عنوان مقاله:

HSA-MIR-ΔΥ٩-ΔΡ promots gastric adenocarcinoma by disturbing interactions of STK ΥΥΑ-AS\ as a lncRNA

محل انتشار:

دوازدهمین همایش ملی و سومین همایش بین المللی بیوانفورماتیک (سال: 1402)

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## خلاصه مقاله:

Gastric cancer (GC) represents the fifth most common tumor and the fourth leading cause ofcancer-related deaths worldwide [\]. Several genetic and epigenetic factors, including microRNAs(miRNAs) and lncRNAs, affect its initiation and progression. MiRNAs are short chains of nucleic acidsthat can regulate several cellular processes by controlling their gene expression, Long noncodingRNA (LncRNA) is a large class of RNA molecules with size larger than Υ·· nucleotides. They exhibitcellular functions although having no protein-coding capability [Υ]. In recent decades, miRNAa andlncRNAs have been studied and considered as impactful biomarkers in cancer. In the present study, microarray analysis was performed on GSEΛ\٩₹λin the field of GC from the GEO database. TheSERPINE\ gene was selected as a gene with significant over expression after checking with ENCORland GEPIAY databases. The signaling pathways in which the SERPINE\ gene was active and waschecked by KEGG database. The protein- protein interaction of the gene was analyzed by usingSTRING database. The interaction between the desired gene and its related miRNAs was checked bymiRWalk database. After analyzing the desired gene with its related miRNAa, hsa-mir-ΔΥ٩-Δp wasselected as the miRNA affecting the YUTR region. STKYYA-AS\ lncRNA was selected in thelncRResearch database as the lncRNA associated with the SERPINE\ gene. This up-regulted gene(SERPINE\) has correlation with a down-regulated gene which is DNER. In conclution, the interactionbetween the selected lncRNA and its related miRNAa was studied. After microarray analysis .onSERPINE\ gene, the result of this study showed that the gene which was mentioned has a significant increase in expression in gastric cancer

كلمات كليدى:

Gastric cancer, gene expression, SERPINE\ gene, GSEA\94A

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