

Proteomic Technologies for the Discovery of Type 1 Diabetes Biomarkers

Wenbo Zhi, Ph.D., Sharad Purohit, Ph.D., Colleen Carey M.S., Meiyao Wang, Ph.D., and Jin-Xiong She, Ph.D.

Abstract

In this review, we discuss several important issues concerning the discovery of protein biomarkers for complex human diseases, with a focus on type 1 diabetes. Serum or plasma is the first choice of specimen due to its richness in biological information and relatively easy availability. It is a challenging task to comprehensively characterize the serum/plasma proteome because of the large dynamic range of protein concentration. Therefore, sample pretreatment is required in order to explore the low- to medium-abundance proteins contained in serum/plasma. In this regard, enrichment of low-abundance proteins using random hexapeptide library beads has distinct advantages over the traditional immune-depletion methods, including higher efficiency, higher binding capacity, and lower cost. In-depth mining of serum/plasma proteome using different separation techniques have also been evaluated and are discussed in this review. Overall, the shotgun proteomics—multidimensional separation of digested peptides followed by mass spectrometry analysis—is highly efficient and therefore has become a preferred method for protein biomarker discovery.

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Author Affiliation: Center for Biotechnology and Genomic Medicine, Medical College of Georgia, Augusta, Georgia

Abbreviations: (2D) two dimensional, (3D) three dimensional, (AbP) autoantibody-positive, (DIGE) difference gel electrophoresis, (GeLC) gel-based liquid chromatography, (HPLC) high-performance liquid chromatography, (IEF) isoelectric focusing, (PM) ProteoMiner, (PTM) posttranslational modification, (RP) reverse phase, (SDS-PAGE) sodium dodecyl sulfate polyacrylamide gel electrophoresis, (SELDI-TOF) surface-enhanced laser desorption and ionization time-of-flight, (T1DM) type 1 diabetes mellitus

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Corresponding Author: Jin-Xiong She, Ph.D., Center for Biotechnology and Genomic Medicine, Medical College of Georgia, 1120 15th Street, Augusta, GA 30912; email address jshe@mail.mcg.edu