Differential Expression Analysis and Transcriptomic Characterization of Glioma Progression

Lee, Matthew (School: East Brunswick High School)

Gliomas make up nearly a third of all brain tumors and are extremely aggressive in later stages, with only a 5% five-year survival rate. Each year, approximately 20,000 people are diagnosed with glioma in the US. Publicly available RNA-Seq data was used to identify differentially expressed genes (DEGs) and survival analysis was performed to validate their effects on patient prognosis. Gene expression levels were compared between varying grades of glioma and to normal brain samples. 41 out of the top 100 most significant DEGs were associated with increased patient mortality. Analysis showed glioma progression is strongly correlated with increases in expression of SAA1, PLA2G2A, and H19 genes over 17-fold (hazard ratio of 15); and decreases in expression of HPSE2, SELL, and SFRP2 genes over 4-fold (hazard ratio of 12). Expression levels of these genes could potentially act as biomarkers for screening tests. Samples were then grouped by the presence or absence of mutations and methylation, and analyzed using Gene Set Enrichment Analysis. Results showed positive enrichment of G2/M cell cycle checkpoint genes, E2F transcription factors, and MYC gene sets across all groups. Normalized enrichment scores were similar across all groups, indicating the presence of mutations and methylation do not have large impacts on patterns of gene expression. Pathway analysis showed retinoic acid receptor signaling and ribosome assembly are heavily upregulated throughout the entirety of glioma progression in all patients, making these pathways attractive targets for interventions in future studies and drug development.

Awards Won:
Fourth Award of $500
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