CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Award ID:
RP121018

Project Title:
Rapid and sensitive diagnostic testing for somatic mutations in cancer

Award Mechanism:
Bridging the Gap: Early Translational Research Awards

Principal Investigator:
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Entity:
Baylor College of Medicine

Lay Summary:

Cancer is a disease of the genome. That means, no matter what organ the cancer appears in, cancers share the common feature of mutations in the DNA that have been acquired at random during the lifetime of the individual and the during the development of cancer. Although every individual's cancer has a set of mutations unique to the individual, the cancers of a given organ tend to have specific genes mutated in common, thereby forming a "gene mutation profile" characteristic of a given cancer. Some of the recurrently mutated genes for common cancers, such as breast, colon and lung cancers, have become the targets for highly specific drug therapies, for example, Gleevec for treatment of leukemias.

The key strategy enabled by the "genomics era" is to determine the DNA sequence of an individual's tumor genome and use the information obtained to make treatment decisions based on the repertoire of targeted therapies available. Thus rapid DNA sequencing of patient's genomes is revolutionizing our approach to the disease. We have learned in the past 5 years that there are approximately 200 genes, occupying only 0.0003% of the genome, which when mutated contribute to the majority of cancer. This proposal seeks to accelerate the clinical application of the revolutionary DNA sequencing technologies by focusing on the 0.0003% of the genome we know is most relevant to the disease. We will accomplish this by developing and refining technologies that restrict the genome sequencing to the desired target genes. The objective is to shrink the 30-60 days required for a whole genome analysis, to 4 days so that the patient's mutations content can inform front line treatment. The test will be applicable to resected tumors and to biopsy samples in which there is the small tumor number of tumor cells presence. In either case, high sensitivity to mutation is a key requirement so that the physician can make the most informed decision about therapy.