Transcriptomic landscape of immune system in brain tumors

Jiin Choi[1], Hee Jin Cho[1,2,*]

[1]Department of Biomedical Convergence Science and Technology, Kyungpook National University, Daegu 41566, Korea

[2]Cell and Matrix Research Institute, Kyungpook National University, Daegu 41944, Korea

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Abstract

Background: Various types of brain tumor occur in both children and adults, and they showed different characteristics such as malignancy, cellular lineage and originated location as well as genomic profiling. Due to the locational limitation for surgical removal, additional therapies are often followed by resection. Recently, immunotherapy is in the spotlight as a treatment for tumors, by manipulating immune cells in tumor microenvironment (TME) to kill tumor cells. Here we analyzed the transcriptomic architecture of the immune systems in brain tumors to provide the potential guideline of immunotherapy for brain tumors.

Methods: We decomposed the population of immune cells among six brain tumor types (meningioma, pilocytic astrocytoma, ependymoma, medulloblastoma, glioblastoma, and lower grade glioma) using publicly available microarray datasets. We also analyzed publicly available single cell RNA sequencing (scRNA-seq) datasets of brain tumors to delineate the immune cell infiltration within these brain tumors at a single cell level.

Results: Transcriptome-based immune cell profiling revealed the infiltrated immune cell types in brain TME were distinguished by tumor type, malignancy, and location, particularly in M2 macrophage, CD8+ T cell, and CD4+ T cell. Our findings from bulk microarray datasets were confirmed by analyzing scRNA-seq datasets.

Conclusions: Our results unveil the distinct immunoprofiles across brain tumor types and may contribute to realize future precision medicine, providing the basic rationale for the immunotherapy in brain tumors.