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Genomic, epigenomic and transcriptomic landscape of glioblastoma

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Abstract

The mostly aggressive and extremely malignant type of central nervous system is Glioblastoma (GBM), which is characterized by an extremely short average survival time of lesser than 16 months. The primary cause of this phenomenon can be attributed to the extensively altered genome of GBM, which is characterized by the dysregulation of numerous critical signaling pathways and epigenetics regulations associated with proliferation, cellular growth, survival, and apoptosis. In light of this, different genetic alterations in critical signaling pathways and various epigenetics regulation mechanisms are associated with GBM and identified as distinguishing markers. Such GBM prognostic alterations are identified in PI3K/AKT, p53, RTK, RAS, RB, STAT3 and ZIP4 signaling pathways, metabolic pathway (IDH1/2), as well as alterations in epigenetic regulation genes (MGMT, CDKN2A-$p16^{INK4a}$CDKN2B-$p15^{INK4b}$). The exploration of innovative diagnostic and therapeutic approaches that specifically target these pathways is utmost importance to enhance the future medication for GBM. This study provides a comprehensive overview of dysregulated epigenetic mechanisms and signaling pathways due to mutations, methylation, and copy number alterations of in critical genes in GBM with prevalence and emphasizing their significance.

Keywords: Brain Cancer; Epigenetics/ Epigenomics; Genomics; Glioblastoma; Glioma; Signaling pathway.