

A Method for Comprehensive and Quantitative Proteome Analysis Using 1-D and 2-D DIGE Combined with MicroSol IEF Prefractionation

한미정^{1,2,*}

¹동양대학교 생명화학공학과; ²The Wistar Institute

(mjhan75@dyu.ac.kr*)

Current methods for quantitatively comparing complex protein profiles such as two-dimensional gel electrophoresis (2-DE), 2-D differential in-gel electrophoresis (DIGE), and liquid chromatography (LC)-mass spectrometry (MS) have still limited resolution and dynamic ranges. In this study, we introduce a new method of 1-D/2-D DIGE combined with microscale solution isoelectric focusing (MicroSol-IEF) fractionation. The method has advantages over sample prefractionation and conventional 2-D DIGE technique including high reproducibility, high resolution, and a much wide linear dynamic ranges for detection. To illustrate its utility, this method was applied to analysis of human melanoma cell lines and mouse lung tissue extracts. Thus it is a powerful method for more comprehensive and quantitative comparison of protein profiles of very complex proteomes. [This work was supported by Basic Science Research Program through the National Research Foundation of Korea(NRF) funded by the Ministry of Education, Science and Technology(2010-0008826)]