Chinese Glioma Genome Atlas

see also The Cancer Genome Atlas (TCGA)

http://www.cgga.org.cn

In the year 2004, under the guide of Academician, Zhongcheng Wang, the first comprehensive glioma center was built in China. Dr. Tao Jiang is the director of comprehensive Glioma center. Dr. Jiang's research mainly focuses on translational medicine and molecular classification of gliomas. And through nearly ten years' sample collection, Dr. Jiang has built the largest glioma tissue bank with particular follow-ups in China. Hundreds of samples have been subjected to whole-genome sequencing (WGS), whole-exome sequencing (WXS), DNA methylation microarray detection, microRNA, circRNA and mRNA sequencing, etc. In the year 2012, Chinese Glioma Genome Atlas (CGGA) was built, which represented a landmark to glioma research in China. And this will provide massive amounts of data for the research both in basic and clinical research of gliomas.

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 signature was established using dataset from CGGA and tested in TCGA database. Subsequently, we 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)].

Jagged1 is the ligands of the Notch signaling and has been shown to promote glioma stem cells in glioblastoma.

Survival data from R2 genomics analysis, the Cancer Genome Atlas (TCGA), the Chinese Glioma Genome Atlas (CGGA) and visualization platform database were used to evaluate the effects of Jagged1 on overall patient survival. Hai et al., investigated Jagged1 induced the glioma stem cells invasion by matrix degradation assays and Transwell cell invasion assays in vitro, then they further explored the underlying molecular mechanisms using Co-immunoprecipitation (co-IP) analysis.

High expression of Jagged1 in human glioma was associated with poor survival. Clinical data analysis showed that the Jagged1 was positively correlated with NF-κB(p65). Jagged1-induced invasion of

glioma stem cells through activation of NF-κB(p65) pathway. In vivo, knockdown of Jagged1 could suppress the tumorigenicity of GICs cells through NF-κB(p65) signaling.

Insights gained from these findings suggest that Jagged1 plays an important oncogenic role in GICs malignancy by activation of NF-κB(p65) signaling, and Jagged1 could be employed as an effective therapeutic target for GICs [2].

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2)
Hai L, Liu P, Yu S, Yi L, Tao Z, Zhang C, Abeysekera IR, Li T, Tong L, Ma H, Liu B, Xie Y, Zhou X, Lin Y, Zhu M, Zhang K, Ren B, Ming H, Huang Y, Yang X. Jagged1 is Clinically Prognostic and Promotes Invasion of Glioma-Initiating Cells by Activating NF-κB(p65) Signaling. Cell Physiol Biochem. 2018 Dec 21;51(6):2925-2937. doi: 10.1159/000496044. [Epub ahead of print] PubMed PMID: 30580328.