Revolutionizing Healthcare: The Proteomics Paradigm in Molecular Medicine

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Proteomics, the comprehensive study of function, composition, structures, and interactions of proteins in biological systems, has emerged as a revolutionary force in the field of molecular medicine. Over the last few decades, this rapidly developing field has played a decisive role in decoding the complex molecular mechanisms underpinning health and disease. In this editorial, we explore the crucial role that proteomics plays in the field of molecular medicine, emphasizing how it has transformed diagnostic/prognostic biomarker discovery, therapeutics, and our basic knowledge of the human body.

The Human Genome Project (HGP) has been the prime focus in past decades and has provided a plethora of knowledge. However, a significant drawback of genomic studies is that they does not correlate with proteins, an executor of cellular processes. Therefore, proteomics bridges the gap of genomics to provide a holistic view of the molecular mechanism of the disease. Almost a decade ago in 2010, to get deep insight into the proteome intricacies, including post-translational modifications, proteoform, and interactome, the Human Proteome Project (HPP) was launched. According to a recent draft, over 90% blueprint of the human proteome has been mined, yet further information stored in the proteome remains to be discovered¹.

Biomarkers play a promising role in the early diagnosis, prognosis, and therapy response. The advancement in proteomics techniques particularly mass spectrometry has redefined biomarker discovery. Recently in 2022 FDA approved the first in vitro test that measures the ratio of β-amyloid 1-42 and β-amyloid 1-40 in cerebrospinal fluid for early detection of amyloid plaques associated with Alzheimer's disease. Another recent breakthrough is the FDA clearance of the Roche test that measures β-amyloid and tau proteins to confirm pathological changes in Alzheimer's disease. Moreover, a recent study published by Luan, Yi, et al. concluded a panel of seven proteins from the blood for early detection of multiple cancer by using an electro-chemiluminescence immunoassay analyzer and Oncoseek, an artificial intelligence (AI) algorithm². Researchers are now developing next-generation strategies for pan-cancer proteome profiling to establish novel cancer-specific protein signatures³. The continuing advancements in mass spectrometry-based diagnostic methods are escalating the diagnostic landscape. Numerous methods have been approved by the FDA in the past decade including vitamin D assay, newborn screening, therapeutic drug quantification, and pathogen identification.

Furthermore, the technological advancements in proteomics have extended it applications in drug target identification, mechanism, efficacy, resistance, and toxicity. Pharmacoproteomic is essential in suggesting potential therapeutic strategies by proteomic characterization in response to medications. A study by Henry et al. identified 7 druggable targets for heart failure⁴. A wide variety of proteomic methods from conventional to advanced techniques are currently available including 2D-DIGE, high-resolution MS, TMT, iCAT, SILAC, iTRAQ, protein microarrays, N-terminomics, next-generation tissue microarrays, single-molecule proteomics, aptamer-based assays, single-cell proteomics, proximity extension assay, etc. to solve the mysteries. Moreover, breakthroughs in machine learning and deep learning for big data analysis will further help in translating the concept of proteomics from bench to bedside⁵.

In conclusion, the future of proteomics holds great promise in exploring new dimensions in the field of molecular medicine. In Pakistan, where health challenges persist, proteomics can offer significant contributions by identifying specific proteins associated with prevalent diseases or protein profiles in different patient populations thus aiding in early diagnosis and prognosis. Likewise, considering the genetic diversity of Pakistan, proteomics can aid in tailoring drug treatment by identifying drug targets and drug resistance mechanisms to improve the effectiveness of exciting treatments. However, a strong collaboration between scientists, clinicians, healthcare industries, and policymakers is crucial to translating these advancements into practical applications that can positively impact public health.

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REFERENCES

1. Adhikari S, Nice EC, Deutsch EW, Lane L, Omenn GS, Pennington SR, Paik YK, Overall CM, Corrales FJ, Cristea IM, Van Eyk JE. A high-stringency blueprint of the human proteome. Nature communications. 2020;11(1):5301. doi: 10.1038/s41467-020-19045-9.

2. Luan Y, Zhong G, Li S, Wu W, Liu X, Zhu D, Feng Y, Zhang Y, Duan C, Mao M. A panel of seven protein tumor markers for effective and affordable multi-cancer early detection by artificial intelligence: a large-scale and multicentre case–control study. eClinicalMedicine. 2023;61 :102041. doi: 10.1016/j.eclinm.2023.102041.

3. Álvez MB, Edfors F, von Feilitzen K, Zwahlen M, Mardinoglu A, Edqvist PH, Sjöblom T, Lundin E, Rameika N, Enblad G, Lindman H. Next generation pan-cancer blood proteome profiling using proximity extension assay. Nature Communications. 2023;14(1):4308. doi: 10.1038/s41467-023-39765-y.

4. Henry A, Gordillo-Marañón M, Finan C, Schmidt AF, Ferreira JP, Karra R, Sundström J, Lind L, Ärnlöv J, Zannad F, Mälarstig A. Therapeutic targets for heart failure identified using proteomics and Mendelian randomization. Circulation. 2022;145(16):1205-1217. doi: 10.1161/CIRCULATIONAHA.121.056663.

5. Cui M, Cheng C, Zhang L. High-throughput proteomics: a methodological mini-review. Laboratory Investigation. 2022;102(11):1170-1181. doi: 10.1038/s41374-022-00830-7.

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