

Role of Protein Biomarkers in Performing Accurate Disease Diagnosis

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ABSTRACT

Protein biomarkers are detectable signs in a patient's blood that correlate with significant events or signal specific stages in a biological process, such as disease progression. Better biomarkers are desperately needed to better diagnosis, guide molecularly focused therapy, and track activity and therapeutic response across a broad range of diseases. Proteomics technologies based on mass spectrometry hold particular potential for the development of novel biomarkers that could form the basis for new clinical blood tests, but their contribution to the diagnostic arsenal has been unsatisfactory thus far. This is due in part to the lack of a unified pipeline that connects marker discovery with well-established validation approaches. Candidate identification, qualification, verification, research assay optimization, biomarker validation, and commercialization may now be built into a comprehensive biomarker pipeline.

Keywords: Protein biomarkers; Non-invasive testing; Disease diagnosis; Diagnostic tests

DESCRIPTION

Proteins are important because they are typically easier to measure than the complicated actions they reflect. Proteins are particularly helpful as biomarkers since they are frequently the cause of diseases and the focus of therapeutic interventions. Healthcare professionals can use protein biomarker panels to accomplish reliable illness diagnosis through non-invasive testing. Improved experimental study design, as well as a better understanding of the overall process of biomarker discovery and validation, as well as the challenges and strategies inherent in each phase, should improve biomarker development efficiency and facilitate the delivery and deployment of novel clinical tests. Diagnostic testing is critical in modern medicine, as it assists doctors in making educated decisions about disease diagnosis and treatment. Currently, spectrophotometric or immunologic analysis is used in the majority of routine chemical assays [1-4]. However, there is a growing realization that effective diagnostic assays will require *in vitro* diagnostic multivariate index assays and the inherent ability of mass spectrometry (MS) to multiplex analytes efficiently and precisely, rather than screening for individual markers. MS-based protein biomarker discovery has risen to the forefront of molecular diagnostics research as a result of this. Over the last two decades, a lot of development has

been done. The latest advances in proteomics technologies, such as advances in MS technology and tandem mass tag reagents, as well as the creation of powerful bioinformatics software, spectral libraries, and peptide databases, are opening up new avenues for the development of protein biomarkers for disease diagnosis, prognosis, and therapeutic response prediction. Despite the huge number of candidate protein biomarkers published, a well-documented gap exists between the number of candidate biomarkers identified and those cleared or licensed for clinical use by the FDA. We look at whether using robust quality control (QC) measures and robust experimental design may help bridge this gap and speed up biomarker translation from bench to bedside. Proteomics technology used to detect new protein biomarkers have advanced significantly over the last two decades. Thousands of potential protein biomarkers have been identified as a result of research. However, only a small percentage of these candidates have progressed to FDA-approved clinical diagnostic tests. Biomarkers discovered in initial discovery investigations are frequently found to have inconsistent activity during subsequent validation. Biomarker panels are used more widely in clinical diagnostics, resulting in more tailored and effective illness therapy. However, there is a considerable translational gap between proteomic biomarker discovery and validation that must

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be bridged if sensitive and selective biomarkers are to advance more quickly from the research lab to the clinic.

REFERENCES

1. Crutchfield CA, Thomas SN, Sokoll LJ, Chan DW. Advances in mass spectrometry-based clinical biomarker discovery. *Clin Proteomics*. 2016;13(1):1-2.
2. Füzéry AK, Levin J, Chan MM, Chan DW. Translation of proteomic biomarkers into FDA approved cancer diagnostics: issues and challenges. *Clin Proteomics*. 2013;10(1):1-4.
3. Hernández B, Parnell A, Pennington SR. Why have so few proteomic biomarkers “survived” validation?(Sample size and independent validation considerations). *Proteomics*. 2014;14(13-14): 1587-92.
4. Pepe MS, Feng Z, Janes H, Bossuyt PM, Potter JD. Pivotal evaluation of the accuracy of a biomarker used for classification or prediction: standards for study design. *J Natl Cancer Inst*. 2008;100(20):1432-8.