Predicting Dose Level and Length of Time for Radiation Exposure Using Gene Expression

Authors : Chao Sima, Shanaz Ghandhi, Sally A. Amundson, Michael L. Bittner, David J. Brenner

Abstract : In a large-scale radiologic emergency, potentially affected population need to be triaged efficiently using various biomarkers where personal dosimeters are not likely worn by the individuals. It has long been established that radiation injury can be estimated effectively using panels of genetic biomarkers. Furthermore, the rate of radiation, in addition to dose of radiation, plays a major role in determining biological responses. Therefore, a better and more accurate triage involves estimating both the dose level of the exposure and the length of time of that exposure. To that end, a large in vivo study was carried out on mice with internal emitter caesium-137 (^{137}Cs). Four different injection doses of ^{137}Cs were used: 157.5 µCi, 191 µCi, 214.5µCi, and 259 µCi. Cohorts of 6~7 mice from the control arm and each of the dose levels were sacrificed, and blood was collected 2, 3, 5, 7 and 14 days after injection for microarray RNA gene expression analysis. Using a generalized linear model with penalized maximum likelihood, a panel of 244 genes was established and both the doses of injection and the number of days after injection were accurately predicted for all 155 subjects using this panel. This has proven that microarray gene expression can be used effectively in radiation biodosimetry in predicting both the dose levels and the length of exposure time, which provides a more holistic view on radiation exposure and helps improving radiation damage assessment and treatment.

Keywords : caesium-137, gene expression microarray, multivariate responses prediction, radiation biodosimetry

Conference Title : ICPB 2018 : International Conference on Proteomics and Bioinformatics

Conference Location : Osaka, Japan

Conference Dates : March 29-30, 2018