Functional Role of Long Non-Coding RNA LINC01896 in Glioblastoma

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Glioblastoma multiforme (GBM) is one of the most aggressive and rapidly progressing brain tumors. Due to its molecular heterogeneity, it exhibits strong resistance to therapy. Recent studies have shown that long non-coding RNAs (lncRNAs) play key regulatory roles in protein-coding gene expression, thereby influencing cancer development. Single-cell RNA sequencing (scRNA-seq) has emerged as a powerful tool for cancer research by enabling detailed investigation of cellular heterogeneity within tumors. In the computational phase of this project, publicly available scRNA-seq datasets from 13 GBM patients were analyzed to distinguish malignant from non-malignant cell populations. Our analyses demonstrated that, among 12,133 lncRNAs, LINC01896 is significantly overexpressed in malignant cells compared to non-malignant cells. Furthermore, LINC01896 was found to exert regulatory effects on genes involved in key cellular state dynamics, including malignancy, multicellular signaling, migration and cell-cycle transitions. However, there are no experimental studies investigating the role of LINC01896 in GBM in the literature. Therefore, in the second phase, the functional effects of LINC01896 were experimentally examined using healthy astrocytes and GBM cell lines. Overexpression of LINC01896 and changes in the expression of genes associated with key cellular state dynamics following its deletion via CRISPR-Cas9 were validated by RT-qPCR. In addition, the effects of LINC01896 loss on cell viability, migration, apoptosis, and cell cycle progression were evaluated. Overall, our findings indicate that LINC01896 promotes tumorigenesis by regulating the expression of genes critical to GBM development, highlighting this lncRNA as a potential therapeutic biomarker and treatment target.

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