

Using metagenomic sequencing to quickly identify pathogens in body fluids

10 November 2020, by Bob Yirka



Credit: Pixabay/CC0 Public Domain

A team of researchers from the University of California San Francisco, Leeds Teaching Hospitals NHS Trust, and Chan Zuckerberg Biohub has found that it is possible to use metagenomic sequencing to quickly identify pathogens in human body fluids. In their paper published in the journal *Nature Medicine*, the group describes testing they conducted with a host of bodily fluids from a wide range of people, most of whom were hospitalized with an illness.

The current means for diagnosing a patient with a possible infection is to collect blood or [tissue samples](#) and send them to a lab for testing. Testing in most cases falls into one of two categories: culturing to see if a virus, fungus or bacteria grows, or [polymerase chain reaction](#) (PCR), in which DNA is tested to identify foreign bodies. As the researchers note, cultures take time to grow and PCR can only be used when a doctor has already determined the nature of an infection. In this new effort, the researchers report that [metagenomic sequencing](#) can speed up identification of infectious agents.

In metagenomic sequencing, [genetic material](#) is retrieved from [environmental samples](#) such as urine, pus or cerebral fluids and then sequenced. In this new effort, the researchers tested the possibility of using metagenomic sequencing as a means of quickly identifying bacterial, fungal or viral infections.

The work involved collecting a wide variety of bodily fluids from 158 patients, the majority of whom had been admitted to a hospital for treatment. Of those patients, 127 had already been diagnosed with a specific pathogen, while nine had been found not to be infected via culture testing but whose PCR results were positive.

To [test](#) the samples, the researchers came up with a new sequencing approach using either nanopore or Illumina sequencing. They called it metagenomic next-generation sequencing (mNGS). Testing showed it to be accurate and much faster than other methods. They found it to be 79.2% accurate with bacterial sensitivity, 90.6% specific when they used Illumina sequencing and 75% sensitive and 81.4% specific when using nanopore sequencing. They also found that such testing could be done within a matter of hours.

More information: Wei Gu et al. Rapid pathogen detection by metagenomic next-generation sequencing of infected body fluids, *Nature Medicine* (2020). [DOI: 10.1038/s41591-020-1105-z](https://doi.org/10.1038/s41591-020-1105-z)

[Press release](#)

© 2020 Science X Network

APA citation: Using metagenomic sequencing to quickly identify pathogens in body fluids (2020, November 10) retrieved 24 November 2020 from <https://medicalxpress.com/news/2020-11-metagenomic-sequencing-quickly-pathogens-body.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.