

**Bioinformatic Analysis proteins membrane transducers
of *Candidatus Liberibacter asiaticus* spp.**

**Cynthia G. Rodríguez-Quibrera¹, Aldo Segura-Cabrera¹, Isidro H. Almeyda-León²
and Alberto Mendoza-Herrera¹.**

¹CBG-IPN, Boulevard del Maestro s/n esq. Elías Piña, Col. Narciso Mendoza, Cd. Reynosa,
Tamaulipas, C.P. 88710, México. Tels: +52(899)924 3627.

²INIFAP-CIRNE, Km. 61 Carretera Matamoros- Reynosa C.P. 88900, Cd. Río Bravo, Tamaulipas.
crodriguezq1200@alumno.ipn.mx

In this study, some transmembrane proteins of *Candidatus Liberibacter asiaticus* spp were analyzed by using bioinformatics tools. Our main objective is to find potential transmembrane antigenic proteins. By using UniProtKB platform, 90 proteins were found, from there, only 12 transmembrane proteins were selected and by the obtained amino acid sequences an analysis of Blast2go800 (Run Blast, Mapping, Annotation and Inter ProScan) was performed, resulting that the majority of these proteins were not characterized. Based on these results, a more comprehensive study was performed by the software HHPred / HHSearch getting the hit numbers of the 12 proteins in question. For 10 proteins we got a protein function prediction with a probability of 97 to 100 %. For the other two proteins the results were not reliable. HHPred predicts the structure of proteins and detecting remote homologs HHSearch protein, generates high quality alignment homology modeling and prediction function comparing pairs of hidden Markov models (HMMs), according to STML non redundant library, were considered those showing at least a 70% identity. Construction, recording and calibration of HMM were performed by HHSearch v1.5.01. According to our results it is concluded that the bioinformatics analysis of membrane proteins present in *Candidatus Liberibacter asiaticus* spp. genome revealed that some of them are associated as surface antigens.