Aggressive form of breast cancer influenced by dual action of genes and RNA

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Women with an aggressive, less-common type of breast cancer, known as triple-negative, versus a more common form of the disease, could be differentiated from each other by a panel of 17 small RNA molecules that are directly influenced by genetic alterations typically found in cancer cells.

Researchers lead by Luciane Cavalli, Ph.D., at Georgetown Lombardi Comprehensive Cancer Center, and colleagues found that variations in how these small RNA, known as microRNA (miRNA), are expressed, at higher or lower levels, could partially explain disparate rates of triple-negative breast cancer (TNBC) in Latina women compared to non-Hispanic white women and potentially lead to more effective treatment options.

That is the finding of a new study that was published October 22, 2019, in *Oncotarget*.

"Due to the variability in expression of miRNA by race or ethnicity, we determined that it was critical to characterize the genomic lineage (or ancestral background) of women with TNBC," said Cavalli, an adjunct professor of medicine at Georgetown University School of Medicine and a faculty member at Instituto de Pesquisa Pelé Pequeno Príncipe in Brazil. "While our focus was on genetics, we remain aware that non-genetic factors, such as social-economic conditions, can significantly impact the incidence rates of TNBC and other subtypes of breast cancer."

Statisticians estimate that TNBC occurs in up to one-third of women in Latin American countries, a rate that is higher than in the United States. The researchers in this study focused on Brazil, in particular, where an estimated 60,000 new cases of breast cancer were diagnosed in 2018.

The scientists discovered that women with TNBC had specific alterations in copies of their genes that directly influenced the expression of 17 miRNAs compared to women with other forms of breast cancer who did not have these alterations. They also found that the expression levels of the majority of these miRNAs were associated with the tumor's clinical aggressiveness (advanced grade and stage).

"The panel of miRNAs we identified indicate potential, critical cancer-related pathways and gene networks that could be targeted for the treatment of TNBC in Latinas, once our findings are validated by larger studies," concluded Cavalli. "Targeting these genetic alterations, that represent the unique biology of their tumors, may lead to more efficient treatments, which could increase the longevity of Latina women who do not have many therapeutic options to fight this very aggressive disease."

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