

**A PROTEOMIC APPROACH TO STUDY HEPG2 HEPATOMA CELL
INFECTED BY DENGUE VIRUS**

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Dengue viruses are among the most prevalent arboviruses in tropical and subtropical areas and are transmitted to humans via *Aedes aegypti*. At present, some 2,5 billion people live in areas of risk. We identified the presence of proteins and peptides secreted by HepG2 cells infected with Dengue virus 2 using proteomics approach. The sample was fractioned in ultrafiltrate, < 10kDa (FU), and concentrated > 10kDa (FC). The FU was analyzed on MALDI-TOF/MS. Our results showed that control and infected cells possess some similar components. The FC was applied in one-dimensional SDS/PAGE. We observed different profiles with 33 bands for each sample. 31 bands of each sample were analyzed by mass spectrometry at present. The data analysis resulted in 113 proteins identifications for control and 120 for infected cells. 56 proteins were present in both samples, 57 were only identified in control and 64 in infected sample. All these components are being characterized by MS/MS. Blood coagulation factors like prothrombin and factor X were investigated on cellular extract of HepG2. Using a Dot Blot approach we observed differences between control and infected cells. These results indicate that the proteomic approach is useful in order to identify peptides or proteins that can be used as biomarkers for disease diagnosis or prognosis.

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