

عنوان مقاله:

Highlight DNA Methylation Biomarkers in Different Cancer Type for Drug Designing

محل انتشار:

فصلنامه اییژنتیک, دوره 3, شماره 1 (سال: 1401)

تعداد صفحات اصل مقاله: 8

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خلاصه مقاله:

Recently the study of epigenetics is related to diverse processes such as chromatin structure, tumorigenesis, transcriptional regulation, and genome integrity. Epigenetics defect is one of a new area of cancer detection. It is a rapidly expanding field of cancer research. Epigenetics is the heritable process that effects the gene expression without alteration in DNA sequences. Epigenetics includes three systems DNA methylation, histone modification, Noncoding RNA associated silencing gene and chromatin changes. Major epigenetics modifications include DNA methylation patterns that are modified in the cancer cell and used to distinguish a cancer cell from normal and strongly involved in the physiological control of genome expression. Cancer results from an aberration in genomic DNA include hypo-methylation and hyper-methylation of DNA. Hyper-methylation exhibit the silencing of Tumor suppressor genes. Hypo-methylation activate transcription of proto-oncogenes, cancer cell metastasis and genomic instability. Due to emergence of powerful technologies the detection of DNA methylation accelerated cancer research. DNA methyltransferases DNMT1 and DNMTrB catalyzed DNA methylation. DNA methylation associated with loss of gene expression. Different DNA Methylation biomarkers associated with different cancer types. This review highlights different DNA methylation biomarkers in different types of cancer which are helpful for diagnosis, prognosis and drug .designing for curing different types of cancer

کلمات کلیدی:

DNA Methylation, epigenetics mechanism, hypo-methylation, hyper-methylation, biomarkers in different cancer types

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