عنوان مقاله:

In-silico analysis of rs1836724 and its related microRNAs in breast cancer

محل انتشار:

دهمین کنگره بین المللی سرطان پستان (سال: 1393)

تعداد صفحات اصل مقاله: 1

نویسندگان:

Fatemeh bagheri - *Biochemistry Division, Biology Department, Faculty of Science, Payame noor University of Taft, Yazd,Iran*

Mansooreh Azadeh - *Zistfanavari Novin biotechnology institute, Isfahan, Iran*

Kamran Ghaedi - *Cellular and Molecular Biology Divisions, Biology Department, Faculty of Sciences, University ofIsfahan, Isfahan, Iran*

Hossein Tabatabaeian - *Genetics Division, Biology Department, Faculty of Sciences, University of Isfahan, Isfahan, Iran*

خلاصه مقاله:

Breast cancer is the most common cause of cancer death among women worldwide.Aberration in signal transduction pathway of ErbB family in human tumors is a common phenomenon. ErbB4 as an oncogene and also tumor suppressor is one of the members of ErbB family. ErbB4 overexpression has been observed in approximately 50% of breast cancer cases. miRNAs are the large subgroup of noncoding RNAs with 18-25 nucleotides inhibiting the expression of target genes by means of binding to their 3'UTR. They also can play role as an oncogene and/or tumor suppressor. In recent years, the association of some SNPs located in either miRNA seeds or 3'UTR of their target genes with the risk of breast cancer have been proved in some populations. Material and method: miRNASNP database was used to identify the miRNAs with the ability to bind to the 3'UTR of ErbB4 transcripts. In next step, miRTarBase and DAVID databases were used to investigate the function and the related signaling pathways of obtained miRNAs.Results: In silico investigation of SNPs in the 3'UTR of ErbB4 gene showed that rs1836724 could alter the binding properties of miR-665, miR-708 and miR-335. Due to rs1836724, the binding activity of miR-335 (as an oncomiRNA) and miR-665 (as a tumor suppressor) undergoes gain and lossrespectively; consequently, this SNP could act as a poor-prognostic factor. On the other hand, the binding affinity of miR-708 (as an oncomiRNA) alleviates as a result of rs1836724; therefore, rs1836724 could also acts as good-prognostic factor.Conclusion: Bioinformatically, rs1836724 could have association with breast cancer, especially with prognosis of patients.

کلمات کلیدی:

Breast Cancer, ErbB4, microRNA, Prognosis, rs1836724

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