GLOBAL PROTEOME ANALYSIS OF THE HUMAN PLASMA REVEALS NEW BIOLOGICAL FEATURES: A REVIEW OF EVOLUTIONARY IMPLICATIONS

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Coding capacity of the genome determines primary amino acid sequence of proteins. However, the human proteome space, is not limited to the primary peptide sequence coded by the approximately 25 000 protein coding genes, complexity is estimated to be at least 10^2 - 10^3 fold higher. This, “added” proteome complexity is at least partly due to the variability introduced by splice variation and other genetically coded differences. However, genetically non coded variability, like protein-portein interactions, post translational modifications, and folding state heterogeneity also influence protein function. Thus, while deciphering primary peptide sequence and its' variability is important, however, it is insufficient for understanding protein function, especially in the case of complex protein mixes like the human blood plasma, or i.e. the hemolymph of drosophilidae. Popular global, mass spectrometry based proteome analysis tools do not provide sufficient insight into protein complexity.

Similarly to domains carrying functional activity, antigenic epitops of proteins are also influenced by secondary and tertiary structure, splice variation, genetic variation and genetically non-coded variability (protein interactions, folding variation). In order to test whether the quasi global analysis of medium and highly abundant human plasma proteome by non redundant (at the epitome level) mAB libraries would detect at least some of addressed protein features we performed monoclonal antibody proteomics profiling of the human plasma proteome. Initial results indicate that our approach my shed light to novel aspects of proteome heterogeneity with considerable biological relevance from human to insects.