

JOINT EVENT

10<sup>th</sup> International Virology Summit  
&  
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**Dengue virus (DENV) insights using comparative genomics****Mansi Verma**

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**D**ENV is a positive stranded RNA virus composed of three structural proteins which forms the components of virion and seven non-structural proteins which control various functions like viral replication, immunity and pathogenesis. There are five different serotypes of virus namely DENV-1 to DENV-5. So far, no vaccine with higher efficacy has been known for treating all serotypes of dengue. In the present study, comparative genomics of Dengue virus was conducted to explore potential candidates for novel vaccine targets. All ten proteins of all four serotypes of dengue virus were downloaded and analysed for conserved motifs using MEME software. Several B-cell epitopes were predicted using Immune Epitope Database B-cell prediction tool & Bepipred. Overlapping epitopes sequences were analysed for surface accessibility and conservancy. Based on our studies, we could find several conserved epitopes which are antigenic in nature. Using *in silico* analysis, we could successfully obtain many conserved epitopes common to all serotypes of dengue virus, which seems promising for designing novel vaccine targets.