

51: Increased epigenetic age in normal breast tissue from luminal breast cancer patients Hofstatter, E.W. et al., 2018

Increasing age is one risk factor for developing breast cancer. Your chronological age is one factor, but researchers also are looking at biological age, or how your chromosomes are changing over time. The authors of this study wanted to see if faster biologic, or epigenetic, aging also is a risk factor for breast cancer.

Methods:

The researchers used 96 normal breast cancer tissue samples from 88 subjects. The normal tissue came from the non-tumor sites of primary mastectomy patients as well as samples from unaffected women obtained from the Komen Tissue Bank and some non-cancer related breast surgery specimens.

The researchers divided the samples into four groups: Women younger than 50 with and without breast cancer and women older than 50 with and without breast cancer. They created DNA profiles using an established biomarker of aging to arrive at a “DNA methylation age.”

Our bodies use DNA methylation to control gene expression, to turn off or on genes that may threaten our health. DNA methylation age can assess the frequency and degree to which this happens, especially when trying to counteract cancer. In previous work, researchers had used DNA methylation to determine that breast tissue ages faster than blood in unaffected women. For this study, they wanted to see how DNA methylation affects tissue specifically.

Findings:

The researchers found that the normal breast tissue of patients never diagnosed with breast cancer was strongly correlated with chronological age. Compared to this group, women already diagnosed with breast cancer showed significant age acceleration in their normal tissue that wasn't affected by the cancer. Their normal tissue seemed about half a decade older than the women who never have had breast cancer. The breast tissue was aging at a faster epigenetic (biologic) rate than the patient's chronological age.

The study supports its hypothesis because it looks as if significant age acceleration in the breast cancer patients' normal tissue increases at a higher rate than those unaffected by breast cancer.

Though the study did not set out to look at smoking in particular, the researchers found a strong correlation between smoking and biological age.

Why this study is important:

As researchers continue to look for ways to predict breast cancer risk and outcome, exploring genetic methods and triggers has come to the forefront. This study suggests that having a breast tissue biomarker of accelerated aging could lead to future development of breast cancer. Looking at these biomarkers may be another way to assess breast cancer risk.