Comparative Analysis of Genetic Mutations and Overall Survival in Patients with Glioblastoma Multiforme: A Retrospective Cohort Study

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Glioblastoma multiforme (GBM) is a highly aggressive and rapidly growing brain cancer that affects the central nervous system and typically leads to death within 15 months of diagnosis. It is the most malignant primary brain tumor with an incidence of roughly 2-3 per 100,000 people annually, mostly in adults between the ages of 45-70. The objective of this study was to identify the leading genetic mutations that occur in patients with GBM and compare overall patient survival rates by each respective mutation. Clinical and proteogenomic data from cBioPortal, TCGA PanCancer Atlas, and NIH GDC Database was analyzed to identify prevalent gene mutations in a cohort of 236 GBM patients and in sub-cohorts of patients based on overall survival. Mortality rates, sex, race, and age at diagnosis were evaluated using R/RStudio. Log-rank significance tests were performed to compare survival distributions. Mutations in TP53 (33%), PTEN (31%), EGFR (20%), ATRX (12.4%), and NF1 (11.4%) genes were the most prevalent in the overall cohort. The mortality rates by mutation were 56.5% TP53, 66.2% PTEN, 71.7% EGFR, 42.3% ATRX, and 70.8% NF1. Mutation hotspots were discovered for the TP53 mutation at the codon positions R248Q and R175H, the PTEN mutation at R130Q, and the EGFR gene at A289V. Overall, there are several genetic mutations associated with GBM, the majority of which may be associated with poor prognosis. The unique mutation hotspots identified in this study can contribute to future efforts in developing genetic screening and targeted drug therapies for slowing disease progression and improving survival rates. Further research should aim to analyze the role of genetic mutations in GBM pathophysiology, as well as potential confounding variables through multivariate modeling.