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Serum proteomic based biomarkers identification in diabetic patients

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Diabetes is one of the most challenging health problems. The global prevalence of diabetes in the adult population is 8.5, and it caused 1.6 million deaths worldwide in 2015. In human serum, for example, albumin and immunoglobulin comprise over 50% of total serum protein mass. The current proteomic technique is limited by the high dynamic range of protein concentration. In most of the biological sample, the dynamic range of protein concentration spans more than 10 orders of magnitude. This large range of concentration exceeds the analytical capabilities of most proteomic technique, hindering the detection of those low abundant, but important, proteins. To tackle this challenge, our research group is focusing on the technique of detecting the low abundant proteins in the complex biological sample. For example, in a serum biomarker discovery study for early diagnosis of diabetic complication, we have reduced the sample complexity by two pretreatment methods separately: 1) ligands competition and 2) depleting the high abundant proteins by immunodepletion. Interestingly, these two pretreatment methods result in two very different proteome profiles, whereas only <6% of proteins were identified by both methods. Besides, we have found that a more comprehensive proteome profile could be generated by combining the data from both matrix-assisted laser desorption/ionization (MALDI) and electrospray ionization (ESI) based mass spectrometry, which could enhance the detection of low abundant proteins. By comparing the proteome profile between the sera from patients with and without diabetic complications, we have identified several potential biomarkers, including the high-abundant proteins (e.g. haptoglobin and transferrin); as well as the low-abundant proteins (e.g. R3HCC1L and zinc-alpha-2-glycoprotein).

Biography

Ngai Sai Ming has completed the degree of PhD from the University of Alberta, Canada. He is the Associate Professor at School of Life Sciences of Chinese University of Hong Kong (CUHK). Professor NGAI is the Director of The Chinese Medicinal Fungal Proteomics Laboratory (CUHK) and Investigator of State Key Laboratory for Agrobiotechnology in CUHK. His research interest includes bioinformatics, proteomics, protein/peptide structural and functional studies, research and development on Modern Chinese Medicine.

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