

Summary of: Single-cell analysis identifies conserved features of immune dysfunction in simulated microgravity and spaceflight

****Key Findings and Quantitative Results:****

****Single-Cell Analysis:**** - ****Microgravity vs. 1G Conditions:**** Single-cell analysis of PBMCs exposed to simulated microgravity (25 hours) showed altered gene expression patterns compared to 1G conditions. - ****Gene Expression Patterns:**** Over 4500 genes were differentially expressed between unstimulated and stimulated conditions. - ****Core Gene List:**** A core gene list of ~375 genes was identified, with additional cutoffs for $|\log_2FC| > 0.1$ and $\text{adj. } p < 0.05$. - ****Pathway Analysis:**** Major pathways altered include interferon response, pyroptosis, oxidative stress, sirtuin signaling, etc.

****Validation Experiments:**** - ****Bulk RNA-seq:**** Bulk RNA-seq analysis of PBMCs from young donors showed 2149 differentially expressed genes. - ****Comparison:**** The core gene list from single-cell analysis was validated against bulk RNA-seq data, showing a high correlation in gene counts. - ****Overlap Analysis:**** Over 28% of core genes were identified as overlapping between single-cell and bulk RNA-seq datasets.

****Simulated Microgravity vs. Spaceflight:**** - ****iAge Index:**** iAge index was significantly reduced in simulated microgravity compared to spaceflight. - ****SenMayo Score:**** SenMayo score was also reduced in simulated microgravity. - ****IL-1 β , IL-6, IL-8:**** Elevated levels of IL-1 β , IL-6, and IL-8 were observed in simulated microgravity. - ****ROS Levels:**** Increased ROS levels were observed in simulated microgravity. - ****Inflammasome Activation:**** Pyroptosis and inflammasome activation were downregulated in simulated microgravity.

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