Novel Method for Finding Low Abundance Sequences By Hybridization

Tech ID: 27070 / UC Case 2017-021-0

INVENTION NOVELTY

This invention describes a novel method for enriching rare sequences in nucleic acid libraries.

VALUE PROPOSITION

Current methods for enriching low-abundance sequences in complex sequencing libraries involve either multiplex PCR or hybridization to labeled oligonucleotides. Such methods lack efficiency, are expensive and difficult to optimize. They are also limited in the number of sequences that can be enriched in a given sample.

This invention overcomes above limitations and provides the following advantages:

- Large number of sequences can be targeted simultaneously
- Applicable to sample of any origin
- Compatible with use in any next-generation sequencing platform

TECHNOLOGY DESCRIPTION

UCSF researchers have developed a novel technique, to cut specific sites of interest in a DNA library or other samples prior to sequencing or other molecular counting applications. The newly exposed ends of the DNA are then ligated to specific adapter sequences that allow them to be amplified. A single PCR step using only a pair of primers specific to the adaptors can therefore amplify hundreds, thousands, or millions of different sequences, in a fully programmable way. Using this method to target antibiotic resistance genes, UCSF researchers have demonstrated enrichment of low-abundance genes by over ten-fold compared to randomly fragmented cDNA libraries derived from patient samples.

LOOKING FOR PARTNERS

To commercialize the technology as a research tool and diagnostic

STAGE OF DEVELOPMENT

Pre-clinical

DATA AVAILABILITY

Under CDA / NDA

PATENT STATUS

Country	Type	Number	Dated	Case
United States Of America	Issued Patent	11,046,995	06/29/2021	2017-021

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OTHER INFORMATION

CATEGORIZED AS

- Medical
  - Diagnostics
  - Research Tools
- Research Tools
  - Nucleic Acids/DNA/RNA

RELATED CASES

2017-021-0

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