عنوان مقاله:

In Silico Analysis Of MiRNA-150 And Its Related Targets In Breast Cancer

محل انتشار:

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خلاصه مقاله:

Background: Breast cancer is the most common cause of cancer death among women worldwide.miRNAs are the large subgroup of non-coding RNAs with 18-25 nucleotides inhibiting the expressionof target genes by means of binding to their 3'UTR. They can also have tumor suppressor oroncogenic role in cell cycle pathways. Recently, relations between breast cancer risks and someSNPs are located in miRNA seeds or 3'UTR of their target, in some populations have been shown.Aberration in signal transduction pathway of Znf350 family in human tumors is a commonphenomenon. Znf350 as an oncogene and also tumor suppressor gene is a member of Znf350 family.miRWalk2 database was used to identify the has-miR-150 predicted target genes. In next step,DAVID database were used to investigate the function and the related signaling pathways ofobtained has-miR-150 target genes. In silico investigation of SNPs in the 3'UTR of Znf350 geneshowed that rs2278414 could alter the binding properties of has- miR-150. Due to bindinginformation of rs2278414 to has-miR-150 based on G, the binding activity of this microRNA (asoncomiR) undergoes respectively; this SNP could act as a good-prognostic factor. It also appearedthat predicted target genes of our microRNA are related to the most probably cancer pathways suchas ERBB SIGNALING PATHWAY and PATHWAYS IN CANCER . Bioinformatically rs2278414 couldhave association with breast cancer, especially with prognosis of patients. Since has-miR-150 bindsto rs2278414 within ZNF350 and based on in silico information this microRNA involves in cancerpathways, it is predicted that the regulation of ZNF350 by hsa-miR-150 .influences the developmentof breast cancer

کلمات کلیدی: