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Perspective

A Brief Note on Human Plasma Proteome

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DESCRIPTION

Plasma is not only the most common clinical specimen, but it also contains the most comprehensive version of the human proteome found in any sample. It contains all tissue proteins as well as a large number of distinct immunoglobulin sequences, and it has an incredible dynamic range, with more than 10 orders of magnitude in concentration separating albumin from the rarest proteins now measured clinically. If substantial obstacles in proteomics and associated fields can be overcome, the human plasma proteome has the potential to revolutionise illness diagnosis and treatment monitoring.

Although traditional proteomic technology's limited dynamic range has limited its contribution to the list of 289 proteins found in plasma to date, current developments in multidimensional survey techniques promise to at least quadruple this number in the near future. Proteomics and other scientific data shows that among them are proteins whose abundances and structures alter in ways that is suggestive of many, if not all, human disorders. Despite this, just a few proteins are now utilised in normal clinical diagnosis, and the number of new protein tests authorised by the US Food and Drug Administration (FDA) has dropped to less than one new protein diagnostic marker per year during the previous decade. We hypothesise on the causes for the enormous gap between the expectations deriving from proteomics and the realities of clinical diagnostics, and we propose methods for more efficiently translating protein-disease relationships into diagnostic tools in the future.

In many ways, the proteome of blood plasma is unusual. It's the most complicated human proteome, with subsets of different tissue proteomes. It's harvested in large quantities for the production of protein therapeutics. Because of the large proportion of albumin (55%), the wide dynamic range in abundance of other proteins, and the tremendous heterogeneity of its predominant glycoproteins, with hundreds of millions of tubes taken every year for medical diagnosis, it is the most sampled proteome, making it clinically the most significant.

After seeing the recent superlatives of the human genome effort(s) and the expectations that they produced, it may seem foolish to utilise such exaggeration in the more humble realm of proteins and proteomics. In reality, the special character of plasma prevents us from committing the sin of self-congratulation because we are not in imminent danger of finishing its analysis or even maximising its diagnostic capabilities. The combination of extreme analytical difficulty and well-founded hopes for radical improvements in disease diagnosis makes a compelling case for increased research effort at this point, particularly some systematic means of speeding up an investigation that has been ongoing for decades. Molecular biology, including genome and proteome projects, is changing biological and medical sciences, promising a complete knowledge and effective treatment of all human ailments. These efforts exemplify reductionist biology's ultimate goal. A comprehensive investigation and description of biological systems at the molecular level. Billions of dollars were raised, tens if not hundreds of thousands, of patents were submitted, and new large integrated laboratories were built and managed on a crash basis in the one case quasi-completed so far.

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