Mayo Clinic genomic analysis lends insight to prostate cancer

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Mayo Clinic researchers have used next generation genomic analysis to determine that some of the more aggressive prostate cancer tumors have similar genetic origins, which may help in predicting cancer progression. The findings appear online today in the journal *Cancer Research*.

"This is the first study to examine DNA alterations using next generation sequencing in adjacent Gleason patterns in the same tumor allowing us to correlate genomics with changes in pathology," says John Cheville, M.D., Mayo Clinic pathologist and one of the authors on the paper.

The standard method of evaluating prostate cancer biopsy samples is a numerical scoring system called Gleason grading. A pathologist examines the tumor sample under the microscope, giving it a Gleason score based on the pattern of its cells. Since many prostate cancers contain more than one pattern, the two most common patterns are added together to provide the Gleason score. The Gleason score is the strongest predictor of outcome, with high scores indicating more aggressive prostate cancer. This study focused on Gleason patterns of three and four (Gleason score 7), a combination that indicates a cancer with increased risk of progression.

"While each pattern had its own breakpoints, they shared identical ones, which implies a common origin," Dr. Cheville says. DNA changes associated with aggressive prostate cancer were identified in the lower Gleason pattern, indicating that genomic changes occurred before they could be recognized by a pathologist. By understanding these lineage relationships within a tumor, he says, physicians will be better able to predict progression of the cancer and, in turn, better manage patients including those who chose no treatment but enter a follow-up program called active surveillance.

To determine relationships among the Gleason patterns of each tumor sample the team used laser capture micro dissection, whole genome amplification and next generation sequencing. They examined 14 tumors and found over 3,000 unique chromosomal alterations among all tumors and 300 that appeared in at least two of the tumors. They also found that Gleason pattern 3 in each tumor had more alterations in common with its corresponding Gleason pattern 4 than it did with Gleason pattern 3 from other patients.

Provided by Mayo Clinic

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