

Adenoviral Tumor Diagnostics

INVENTION: Dr Clodagh O'Shea at Salk is developing a powerful diagnostic solution that detects circulating tumor cells (CTCs) from a blood biopsy using viral labeling, and can sort and array those cells based on pathway-specific viruses. These viruses can then be used to define the malignant phenotype of the cells, and functionally determine their ability to respond to different therapies. This approach will not only facilitate repeat analysis, but also potentially capture a wider picture of the multiple primary and metastatic clones in the tumors, quantifying their malignant potential and rapidly identify the therapies that are most effective in ablating an individual patient's tumor. This is a powerful technique to identify therapeutic targets associated with specific pre-selected cancer types, to identify the correct therapeutic approach for individual patients and to stratify patients in clinical testing, ultimately accelerating the development of designer therapeutics.

APPLICATIONS:

- Precision and personalized medicine in cancer
- Development of targeted therapies
- Identification of therapeutic targets specific to selected tumor types
- Phenotypic interrogation of the defective pathways in circulating tumor cells, tissue samples and other material

ADVANTAGES:

- Rapid, customizable diagnostic platform
- Ability to interrogate the malignant phenotype of cells- not just the genotype
- Generates a wider picture of multiple primary tumor clones than traditional genotyping
- Can identify specific mutants
- Technology discriminates live cells from dead cells, which can't be done with EPCAM Ab
- Provides for simple sample collection, and repeat analysis
- Efficient assembly of viral reporters to probe multiple transcriptional and molecular markers
- Ability to manipulate the 36kb viral genome rapidly and systematically
- Orthogonal approach to personalized medicine - integrate genomic analysis, activity, develop personalized therapeutic, and patho-physiologic outcomes

DEVELOPMENT STAGE: The diagnostic solution was tested in patient samples, now ready for scale-up.

BACKGROUND: Genome sequencing has accelerated our understanding of how molecular alterations determine a tumor's response to targeted drugs, leading to the development of personalized therapies. There are a number of challenges remaining including tumor heterogeneity, polygenic drug resistance and the need for more predictive prognostic markers. The diagnostic solution above has been made possible through the development of a modular adenovirus assembly platform, which facilitates the creation of diagnostic viruses that infect and phenotype a patient's CTCs. Using these viral reporters, the molecular lesions and malignant characteristics of any given CTC will be rapidly discerned (within 24 hours) and scored via a standardized automated platform.

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PATENT STATUS: U.S. patent application US-2015-0005397 A1 is pending

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