Crosstalk

In electronics, crosstalk is any phenomenon by which a signal transmitted on one circuit or channel of a transmission system creates an undesired effect in another circuit or channel.

Biological crosstalk refers to instances in which one or more components of one signal transduction pathway affects another. This can be achieved in a number of ways with the most common form being crosstalk between proteins of signalling cascades. In these signal transduction pathways, there are often shared components that can interact with either pathway. A more complex instance of crosstalk can be observed with transmembrane crosstalk between the extracellular matrix (ECM) and the cytoskeleton.

While accumulating studies have investigated coding gene-associated biomarkers in malignant glioma, research on comprehensive coding and non-coding RNA-associated biomarkers is lacking. Furthermore, few studies have illustrated the crosstalk signalling pathways among these biomarkers and mechanisms in detail.

Huang et al. identified differentially expressed genes and Competing endogenous RNA (ceRNA) networks in malignant glioma and then constructed Cox/Lasso regression models to further identify the most valuable genes through stepwise refinement. Top-down comprehensive integrated analysis, including functional enrichment, SNV, immune infiltration, transcription factor binding site, and molecular docking analyses, further revealed the regulatory maps among these genes. The results revealed a novel and accurate model (AUC of 0.91 and C-index of 0.84 in the whole malignant gliomas, AUC of 0.90 and C-index of 0.86 in LGG, and AUC of 0.75 and C-index of 0.69 in Glioblastoma) that includes twelve ncRNAs, 1 MicroRNA and 6 coding genes. Stepwise logical reasoning based on top-down comprehensive integrated analysis and references revealed cross-talk signalling pathways among these genes that were correlated with the circadian rhythm, tumour immune microenvironment and cellular senescence pathways. In conclusion, our work reveals a novel model where the newly identified biomarkers may contribute to a precise diagnosis/prognosis and subclassification of malignant glioma, and the identified cross-talk signalling pathways would help to illustrate the noncoding RNA-associated epigenetic regulatory mechanisms of glioma tumorigenesis and aid in targeted therapy 1).

1)
Huang Y, Gao X, Yang E, Yue K, Cao Y, Zhao B, Zhang H, Dai S, Zhang L, Luo P, Jiang X. Top-down stepwise refinement identifies coding and noncoding RNA-associated epigenetic regulatory maps in malignant glioma. J Cell Mol Med. 2022 Feb 22. doi: 10.1111/jcmm.17244. Epub ahead of print. PMID: 35194922.