52: Estimating breast tissue-specific DNA methylation age using next-generation sequencing data
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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. This study aims to develop a model to estimate breast tissue-specific biological age.

Methods:

Our bodies use DNA methylation to control gene expression, to turn off or on genes that may threaten our health. DNA methylation age (DNAm) can assess the frequency and degree to which this happens. Scientists already use a method called the Horvath clock to estimate DNAm, but it is not as effective in breast tissue as other tissues. This study seeks ways to develop a better method of gauging DNAm in breast cancer tissue.

To do this, the researchers used 459 normal, 107 tumor and 45 adjacent-normal breast tissue samples to develop a model to estimate DNAm age in different breast tissues type and tumors.

Findings:
Researchers found that DNAm age is much the same as chronological age in normal breast tissue. In breast tumor tissue samples, they found DNAm was on average seven years older than respective chronological age and appeared 12 to 13 years older than adjacent-normal and normal breast tissue.

They also looked further at other tumor attributes. Both HER2+ and hormone-receptor positive tumors showed acceleration in DNAm ages, but triple negative tumors showed no DNAm age acceleration. Early-stage tumors showed DNAm acceleration, but late-stage tumors showed a non-significant negative acceleration.

Why this study is important:
We already know that female breast tissue ages faster than other parts of the body, and that age is an established risk factor for breast cancer. A new model that can pinpoint DNAm age could help us understand how aging breast tissue contributes to cancer development. Such a tool also could be used to assess a patient's breast cancer risk.