

Gene Expression Profile Helps Predict Chemotherapy Response In Ovarian Cancer Patients

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Gene Expression Profile Helps Predict Chemotherapy Response In Ovarian Cancer Patients

A newly identified gene expression profile could help predict how patients with advanced ovarian cancer will respond to chemotherapy treatment. Described in a study in the November 1, 2005 issue of The Journal of Clinical Oncology (JCO), the new findings further establish an important role for microarray gene profiling as a predictor of clinical outcome in ovarian cancer, and could eventually provide clinicians with insights into the mechanisms of drug resistance.

"In many patients with advanced ovarian cancer, post-operative treatment with first-line chemotherapy will result in an excellent clinical response," says senior author Stephen A. Cannistra, MD, director of gynecologic oncology at Beth Israel Deaconess Medical Center (BIDMC) and professor of medicine at Harvard Medical School.

"However," he adds, "due to the lingering presence of chemotherapy-resistant cancer cells, most patients will unfortunately experience a relapse. The goal of our current research is to help determine which patients will relapse and which will not, and to better understand the reasons for this."

Cannistra's group has been working to develop a genetic profile of ovarian cancer that will enable clinicians to more accurately determine a patient's prognosis. As a first step in this process, he and his colleagues last year identified a gene expression profile known as the Ovarian Cancer Prognostic Profile (OCPP), which is predictive of survival in patients with advanced ovarian cancer. (These study results appear in the December 2004 issue of the JCO.)

Their work makes use of a DNA technology known as microarray analysis, in which genes expressed by cancer cells are labeled and applied to a glass

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slide containing embedded sequences of thousands of known human genes. The genes that are present in the tumor cell bind to their counterpart sequences on the slide and can then be identified through computer analysis.

In this new study, the authors conducted microarray testing on samples from 60 ovarian cancer patients treated at BIDMC and Memorial Sloan-Kettering Cancer Center to determine if tumor tissue obtained at a patient's initial diagnosis expressed a gene profile predictive of findings at second-look surgery. (Second-look surgery is currently the most sensitive investigation