

A new test may better predict ovarian cancer survival

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Intermediate magnification micrograph of a low malignant potential (LMP) mucinous ovarian tumour. H&E stain. The micrograph shows: Simple mucinous epithelium (right) and mucinous epithelium that pseudo-stratifies (left - diagnostic of a LMP tumour). Epithelium in a frond-like architecture is seen at the top of image. Credit: Nephron /Wikipedia. CC BY-SA 3.0

Scientists may have found a better way to estimate survival for women with aggressive ovarian cancer, according to a new study by USC researchers and international colleagues.

The findings, which appear Monday in the print edition of the journal *Annals of Oncology*, could focus the development of targeted therapeutic approaches and identify [women](#) who might benefit from clinical trials.

An estimated 21,750 American women will be diagnosed with [ovarian cancer](#) this year. Average survival for women with the most common and aggressive form is around four years. But survival varies widely between patients, underscoring the need to estimate who is facing a fast-moving or slower disease.

In this study, researchers discovered that a [tumor](#) gene test, which is based on tissue removed during cancer surgery, is better at predicting survival among women with ovarian cancer than making estimates the usual way, which is based on a patient's age and cancer stage.

"We envisioned a test to use at the time of diagnosis—to identify patients unlikely to benefit from [current treatments](#) and potentially offer them alternatives," said Joshua Millstein, an associate professor of research in [preventive medicine](#) at the Keck School of Medicine of USC and the study's first author. "For example, those patients might be good candidates for clinical trials or for different treatments that might improve their survival."

Tumor gene test can predict ovarian cancer survival rate

To start, researchers gathered preserved tumor samples and data about duration of survival after diagnosis from nearly 4,000 women worldwide whose information had been collected for previous studies.

They custom-designed a test to measure each sample for the expression of 500 genes linked to the ovarian cancer disease process. Genes

"express" proteins and other molecules, based on the gene's particular DNA, to perform particular functions. They then "trained" the test with a portion of the tumor samples, inputting gene expression data from each tumor as well as the number of years the patient survived after their diagnosis.

Soon, the tumor gene [test](#) could accurately predict a patient's five-year survival rate based on their tumor's gene expression profile alone. This important information could help newly diagnosed women and their doctors make treatment decisions as well as set targets for developing new therapies.

"Some of the [genes](#) we identified as being predictors for good or poor survival may be potential targets for new treatments," said senior author Susan Ramus, an ovarian cancer researcher previously at the USC Norris Comprehensive Cancer Center and now a professor at the University of New South Wales in Sydney.

"At the moment, the majority of ovarian cancer patients get the same treatment. It's not like breast [cancer](#) or other cancers where they look at your tumor and select from a range of treatments," she added. "So this is a way to stratify patients and potentially give more personalized treatment down the track."

Provided by University of Southern California

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