MSR1

Macrophage scavenger receptor 1, also known as MSR1, is a protein which in humans is encoded by the MSR1 gene. MSR1 has also been designated CD204 (cluster of differentiation 204).

The differential expression of MSR1 was analyzed in Low-Grade Glioma (LGG) patients with different clinicopathological characteristics. Kaplan-Meier survival analysis, a time-dependent receiver operating characteristic (ROC) curve, and Cox regression analysis were used to assess the prognostic value of MSR1. Differentially expressed genes (DEGs) were screened between the high and low expression groups of MSR1. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) were used to annotate the function of these DEGs. Hallmark gene sets were identified based on MSR1 by Gene Set Enrichment Analysis (GSEA). Difference analysis and correlation analysis were used to study the relationship between MSR1 and TME-related scores, tumor-infiltrating immune cells (TIICs), immune-related gene sets, and immune checkpoints (ICPs). The single-cell sequencing data were processed to identify the cell types expressing MSR1. The quantification of TIICs in TME was calculated by single-sample gene set enrichment analysis (ssGSEA). The differential expression of MSR1 in LGG and control brain tissues was verified by experiments.

There were significant differences in the expression level of MSR1 in different types of tissues and cells. MSR1 has a high prognostic value in LGG patients and can be used as an independent prognostic factor. MSR1 is closely related to TME and may play an important role in the immunotherapy of LGG patients.

The result of the study demonstrated that MSR1 is an independent prognostic biomarker in LGG patients and may play an important role in the tumor microenvironment (TME) of LGGs [1].

CD204 is a specific marker of tumor-associated macrophages (TAMs) in glioma. However, the expression levels of CD204 and its involvement in glioma are not fully understood. In this large-scale study, we assessed the expression and function of CD204 in whole-grade glioma molecularly and clinically. In total, 1323 glioma samples, including 301 microarray data and 325 RNA-seq data from the Chinese Glioma Genome Atlas (CGGA) dataset and 697 RNA-seq data from The Cancer Genome Atlas (TCGA) dataset, were utilized. The statistical analysis and graphical work were mainly performed using the R software. Univariate and multivariate Cox analysis demonstrated that CD204 was an independent prognosticator in glioma patients. CD204 expression was positively correlated with the grade of malignancy. CD204 was consistently upregulated in wild-type isocitrate dehydrogenase glioma and highly expressed in mesenchymal glioblastoma. Gene ontology of CD204-related genes showed that CD204 was most enriched in inflammatory response and immune response. It was associated with the stromal and immune populations, especially the monocytic lineage, fibroblasts, and T cells. Circos plots revealed that CD204 was closely associated with many immune checkpoint regulators, especially TIM-3. CD204 expression is consistent with the malignant phenotype of glioma and independently predicts poor outcomes in glioma patients [2].

1)
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2)

Yuan Y, Zhao Q, Zhao S, Zhang P, Zhao H, Li Z, Du Y, Tian X, Lu J. Characterization of transcriptome profile and clinical features of a novel immunotherapy target CD204 in diffuse glioma. Cancer Med. 2019 Jul;8(8):3811-3821. doi: 10.1002/cam4.2312. Epub 2019 May 29. PMID: 31140757; PMCID: PMC6639170.