Identification of cuproptosis-related lncRNAs for prognostic markers in glioma

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Glioma represents a frequent intracranial malignancy characterised by a dismal clinical outcome. Cuproptosis, a recently identified type of cellular demise, has garnered significant interest within the oncological community. The specific functions of cuproptosis-associated genes in glioma remain undefined. Herein, we utilised Cox regression modelling to detect 7 prognostic long non-coding RNAs (lncRNAs) and developed a risk framework based upon those molecules. Patients were stratified into high-risk and low-risk groups based upon the median risk score. Regardless of personal age, gender, tumour grade, or O^6-methylguanine-DNA methyltransferase methylation state, the survival prospects of the high-risk cohort were considerably poorer compared to those of the low-risk cohort. Cox proportional hazards modelling verified that this model functions as an independent prognostic tool for glioma patients. Receiver operating characteristic curve evaluation indicated that this system maintains superior accuracy for predicting survival among the Cancer Genome Atlas participants. Functional enrichment analysis using Gene Ontology and Kyoto Encyclopedia of Genes and Genomes was performed to determine the biological roles of differentially expressed genes. Furthermore, it was noted that the cuproptosis-related lncRNAs risk signature correlates with tumour mutation burden and the immune landscape. To summarise, we developed a prognostic risk model centred around cuproptosis-associated lncRNAs, which demonstrates solid capacity for predictive assessment.

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year survival statistics for this deadly cancer tend to be relatively poor[2]. The intricacy of glioma manifests not just through its elevated heterogeneity and virulence but additionally via the absence of potent biomarkers. Accurate management and customised interventions still encounter significant difficulties. Consequently, identifying novel markers and prospective therapeutic goals is profoundly important for enhancing the therapeutic success of glioma.

In recent times, exploring long non-coding RNAs (lncRNAs) present in gliomas has emerged as a primary area of academic investigation. Particularly, progress concerning lncRNAs linked to cuproptosis (CRlncRNAs) in this disease has attracted considerable focus. Cuproptosis represents an emerging type of regulated cell demise that is intimately tied to the internal levels of copper ions and redox equilibrium[3]. Within gliomas, these CRlncRNAs might influence the viability and growth of tumour cells by modulating intracellular copper homeostasis and redox conditions. For instance, specific lncRNAs could modify the responsiveness and resistance of glioma cells toward copper ions through adjusting the levels of genes involved in copper turnover, thus impacting their overall survival and replicative potential[4]. As research into cuproptosis and innovative oncological treatments progresses, novel roles for lncRNAs continue to be uncovered continuously.

Within our research, we examined information regarding glioma sufferers from the Cancer Genome Atlas (TCGA) and Chinese Glioma Genome Atlas (CGGA) cohorts to explore the mutual association between cuproptosis-related genes and lncRNAs in glioma and to pinpoint cuproptosis-involved lncRNAs associated with glioma prognosis, providing fresh perspectives and potential targets for glioma treatment.

Materials and methods