Abstract

Extrapolation of known radiation risks to the risks from low dose and low dose-rate exposures of human population, especially prolonged exposures of astronauts in the space radiation environment, relies in part on the mechanistic understanding of radiation induced biological consequences at the molecular level. While some genomic data at the mRNA level are available for cells or animals exposed to radiation, the data at the protein level are still lacking. Here, we studied protein expression profile changes using Panorama antibody microarray chips that contain antibodies to 224 proteins (or their phosphorylated forms) involved in cell signaling that included mostly apoptosis, cytoskeleton, cell cycle and signal transduction. Normal human fibroblasts were cultured until fully confluent and then exposed to 2cGy of 150MeV protons at high-dose rate. The proteins were isolated at 2 or 6h after exposure and labeled with Cy3 for the irradiated cells and with Cy5 for the control samples before loading onto the protein microarray chips. The intensities of the protein spots were analyzed using ScanAlyze software and normalized by the summed fluorescence intensities and the housekeeping proteins. The results showed that low dose protons altered the expression of more than 10% of the proteins listed in the microarray analysis in various protein functional groups. Cell cycle (24%) related proteins were induced by protons and most of them were regulators of G1/S-transition phase. Comparison of the overall protein expression profiles, cell cycle related proteins, cytoskeleton and signal transduction protein groups showed significantly more changes induced by protons compared with other protein functional groups.