One single biopsy not sufficient to guide treatment decisions in prostate cancer

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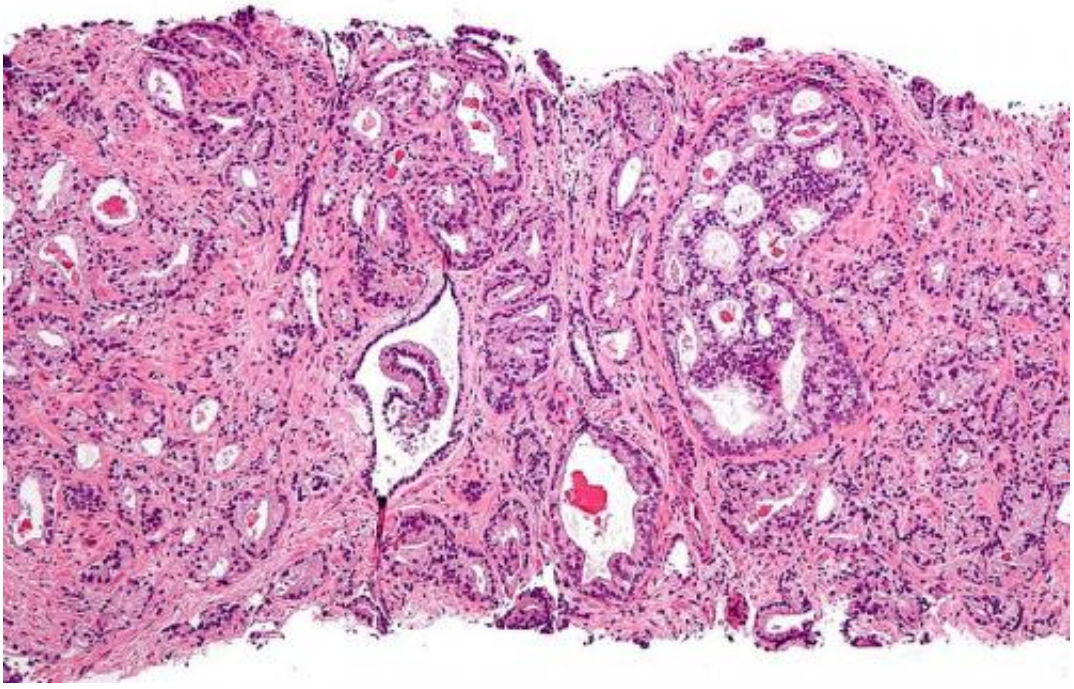

Micrograph showing prostatic acinar adenocarcinoma (the most common form of prostate cancer) Credit: Wikipedia, CC BY-SA 3.0

While the majority of prostate cancers are slow growing and not fatal, some are aggressive and lethal. Genomic fingerprinting can help predict a tumor's aggressiveness and tailor treatment plans; however, in the majority of cases involving multiple prostate tumors, only the largest tumor is typically fingerprinted – resulting in more aggressive tumors potentially going undetected.

Writing in the journal *European Urology*, a research team led by Hannelore Heemers, Ph.D., of Cleveland Clinic's Lerner Research Institute Department of Cancer Biology, and James Mohler, M.D., chair of the Department of Urology at Roswell Park Cancer Institute in Buffalo, has demonstrated that when genomic fingerprinting is performed on only a single tumor sample, a smaller but more aggressive tumor could potentially be missed.

The finding underscores the importance of new evidence that prostate tumors can be genetically different within an individual patient, which carries important implications for patients and oncologists.

For the study, "Intratumoral and Intertumoral Genomic Heterogeneity of Multifocal Localized Prostate Cancer Impacts Molecular Classifications and Genomic Prognosticators," the team used next-generation sequencing techniques to genotype prostate tumors from four men who underwent radical prostatectomy at Roswell Park. They also examined public data from the Cancer Genome Atlas to confirm their findings.

"We examined the molecular composition of heterogeneous cancerous tumors in a patient's prostate. We found a lot of genetic differences among these tumors, and concluded that information from a single cancer biopsy is not sufficient to guide treatment decisions," said Dr. Heemers. "Precise treatment is more complicated and the findings demonstrate a weakness in current genetic fingerprinting in prostate cancer."

"High risk prostate cancers differ genetically among patients, among the different tumors within an individual patient and even within different sections of a single tumor," said Dr. Mohler. "Clinicians need to be careful about using the information from a gene-based test, because the analysis may not have been performed on the most aggressive portion of a man's prostate cancer."

In "*Disrupting the Status Quo in Prostate Cancer Diagnosis,*" an editorial published in the same journal, Alastair David Lamb, MB.ChB., Ph.D., of Cambridge University Hospitals, and co-authors write: "Several aspects of this study are impressive. [The authors] addressed an important clinical and molecular question: What effect does tumor heterogeneity have on decision making in prostate cancer, specifically, with respect to molecular taxonomies of the disease?"

The study authors note that the use of genomic analysis to personalize treatment plans is in its infancy and that many more large studies will be required to develop next-generation prognostic tools that can be relied on to guide treatment selection and planning for men with prostate cancer.

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