

Rapid diagnosis of lower respiratory infection using nanopore-based metagenomic sequencing

Lower respiratory tract infections are the leading cause of death from infectious disease worldwide, causing three million deaths in 2016. A wide range of pathogens cause these infections, making quick diagnosis and prescribing decisions a challenge. Culture is required to diagnose bacterial infections and results can be slow or uncertain, resulting in over-use of broad spectrum antibiotics. Researchers at the Quadram Institute of Bioscience in Norwich, and colleagues, used nanopore sequencing to explore a metagenomic sequencing approach directly from patient respiratory samples to facilitate quicker identification of bacterial pathogens and accurate detection of resistance genes.

Using the MinION™, the researchers developed a pipeline that was capable of removing up to 99.99% of host nucleic acids from the clinical samples, was 96.6% concordant with culture in terms of pathogen detection, and could accurately detect resistance genes within six hours.

Read the preprint at <http://bit.ly/rapiddiag>

Sample preparation

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Host DNA depletion ~ 50 minutes
Bacterial lysis and DNA extraction ~ 50 minutes

Optimised method: host DNA depletion

