MedicalXpress

Common genetic fusion event may be associated with low-risk prostate cancer

November 10 2017

Establishing the way in which a genetic alteration called a TMPRSS2-ERG gene fusion forms in a prostate cancer, rather than the presence of the gene fusion itself, could help identify patients with prostate cancer with a low risk of spreading, which might determine the best course of treatment for the patient.

The study is published in *Cancer Research*, a journal of the American Association for Cancer Research, by John C. Cheville, MD, professor of pathology at the Mayo Clinic in Rochester, Minnesota.

A Gleason score provides information on how aggressive a prostate cancer is. It is calculated when a prostate needle biopsy specimen is examined under a microscope. Depending on how normal or abnormal the cancer looks, it is assigned a number from 1 to 5, with 5 being the most abnormal and most aggressive. Different areas of a tumor may have different patterns, and the two highest patterns are added together to give the Gleason score. Most prostate cancers are Gleason score 6 (composed entirely of pattern 3) and men with Gleason score 6 are considered at low risk of having their tumors progress.

Cheville explained that active surveillance is a common approach to caring for patients with prostate cancer with a Gleason score of 6. Men on active surveillance receive no treatment and are followed. Some of these men are later found to have clinically significant disease that requires treatment. Identifying a biomarker that, in addition to Gleason score, distinguishes men at increased risk for disease progression from

those whose prostate cancer never becomes a clinically significant problem could help improve patient care, added Cheville.

To look for genetic biomarkers of clinically significant or insignificant disease, Cheville and colleagues used whole-genome mate pair sequencing to study gene fusions in prostate cancer tissue samples obtained from 133 patients who underwent a radical prostatectomy at the Mayo Clinic. The prostate cancers were divided into four groups: 53 low volume Gleason 6 tumors were classed as very low risk for progression; 26 high volume Gleason 6 tumors were classed as low risk for progression; 29 Gleason 7 tumors were classed as intermediate risk for progression; and 25 Gleason 8 or higher tumors were classed as high risk for progression.

The researchers detected TMPRSS2-ERG fusions in 45 percent of the prostate cancers analyzed, which is consistent with prior studies, according to Cheville. Fusions were detected in 43 percent, 49 percent, 52 percent, and 24 percent in the very-low risk, low-risk, intermediate-risk, and high-risk groups, respectively.

Among the 60 prostate cancers with TMPRSS2-ERG fusions, 39 had deleted the interstitial genes between TMPRSS2 and ERG during the fusion event and 21 had retained these genes. Eighteen of the 21 prostate cancers that had retained the interstitial genes during TMPRSS2-ERG gene fusion were in the very-low risk and low-risk groups.

Information on whether a patient went on to have a biochemical recurrence was available for 34 patients who had prostate cancer with a TMPRSS2-ERG gene fusion with interstitial gene deletion and 22 patients who had prostate cancer with a TMPRSS2-ERG gene fusion with interstitial gene retention. In univariate, but not multivariate, analysis, biochemical recurrence was significantly lower if the prostate cancer had a TMPRSS2-ERG gene fusion with interstitial gene retention

compared with those that had interstitial gene deletion.

"Our data support results from other studies in that the presence or absence of a TMPRSS2-ERG gene fusion was not predictive of outcome," Cheville said. "But how the gene fusion formed was important; the retention of interstitial genes during the fusion event was more common in very-low risk and low-risk cancers, and there may be genes in this region that suppress or limit tumor growth. There is potential utility for determining the status of interstitial genes in stratifying men with prostate cancer into more well-defined risk groups, but this will require further study before it can be incorporated into clinical practice.

"The loss or retention of interstitial genes was tied closely to Gleason score, and we did not have enough cases to determine whether or not the type of fusion was an independent marker for biochemical recurrence," continued Cheville. "We need to look at many more samples and also look at patients with higher Gleason scores to determine the extent to which loss of interstitial genes is associated with disease progression."

According to Cheville, the main limitation of the study is the relatively small number of patients analyzed in each group.

This study was supported by James and Dorothy Nelson Benefactor Funds and the Mayo Clinic Center for Individualized Medicine. Cheville declares no conflicts of interest.

Provided by American Association for Cancer Research

Citation: Common genetic fusion event may be associated with low-risk prostate cancer (2017, November 10) retrieved 9 April 2024 from https://medicalxpress.com/news/2017-11-common-genetic-fusion-event-low-risk.html

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.