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HYPOTHETICAL LOC GENES AS BIOMARKERS OF SPACEFLIGHT ADAPTATION: A COMPARATIVE STUDY FROM ISS, SUBORBITAL, AND EARTH-BASED EXPERIMENTS

Abstract

The long-term effects of microgravity on human biology remain a critical challenge for space exploration and astronaut health. Recent transcriptomic analyses from Axiom-3 and the MESSAGE Science Mission have identified uncharacterized and hypothetical LOC genes that exhibit differential expression in microgravity, particularly in long-duration ISS missions compared to suborbital flights and Earth-based controls.

This study focuses on the LOC gene family, a set of poorly characterized genes identified through genomic annotation, whose biological functions remain largely unknown. Among the key findings, LOC101928742, LOC105377546, and LOC285419 were significantly upregulated in ISS microgravity, suggesting a potential role in stress adaptation, metabolic regulation, and cellular resilience mechanisms. Conversely, LOC100996732, LOC101927091, and LOC102724836 were downregulated, indicating a possible link to immune suppression, energy conservation, or inhibited cellular proliferation under prolonged spaceflight conditions.

By integrating data from suborbital missions, ISS experiments, and Earth-based reference samples, this study provides a comparative analysis of gene expression patterns across different gravitational environments. Unlike transient microgravity exposure in suborbital flights, the ISS environment induced sustained changes in LOC gene expression, indicating that prolonged microgravity may activate novel genetic pathways essential for long-term physiological adaptation.

These findings contribute to a deeper understanding of gravitational stress responses at the molecular level, offering new insights into space medicine, astronaut health monitoring, and biotechnological applications. Identifying LOC genes as potential biomarkers of space adaptation could facilitate the development of genetic and pharmacological countermeasures for future long-duration space missions and planetary colonization efforts. Further functional studies, CRISPR-based gene editing, and bioinformatics analyses will be essential to unravel the specific roles of these genes and their implications for human biology in space.