

NEXT-GENERATION BIOAEROSOL DETECTION & IDENTIFICATION

Bioaerosol Threat Surveillance Via Untargeted Nanopore Sequencing Technology

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In the future, the ideal biological surveillance technology is a fully automated and untargeted sequencing device for continuous aerosol monitoring for both indoor and outdoor locations. This sequencing system would enable the identification of any biological threat (threat agnostic) including those that are emerging or genetically modified. Required modules for this system include an aerosol collector, a sample/library preparation module, the sequencer itself, and computational hardware. These modules could be upgraded based on continued technological advances and they could also be combined with other biological surveillance technologies, if desired, such as biological detectors/triggers or PCR technologies.

In addition to being small, inexpensive, and portable, nanopore sequencing technology lends itself to automation and recent progress has been made in this area. Nanopore sequencing workflows have also been developed for biothreat identification from aerosol samples. However, much more progress is needed, especially when it comes to understanding the natural microbial background in air. This can only be accomplished using large-scale, international collaboration since the microbial background varies with location, season, time of day, and fluctuations in weather among other factors. A proof-of-concept study was conducted to monitor the bioaerosol background in two locations: a mid-Atlantic site (Aberdeen Proving Ground, Maryland) and a desert site (Dugway Proving Ground, Utah). In collaboration with NATO, future studies will aim to characterize the background at many different locations around the world. Knowing the natural biological background will reduce false alarms and allow for the detection of true biological anomalies. Another focus area is on the bioinformatics analyses for metagenomic sequencing data generated from aerosol samples. How to effectively analyze, interpret, and present the data is a difficult challenge. Microbial standards are being developed and applied to effectively compare sequencing data that is generated by researchers across the globe. In addition, software tools are being developed to detect biological threats from nanopore sequencing data, irrespective of taxonomic identity.

This research was funded by the Defense Threat Reduction Agency (DTRA)/Joint Science and Technology Office (JSTO), the Director, Combat Capabilities Development Command Chemical Biological Center under the authorities and provisions of Section 2363, and the Joint Program Executive Office for Chemical, Biological, Radiological and Nuclear Defense (JPEO-CBRND).