Potential biomarkers for ischemic heart damage identified by comparative proteomics of a rabbit model: mitochondrial protein expression

Hyoung kyu Kim, Nari Kim, Hyun Joo, Jae boum Youm, Won sun Park, Sunghyun Kang, Dang Van Cuong, Teaho Kim, Hyunju Kim, Hyejin Moon, Hyunsuk Lee, Tran Minh Khoa, Vu Thi Thu, Euiyong Kim and Jin Han*

Abstract

Brief nonlethal episodes of ischemia in the mammalian heart provide cardioprotection against the detrimental effects of a longer duration ischemia. But the mechanism of this protection on a protein level is still unclear. We used proteomics to detect regional differences in protein expression levels from mitochondrial fractions of normal, ischemiareperfusion (IR), and ischemic preconditioned (IPC) rabbit hearts. Using two-dimensional gel electrophoresis (2-DE), we identified twenty mitochondrial proteins that were expressed differentially in the IR heart compared with the normal and IPC hearts. And these spots were confirmed by Western blotting. These proteins included 3-hydroxybutyrate dehydrogenase (3-HBD), prohibitin, 2-oxoglutarate dehydrogenase, ATP synthase, NADH oxidoreductase, translation elongation factor, actin alpha, malate dehydrogenase, NADH dehydrogenase and the voltage-dependent anion channel (VADC). Interestingly, these several proteins are associated with the mitochondrial respiratory chain and energy metabolism. The successful use of multiple techniques, including 2-DE, matrix assisted laser desorption ionizationtime-of-flight mass spectrometry (MALDI-TOF-MS) and western blot, demonstrates that proteomic analysis can be an appropriate means of identifying cardiac markers to detect ischemia-induced cardiac injury.

Key words; Proteomic analysis, Ischemic preconditioning, ischemia-reperfusion injury, Cardiac biomarker.