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TRANSCRIPTOMIC ANALYSIS OF ANGIOGENESIS ON DATASETS DERIVED FROM
EXPERIMENTS PERFORMED ON MICE IN SPACE

Abstract

Studies have shown that wound healing in microgravity is highly affected. To understand the extent to which genetic background plays a role in determining the course of angiogenesis, we compared the RNA-Seq data of dorsal skin samples of two different inbred mice strains, Balb/c and C57BL/6J from two distinct missions namely RR5 and RR6. In-silico analysis was done to identify biomarkers of endothelial dysfunction responsible for delayed wound healing responses under microgravity. With the help of bioinformatics, differentially expressed genes (DEGs) and enriched pathways were identified. Further, using these DEGs, several transcription factors (TFs) and kinases were statistically predicted. E2F1, a significant TF involved in angiogenesis, and MAPK1, an important kinase involved in the post-translational modification of VEGF were some of the potential therapeutic targets to regulate wound healing. Potential countermeasures such as photobiomodulation, (lasers emitting red/IR radiation) on the mentioned targets are currently being studied to optimize reparative angiogenesis.