Gene Methylation Is a Driver of Cellular Differentiation for Intrinsic Subtype of Breast Cancer During Carcinogenesis

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The intrinsic subtype of breast cancer is a major factor considered in the development of individualized treatment regimens for patients. An understanding of when and which molecular changes drive the different intrinsic subtypes of breast cancer may lead to being able to create a better strategy for managing breast cancer patient individualized treatment in the clinical setting. In a previous study, I found that PAM50 genes associated to the HER2 subtype of breast cancer are expressed through gene amplification (unpublished data). Additionally, I demonstrated that the expression of luminal and triple negative subtype associated PAM50 genes is controlled by gene methylation (unpublished data). In this study, I analyzed gene methylation data of normal breast tissue, ductal carcinoma in situ (DCIS), and invasive ductal carcinoma (IDC) of intrinsic subtype genes through hierarchical (HCA) and multidimensional clustering (MCA). The data shows that there is a statistically significant difference in gene methylation in normal breast tissue but differentiation of intrinsic subtype may occur during carcinogenesis with increasingly prominent differences of gene methylation level seen between DCIS and IDC.

Awards Won:
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