

Gene Expression Analysis in Circulating Tumor Cells from Prostate Cancer Patients using the NanoVelcro Assay

Yu Jen Jan¹, Jie-Fu Chen¹, Sungyong You¹, Shirley Cheng¹, Nu Yao¹, Michael R. Freeman¹, Hsian-Rong Tseng², Edwin. M. Posadas¹

¹ Urologic Oncology Program & Translational Oncology Program, Samuel Oschin Comprehensive Cancer Institute, Cedars-Sinai Medical Center (CSMC).

² California NanoSystems Institute, University of California, Los Angeles (UCLA).

Background: Circulating tumor cells (CTCs) are tumor cells shed from all present disease sites, including primary and metastatic tumors. CTCs have been used to identify important transcriptomic features such as androgen receptor (AR) splicing variants in prostate cancer (PCa). Newer transcriptomic profiles such as the prostate cancer classification system (PCS) have been developed that may be useful clinically. However, the low abundance of CTCs and the fragility of the genetic materials create a need for tools that obtain high-quality signals with great efficiency usable for these approaches. Over the past decade, we have been developing the NanoVelcro CTC purification system which includes 3 different stimuli-responsive strategies (temperature-dependent, glycan-stimulated, click chemistry-mediated) to capture and release viable CTCs with intact RNA. The CTCs purified by the NanoVelcro devices can then be subjected to modern transcriptomic analysis. In this study, we benchmarked the efficiency of these platforms for purification of CTCs from blood specimens and the feasibility of using this approach for detection of PCa-related RNA signatures from purified CTCs.

Methods: The efficiency of NanoVelcro CTC Purification System was tested using PCa cell lines and artificial blood samples. Transcriptomic analyses were performed using qPCR, ddPCRTM, the Nanostring nCounter[®] platform to detect PCa-specific RNA targets in purified CTCs obtained from PCa patients.

Results: The NanoVelcro CTC assays yielded cell capture efficiency above 80% in artificial blood samples. In patient samples, PCa-related RNA signals (including Arv7) were detected 16 of 17 PCa patients including 3 of 4 non-metastatic patients. We also developed a modified PCS panel adapted to the Nanostring nCounter[®] platform. Unbiased clustering of the PCS signature genes grouped patients in a manner which strongly associated with clinical status.

Conclusions: Using the NanoVelcro system, it is possible to purify viable CTCs with intact RNA suitable for measurement of PCa-specific transcripts. This non-invasive, blood-based approach could be used to detect and monitor transcriptomic alterations related to disease evolution addressing an unmet need in prostate cancer.

Conflict of Interest: N/A

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