8a Plenary: Drilling Deeper into the Proteome

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Genome sequencing projects have revealed that the human genome encodes for approximately 30,000 genes. An estimate of the scope of the proteome arising from these genes is up to ten times higher due to gene-processing, variants and post-translational modifications. The concept of proteomics is now 10 years young, and while great strides have been made in analysing proteomes we are orders of magnitudes removed from complete proteome characterisation (e.g., Anderson et al Mol. Cell. Proteomics 3, 2004, where 1175 non-redundant proteins were identified in human plasma). Early efforts by APAF and others towards drilling into the proteome utilised sample pre-fractionation based on protein solubility and various electrophoretic separation parameters (e.g., pI). In an effort focused towards protein biomarkers in human biofluids, APAF is developing an approach to remove at least the 100 most abundant proteins from human serum - paving the way to detect less abundant proteins that may have diagnostic potential. This strategy known as cyclic abundant protein immunodepletion (CAPI) utilizes suites of polyclonal IgY antibodies and involves successive rounds of immunization with pre-fractionated serum/plasma then depletion of high abundant proteins from the original antigen followed by additional cycles. A second approach for deeper drilling involves using improved MALDI capture targets (i.e., LumiCyte STS-biochips) that provide higher sensitivity for protein identification. Deeper drilling of the proteome will augment the systems biology approach of using bioinformatics to weave together data from disparate experimental approaches to provide a holistic view of biological activity.