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Whole transcriptome analysis revealed a stress response to deep underground environment conditions in Chinese Hamster V79 lung Fibroblast Cells

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Background: Prior studies have shown that the proliferation of V79 lung fibroblast cells could be inhibited by low background radiation (LBR) in deep underground laboratory (DUGL). In the current study, we revealed further molecular changes by performing whole transcriptome analysis on the expression profiles of long non-coding RNA (lncRNA), messenger RNA (mRNA), circular RNA (circRNA) and microRNA (miRNA) in V79 cells cultured for two days in a DUGL

Methods: Whole transcriptome analysis including lncRNA, mRNAs, circ RNA and miRNA was performed in V79 cells cultured for two days in DUGL and above ground laboratory (AGL), respectively.The differentially expressed (DE) lncRNA, mRNA, circRNA and miRNA in V79 cells were identified by the comparison between DUGL and AGL groups. Quantitative real-time polymerase chain reaction(qRT-PCR)was conducted to verify the selected RNA sequencings. Then, Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway was analysed for the DE mRNAs which enabled to predict target genes of lncRNA and host genes of circRNA.

Results: With $|\log2(\text{Fold-change})| \geq 1.0$ and $p < 0.05$, a total of 1257 mRNAs (353 mRNAs up-regulated, 904 mRNAs down-regulated), 866 lncRNAs (145 lncRNAs up-regulated, 721 lncRNAs down-regulated), and 474 circRNAs (247 circRNAs up-regulated, 227 circRNAs down-regulated) were significantly altered between the two groups. There was no significant difference in miRNA between the two groups. The altered RNA profiles were mainly discovered in lncRNAs, mRNAs and circRNAs. DE RNAs were involved in many pathways including ECM-RI, PI3K-Akt signaling, RNA transport and the cell cycle under the LBR stress of the deep underground environment.

Conclusion: Taken together, these results suggest that the LBR in the DUGL could induce transcriptional repression, thus reducing metabolic process and reprograming the overall gene expression profile in V79 cells.

Key words: Deep underground environment, V79 cells, mRNA, lncRNA, circRNA

Recent Publications

1. Proteomics provides insights into the inhibition of Chinese hamster V79 cell proliferation in the deep underground environment

2. Should Contralateral Nodules Be an Indication of Total or Completion Thyroidectomy for Patients with Unilateral Papillary Thyroid Carcinoma? Front. Endocrinol., 09 August 2021 | https://doi.org/10.3389/fendo.2021.723631.

3. Intraoperative dexmedetomidine-related polyuria: A case report and review of the literature2022 Apr;60(4):188-191. doi: 10.5414/CP204129.

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