

DNA Methylation Levels and the Effect on Gene Expression of Several Genes Involved in Breast Cancer Using PCR Array

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Abstract

The levels of DNA methylation and its role in gene expression are key factors that could affect the diagnosis, prognosis and treatment options for breast cancer. In this study, the methylation levels of 22 genes that are mostly correlated to breast cancer were determined using, EpiTect methyl II PCR array. This analysis was done on three breast cancer cell lines (MCF7, MDA-MB-231 and T47-D). Different passage numbers of MCF7 cells were also studied in addition to studying the effect of antibiotics on methylation levels in all cell lines. After analysis, ten genes (*ADAM23*, *CCND2*, *CDH13*, *GSTP1*, *HIC1*, *RASSF1*, *PYCARD*, *TNFRSF*, *SLIT2* and *THBS1*) were found to be hypermethylated and were chosen to follow their gene expression levels after demethylation using 5-Aza.

This study shows that the presence of antibiotic within cultured media, cell line's passage number and cell line type could greatly affect the methylation levels. A strong linkage between DNA methylation and breast cancer is observed. Since it is the first time EpiTect methyl II PCR array technique is used, the obtained results would be more reliable to demonstrate the DNA methylation levels among genes involved in breast cancer.