Transcript Details

This is a transcript of a continuing medical education (CME) activity. Additional media formats for the activity and full activity details (including sponsor and supporter, disclosures, and instructions for claiming credit) are available by visiting:
https://reachmd.com/programs/cme/Molecular-Profiling-in-mHSPC-Informing-Treatment-Selection/57199/

Released: 06/16/2026
Valid until: 06/16/2027
Time needed to complete: 43m

ReachMD
www.reachmd.com
info@reachmd.com
(866) 423-7849

Molecular Profiling in mHSPC: Informing Treatment Selection

Announcer:
This activity is provided by **Global Learning Collaborative** and is part of our MinuteCE curriculum.

Prior to beginning the activity, please be sure to review the faculty and commercial support disclosure statements as well as the learning objectives.

Dr. Tagawa:
This is CE on ReachMD, and I'm Dr. Scott Tagawa. It's a pleasure to welcome Dr. Mary-Ellen Taplin to the program. Let's turn to the role of molecular profiling. Dr. Taplin, what genetic alterations can inform treatment selection in metastatic HSPC?

Dr. Taplin:
Thank you, Dr. Tagawa. First off, I just want to say that it's difficult to change our practice patterns, but it's of utmost importance in our metastatic prostate cancer patients now to consider both germline and somatic testing very early on; I would say at the time of initial diagnosis. Because as the data evolves to support additional treatments such as PARP inhibitors or AKT inhibitors, we won't be able to deliver those treatments to the patients who will most benefit unless we do the testing.

So, for me, the first thing I do is recommend germline testing for my patients. At Dana Farber we have a genetics group that helps us with that type of testing, but there is multiple germline panels that can be recommended to patients in testing ordered by the treating physicians. Results return in about 3 weeks and can be shared with the patient and integrated into treatment decision-making.

Also important, in addition to germline testing, is somatic testing of the tumor itself. And all of our patients have a prostate biopsy at the time of diagnosis, I'll say the vast majority. Additionally, some patients have other types of tumor tissue available, such as prostatectomy tissue or a metastatic biopsy tissue.

But the bottom line is: it's really important to get molecular sequencing of a patient's tumor. The site that you choose is less important than the fact that the tumor sequencing is done and available.

And why are we doing the sequencing? The reason that we're doing it is because there are actionable alterations in genes that are driving the growth of our patients' prostate cancer. And by doing the sequencing, we're identifying which patients have these alterations that we can impact by assigning a specific therapy to a specific mutation.

So, for instance, one of the things we're looking for is mutations in the DNA repair pathway. And there's a long list of possible mutations in the DNA repair pathway, but the most actionable one is the BRCA2 mutation. And BRCA2 mutations are seen in about 10% of prostate cancer patients. And patients with these mutations have, in general, an excellent response to PARP inhibitors, and now there's data to consider PARP inhibitors in combination with androgen pathway inhibitors as the first treatment in metastatic hormone-sensitive

prostate cancer. [One example] would be abiraterone and niraparib. So very important to get the information so if you have one of these patients, you can apply the right therapy.

In addition, there's other evolving data about the AKT pathway and PTEN loss. PTEN loss, to some degree—let's just say, by immunohistochemistry—can be seen in about 30% of prostate cancers, [which is] a healthy number. And there's evolving data that patients with significant loss of this pathway have response to an AKT inhibitor, and thus we need to get the data to consider this type of therapy and, again, match to the right patient.

And now, as the clinical data from clinical trials show us the benefit of matching therapy to specific mutations, it becomes of utmost importance for us, on every patient, to sequence their tumor and germline [testing], and apply the right therapies based on what we find.

Dr. Tagawa:
Thank you very much, Mary-Ellen. I completely agree that for essentially 100% of our patients, we test both germline as well as somatic alterations.

And having the prognostic information that we get from a lot of these—and now turning into, potentially, predictive information for certain types of therapy—is even more important.

We hope this has been helpful in your clinical practice. See you next episode.

Announcer:
This activity is provided by **Global Learning Collaborative** and is part of our MinuteCE curriculum.

To receive your free CE credit, or to download this activity, go to ReachMD.com/**CME**. Thank you for listening.