Team identifies genes that increase risk for triple-negative breast cancer

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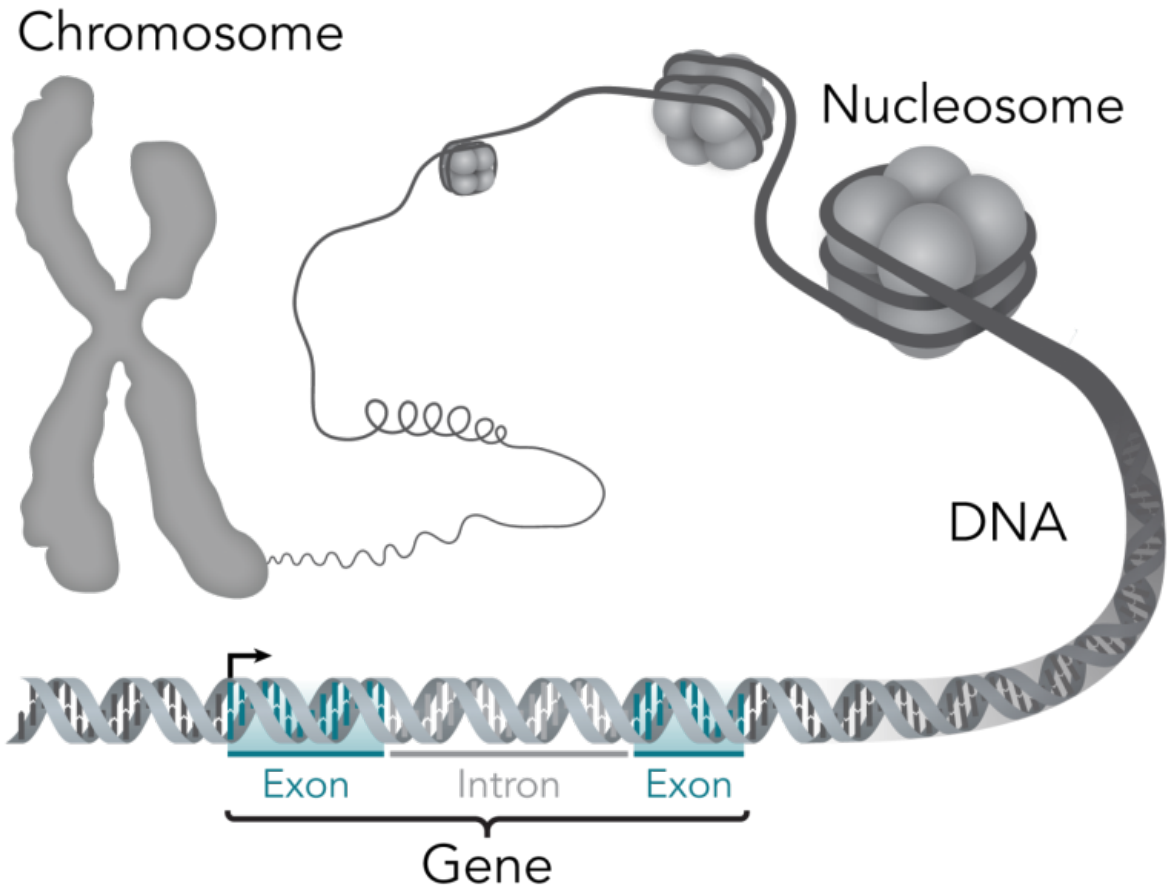

This stylistic diagram shows a gene in relation to the double helix structure of DNA and to a chromosome (right). The chromosome is X-shaped because it is dividing. Introns are regions often found in eukaryote genes that are removed in the splicing process (after the DNA is transcribed into RNA): Only the exons encode the protein. The diagram labels a region of only 55 or so bases as a gene. In reality, most genes are hundreds of times longer. Credit: Thomas

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A research team led by Fergus Couch, Ph.D., a geneticist at Mayo Clinic, has identified specific genes associated with an increased risk for developing triple-negative breast cancer. Their research was published in the *Journal of the National Cancer Institute*.

"Triple-negative breast cancer is an aggressive type of cancer that cannot be treated using targeted therapies," says Dr. Couch. "It accounts for 15 percent of breast cancer in the Caucasian population and 35 percent in the African-American population. It is also associated with a high risk of recurrence and a poor five-year survival rate. Our findings provide the basis for better risk management."

Dr. Couch says germ line genetic testing, which evaluates inherited genetic changes that increase the risk of certain cancers in an individual, has helped identify women at increased risk of breast cancer. However, he says it has been more difficult to identify women at elevated risk of triple-negative breast cancer because only inherited mutations in BRCA1 have been linked to this subtype of breast cancer.

Dr. Couch and his colleagues performed genetic testing on 10,901 patients with triple-negative breast cancer from two studies. They tested 21 cancer predisposition genes in 8,753 patients and 17 genes in the remaining 2,148 patients. They found that alternations in BARD1, BRCA1, BRCA2, PALB2 and RAD51D genes were associated with a high risk for triple-negative breast cancer and a greater than 20 percent lifetime risk for overall breast cancer among Caucasians. They observed a similar trend among African-Americans. In addition, mutations in the BRIP1 and RAD51C genes were linked to a more moderate risk of triple-negative breast cancer.

"This study is the first to establish which genes are associated with high lifetime risks of triple-negative breast cancer," says Dr. Couch. "While previous studies have found genetic variants in BARD1, BRIP1, PALB2 and RAD51C triple-negative breast cancer patients, the current study shows this in more detail, and identifies new specific and strong associations between the susceptibility genes RAD51D and BARD1, and triple-negative breast cancer risk."

Dr. Couch says these findings will enable expanded genetic testing to identify women at risk for triple-negative breast cancer and may potentially lead to better prevention strategies.

Dr. Couch says the new findings also may lead to revisions to the National Comprehensive Cancer Network screening guidelines, which currently recommend only BRCA testing when a patient has a family history of breast cancer or is diagnosed at age 60 or younger.

Provided by Mayo Clinic

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