# Pros and Cons of the Proteomics

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The number of proteins produced by the 30,000-40,000 genes of the human genome is estimated to be three or four orders of magnitude higher. Proteomics is a rapidly developing science. In principle, two main areas in the field of proteomics have been developed, each of them having its pros and cons. These fields are profiling and functional proteomics. The aim of the proteomic profiling is to describe and index the whole set of proteins of a biological sample, which could be an organism, an organ, or a cell, or parts there of like individual's tissue or organelles. In our understanding, both types of proteomics (profiling and functional) are valuable tools complementing other biological methodologies. *(Biomed J 2014;37:163-164)*

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At present, proteomics seems to be the most promising tool for global quality assessment of the production process of blood components and blood derivatives. Table 1 lists the various assays being used to follow changes in platelets with processing and storage of platelet storage lesion. The potential of proteomics as a viable tool for the identification of the platelet storage lesion has since increased dramatically with the development of mass spectrometry (MS), and has required the development of quantitative proteomic techniques such as differential gel electrophoresis (DIGE), isotope-coded affinity tagging (ICAT), and isotope tagging for relative and absolute quantitation (iTRAQ). Proteomics offers the power to characterize protein mixtures in such systems, determine relationships between proteins, resolve their function, and identify protein–protein interactions of interest in the platelet storage lesion process. In this regard, 2D gel electrophoresis, DIGE, iTRAQ, and ICAT can be used to identify protein isoforms that may enable platelets to be stored longer, and resolve conditions under which such platelets store better. As many differential effects on proteins themselves come from post-translational modifications (PTMs) such as phosphorylation or glycosylation, monitoring these will contribute to a better understanding of how platelets function under various storage conditions.

The term "proteome" (PROTEins expressed by agenOME) was coined by Wilkins and colleagues in 1996.[1] Initially the word proteomics referred to the techniques used to analyze a large number of proteins at the same time, but at present, this word covers any approach that yields information on the abundance, properties, interactions, activities, or structures of proteins in a sample.[2] The number of proteins produced by the 30,000-40,000 genes of the human genome is estimated to be three or four orders of magnitude higher.[3] The reasons for this numerical superiority and complexity are: i) differential splicing of mRNA gene transcripts, which allows a single gene to produce multiple protein products; ii) the capability many proteins have of associating with other proteins to form complexes; and iii) PTMs, which are additional changes that proteins initially translated within a cell may undergo. These are covalent modifications that regulate protein functions, determining their activity state, cellular location, and dynamic interactions with other proteins; the most important and best-studied PTMs are phosphorylation and glycosylation, but many others are common (acetylation, methylation, lipid attachment, sulphation of tyrosine, ubiquitination, and disulfide bond formation) among over 300 different known types.[4]

Proteomics is a rapidly developing science, and allows a much more precise assessment of the quality of the blood products transfused to patients. In principle, two main areas in the field of proteomics have been developed, each of them having its pros and cons. These fields are "profiling" and "functional" proteomics.[5] The aim of the proteomic profiling is to describe and index the whole set of proteins of a biological sample, which could be an organism, an organ, or a cell, or parts thereof like individual's tissue or organelles. Profiling also includes differential protein expression levels under specific experimental conditions

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**Table 1:** Assays for quantification and characterization of platelet storage lesion

| Type of analysis | Method |
|---|---|
| Routine assays in transfusion Practice | Visual inspection |
| | Qualitative swirling |
| | Platelet count |
| | Concentrate volume |
| | pH* and leukocyte content |
| Assays primarily for research application | Morphology score* |
| | Mean platelet volume (MPV) |
| Platelet morphology | Extent of shape change (ESC)* |
| | Hypotonic shock response (HSR)* |
| GP expression | Expression of CD41 and CD61 |
| Metabolic activity | pH, pO2, pCO2, HCO3 changes |
| | Lactate production |
| | Glucose consumption |
| | Intracellular calcium |
| | ATP/ADP ratio* |
| Platelet aggregation | Spontaneous aggregation |
| | Response to dual agonists |
| Coagulation | Fibrinogen binding |
| Platelet activation | CD62 P-selectin expression |
| | Annexin V binding |
| Platelet lysis | Supernatant LDH content |
| | Lysate vWF: Ag levels |
| UV and gamma irradiation | Nucleic acid core |
| | RNA crosslinking |
| Proteomics | Differential gel electrophoresis (DIGE) |
| | Isotope-coded affinity tagging (ICAT) |
| | Isotope tagging for relative absolute quantitation (iTRAQ) |
| *In vivo* assays | Corrected count increment (CCI) |
| | Bleeding time studies |
| | Radiolabeled survival (Cr-51, In-111) |
| | Biotin-labeled survival |

**In vitro* tests correlating with platelet viability

or the comparison of different types or origins of sample material. Thus, proteomic profiling describes the inventory of proteins at a particular point of time. In contrast to the more static approach of proteomic profiling, the term "functional proteomics" encompasses direct functional aspect, like enzyme activity, protein interactions, and PTMs. Although these two experimental approaches cannot be seen completely separate, profiling has been regarded to be of minor biological relevance due to its descriptive nature. However, such an opinion does not seem justified, since the cataloging of existing proteins is a basis to generate new hypotheses which trigger further biological investigations; on the other hand, functional proteomics is based on protein profiling, since one needs to know which protein to search for when it is intended to focus on a subset of proteins that are functionally coupled. In our understanding, both types of proteomics ("profiling" and "functional") are valuable tools complementing other biological methodologies.

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