

Pathogen Detection Through Genetic Sequence Enrichment



BACKGROUND

There is an increasing demand for public health laboratories to provide diagnoses of human pathogens in an accurate and timely manner, particularly in the context of an infectious disease outbreak. A large challenge with traditional diagnosis has been a requirement to know or assume what pathogen to look for.

DESCRIPTION

The inventors have developed a technology that can be used to greatly enrich pathogenic sequences in human clinical samples. This technology does not require prior knowledge of the pathogen or assumption of the infection, and therefore, provides a fast and sequence-independent approach to identify human pathogens. Advantageously, this technology can be widely used in clinical laboratories for the detection of human viral pathogens such as HIV, HCV, and the influenza virus while also significantly lowering the cost per sample by reducing the overall number of samples requested. This technology uses a set of "non-human primers" that do not match the most abundant human transcripts and are able to preferentially amplify non-human (and presumably pathogenic) sequences. Using this technology, pathogenic sequences have been enriched up to 200-fold in the final sequencing library. Pathogenic sequences can be further enriched by subtractive hybridization against reference human transcripts.

ADVANTAGES

- Pathogen-independent detection
- Lowers the cost per sample

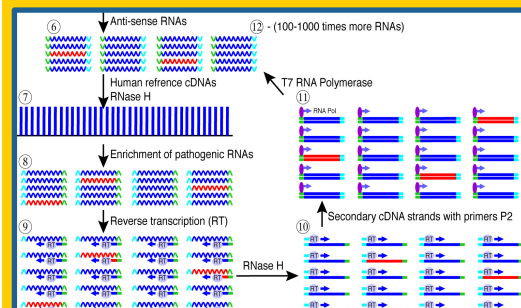
APPLICATIONS

- Diagnostic and clinical laboratories
- Detection kits

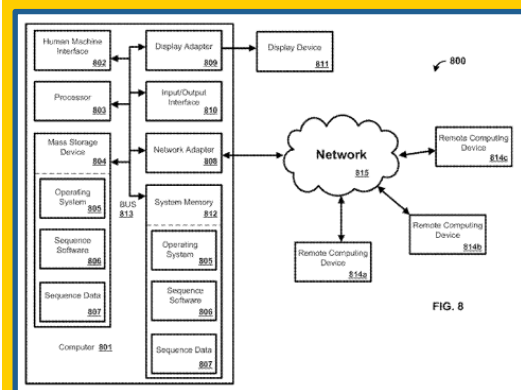
INTELLECTUAL PROPERTY

- US Patent Application No. 15/101,590
- Patent pending

CASE ID: UA 272-14



Detection method.



Detection system.

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