

Gravity affects the function and maintenance of organs, such as bones, muscles, and the heart. Several studies have used DNA microarrays to identify genes with altered expressions in response to gravity. However, it is technically challenging to combine the results from various microarray datasets because of their different data structures. We hypothesized that it is possible to identify common changes in gene expression from the DNA microarray datasets obtained under various conditions and methods. In this study, we grouped homologous genes to perform a meta-analysis of multiple vascular endothelial cell and skeletal muscle datasets. According to the t-distributed stochastic neighbor embedding (t-SNE) analysis, the changes in the gene expression pattern in vascular endothelial cells formed specific clusters. We also identified candidate genes in endothelial cells that responded to gravity. Further, we exposed human umbilical vein endothelial cells (HUVEC) to simulated microgravity (SMG) using a clinostat and measured the expression levels of the candidate genes. Gene expression analysis using qRT-PCR revealed that the expression level of the prostaglandin (PG) transporter gene *SLCO2A1* decreased in response to microgravity, consistent with the meta-analysis of microarray datasets. Furthermore, the direction of gravity affected the expression level of *SLCO2A1*, buttressing the finding that its expression was affected by gravity. These results suggest that a meta-analysis of DNA microarray datasets may help identify new target genes previously overlooked in individual microarray analyses.