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GENE PAIR CORRELATIONS AS NOVEL DIAGNOSTICS FOR ASTRONAUTS

Abstract

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Space travel exposes astronauts to a wide range of environmental stresses, including sustained microgravity and cosmic radiation. This is extremely harmful to astronauts' health and is associated with significant pathophysiological changes such as loss in muscle mass, reduction in bone density, compromised immune system, cancer and cardiovascular diseases. Monitoring the genetic dynamics behind these changes can help engage genomic medicine in clinical care and improve health outcomes for the astronauts. Advances in transcriptomic technologies now allow us to monitor these alterations at the genomic level and can help identify genes responsible for these ailments. However, sample size is a limitation for correlating and mapping gene expression alterations in astronauts to spaceflight. This is further confounded by the limited availability of data in the public domain.

This study analyzes transcriptomic data from GLDS 174 - "Effects of a closed space environment on gene expression in hair follicles of astronauts in the International Space Station" from the NASA GeneLab open data repository. We downloaded and analyzed the microarray dataset (E-GEOD-74708) which provides access to the gene expression information for 10 astronauts in three stages: Pre-flight (6 months to 2 weeks before launch), In-flight (while staying in the ISS), and Post-flight (2 days to 3 months after returning from the ISS). This is the largest gene expression dataset for astronauts in spaceflight in the public domain.

In this study, we developed and detailed a novel method of expression analysis called gene-pair correlation analysis, which is a measure of the mathematical concept of correlation coefficients when applied to individual genes and the genome as a whole. We analyzed the differential gene expression, as well as the gene expression correlation values of 20,000 transcripts in this dataset.

Our results show a significant and noticeable loss in overall genome correlation. Genes showing significant changes in expression during spaceflight were identified and shown to be involved in important biological pathways. These were further analyzed to classify gene pairs based on the strength of correlation. This procedure helped us identify 32 key genes which could potentially play critical roles in the pathophysiological changes reported above during spaceflight. This study is the first to propose the development of a scalable genome-based rapid assay kit (based on alterations in genome correlations) to monitor astronaut health in space. This proposed methodology could be further developed (with the analyses of more datasets) to provide revolutionary point-of-care diagnosis and treatment methods for astronauts in spaceflight.