Genetic predictor of breast cancer response to chemotherapy

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Chemotherapy is a major first line defense against breast cancer. However a patient's response is often variable and unpredictable. A study published in BioMed Central's open access journal *BMC Medical Genomics* shows that 'gene expression signatures' for TOP2A and ?-tubulin can be used to predict the outcome of chemotherapy.

The goal of personalized medicine in cancer treatment is to target therapy to the characteristics of the individual tumor. For example Herceptin treatment is of most benefit to patients whose cancer is driven by HER2 and antiestrogens benefit patients whose breast cancer is hormonally driven. Gene signatures are increasingly available for different cancer types and can be used to predict patient prognosis.

Researchers from McMaster University, in association with the Juravinski Hospital and Cancer Center, analyzed the expression of the enzyme TOP2A (DNA topoisomerase) and ?-tubulin, which are the targets of commonly used chemotherapy drugs (anthracycline and taxane) in hundreds of breast tumors. Combining the results from the tumor samples analyses allowed the researchers to build gene expression 'signatures' that measure the susceptibility of tumor cells to chemotherapy.

Both of the 'signatures' were separately able to predict which patients achieved a complete response (where invasive or metastatic cancer could no longer be detected) and together the two indices together were even more accurate at predicting response to chemotherapy.

Prof John Hassell, who led this study, commented, " Our results clearly demonstrate the practicality of using gene expression to personalize chemotherapy treatment for breast cancer patients. Identifying patients who will not benefit from a specific treatment means that they can be moved to a different treatment plan, and the earlier appropriate treatment is started the more likely it is that the patients will benefit from it."

More information:
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