

Validation of AR-V7 as a Treatment-Specific Biomarker at Decision Points in Management of **Castration-Resistant Prostate Cancer** Howard I. Scher^{1,2}, David Lu³, Nicole Schreiber¹, Jessica Louw³, Ryon Graf³, Hebert Vargas¹, Ann Johnson³, Adam Jendrisak³, Richard Bambury¹, Daniel Danila¹, Brigit

¹ Sidney Kimmel Center for Prostate and Urologic Cancers, Memorial Sloan-Kettering Cancer Center, New York, NY ² Department of Medicine, Weill Cornell Medical College, New York, NY ³ Epic Sciences, Inc., San Diego, CA

Background

Androgen receptor signaling directed therapies (AR Tx), including Abiraterone Acetate + Prednisone (A) and Enzalutamide (E), prolong survival in patients with mCRPC and are FDA approved. The presence of the splice variant AR-V7 mRNA in EpCAM selected CTCs has been prospectively linked to resistance to A & E¹ but not to taxane chemotherapy (T)². AR-V7 may provide clinical utility in therapy selection between A & E or T. A key limitation to the predictive value of an AR-V7 mRNA assay in CTCs is the analytical validation of the measurement of low frequency and labile mRNA in CTCs, and to be able to meet diagnostic workflows amenable to community practices. Separately, EpCAM based CTC isolation and capture methods will not detect EpCAM(-) cells, potentially leading to under-sampling of the AR-V7 biomarker. We developed an AR-V7 immunofluorescent test for use in fixed single CTCs that is inclusive of all CTC subtypes which was evaluated in blood samples from men with progressive mCRPC patients in need of a change in therapy. The context of use is to inform the selection of treatment. The Epic CTC platform was designed for global diagnostic workflows with a rapid turnaround time. The focus was the association between the pre-therapy detection of nuclear localized AR-V7(+) CTCs and objective clinical outcomes following treatment with the most frequently, approved drug classes for management of mCRPC: AR Tx and taxanes. The goal is the development of predictive biomarkers for use at the point a treatment decision is needed that will enable broad adoption from global clinical sites.

Methods

193 mCRPC patient blood samples were collected prior to starting Abiraterone (44); Enzalutamide (81), Docetaxel (46) Cabazitaxel (13), and Paclitaxel (2). PSA Outcomes were recorded as Sensitive (S): Patterns 1 and 2, or Resistant (R): Pattern 3 (A)⁶. Patients were monitored for up to 2.3 yrs to assess rPFS and OS outcomes. Samples were processed utilizing the Epic Sciences platform (B).



- 1) Nucleated cells from blood sample placed onto slides and stored in a 4) CTC candidates detected by a multi-parametric digital
 - 5) Human reader confirmation of CTCs & quantitation of
 - - Patient Demographics



References: 1) Antonarakis, Emmanuel S., et al. New England Journal of Medicine 371.11 (2014): 1028-1038. 2) Antonarakis, Emmanuel S., et al. J Clin Oncol 33, 2015 (suppl 7; abstr 138). 3) Efstathiou, E., et al. Annals of Oncology 2014 (25 suppl 4) 4) Bambury, Richard M., et al. Annuals of Oncology 2014 (25 suppl 4) 5) Scher, Howard I., et al ASCO GU Abstract #147 6) Scher, Howard I., et al. Cancer J. 2013 Jan-Feb;19(1):43-9

-80°C biorepository

- 2) Slides stained with cytokeratin (CK), CD45, DAPI, AR-V7 Slides scanned
- pathology algorithm
- biomarker expression

McLaughlin¹, Justin Wahl³, Stephanie Greene³, Glenn Heller¹, Dena Marrinucci³, Martin Fleisher¹, Ryan Dittamore³

3) SCANNING

Analytical Validation: Specificity of AR-V7 Detection The specificity of AR-V7 protein detection in single prostate cancer cell line cells spiked into whole blood was corroborated by single-cell mRNA analyses (C, D). The requirement for AR-V7 protein signal localization in the nucleus is consistent with AR-V7-mediated ligand-independent proliferation in preclinical models. Nuclear AR-V7 localization was required to be considered AR-V7+ in all patient samples.

Specificity of AR-V7 in Patient Samples

Parallel AR Assays (N-terminal and AR-V7) were utilized, and the incidence of CTCs positive for either biomarker on sister slides is shown to the right. Comparison of stained sister slides per sample with different assays is subject to some stochastic differences in CTC incidence across slides in samples. (E). However, the much greater incidence of AR N-terminal CTCs is consistent with previous studies on AR-V7 prevalence in relation to total AR gene product.



Prevalence and Frequency of AR-V7 CTC Positivity **Increases by Line of Therapy**

AR-V7 Is Expressed in Multiple CTC Subtypes AR-V7 nuclear expression was found on a variety of CTC subtypes, including "traditional" CK(+) single CTCs (F), CTC clusters (G), and CK(-) CTCs (H). CTCs not expressing AR-V7 were also found (I).



resistant posttherapy PSA change. None of the 47 with sensitive posttherapy PSA changes had AR-V7(+) CTCs (0%, 95% CI: 0.0%-9.41%). In contrast, of the 81 with resistant PTPC, 16 had AR-V7(+) CTCs (20%, 95% CI: 12.1%–30.4%) prior to therapy (N). This was not the case for pre-taxane samples, where posttherapy PSA changes were not significantly different by AR-V7 status. (O).

Prevalence and Frequency of AR-V7 CTC Positivity Increases by Line of Therapy Most of the CTCs detected from 191 evaluable



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