Mobile DNA sequencer shows potential for disease surveillance

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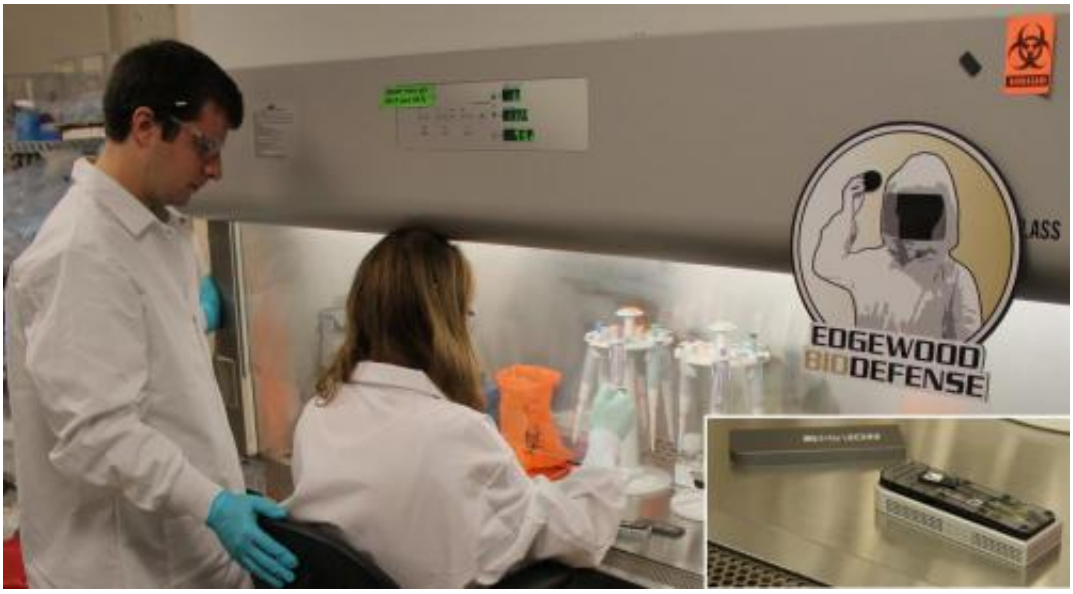

Edgewood group using MinION. Credit: Andrew Kilianski

A pocket-sized device that can rapidly determine the sequence of an organism's DNA has shown its potential in disease detection, according to a study published in the open access, open data journal *GigaScience*.

In the first analysis of its kind, researchers were able to use the device to accurately identify a range of closely-related bacteria and viruses within six hours, demonstrating the potential for this technology to be used as a mobile diagnostic clinic during outbreaks.

The MinION 'Nanopore sequencer' is a low-cost palm-sized sequencing device from Oxford Nanopore Technologies that has been made available to some research groups for testing. It is powered and operated via a USB connection plugged into a laptop, which means that it could potentially be used for on-site clinical analyses in remote locations, negating the need for samples to be sent off to laboratories.

Lead author Andrew Kilianski from Edgewood Chemical Biological Center, USA, whose team tested the device in joint collaboration with Signature Science, LLC, said: "Our findings are important because we have for the first time communicated to the community that this technology can be incredibly useful in its current state.

"Being able to accurately identify and characterize strains of viruses and bacteria using a mobile platform is attractive to anyone collecting biological samples in the field. And we expect that as the technology improves, the sequencing will generally become cheaper, faster and more accurate, and could have further clinical applications."

The researchers were able to use the MinION to accurately identify and differentiate viral and bacterial species from samples. Within six hours, the device generated sufficient data to identify an *E. coli* sample down to species level, and three poxviruses (cowpox, vaccinia-MVA, and vaccinia-Lister) down to strain level. The device was able to distinguish between the two vaccinia strains despite them being closely related and over 98% similar to each other.

Close up of MinION. Credit: Andrew Kilianski

The technology relies on protein 'nanopores' to determine the sequence of a strand of DNA. At the core of the protein is a hollow tube only a few nanometres in diameter, through which a single DNA strands can pass. As the DNA strand passes through the nanopore, it causes characteristic electrical signatures, from which bases can be identified, and the sequence of the strand determined.

Despite MinION's observed read error rate of 30%, which is higher than that of other DNA sequencing methods, the team was able to overcome some of the current limitations by utilizing an approach based on amplified DNA (an 'amplicon' approach). This allowed them to confidently differentiate between closely-related strains.

MinIONs and laptops. Credit: Scott Edmunds

The amplicon approach allows for the analysis of more complex mixed samples containing a range of organisms in a short runtime. For whole genome sequencing approaches in less pure samples, they note that improvements will need to be made as the technology matures.

The authors state it would be difficult to accurately characterize pathogens within a complex sample in six hours without applying the amplicon methodology.

More information: Andy Kilianski, Jamie L Haas, Elizabeth J Corriveau, Alvin T Liem, Kristen L Willis, Dana R Kadavy, C Nicole Rosenzweig and Samuel S Minot, Bacterial and viral identification and

differentiation by amplicon sequencing on the MinION nanopore sequencer, *GigaScience* 2015, DOI: 10.1186/s13742-015-0051-z

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