Dried Blood Spot Sequencing to Identify RNA Biomarkers

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Technology description

Researchers at TGen have developed a simple and non-invasive approach to sequence RNA biomarkers from a single dried blood spot. Using this RNA biomarker technology enables a relatively small volume biofluid sample from a patient (e.g., a drop of blood) to provide significant clinical information, such as identification, severity, stage, outcome, etc., of various diseases, conditions, and medical states based on the expression of the RNAs. With this technology, not only could multiple samples from a patient be easily obtained over an extended period of time for monitoring a disease, condition, or medical state, but the samples could be taken remotely by the patient themselves and mailed to a laboratory for analysis.

The discovery and reliable detection of biomarkers for any type of disease or condition may be complicated by the relative inaccessibility of some forms of tissue (e.g., central nervous system tissue) or an inability to biopsy or test tissue. The ability to meaningfully profile more easily accessible peripheral biofluids to monitor and gain insights about the underlying conditions and diseases would bring significant benefits to monitoring disease progression and treatment efficacy. However, the profiling of peripheral biofluids is also challenging due to concerns regarding sampling from cerebrospinal fluid (CSF) (e.g., extensive numbers of punctures of the spinal column), the large volumes of urine needed for biomarker extraction, and the difficult collection regimens with which patients may have to comply (e.g., saliva collection). This approach using a single dried blood spot on a solid substrate provides a simple and easily usable methodology for the ready collection of biofluids and downstream RNA isolation and processing.

TGen researchers have surveyed the stability of different RNAs in collected samples (e.g., dried blood spots) by sequencing technical replicates and calculating the coefficient of variance (CV) for each transcript. By calculating the CV, the inventors were able to gather information related to each RNA’ s stability during the drying process and determine each RNA’ s potential accuracy as a biomarker. The CV information can be used to filter sample-specific technical variance so that the best RNAs can be selected as markers for medical purposes, for example: determining the sex of an in utero fetus, predicting the onset of a migraine, or tracking athletic performance.

Institution

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