Enriching non-human DNA in body fluid samples for diagnosis

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Technology description

Researchers from the University of Arizona and TGen have developed a method of rapidly and accurately diagnosing microbes and pathogens causing conditions such as sepsis from body fluid samples. By leveraging the difference in size between human and non-human DNA fragments, the method facilitates a more efficient sepsis diagnosis with reduced turnaround time, reduced costs of sequencing, and increased on-target rates.

In patients with infections sepsis, current methods of identifying the pathogen causing sepsis include blood culture and urine cultures. Culturing approaches are slow, taking 4-5 days for results, and lack sensitivity. Cell-free (cfDNA) in body fluids carries non-human DNA from microbes and pathogens, however while sequencing of cfDNA to identify microbes and pathogens is more sensitive that culturing methods, whole genome sequencing of a body fluid sample for identifying microbes and pathogens can be expensive and time consuming because over 98% of the cfDNA in body fluids is human DNA.

Researchers from the University of Arizona and TGen developed a method of selecting cfDNA fragments based on size to enrich the body fluid sample for non-human cfDNA (up to 100-fold) prior to sequencing to increase the yield of microbial and pathogenic DNA in the body fluid sample. The method may further facilitate delineation of antibiotic resistance by increasing the coverage of microbial DNA in plasma samples, and microbiome analysis in cancer patients.

Institution

The Translational Genomics Research Institute

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