivers sophisticated analysis such as whole-genome alignments, conservation and variation, CpG islands, codon context, usage bias and phylogenetic inferences at whole genome and proteome level [7]".

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