Identifying DNA Methylation Variation Patterns for Breast Cancer Biomarker Genes

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Patterns of DNA methylation in human cells are crucial in regulating tumorgenesis and can be indicative of breast cancer susceptibility. In our research, we pinpoint genes with significant methylation variation in the breast cancer epigenome to be used as potential novel biomarkers for breast cancer susceptibility. Using the statistical software package R, we compare DNA methylation sequencing data from 7 normal individuals with 8 breast cancer cell lines. This is done by selecting CG sites, or cytosine-guanine pairings, at which normal cell and cancer cell variation fall in different ranges, and by performing upper one-tailed chi-square tests with a significance value of 0.01. Due to multiple-testing error, the Bonferroni correction method was applied for equivalent adjustments to each p-value for accurate significance conclusions. These selected CG sites, which were significant in chi-square testing, are mapped to their corresponding genes. Genes with over 100 significant CG sites are chosen as potential genes of interest. Using the ConsensusPath Database software, we generate genetic pathways with our data to study biological relations between our selected genes and tumorgenenic cellular mechanisms. Using breast cancer-related genes from the PubMeth and GeneCards databases, we have discovered 26 potential biomarker genes which are biologically linked to genes known to be associated with breast cancer. Our results have numerous implications for early screening and detection measures for breast cancer susceptibility. Furthermore, novel treatments may be developed as more research is conducted exploring the biomarker genes' association with stimulating tumorgenesis.

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