An efficient method for system-level proteome analysis of heart muscle in a rat model of myocardial ischemia/reperfusion

한미정*
동양대학교
(mjhan75@dyu.ac.kr*)

Within the past decade numerous methods for quantitative proteome analysis have been developed of which all exhibit particular advantages and disadvantages. Isobaric mass tagging (e.g., TMT and iTRAQ) is a precise and sensitive multiplexed peptide/protein quantification technique in mass spectrometry. In this study, heart muscle proteomes were analyzed using TMT protein labeling followed by digestion, separation, identification and quantification of proteins extracted from normal and hypoxic-reperfusion rats. A dye-swapping for each sample was carried out to minimize technical variances. The results show 185 of 1018 proteins identified were found to be differentially expressed when compared normal samples with hypoxic-reperfusion samples. Most of the proteins were myocardial infarction related and involved in energy metabolism, oxidative stress, detoxification, or transport. We were able to verify with existing literature many of our differentially expressed proteins as candidate hypoxic biomarkers and, most importantly, reveal several new candidate biomarkers. These results will be presented in detail.