



In Deep Proteomic Characterization of an OMV Based Vaccine Against *N. meningitidis*

Jeovanis Gil Valdés

Department of Proteomics, Biomedical Researches, Centre for Genetic Engineering and Biotechnology,
Havana, Cuba

At present one of the efforts devoted to the development of an effective vaccine against *Neisseria meningitidis* serogroup B have been focused in the proteomic studies of outer membrane vesicles (OMV). This work presents the results from a detailed study of the protein composition of OMV from VA-MENGOC-BC™ (Finlay Institute, Cuba). The characterization of this protein preparation is a challenge because of it is enriched in lipids and membrane proteins and only a few number of proteins represent about 70 % of the total protein mass. Proteins were identified by, combining two-dimensional gel electrophoresis of proteins and peptides and mass spectrometry, and the application of non-gel based approaches starting from the tryptic digest of the OMV preparation followed by (1) the Selective Capture of Peptides (SCAPE-nHnR), and (2) equalization of the peptide mixture by using peptide libraries and fractionation by reverse phase liquid chromatography at basic pH before LC-MS/MS analysis. Most of the applied methods have been developed in our group. This study resulted in the identification of more than three hundred proteins. Bioinformatics analysis of the identified components allowed the selection of potential antigens for cloning, expression, purification and immunological studies, which were part of a wider project aimed to the development of a new vaccine based on a defined protein composition.