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·Letter to the Editor·

Proteomic analysis in diabetic retinopathy

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Dear Sir,

I am Prof. Beuy Joob from Sanitation 1 Medical Academic Center, Bangkok, Thailand. I write to discuss the recent publication on proteomic analysis in diabetic retinopathy(DR).Liu *et al*[1] concluded that their approach by two dimensional fluorescence difference gel electrophoresis (2D-DIGE) combined with matrix-assisted laser desorption/ionization time of flight tandem mass spectrometry (MALDI-TOF MS) could be useful in proteomic study, with some limitations, for DR and further claimed that this could be the way to find the candidate biomarker on DR diagnosis. First, it is no doubt that the use techniques, which are the basic proteomics techniques, can be useful in proteomic study. However, it has to be noted that proteomics study is the study of the already expressed proteins, not the genes. Hence, the exact pathogenesis might not be completely revealed from this approach. Finding proteins from proteomics study might be the exact proteins from the focused disease, which hereby is DR, or from other confounding diseases. In this work, there is no ruling out of other possible concomitant diseases such as renal disease. The simple question is whether the detected proteins in this work are actually due to the DR or other disorders that are not clarified in this work. Also, the conclusion that this work can be a way to find candidate biomarker for DR should be discussed. With the already mentioned concerns, the detected proteins might not be good biomarkers. In addition, the next question is whether the blood biomarker is reliable and acceptable in the specific case of DR. As a gold standard, retinopathy has to be diagnosed based on the opthalmological assessment. The finding of protein which is the biochemical assessment might not be as good as anatomical eye assessment.

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