Molecular Genetic Analysis of Neural Stem Cells After Space Flight And Simulated Microgravity on Earth

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Abstract

Understanding how stem cells adapt to space flight conditions is fundamental for human space missions and extraterrestrial settlement. We analyzed gene expression in boundary cap neural crest stem cells (bNCSCs), which are attractive for regenerative medicine by their ability to promote proliferation and survival of co-cultured and co-implanted cells. bNCSCs were launched to space (Space cells), onboard Sounding rocket as free-floating neurospheres or in bioprinted scaffold. For comparison, bNCSCs were placed in random positioning machine to simulate microgravity (Microgravity cells) or cultured under Earth conditions. Using Next-Generation RNA sequencing and data post-processing, a list of genes that were at least two-fold changed between control cells and Space cells were selected for further analysis. Functional clusters of enriched genes were obtained by gene ontology bioinformatics, using the DAVID program, and Ingenuity Pathway Analysis was used to predict functional implications of the identified gene expressions. Space cells upregulated genes related to proliferation and survival, whereas Microgravity cells upregulated genes associated with differentiation and inflammation. Thus, i) space flight provides unique conditions with distinctly different effects on the properties of bNCSCs compared to Earth controls, and ii) may induce post-flight properties that reinforce the utility of bNCSCs for regenerative medicine and tissue engineering.

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