PHARMA Pharmacologia

OPEN ACCESS

News & Comments

Pathway of SNHG1 on BC cells that can be beneficial for cancer research

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Due to its rising prevalence, breast cancer has caught the public's attention. Age, profession, and hereditary variables are all strongly correlated with the development of breast cancer. Non-coding RNAs, which are important in the development of cancer, have received a lot of attention because of the rising incidence of breast cancer. It is difficult to understand how SNHG1 influences physiological functions and the development of disease. By complementarily binding to its target miRNAs, SNHG1 performs the biological activity. Determining whether SNHG1 regulated the malignant phenotype of breast cancer cells by targeting miR-101 and examining its associated mechanism were the goals of the current investigation.

This research project was conducted in Baoding First Hospital Lab China. Using the Trizol reagent, total RNA was extracted from breast cancer tissue samples or cells. Shanghai Suobao Biological Technology Co., Ltd.'s Transcript or First Strand cDNA Synthesis Kit and the miRNA RT kit were used to create the cDNA (TaKaRa). A Thermo Real-time PCR Master Mix system was used to carry out the PCR experiment. The MDA-MB-231 cell line was used for the in vitro breast cancer cell research. A Cell Viability Assay was carried out under the MTT assay kit (Sangon Biotech, Shanghai, China). The cell apoptosis was assessed using FCM. To confirm the target interaction between SNHG1 and miR-101, a Dual-luciferase reporter experiment was carried out. SPSS 21.0 was used to analyse all the data. The measurement information was displayed as Mean SD.

The qRT-PCR was used to assess the expression levels of SNHG1 and miR-101 in breast tumour tissues. The findings demonstrated that miR-101 expression levels were higher in the miR-mimics group (1.840.12) than in the NC group and miR-inhibitors groups. By using the MTT assay, the impact of SNHG1 targeting miR-101 on BC cell growth was examined. Proto-oncogene activation and suppressor gene degradation are two examples of anomalies in gene expression that may contribute to the advancement of BC. Diverse cancer stages exhibit different patterns of gene expression. Recent research on the role of SNHG1 reveals that via interacting with its target miRNAs, such as miR-1548, miR-33814, miR-32615, and miR-137, SNHG1 performs a range of biological roles in various tumour tissues.

According to the experimental findings, SNHG1 and miR-101 have a specific regulatory interaction since reducing miR-101 expression entirely counteracted the effect of SNHG1 inhibition on BC cell proliferation and death. This study is the first to confirm the role of miR-101 in BC and its targeted

regulation relationship with SNHG1, which lays the groundwork for molecular targeted therapy from the perspective of SNHG1 in the future and provides a more accurate baseline for subsequent studies. Previous studies have discovered that lncRNA SPRY4-IT1 and MALAT1 affect the biological behaviour of tumour cells such as osteosarcoma and oral cancer through miR-101.

JOURNAL REFERENCE

Zhu, L., H. Chen, Y. Yang, Y. Miao, J. Lu and J. Zhang, 2022. The role of lncRNA SNHG1 in breast cancer cells by targeting miRNA-101. Int. J. Pharmacol., 18: 924-931.

KEYWORDS

Breast cancer, SNHG1, miR-101, invasion, apoptosis, proliferation, target interaction