Glioblastoma IDH Mutant

No longer exist.

see Astrocytoma IDH-mutant or Oligodendroglioma IDH-mutant and 1p/19q-codeleted

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While glioblastoma was historically classified as isocitrate dehydrogenase (IDH)-wildtype and IDH-mutant groups, the Consortium to Inform Molecular and Practical Approaches to CNS Tumor Taxonomy (cIMPACT-NOW) and the World Health Organization Classification of Tumors of the Central Nervous System 2021 clearly updated the nomenclature to reflect glioblastoma to be compatible with wildtype IDH status only.

Old literature

Isocitrate dehydrogenase (IDH) mutant glioblastoma (Glioblastoma), accounts for ~10% Glioblastomas, arises from lower grade diffuse glioma and preferentially appears in younger patients.

MGMT promoter methylation has predictive value in IDH-mutant glioblastoma, but its cutoff value should be higher than that for IDH-wildtype glioblastoma [1].

Wu et al., aimed to establish a robust gene expression-based molecular classification of IDH-mutant Glioblastoma. A total of 33 samples from the Chinese Glioma Genome Atlas RNA-sequencing data were selected as training set, and 21 cases from Chinese Glioma Genome Atlas microarray data were used as validation set. Consensus clustering identified three groups with distinguished prognostic and molecular features. G1 group, with a poorer clinical outcome, mainly contained TERT promoter wild-type and male cases. G2 and G3 groups had better prognosis differed in gender. Gene ontology analysis showed that genes enriched in G1 group were involved in DNA replication, cell division and cycle. On the basis of the differential genes between G1 and G2/G3 groups, a six-gene signature was developed with a Cox proportional hazards model. Kaplan-Meier analysis found that the acquired signature could differentiate the outcome of low- and high-risk cases. Moreover, the signature could also serve as an independent prognostic factor for IDH-mutant Glioblastoma in the multivariate Cox regression analysis. Gene ontology and gene set enrichment analyses revealed that gene sets correlated with high-risk group were involved in cell cycle, cell proliferation, DNA replication and repair. These finding highlights heterogeneity within IDH-mutant Glioblastomas and will advance our molecular understanding of this lethal cancer [2].

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Chai R, Li G, Liu Y, Zhang K, Zhao Z, Wu F, Chang Y, Pang B, Li J, Li Y, Jiang T, Wang Y. Predictive value of MGMT promoter methylation on the survival of TMZ treated IDH-mutant glioblastoma. Cancer Biol Med. 2021 Feb 15;18(1):272-282. doi: 10.20892/j.issn.2095-3941.2020.0179. PMID: 33628600; PMCID: PMC7877176.
2)

Wu F, Chai RC, Wang Z, Liu YQ, Zhao Z, Li GZ, Jiang HY. Molecular classification of IDH-mutant glioblastomas based on gene expression profiles. Carcinogenesis. 2019 Feb 13. pii: bgz032. doi: 10.1093/carcin/bgz032. [Epub ahead of print] PubMed PMID: 30877769.