Genetics may influence risk for breast cancer after chest radiotherapy to treat childhood cancer

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Among females who received radiotherapy to the chest as part of treatment for a childhood cancer, those who had either of two specific genetic variants were at significantly higher risk of developing breast cancer later in life, according to research presented here at the AACR Annual Meeting 2016, April 16-20.

"It has been well established that female survivors of childhood cancer who received radiotherapy to the chest as part of their treatment have a higher risk of developing breast cancer later in life, compared to survivors who did not receive radiotherapy," said Lindsay M. Morton, PhD, senior investigator in the Radiation Epidemiology Branch of the Division of Cancer Epidemiology and Genetics at the National Cancer Institute in Bethesda, Maryland. "We set out to investigate whether inherited genetic susceptibility variants may influence which survivors go on to develop breast cancer."

Morton and colleagues found that specific variants in two regions of the genome were associated with increased risk of breast cancer after childhood cancer among survivors who received 10 or more gray [a measure of radiation dose] of chest radiotherapy. A variant at position q41 on chromosome 1 was associated with nearly two-fold increased risk and one at position q23 on chromosome 11 was associated with a more than three-fold increased risk for each copy of the risk alleles.

"Although breast cancer risk was increased significantly for each copy of the risk alleles, they didn't appear to have an effect among survivors who did not receive chest radiotherapy," said Morton. "Because this is a discovery study it is very important to replicate our findings in independent populations.

"If the findings are confirmed, we hope that we will be able to identify more precisely the risks and benefits of radiotherapy at the time of childhood cancer diagnosis," she added. "In addition, for patients who have already been treated, the results could be used to identify the survivors who have the highest risks of developing breast cancer and therefore might benefit the most from screening."

The researchers conducted genomic analyses of DNA obtained from blood or saliva samples collected from 3,002 female childhood cancer survivors from two independent cohorts followed by investigators at the St. Jude Children's Research Hospital, the Childhood Cancer Survivor Study and the St. Jude Lifetime Cohort. The children in these cohorts have been followed for a median of 25 years and 207 cases of breast cancer have been diagnosed.

According to Morton, despite the size of the study population, there were not enough participants to provide statistical power to identify regions of the genome that may be associated with smaller risks. She also noted that another limitation of the study was that the researchers did not have information about the type of breast cancers diagnosed in these survivors.

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