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Center and other centers identified genetic mutations and pathways that distinctly set the disease apart not only from other types of ovarian cancer, but from other solid tumors as well. The findings, reported in the June 30, 2011 issue of *Nature*, may be useful in helping doctors to choose experimental treatments that are most likely to effectively target molecular alterations in patients with this type of ovarian cancer, called high-grade serous ovarian adenocarcinoma. [PubMed Abstract]

The research was a project of The Cancer Genome Atlas (TCGA), a collaborative study that is one of the most comprehensive national efforts to collect, process, and analyze the largest set of tumor samples to date using state-of-the-art genomic and molecular techniques. Memorial Sloan Kettering provided the greatest number of ovarian tumor samples for this study and served as one of the main centers that generated and analyzed the genomic data.

The investigators analyzed genetic abnormalities in nearly 500 high-grade serous ovarian tumors. Memorial Sloan Kettering researchers are now building on the findings by studying whether some of these genetic alterations affect the way cells behave and respond to certain targeted agents. In particular, the team showed that alterations in *BRCA1*, *BRCA2*, and related genes, some of which predict responsiveness to a new class of agents called PARP inhibitors, are present in half of all ovarian cancer patients. Center investigators are now translating these findings into clinically useful tests that may be applied to ongoing and planned clinical trials.

“This unprecedented work provides a much-needed framework upon which future discoveries in the understanding and treatment of ovarian cancer will be built,” says Douglas A. Levine, co-chair of TCGA Ovarian Disease Working Group and part of the Memorial Sloan Kettering multidisciplinary team, along with molecular pathologist Marc Ladanyi and computational biologist Chris Sander.

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