The Chinese Glioma Genome Atlas (CGGA) and The Cancer Genome Atlas (TCGA) databases with RNA sequencing and corresponding clinical data were dichotomized into training group and testing group. The immune-related differentially expressed genes (DEGs) associated with 1p/19q codeletion were screened using Cox proportional hazards regression analyses. A prognostic gene signature was established using dataset from CGGA and tested in TCGA database. Subsequently, Xu et al. explored the correlation between the prognostic gene signature and immune response. Thirteen immune genes associated with 1p/19q codeletion were used to construct a prognostic signature. The 1-, 3-, 5-year survival rates of the low-risk group were approximately 97%, 89%, and 79%, while those of the high-risk group were 81%, 50% and 34%, respectively, in the training group. The nomogram which comprised age, WHO grade, primary or recurrent types, 1p/19q codeletion status and risk score provided accurate prediction for the survival rate of glioma. DEGs that were highly expressed in the high-risk group clustered with many immune-related pathways. Immune checkpoints including TIM3, PD1, PDL1, CTLA4, TIGIT, MIR155HG, and CD48 were correlated with the risk score. VAV3 and TNFRFSF11B were found to be candidate immune checkpoints associated with prognosis. The 1p/19q codeletion-associated immune signature provides accurate prediction of OS. VAV3 and TNFRFSF11B are novel immune checkpoints [1].

1)
Xu J, Liu F, Li Y, Shen L. A 1p/19q Codeletion-Associated Immune Signature for Predicting Lower Grade Glioma Prognosis [published online ahead of print, 2020 Sep 7]. Cell Mol Neurobiol. 2020;10.1007/s10571-020-00959-3. doi:10.1007/s10571-020-00959-3

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