ABSTRACT

Hum Cell. 2022 Nov;35(6):1976-1992. doi: 10.1007/s13577-022-00791-5. Epub 2022 Sep 21.

Pyroptosis: a novel signature to predict prognosis and immunotherapy response in gliomas.

He G(#)(1), Chen Z(#)(2), Zhuo S(#)(3), Tang J(4), Hao W(2), Yang K(5), Yang C(6).

Author information:
(1)Department of Neurology, Shenzhen Nanshan People's Hospital and the 6th Affiliated Hospital of Shenzhen University Health Science Center, Shenzhen, 518052, Guangdong, China.
(2)State Key Laboratory of Oncogenes and Related Genes, School of Medicine, Renji-Med X Clinical Stem Cell Research Center, Ren Ji Hospital, Shanghai Jiao Tong University, Shanghai, 200127, China.
(3)Department of Neurosurgery, The First Affiliated Hospital of Hainan Medical University, Haikou, 570102, Hainan, China.
(4)Department of Ultrasound, Fudan University Shanghai Cancer Center, Shanghai, 200433, China.
(5)Department of Neurosurgery, The First Affiliated Hospital of Hainan Medical University, Haikou, 570102, Hainan, China. chbyk1379@163.com.
(6)Department of Neurology, Shenzhen Nanshan People's Hospital and the 6th Affiliated Hospital of Shenzhen University Health Science Center, Shenzhen, 518052, Guangdong, China. Yangzyi@126.com.
(#)Contributed equally

Gliomas are the most common primary brain tumors and are highly malignant with a poor prognosis. Pyroptosis, an inflammatory form of programmed cell death, promotes the inflammatory cell death of cancer. Studies have demonstrated that pyroptosis can promote the inflammatory cell death (ICD) of cancer, thus affecting the prognosis of cancer patients. Therefore, genes that control pyroptosis could be a promising candidate bio-indicator in tumor therapy. The function of pyroptosis-related genes (PRGs) in gliomas was investigated based on the Chinese Glioma Genome Atlas (CGGA), the Cancer Genome Atlas (TCGA) and the Repository of Molecular Brain Neoplasia Data (Rembrandt) databases. In this study, using the non-negative matrix factorization (NMF) clustering method, 26 PRGs from the RNA sequencing data were divided into two subgroups. The LASSO and Cox regression was used to develop a 4-gene (BAX, Caspase-4, Caspase-8, PLCG1) risk signature, and all glioma patients in the CGGA, TCGA and Rembrandt cohorts were divided into low- and high-risk groups. The results demonstrate that the gene risk signature related to clinical features can be used as an independent prognostic indicator in glioma patients. Moreover, the high-risk subtype had rich immune infiltration and high expression of immune checkpoint genes in the tumor immune microenvironment (TIME). The analysis of the Submap algorithm shows that patients in the high-risk group could benefit more from anti-PD1 treatment. The risk characteristics associated with pyroptosis proposed in this study play an essential role in TIME and can potentially predict the prognosis and immunotherapeutic response of glioma patients.

DOI: 10.1007/s13577-022-00791-5
PMID: 36129672 [Indexed for MEDLINE]