OMICS Group Conferences
Accelerating Scientific Discovery

3rd World Congress on
Cell Science & Stem Cell Research
November 20-22, 2013 DoubleTree by Hilton Baltimore-BWI Airport, MD, USA

Global gene expression response to acute dose proton radiation in mice: Understanding of early cancer causing events and natural suppression pathways for cancer treatment

Muhammad Akram Tariq[1,2], Shahid Yar Khan[2], Hyunsung John Kim[2], Daniel Carlin[2], Govindarajan T. Ramesh[3], Olufisayo Jejelowo[4] and Nader Pourmand[2]

[1]King Edward Medical University, Pakistan
[2]University of California Santa Cruz, US
[3]Norfolk State University, US
[4]Texas Southern University, US

Astronauts are exposed to proton radiations from space environments, which would have severe health implications for them during interplanetary missions. Radiation is genotoxic and induces DNA lesions in human cells that can lead to cancer and tumor formation. To ensure genomic integrity, cells initiate complex responses that rely on changes in gene expression. The understanding of cellular response to proton radiation would shed a light on the etiology of various cancers. In this study, we evaluated the altered gene expression response to whole-body acute dose proton irradiation (2.0 Gy) of brain, liver and testes tissues of mice by sequencing the whole transcriptome using next-generation sequencing. We observed significant deregulation ($p<0.05$) of a total 622 genes in brain (534 genes upregulated, 88 genes downregulated), 968 genes in liver (456 genes upregulated, 512 genes downregulated) and 763 genes in testis tissues (349 genes upregulated, 414 genes downregulated). The most dysregulated genes in response to radiation in different tissues are involved in significant pathways of tumorgenesis such as cell proliferation, cell growth, invasiveness and metastasis. However, natural response to reverse the effects of radiationwas also observed in the form of activation of cell-cycle arrest, tumor suppressor and apoptotic pathways. We also identified several mRNA transcripts, upregulated upon proton irradiation, in brain, liver and testes tissues, which have not been characterized yet and further investigation of these transcripts and their proteins, may lead us to novel proton radiation responsive genes and enhance our understanding regarding complex cellular radiation response. We further identified functional gene ontology categories associated with proton irradiation. Interestingly, many of the over represented biological processes in response to proton irradiation include induction and regulation of cellular processes, apoptosis, cell death, cell cycle, caspase activity, cell signalling, calcium mediated cell signalling, exocytosis, response to stimulus and endoplasmic reticulum (ER) unfolded protein response to stress. According to our information, this is the first study to provide a comprehensive quantitative catalogue of differentially expressed mice whole transcriptome in response to proton radiation, which may contribute to more accurate estimation of the radiation safety standards in space during space missions and on earth during "proton radiation therapy", increasingly being used for the cancer treatment. Furthermore, this study highlights the early cancer causing events of radiation-based triggers and the natural response to these events bysuppression pathways.The understanding of the early cancer causing events and the natural suppression pathways would provide a promising approach for developing new strategies to treat cancers.

akram@soe.ucsc.edu