

Breast Cancer Family History and Allele-specific DNA Methylation in the LEGACY Girls Study

Hui-Chen Wu, Catherine Do, Irene L. Andrulis, Esther M. John, Mary B. Daly, Sandra S Buys, Wendy K. Chung, Julia A. Knight, Angela R. Bradbury, Theresa H. M. Keegan, Lisa Schwartz, Izabela Krupska, Rachel L. Miller, Regina M. Santella, Benjamin Tycko & Mary Beth Terry

Lay Abstract:

A woman that has a family member with a diagnosis of breast cancer has an increased risk of developing breast cancer herself. Cancer may cluster in families because of shared environments, genetics, and epigenetics. Epigenetic changes, which means the actions of DNA changes without DNA itself changing, can affect how genes work. Environmental exposures like diet and exposure to chemicals throughout life can cause epigenetic changes. Genetic and epigenetic interactions can also occur. Using DNA from girls ages 6-13 in the LEGACY Girls Study, we studied 29 genes and found genetic-epigenetic interactions in two genes, called *ESR1* and *SEC16B*, which are linked to breast cancer and the timing of puberty. We found that changes in these two genes relevant to breast cancer may be present early in life.