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DEVELOPMENT OF EPITOPE BASED VACCINE FOR ZIKA VIRUS AGAINST THE BRAZILIAN HUMAN LEUKOCYTE ANTIGEN BACKGROUND: A BIOINFORMATIC APPROACH

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Increasing infection of Zika virus threatens the infant's life by causing microcephaly in developing countries. Numbers of various approaches have been anticipated to develop a vaccine against Zika virus, but the majority of them proved ineffective. The potency of epitope-based vaccines is directly linked with genotypes of host genetics. In this research article, we have tried to predict most putative Zika virus epitopes which are efficiently restricted by most common HLA alleles in Brazilian population through different computational algorithms. Databases allowed us to develop the consensus sequences from the highly-conserved proteins of Zika virus strains reported from the Brazil. Obtained consensus sequences were used to predict their binding affinities with most prevalent HLA alleles in the Brazilian population. Two Class-I epitopes from E1 region, three from Class-I epitope from NS5, one Class-II epitope from E1 region and one Class-II epitope from NS5 region showed effective binding and proved to be highly putative to boost immune response. A cocktail of these seven has been checked for population coverage and they gave 99.99% for Brazilian populations with no allergenic response. Computational algorithms are robust way to shortlist potential candidate epitopes for vaccine development, but further, *in vivo* and in-vitro studies are required to confirm their immunogenic properties.

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