

## عنوان مقاله:

Breast Cancer Epigenetics

## محل انتشار:

یازدهمین کنگره بین المللی سرطان پستان (سال: 1394)

تعداد صفحات اصل مقاله: 1

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## خلاصه مقاله:

Stable molecular changes during cell division without change the sequence of DNA molecules is known as epigenetic. Molecular mechanisms involved in this process, including histone modifications, methylation of DNA, protein complex and RNA antisense. Cancer genome changes happen through a combination of DNA hypermethylation, long-term epigenetic silencing with heterozygosis loss and genomic regions loss. Different combinations of N-terminal changes cooperation with histone variants with have a specific role in gene regulation have led to load a setting histone that determine transcription potential of a particular gene or genomic regions. DNA methylation analysis in genome region using methylation-specific digital karyotyping of normal breast tissue detect gene expression patterns and DNA specific methylation can be found in breast carcinoma too. More than 100 genes in breast tumors or cell lines of breast cancer are reported hypermethylated. Important of DNA methylation on cancer has been concentrated CpG islands Hypermethylation. The most of the techniques are able to identify hypermethylated areas. Recent studies have showed the role of epigenetic silencing in the pathogenesis of breast cancer in which tumor suppressor genes have been changed by acetylation and DNA deacetylation. Histone deacetylase inhibitors have different roles in cancer cells and could show the ways of new treatment for breast cancer. In this review, various aspects of breast .cancer epigenetics and its applications in diagnosis, prediction and treatment are described

## کلمات کلیدی:

Epigenetics, breast cancer, DNA methylation, histone changes

## لینک ثابت مقاله در پایگاه سیویلیکا:

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