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Gene signature for cancer stem cells may provide drug targets

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A subset of tumor cells that remain after a woman with breast cancer undergoes treatment with either anti-cancer or anti-hormone therapy shows a "gene signature" that could be used to define targets for developing new drugs against the disease, said a consortium of researchers led by Baylor College of Medicine. The report appears in the current issue of the *Proceedings of the National Academy of Sciences*.

"We have found that gene expression patterns in a subset of these resistant cancer cells differ from those associated with the bulk of the epithelial cells in the tumor. These patterns resemble expression patterns more closely associated with cells with a mesenchymal (a form of connective tissue) phenotype (or appearance)," said Dr. Jenny Chang, medical director of the Sue and Lester Smith Breast Center at BCM and a professor of medicine. Chang is a senior author of the paper along with Drs. Michael Lewis and Jeffrey M. Rosen, both of BCM and the Dan L. Duncan Cancer Center as well as the Breast Center.

In a previous paper, the authors showed that after patients received conventional chemotherapy, the remaining tumor contained a higher percentage of tumor-initiating cells, also known as breast cancer stem cells. These remaining tumor-initiating cells were therefore largely resistant to conventional treatments.

They found that gene expression patterns in these chemoresistant cells represented a tumor-initiating gene signature, which was not only more easily detectable in a newly-defined breast cancer subtype called

"claudin-low", but also enriched in human breast tumors after they had been treated with anti-cancer drugs that target the signals of hormones, said Chang. They also found that genes associated with the mesenchymal cell phenotype were increased in breast tumors after hormone treatment.

"This study supports a growing body of evidence that there is a particular subpopulation of cells in breast cancer that may be responsible for disease recurrence, resistance to treatment, and perhaps metastasis (cancer spread)," said Chang.

In the future, she said, the group will be looking at ways to use the gene signature they have identified to develop drugs that can combine with conventional therapy to eradicate all populations of cells within tumors.

Source: Baylor College of Medicine (news : web)