Proteomics Technologies for the Identification of Disease Biomarkers: Application to Infectious Diseases and Cancer

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Proteomics is the study of the function of all expressed proteins. Tremendous progress has been made in the past few years in generating large-scale data sets for protein–protein interactions, organelle composition, protein activity patterns and protein profiles in cancer patients. Proteomics complements other functional genomics approaches, including microarray-based expression profiles, systematic phenotypic profiles at the cell and organism level, systematic genetics and small-molecule-based arrays. The ability of mass spectrometry to identify ever smaller amounts of protein from increasingly complex mixtures is a primary driving force in proteomics.

We have used mass-spectrometry based proteomic chip technology in order to define differential protein expression profiles in sera from HTLV-1 (Human T Cell Leukemia Virus Type 1)-infected individuals and determine the resulting proteomic changes that define ATL (HTLV-1 –associated Adult T Cell Leukemia) and HAM/TSP (HTLV-1 –associated neurodegenerative disease).

HTLV-1 is estimated to currently infect close to 20 million people worldwide. Our approach is to develop disease-specific protein expression profiles, which can be used as predictors of disease outcome and as biomarkers.