عنوان مقاله:

Alterations of Genetic Variants and Transcriptomic Features of Response to Tamoxifen in the Breast Cancer Cell Line

محل انتشار:

پنجمین کنگره بین المللی سرطان (سال: 1400)

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خلاصه مقاله:

Introduction: In current study, two hypotheses of Tamoxifen consumption in breast cancer cell line (MCF۷) were investigated. First, the effect of Tamoxifen on genes expression profile at transcriptome level was evaluated between the control and treated samples. Second, due to the fact that Tamoxifen is known as a mutagenic factor, there may be an association between the alterations of genetic variants and Tamoxifen treatment, which can impact on the drug response. Method: In current study, the whole-transcriptome (RNA-seq) dataset of four investigations (۱۹ samples) were derived from European Bioinformatics Institute (EBI). At transcriptome level, the effect of Tamoxifen was investigated on gene expression profile between control and treatment samples. Moreover, its contribution to alterations of genetic variants and drug response were examined. Results: RNA-seq analysis indicated the contribution of several candidate genes to tumor suppression process and consequently, the achievement of an effective treatment. For instance, XIAP-associated factor ۱ (XAF۱) was reported as an up-regulated gene under Tamoxifen therapy. XAF۱ is a tumor suppressor that contributes to the apoptosis induction and tumor growth inhibition along with TP۵۳. Findings achieved from evaluating Tamoxifen mutagenicity effect on drug response was not confirmed perfectly. Conclusion: At transcriptome level, Tamoxifen consumption in MCF۷ cell line could be associated with candidate genes that contribute to the apoptosis, proteolysis, and tumor suppression. The most reported candidate genes, which were related to differential genetic variants, played the oncogene and tumor suppressor dual .roles and also their exact roles in breast cancer were not investigated precisely

کلمات کلیدی:

.Tamoxifen, breast cancer, genetic variants, RNA-seq