SUMOylation

Small Ubiquitin-like Modifier (or SUMO) proteins are a family of small proteins that are covalently attached to and detached from other proteins in cells to modify their function. This process is called SUMOylation (sometimes written sumoylation). SUMOylation is a post-translational modification involved in various cellular processes, such as nuclear-cytosolic transport, transcriptional regulation, apoptosis, protein stability, response to stress, and progression through the cell cycle.

SUMOylation is one of the post-translational modifications. The relationship between the expression of SUMOylation regulators and the prognosis of glioblastoma is not quite clear.

Materials and methods: The single nucleotide variant data, the transcriptome data, and survival information were acquired from The Cancer Genome Atlas, Gene Expression Omnibus, and cBioportal database. Wilcoxon test was used to analyze differentially expressed genes between glioblastoma and normal brain tissues. Gene set enrichment analysis was conducted to find the possible functions. One risk scoring model was built by the least absolute shrinkage and selection operator Cox regression. Kaplain-Meier survival curves and receiver operating characteristic curves were applied to evaluate the effectiveness of the model in predicting the prognosis of glioblastoma.

Results: Single-nucleotide variant mutations were found in SENP7, SENP3, SENP5, PIAS3, RANBP2, USPL1, SENP1, PIAS2, SENP2, and PIAS1. Moreover, UBE2I, UBA2, PIAS3, and SENP1 were highly expressed in glioblastoma, whereas PIAS1, RANBP2, SENP5, and SENP2 were downregulated in glioblastoma. Functional enrichment analysis showed that the SUMOylation regulators of glioblastoma might involve cell cycle, DNA replication, and other functions. A prognostic model of glioblastoma was constructed based on SUMOylation regulator-related molecules (ATF7IP, CCNB1IP1, and LBH). Kaplain-Meier survival curves and receiver operating characteristic curves showed that the model had a strong ability to predict the overall survival of glioblastoma.

This study analyzed the expression of 15 SUMOylation regulators in glioblastoma. The risk assessment model was constructed based on the SUMOylation regulator-related genes, which had a strong predictive ability for the overall survival of patients with glioblastoma. It might provide targets for the study of the relationship between SUMOylation and glioblastoma [1].

1)
Li X, Meng Y. SUMOylation Regulator-Related Molecules Can Be Used as Prognostic Biomarkers for Glioblastoma. Front Cell Dev Biol. 2021 Apr 9;9:658856. doi: 10.3389/fcell.2021.658856. PMID: 33898460; PMCID: PMC8063029.