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Epigenetics of Breast Cancer: biology and clinical implication in the era of Precision Medicine.

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Abstract

In the last years, mortality from breast cancer has declined in western countries as a consequence of a more widespread screening resulting in earlier detection, as well as an improved molecular classification and advances in adjuvant treatment. Nevertheless, approximately one third of breast cancer patients will develop distant metastases and eventually die for the disease. There is now a compelling body of evidence suggesting that epigenetic modifications comprising DNA methylation and chromatin remodeling play a pivotal role since the early stages of breast cancerogenesis. In addition, recently, increasing emphasis is being placed on the property of ncRNAs to finely control gene expression at multiple levels by interacting with a wide array of molecules such that they might be designated as epigenetic modifiers. In this review, we summarize the current knowledge about the involvement of epigenetic modifications in breast cancer, and provide an overview of the significant association of epigenetic traits with the breast cancer clinicopathological features, emphasizing the potentiality of epigenetic marks to become biomarkers in the context of precision medicine.

List of Abbreviations

BC: Breast Cancer
ER: Estrogen Receptor
PgR, PR: Progesteron Receptor
HER-2: Human Epidermal growth factor Receptor 2
TNBC: Triple Negative Breast Cancer
ncRNA: non coding RNA
CpG(s): Cytosine-phosphate-Guanine dinucleotide(s)
5-me-C: 5-methyl-Cytosine
DNMT(s): DNA-Methyl Transferase(s)
DH: Ductal Hyperplasia
ADH: atypical hyperplasia
DCIS: *in situ* carcinoma
BRCA1: breast cancer 1 gene
PFS: Progression-Free Survival
DSS Disease Specific Survival
OS: Overall Survival