

DIFFERENTIAL PROTEOMICS OF CELLULAR PROTEINS EXPRESSED IN
RESPONSE TO DENGUE VIRUS (SEROTYPE 2) INFECTION OF VERO CELLS.

Chung, J^{1,3}; de Meneses, MDF²; Junqueira, MR^{1,3}; Santos, MF^{1,3}; Ferreira, DF²;
Rebello, MA²; Domont, GB^{1,3}

¹Departamento de Bioquímica. Instituto de Química. UFRJ; ²Departamento de Virologia, Instituto de Microbiologia. UFRJ, ³Rede Proteômica do Rio de Janeiro

Dengue virus is an important human pathogen causing dengue fever and dengue hemorrhagic fever. Four serotypes, DEN-1 to - 4 are known. The ~ 11 kb genome of DEN-2 consists of a single-stranded RNA molecule of positive polarity, enveloped, encoding the polyprotein 5'-C-prM-E-NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5-3', which is cleaved to generate individual proteins. Proteomics techniques were used to investigate the differential protein profiles of DEN-2 infected Vero cells. Pool of infected cells at multiplicity of infection (MOI=0,5) of PFU/cell were recovered 72h post-infection and lysed in 9.6 M urea, 4% CHAPS and 1% Pharmalyte. Samples were analyzed by 2-DE using IPG strips, pH 4-7 and vertical SDS-PAGE. Maps of infected and non-infected (control) cell proteins were visualized by Coomassie G-250. Thirty four differential spots and over-expressed cellular proteins were identified by PMF and MS/MS using a 4700 MALDI-TOF-TOF (ABI). MASCOT platform and NCBI nr database identified three protein groups: metabolic-related, cytoskeleton (e.g. actins, tubulin, vimentin) and heat-shock proteins (HSP70, HSP90, GRP78). These results show that the cytoskeleton participates in viral infection and on the reorganization of the infected cells, and support the importance of HSPs, like HSP70, as a receptor in dengue virus entry. Acknowledgements: CNPq, CAPES, FAPERJ, UFRJ.