**OTR 04 - Identification of targeted epitopes of yellow fever virus based on homology with other species of flavivirus**

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**Introduction:**

The current outbreak of yellow fever virus (YFV) associated with recent outbreaks of old and new viruses (DENV, ZIKAV, CHYV, MAYV) in Brazil has resulted in a massive effort to accelerate the development of new diagnostic methods and specific vaccines. The identification of the epitopes of these viruses and consequently of the immune response in humans would be of extreme importance for the preparation of more specific tests and to understand the mechanism of vaccination. Much has been described about the immune response against the yellow fever virus and the usefulness of the vaccine, however little is known about its antigenic repertoire in humans.

**Objective:**

To predict the epitopes from the yellow fever virus polyprotein and other Flavivirus polyproteins from Brazil

**Methodology:**

While mapping is in progress in our laboratory, we use bioinformatics tools and information from a large number of experimental epitopes from other Flaviviruses available in the IEDB for a comparative analysis against the YFV proteome in order to project targets of the YFV immune response. The complete sequences of the structural and non-structural proteins of the Brazilian vaccine strain and of the other flaviviruses were obtained from EXPASY and the homology with the proteins was determined through the CLUSTAL OMEGA. To analyze sequence conservation among different Flavivirus species, the following method was used: for YFV, zika virus, e dengue virus I, II, III and IV at consensus sequence it was derived from a multiple sequence alignment of all strains matching the respective taxonomic ID (PO3314, Q32ZE1, Q80RP0,

Q8QR27, Q6B523 e H2EJJ4 respectively). The BLAST search was performed using the consensus sequence to identify a representative strain of the following criteria: complete proteome having highest sequence identity to the consensus and full annotation of individual proteins (residue positions).

**Results:**

We found a significant level of overlap between known antigenic sites of other Flavivirus proteins with residues in the YFV polyprotein. E and NS1 proteins shared functional antibody epitopes, whereas regions of T cell reactivity were conserved in NS3 and NS5 for YFV.

**Conclusion:**

The analysis performed based on epitopes described, provided a good orientation of the knowledge of a set and the location of cross-reaction targets of regions of the YVF polyprotein with other flaviviruses. These data may be useful and therefore provide novel approaches for the development of specific B-cell and T-cell antibodies specific for diagnosis, therapy and prophylaxis.

**Keywords: Bioinformatics; Epitope; Prediction**