IVD_17 - Rational design of chimeric proteins using immunoinformatics for the serological diagnosis of Mayaro virus infections

Bianca Corrêa Tinoco[1]; Salvatore Giovanni de Simone[2]; David William Provance Junior[2]; Ana Paula Corrêa Argondizzo[1]; Gabriela dos Santos Esteves[1].
[1]Fiocruz/Bio-Manguinhos
[2]Fiocruz/CDTS

Introduction: Mayaro Virus (MAYV) is responsible for a neglected tropical disease, mayaro fever, that poses a challenge to the public health system. This virus currently circulates in high-density tropical forests or rural areas in Central and South America. However, characteristics of this virus have shown a potential for transmission in urban areas and, along with that, for an epidemic. As MAYV has symptoms similar to those of other arboviruses and is phylogenetically similar to chikungunya virus, clinical and serological diagnoses are difficult. New immunological reagents need to be researched to develop assays that can specifically distinguish between these diseases. Due to the possibility of cross-reactivity from the use of the natural proteins E1 and E2 of MAYV as the main diagnostic targets, immunoinformatics tools were used to identify more specific immunogenic epitopes that were designed into chimeric proteins for use in the specific diagnosis of MAYV.

Objectives: To rationally design chimeric proteins that can be used for the specific diagnosis of MAYV.

Methodology: The MAYV structural polyprotein sequence obtained from the NCBI was introduced into two programs, Bepipred 2.0 and FBCpred, which predict linear epitopes that can be recognized by B lymphocytes. The epitopes predicted by both programs were evaluated for antigenicity by the VaxiJen program. The Rx and Tx chimeras were designed based on the beta barrel structures of Green Fluorescent Protein and Thermal Green Protein, respectively. A third chimeric protein, LATER-MAYV, was designed by expanding the sequence of the epitopes and splicing them with 3-glycine and serine sequences. Chimeras and epitopes were evaluated for similarity with BLASTp and the BioEdit alignment tool. The Rx and Tx sequences were also modeled on the I- TASSER server and visualized using PYMOL to confirm retention of the core barrel structure.

Results: The 10 most antigenic predicted epitopes were used to design Rx and Tx. For the LATER-MAYV protein, 10 antigenic regions were used along with 2 more antigenic epitopes predicted by Bepipred 2.0.

Conclusion: Three chimeras were designed with potential for use in a specific diagnosis of MAYV, requiring experimental validation.

Keywords: Immunoinformatics, Mayaro vírus, Chimeric proteins