



SEEK THE UNKNOWN IN COMPLEX SAMPLES WITH SEQUENCE CAPTURE BY HYBRIDIZATION

#KEYWORDS

Diagnostic tool
Hybridization capture
Exploratory probes
Clinical samples

CONTEXT

Deep exploration of metagenomes remains difficult. In biomedical application, microbial pathogens are a public health concern. Pathogen genomes are generally very small relative to that of their human host.

Therefore, even a modest number of nucleated human cells present in infectious disease samples may result in pathogen DNA representation being dwarfed relative to the host human DNA.

Existing methods for dealing with DNA contamination in infectious disease samples require significant time, money, and/or specific handling of samples at the time of collection.

TECHNOLOGY

***In vitro* diagnostic tool** based on a nucleic acid **hybridization capture in solution** that allows for the enrichment of pathogen DNA sequences in complex samples such as clinical samples from infected patients dominated by human genetic material.

This method is based on a target-specific oligonucleotide probe design, targeting a set of virulence factors and genes. It allows the capture of **large nucleic acid** fragments (minimum 6 000 base pairs) from a sequencing metagenomic DNA library.

ADVANTAGES

- Capture of large nucleic acid fragments (minimum 6 000 base pairs)
- Capture of unknown genetic environments and new combinations of genes
- Facilitated reconstruction of large regions (operons, plasmids, chromosomes)
- Access to scarce genomes
- Increased sensitivity / specificity of metagenomic samples exploration
- Improvement of the sequencing effort on metagenomic samples

INTELLECTUAL PROPERTY

Priority filing in 2016.

PARTNERSHIP

Licencing

RESEARCH TEAM

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