


Integrative Analysis for the Roles of lncRNAs in the Immune Responses of Mouse Peripheral Blood Mononuclear Cell Exposed to Low-Dose Ionizing Radiation-Reply

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Keywords

gene expression, ionizing radiation, lncRNA, low-dose radiation, lymphocytes

Provenance: This is an invited article commissioned by Denise Leonard.

Response to: Yuqing Wang, Shangge Lv, Xiaoqiang Liu, Lei Yan. Bioinformatics Analysis for the Roles of lncRNAs in the Immune Responses of Mouse PBMC Exposed to Low-Dose Ionizing Radiation. School of Medicine, Cheeloo College of Medicine, Shandong University.

First of all, we appreciate the editorial commentary on our published article “Integrative analysis for the roles of lncRNAs in the immune responses of mouse PBMC exposed to low-dose ionizing radiation (LDIR)”.¹

Toxicity and carcinogenesis of LDIR are a lot less obvious, and the probability of severe direct DNA damage after low doses is extremely low, while other, more subtle functional alterations induced by LDIR, such as adaptive response and hormetic effect, have received more attention.² Nevertheless, the understanding on the underlying mechanisms of LDIR-induced immune hormesis is still fragmented and incomplete. The researches on gene expression alterations helped to understand the molecular mechanisms of LDIR-induced immune hormetic effect.³ Accumulating evidence indicates that lncRNAs modulate transcription or post-transcriptional processes, participate in responses modulated by ionizing radiation and transcriptional programs of immune cells, however, lncRNAs in LDIR-induced immune hormesis have been rarely reported, and the functions and molecular mechanisms of lncRNAs in LDIR-induced immune hormesis have not yet been characterized. In this study, to reveal the function of lncRNA in LDIR-induced immune hormesis, we used microarray profiling to determine lncRNA and mRNA expression in BALB/c mice exposed to single- (0.5Gy × 1) and chronic (.05Gy × 10) low-dose γ -rays radiation (Co⁶⁰).

We agree with the editorial author’s view on the characteristics of highly variability and low expression levels of lncRNAs to challenge for the statistical tools for differential expression analysis. However, the quality of the data obtained by microarray technology in this study was superior to RNA-seq for low abundance genes.⁴ And the microarray results were verified by RT-qPCR approach. The editorial author’s concerns on the characteristics of lncRNAs and high false positives are unlikely. A specialized Linear Models for Microarray Analysis (Limma) suggested by editorial author is not quite suitable for LDIR data. Since the changed folds of gene expression caused by LDIR is low, if the differential genes are discarded according to this specialized analysis method, the remaining genes may be too few to reflect the true biological effect induced by LDIR. Therefore, in this study, function pathways for the differentially expressed mRNAs were revealed by Gene Ontology terms and kyoto encyclopedia of genes and genomes database according to the previous report.⁴ To further understand the potential interactions of differentially expressed lncRNAs and mRNAs involved in LDIR-induced immune signaling pathways, we constructed a co-expression network based on a correlation analysis of the differentially expressed lncRNAs and mRNAs.^{4,5}

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Declaration of Conflicting Interests

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Ethical Statement

The author is accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

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