

2023 年臺灣國際科學展覽會 優勝作品專輯

作品編號 090023

參展科別 醫學與健康科學

作品名稱 **Analysis of lncRNA, miRNA, mRNA-associated ceRNA networks include in promoting glioma cancer**

得獎獎項

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關鍵詞

Abstract

The ceRNAs as a class of RNAs act by competitively binding to miRNAs and limiting their regulatory effect on the target genes. Increasing evidences point to the role of ceRNAs in glioma cancer. So far, limited studies have been reported on the role of ceRNA in the development in glioma cancer. In this study, we have analyzed online RNA sequencing data in order to predict the ceRNAs which are putative regulators of in glioma cancer.

Methods

The dysregulated lncRNAs, miRNAs and mRNAs in glioma cancer were screened using SRA algorithms against RNA-sequencing. Finally measure expression of candidate gene in patient samples with qPCR

Result

Our bioinformatics analysis introduced 16 mRNAs, 6 lncRNAs and 149 miRNAs that were up-regulated, while it introduced 622 mRNAs, 263 lncRNAs and 177 miRNAs that were down-regulated in glioma cancer. All of these dysregulated genes were involved in 57 cellular pathway. By constructing regulatory ceRNA network, three axis: LINC00261-mir-33-COL6A3 denitrified as potential ceRNA network involved in glioma cancer.

Conclusion

This study suggested putative ceRNA networks which are involved in glioma cancer, also predict novel promising targets for cancer therapy.

【評語】 090023

By analyzing a public gene dataset , dysregulations of lncRNAs , miRNA , and mRNA in glioma cancer were profiled. Consistent to previous studies , the correlation between the upregulations of LINC00261 and LINC00261 and the malignancy of glioma cell lines were validated. Further evidences showing these lncRNAs as potential therapeutic targets for glioma cancer are required.