Chapter 2
Epigenetic Signature in Breast Carcinoma, a Hidden Language to Dictate Against Genomic Insults

Azad Kumar
Dr. D. Y. Patil Biotechnology and Bioinformatics Institute, India

Devashree Jahagirdar
Dr. D. Y. Patil Biotechnology and Bioinformatics Institute, India

Shruti Purohit
Dr. D. Y. Patil Biotechnology and Bioinformatics Institute, India

Nilesh Kumar Sharma
Dr. D. Y. Patil Biotechnology and Bioinformatics Institute, India

ABSTRACT

The bottleneck in breast carcinoma treatment regimen is actually contributed from inherent genetic and epigenetic signatures present in heterogeneous clonal populations. Epigenetic changes are viewed as permanent and inheritable molecular pattern alterations of a cellular phenotype such as the gene expression profile but do not involve changes of the DNA sequence itself. Epigenetic phenomena are mediated by several molecular mechanisms comprising of histone modifications, DNA methylation and microRNA (miRNA) guided tools. Epigenetic reprogramming may help in protective adaption to environment insults as chemotherapy and radiation therapy either enhance epigenetic tag or erase the epigenetic tag. Such epigenetic tools are being preferably used by several cancer types including breast carcinoma to achieve distinctive proliferation, metastasis and resistance in the wake of genomic insults. In this book chapter, we highlight the summarized findings on implications of epigenetic landscape in breast carcinoma occurrence and presenting as promising avenues for therapeutic intervention.

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INTRODUCTION

Notwithstanding, deepened insights about the genetic, biochemical, signaling and epigenetic implications in breast carcinoma, still this heterogeneous and most complex diseases are elusive in their nature. It is a fact that noticeable threatening aspects of breast carcinoma namely including metastasis, relapse and multidrug resistance are less understood and clinical reasons behind success in treatment and diagnosis (Feinberg & Tycko, 2004; Jeggo et al., 2016). Along with the existing regimen of chemotherapy and radiation therapy approaches, which mainly centered on the creating disturbances in the genomic world of breast carcinoma and ultimately forcing breast carcinoma to death destiny, there is need to extend our ways and observations culminating into new ideas and out of box approaches (Feinberg & Tycko, 2004; Jeggo et al., 2016; Montenegro et al., 2015; Ribezzo et al., 2016). The current regimen of genotoxic drug and radiation therapy based treatment shown promises in some cases, at the same time failures have been widely perceived in the area of breast cancer treatment. As per the literature and scientific evidence, it is true that several carcinomas including breast cancer are highly manipulative for their protective umbrella in the form of dedicated pool of DNA repair protein employing several pathways (Feinberg & Tycko, 2004; Jeggo et al., 2016). The efforts to utilize the knowledge about DNA repair proteins and their selfish act in breast carcinoma will provide opportunities for cocktails of precise drugs/inhibitors directed precisely against one or more aberrant pathways providing protective shield (Montenegro et al., 2015; Ribezzo et al., 2016). The recent findings pointed out the possibilities that a certain breast carcinoma cells may not be initially resistant against genotoxic drug treatment, however in due course of time due to epigenetic heterogeneity accumulation; these cells eventually will acquire drug resistance capability (Jovanovivc et al., 2010; Suvà, Riggi & Bernstein, 2013; Basse & Arock, 2015; Wright, 2013; Shinjo & Kondo, 2015). In recent time, overwhelming attentions are being thrown to epigenome alterations as “Epimutations” specifically centered to DNA repair proteins engaged in creating protective umbrella in case of carcinoma survival strategy to thwart genomic insults caused due to genotoxic drugs and radiation therapy (Brown & Strathdeemail, 2015; Hamm & Costa, 2015; Lv et al., 2016; Bansal, David, Farias & Waxman, 2016). Here, objectives of this book chapter are to encompass the most recent summarized information on the potential of epigenetic mark in the perspectives of breast carcinoma prognosis and treatment.
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