

Evaluating an Upper Respiratory Disease Panel on the Portable MinION Sequencer

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Abstract

The MinION nanopore sequencer was released to community testers for evaluation using a variety of sequencing applications. The MinION was used to evaluate upper respiratory disease infections and was found to have tremendous potential for field use. In this study, we tested the ability of the MinION to accurately identify and differentiate clinical bacterial and viral samples via targeted sequencing and whole genome sequencing. The current nanopore technology has limitations with respect to error rate but has steadily improved with development of new flow cells and library kits. Upper respiratory disease organisms were successfully sequenced, identified and differentiated down to the strain level with 87-98% alignment against our reference genome database. This study offers evidence of the utility of sequencing for identify and differentiate both viral and bacterial species present within clinical samples.

Keywords: Upper respiratory disease, MinION sequencer, Acute respiratory infections, H1N1.

Introduction

Acute respiratory infections (ARI) have been a significant source of disease and nonbattle injury among military forces for centuries. Although mortality from ARIs is low in military populations, the impact of these infections on military readiness in terms of lost work-hours and convalescence is high. Furthermore, novel ARIs have been a periodic source of great morbidity and mortality, such as during the 1918 A/H1N1 ("Spanish") influenza epidemic, the 2002-2003 severe acute respiratory syndrome (SARS) epidemic in Asia and North America, and the 2009-2010 swine-origin A/H1N1 global pandemic. Periodic outbreaks of adenovirus and similar infections have plagued military training centers in recent years, control of which has been hampered until very recently by the unavailability of vaccines [1,2]. Supporting the notion that viral infections play a major role in training and readiness, other studies have demonstrated the rates of ARI in trainees averaged 80%, with hospitalization rates at 20% [3-5]. Despite aggressive vaccination programs, ARI has been noted to be the cause of 70% of U.S. Air Force pilot groundings during Operation Desert Storm [6]. Although influenza is usually the pathogen that captures the attention of the world, other respiratory pathogens have recently garnered the attention of the military. Adenoviruses cause a wide array of symptoms, from conjunctivitis, gastroenteritis, and mild respiratory infections to life-threatening pneumonias in young adults with blood stream and brain

Article Information

Article Type: Analysis

Article Number: JAMBR119

Received Date: 01 April, 2019

Accepted Date: 03 April, 2019

Published Date: 10 April, 2019

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Citation: Lyon WJ, Smith ZK, Geier B, Baldwin J, Starr CR (2019) Evaluating an Upper Respiratory Disease Panel on the Portable MinION Sequencer. J Appl Microb Res. Vol: 2 Issu: 1 (24-31).

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infections in immunocompromised hosts. The Middle East respiratory syndrome-coronavirus (MERS-CoV) outbreak in the Middle East [7] along with the H7N9 influenza outbreak in China [8] has focused our attention on new and emerging pathogens that may be introduced into immunologically naïve populations or recombined into novel forms through human-human or human-animal transmission.

Next-generation sequencing (NGS) technologies are now capable of providing a whole genome sequence or metagenomics for a wide range of organisms [9-15]. NGS is being applied with increasing frequency in clinical microbiology laboratories to detect and characterize pathogens, thereby replacing the currently used Sanger sequencing methods [8,16,17,]. Sanger sequencing has been a reliable and robust method that has served clinical laboratories well for over several decades; however, it is labor intensive, slow, and not easily adapted for processing large genomes or large samples sets. The characterization of upper respiratory disease (URD) viruses would certainly benefit from the use of whole genome sequencing (WGS) and targeted sequencing, providing us with tools for surveillance of highly diverse viral genomes [18-20]. Such data can assist in vaccine development, detection of anti-viral drug resistance, or the identification of new emerging re-assorted viral genomes. These advances may help to mitigate the morbidity and mortality of influenza pandemics or seasonal viral epidemics.

Oxford Nanopore's MinION may therefore provide us with new opportunities to track infectious disease, for example, rapid sequencing of viral genomes would allow us to track early phase influenza pandemics, or determine what coronavirus virus genotypes are present during outbreaks. In addition, sequencing will allow us an opportunity to gain insight into viral genetic drift (single nucleotide polymorphism), emergence of new strains such as SARS-like coronavirus or MERS-CoV, and transmission patterns. To date, a number of pathogenic viral studies have been done with the MinION [18,21-26]. Metagenomic NGS is particularly attractive for surveillance of febrile illness because the approach can broadly detect viruses, bacteria, and parasites in clinical samples in the field [1,7,27]. Although currently limited by a sample-to-answer turnaround time of >24 hours for benchtop sequencers, we report in this study that unbiased pathogen detection using both targeted and whole genomic sequencing can be realized with actionable results for clinical diagnostics [19,20,23,25,26,28- 32] and public health [22,28,30] within 10 h.

NGS platforms such as the Illumina MiSeq and Life Technologies Ion Torrent have been extensively used to provide WGS data for viruses, potentially within 2-3 days of the receipt of a sample [7]. Therefore, there is clearly a place for a portable NGS instrument that can be deployed into the field for surveillance using available field ready kits, single use flow cells (Flongle) and sequencing reagents that are comparable to cost of benchtop sequencer. In addition, analysis of sequencing data is accomplished in real time using an internet-connected laptop. The MinION has been successfully used for WGS and targeted sequencing [8,33,34],

WGS is well suited for the investigation of URD species that high levels of genetic diversity and are difficult to access using targeted sequencing methods [23,25,26]. The purpose of this study was to examine the efficacy of using the MinION to sequence URD organisms present in URD clinical samples.

Materials and Methods

Nucleic acid extraction

Influenza A virus H1N1 (VR1736), parainfluenza virus 1-3 (VR94, VR92, and VR93), coronavirus 229E and OC43 isolates (VR-740 and VR1558), *Mycoplasma pneumoniae* (ATCC 29342), *Haemophilus influenzae* virus (51907), and human adenovirus (VR-1603) were obtained from American Type Culture Collection (ATCC). The nucleic acid isolated from these organisms were used as control nucleic acid (NA) for library preparations and was added as internal control during library preparations. RNA/DNA were extracted from 200 µL viral supernatants or from clinical nasal washes using the Maxwell total viral nucleic acid kits (Promega, Madison, WI) and eluted with 50 µL of RT PCR molecular grade water (Thermo Fisher Scientific, Waltham, MA). De-identified positive nasal washes were obtained from the clinical laboratory at Wright Patterson Air Force Base. Clinical isolates used in this study were influenza A virus, influenza B virus, parainfluenza viruses 1-3, adenovirus, and coronavirus OC043.

Targeted RT-PCR and PCR

Targeted RNA PCR was done per using primers listed in Table 1 using the SuperScript III OneStep RT-PCR system (Thermo Fisher Scientific) per the manufacturer's instructions. Briefly, 10 ng of DNA-free RNA or RNA-free DNA was used for each 50-µL reaction. All PCR reactions were accomplished with 1.0 ul of each primer at 10 uM. RT-PCR thermocycling parameters were as follows: 30 min at 50°C, 2 min at 95°C, and then 35 cycles of 30 s at 95°C, 30 s at 52°C, and 75 s at 72°C, followed with a final extension at 68°C for 5 min. PCR of NA from bacteria or DNA viruses was accomplished using AccuStart II PCR Supermix (Quanta Biosciences, Beverly, MA) as recommended by the manufacturer. Cycling conditions were as follows: 3 minutes at 95°C denaturing, 25 cycles of 30 seconds at 94°C, 30 seconds at 55°C, and 90 seconds at 72°C, followed with a final extension at 72°C for 3 minutes. DNA or cDNA PCR reactions were purified using 1.5X Agencourt Ampure XP beads as described by the manufacturer (Beckman Coulter, Indianapolis, IN) and were quantified using a Qubit 4.0 fluorometer) using either DNA high sensitivity kits. (Thermo Fisher Scientific).

MinION library preparation and sequencing

This work was completed as part of the ONT MinION early access program. During this time the flow cells, flow cell chemistries and library kits changed numerous times during the two-year study. The ONT MinION Sequencing kit that was used to prepare libraries as shown in Table 3. DNA or cDNA libraries were sequenced with various flow cells throughout the study including versions R7, R7.3, and Spot-ON 9.4. The subsequent increase in flow cell

Table 1: Primers used for targeted RT-PCR.

Organism	Gene (URD Panel Name or Source)	Forward Primer 5' to 3'	Reverse Primer 5' to 3'	Instrument Used
Adenovirus				
Influenza A H1N1	CDC ^a Hemagglutinin (HA)	CAACCAAAAAATGAAAG	CCGTCCAGTAGTARTTRATTCT	MinION & MiSeq
Influenza A	polymerase segment 2 (PB2)	CCTCTGGGATTCCTTTCGTCAGTC	GAGAAGTTCGGYGGIAGICTTTG	MiSeq
Influenza A H3N2	CDC (^{HA})	TGTAACACGACGGCCAGTAAAGCAGG GGATAATTCTA	CAATAKATGCTTATTC	MinION & MiSeq
Influenza B	CDC (^{HA})	GCAGACCATTTTCTAA	ACCACACTTTTTGAGG	MinION & MiSeq
Parainfluenza strain 1	URD panel G13 23/25 (Baldwin et al. [1])	ACIGCTATIGCTTGATTGTCTCCTTG	CCAAGAGGGGGTATAGAIGG	MiSeq & Minion
Parainfluenza strain 2	URD panel G2 23/25 (Baldwin et al. [1])	TCTTGTGTAACTGCAATCGCCTG	CAAGGGAGGTATTGAAGGCCTAT	MinION
Parainfluenza strain 3	URD panel G13 23/25 (Baldwin et al. [1])	TCTTGTGTAACTGCAATCGCCTG	CCAAGAGGGGGTATAGAIGG	MinION
Coronavirus 229E	Spike protein (Silva et al. [39])	TACCCTCCGACTTTGCATTC	TACTGCACCCACAAAAGCAC	MinION
Coronavirus HKU14	Spike protein (Silva et al. [39])	TGCTATTGCACCAGGAGTC	TCAGCCATGTCAGGTGTAC	MinION & MiSeq
<i>Mycobacterium pneumoniae</i>	16 S Quast et al. [41]	AGAGTTTGATCMTGGC	GACGGGCGGTGWGTRCA	MinION

number indicates improvements in their flow cells, with Spot-On R9.4 flow cell being the latest improvement. In addition, the ONT MinION library reagents were changed as kit improvements were made during this study (Kit: SQK-MAP0005 for the R7.03 flow cell and Kits: SQK-LSK-209, SQK-RAD 004 (Rapid) for R9.4 or Spot-ON R9.4 flow cells). Barcoding of the DNA fragments was accomplished by using the barcoding kit (EXP-PBC001). Libraries kit used for each of the sequencing libraries are shown in Table 2 and Table 3, as well as, the amount of starting material and flow cells type. The Oxford Nanopore Technologies (ONT; Oxford Nanopore Technologies, Oxford, United Kingdom) MinION Sequencing kit were used to prepare DNA and RNA libraries as described by the manufacturer. Briefly, DNA or cDNA was sheared at 6,000 rpm in a g-TUBE (Covaris). The fragmented DNA was repaired using NEBNext FFPE repair mix (New England BioLabs [NEB], Ipswich, MA). After 15 min of incubation at 20°C with FFPE repair buffer and FFPE repair mix, the repaired DNA was purified using AMPure XP beads in a 1:1 ratio, washed with 80% ethanol, and eluted with nuclease-free water. The DNA fragments were end repaired and deoxyadenosine (dA) tailed using the NEBNext end repair/dA tailing module (NEB). DNA was mixed with DNA CS (positive-control strand), Ultra II end prep reaction buffer and enzyme mix and incubated for 5 min at 20°C and 5 min at 65°C in a thermocycler. DNA was purified using AMPure XP beads in a 1:1 ratio, washed with 80% ethanol, and eluted with nuclease-free water.

End-prepped DNA was incubated with hairpin adapter and NEB blunt/TA ligase master mix (NEB) for 15 min at room temperature, followed by addition of hairpin tether and 10 min of incubation at room temperature. The libraries were incubated with bead binding buffer-washed My One streptavidin C1 beads (Invitrogen, Carlsbad, CA) in a 1:1 ratio

for 5 min at room temperature, washed with bead binding buffer, and eluted with elution buffer prior to loading. Buffer, and eluted with elution buffer prior to loading and were quantified using a Qubit 4.0 fluorometer and DNA high sensitivity kits (Life Technologies). The libraries were transferred to a low-binding 1.5-mL Eppendorf tubes and placed on ice until loaded onto the flow cell.

Rapid 1 D libraries

Rapid 1 D libraries (ONT R9 version; SQK-RAD004) were prepared using whole genomic NA from clinical isolates. Whole genome products were sheared with a Covaris g-tube (Woburn, MA) with fragmentation sizing to approximately 5 kb. Two hundred nanograms of DNA was tagged by incubation with fragmentation mix (FRM) for 1 min at 30°C followed by 1 min at 75°C in a thermocycler. Tagged DNA was then adapter ligated by incubation with rapid adapter mix (RAD) and NEB blunt/TA ligase master mix for 5 min at room temperature and directly loaded for sequencing as described by the manufacturer.

ONT sequencing

A 48-hour sequencing protocols were initiated using the MinION control software, MinKNOW versions 1.1-1.3.24, for flow cells 7.3 and MinKNOW versions 1.4.6-2.4.5 for R9 flow cells, respectively. Read event data were base-called by the Metrichor agent (version 0.46.1.9, which was later updated to EPI2ME) using WIMP application (What In My Pot; 1.2.2 rev 1.5) with appropriate 2D and 1D workflow scripts [35].

Illumina MiSeq library preparation and sequencing

Targeted RT-PCR amplification was completed as described earlier using the same NA extracted for the MinION sequencing experiments. The primers used for targeted RT-PCR are listed in Table 1. Libraries for Illumina MiSeq

Table 2: Targeted Sequencing of URD samples using the MiSeq and MinION.

Descriptor	Influenza A H1N1	Influenza A H1N1	Influenza B	Influenza B	Parainfluenza 1	Parainfluenza 1	Coronavirus OC043	Coronavirus OC043
Flow cell version	MinION R7.3	MiSeq 600 V3	MinION R7.3	MiSeq 600 V3	MinION R7.3	MiSeq 600 V3	MinION R7.3	MiSeq 600V3
Base calling version/ alignment	Metrichor & BWA/SAM Tools Kraken/Bracken	Illumina Basespace MiSeq/ BWA/ SAM Tools	Metrichor & BWA/SAM Tools Kraken / Bracken	Illumina Basespace MiSeq/ BWA/ SAM Tools	Metrichor BWA/SAM Tools Kraken/Bracken	Illumina Basespace MiSeq BWA/SAM Tools	Metrichor BWA/SAM Tools Kraken/Bracken	Illumina Basespace MiSeq/ BWA/ SAM Tool
Library protocol version and amount of starting material	SQK-MAP005 1000 ng	Nextera XT 1.0 ng	SQK-MAP005 1000 ng	Nextera XT 1.0 ng	SQK-LSK109 1000 ng	Nextera XT 1.0 ng	SQK-LSK109 1000 ng	Nextera XT 1.0 ng
Target gene	HA	HA	HA	HA	HA	HA	Spike protein	Spike protein
PCR amplicon base pair length	763	763	886	866	200	150	400	400
Total number of reads passing QC reads	114	202701	7339	230049	404	396725	114	612294
Total number of aligned reads	104	176744	7244	212748	75	365403	104	597202
100 base error rate	1.3E-01	3.63E-02	1.54E-01	7.89E-02	1.01E-01	2.74E-02	1.37E-01	3.47E-3
Percent alignment	87.3	97.5	98.7	93.2	18.6	92.1	91.2	97.5

sequencing were prepared using the Nextera XT library prep kit (Illumina, San Diego, CA). For each library, 1 ng of DNA was added to 10 ul of RSB buffer and 5 ul of ATM. This reaction mixture was incubated at 55°C for 5 min to tagment the DNA and then neutralized with 5 ul of NT buffer. Tagmented DNA fragments were indexed with unique barcode primers and PCR amplified in a 50 ul reaction mixture as follows: 72°C for 3 min, 95°C for 30 s, and 12 cycles of 95°C for 10 s, 55°C for 30 s, and 72°C for 30 s, followed by 72°C for 5 min. PCR cleanup was performed by addition of 30 ul of AMPure XP beads (Beckman Coulter, Brea, CA), followed by 7 min of incubation and then two washings with 80% ethanol and elution into 35 ul of RSB. Nextera libraries for all isolates were multiplexed and sequenced in a paired-end 300-cycle mode on an Illumina MiSeq instrument using 600-cycle reagent kit v. 3 (Illumina). Library preparations were quantified using a Qubit 4.0 fluorometer and DNA high sensitivity kit (Thermo Fisher Scientific).

Sequence data analysis

Read data were extracted from the native HDF5 format (Fast 5) and converted into FASTA using poretools [4] and sequence reads were assessed for quality and trimmed with Nanofilt [36]. Quality reads with a q-score lower than 4 were omitted. Kraken and Bracken bioinformatics packages were used for alignment against a database comprised of fungal, viral and bacterial genomes [32,37-39]. All genomes, viral and bacterial were downloaded from NCBI Ref Seq (May, 2015) and were used to build the Kraken database (version 0.10.4) with k=31. Bracken (Bayesian Reestimation of Abundance after classification with Kraken) estimates species abundances in metagenomic samples. Bracken [38,40] was used to reassign alignments to the species level and visualization was accomplished with Krona [40] using the highest number of hits (lowest e-value) or Metrichor's WIMP application. Illumina reads were assessed for quality using FastQC and trimmed with Trimmomatic 0.36 using the following settings: trim reads: Leading: 3, Trailing: 3,

and Sliding Window: 4:15. Our in-house pipeline aligns the reads using the Kraken and Bracken and the data is visualized with KRONA [40]. Burrows-Wheeler Alignment MEM (BWA; aligned to reference and Human GR2) and SAM Tools was used to extract statistics and error rate per 100 bases [41,42]. Sequence reads were filtered for human sequences and removed prior to visualization. Tables 2 and 3 list the analysis tools used for each data set. Read percentage identity is defined as $100 * \text{matches} / (\text{matches} + \text{deletions} + \text{insertions} + \text{mismatches})$. Fraction of reads aligned are defined as $(\text{alignment length} + \text{insertions} - \text{deletions}) / (\text{alignment length} + \text{unaligned length} - \text{deletions} + \text{insertions})$.

Results

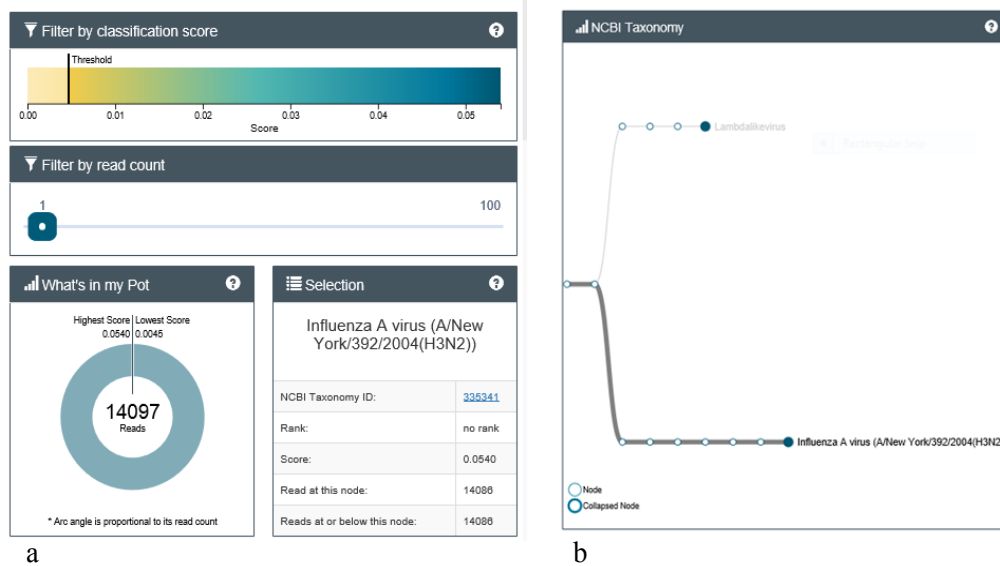
Targeted amplicon sequencing using the MinION

A panel of URD viruses (influenza A virus, influenza B virus, parainfluenza virus 1, parainfluenza virus 2, parainfluenza virus 3, human adenovirus D, coronavirus OC043 and bacterial strains (*M. pneumoniae* and *H. influenzae*) were used in this study. The same NA from each sample was used to generate libraries for both Oxford Nanopore MinION and Illumina MiSeq. All of the organisms listed were successfully sequenced on the MinION and identified correctly using the WIMP application, which uses a cloud-based reference databank. Figure 1 shows a representative example of the data analysis for an influenza A H1N1 isolate listed in Table 1. In addition, BWA MEM and SAM Tools was used to verify the identification of each isolate listed in Table 2 [41,42]. BWA MEM alignment of the reads were in agreement with Metrichor's identification for each of the nasal wash samples listed in Table 2.

Fast 5 files generated by MinKNOW were converted to FASTQ using Poretools [24] then the FASTQ files were FASTQC, trimmed, aligned with Kraken and visualized with KRONA using our in-house pipeline [38,40]. For example, Table 2 shows that sequence reads generated from Influenza

Table 3: Multiplexed Targeted RT-PCR or PCR Amplification.

Descriptor	Human Adenovirus Clinical Isolate	Parainfluenza Strain 1 Clinical Isolate	Parainfluenza Strain 2 Clinical Isolate	Parainfluenza Strain 3 Clinical Isolate	<i>M. pneumoniae</i> ATCC 29342
Flow cell version	R9.4	R9.4	R9.4	R9.4	R9.4
Base calling version	Metrichor 2D version 1.107 RNN	Metrichor 2D version 1.107 RNN	Metrichor 2D version 1.107 RNN	Metrichor 2D version 1.107 RNN	Metrichor 2D version 1.107 RNN
Library protocol version/starting material	SQK-LSK209 2D DNA 1000 ng	SQK-LSK209 2D cDNA 1000 ng	SQK-LSK209 2D cDNA 1000 ng	SQK-LSK209 2D cDNA 1000 ng	SQKLSK209 2D DNA 1000 ng
Average base pair 2D read length	2423	2483	2994	2639	6351
Total number of 2D pass reads	1763	1400	1785	656	2281
Per base error rate	1.09E-01	1.01E-01	9.53E-02	9.08E-02	1.29E-.01
Percent aligned identity	95.9	91.7	94.8	92.5	93.3

**Figure 1:** Target amplification of influenza A virus using the H2N2 primers listed in Table 1. Metrichor WIMP application was used for identification of the Influenza A H3N2 virus.

A H1N1 cDNA resulted in 114 high quality reads and 104 of these reads aligned (87.3%) to Influenza A H1N1 (Table 2). MinION sequence data for viruses Influenza B, Parainfluenza 1 (PAIV1) and Coronavirus OC043 had a percent identity of 98.7, 18.6 and 91.2, respectively (Table 2). Interestingly, there were small differences between the sequencing data quality in terms of alignment error. Influenza A H1N1, Influenza B, Parainfluenza 1 (PAIV1) and Coronavirus OC043 had alignment error of $1.15\text{E-}01$, $1.54\text{E-}01$, $2.74\text{E-}02$ and $1.37\text{E-}01$, respectively (Table 2). The Nanopore kits used early in this study resulted a low number of sequence reads, which is probably due improper NA fragment to adapter ratios during ligation step in the library preparations Figure 2.

Multiplexing Targeted PCR Libraries

NA extracted from clinical nasal washes and the isolated RNA (200 ng/ul) or DNA (200 ng/ul) were used in library preparation. Direct cDNA sequencing kit was used to prepare the RNA for sequencing. The individual libraries were barcoded and mixed in equal molar concentrations prior to being loaded onto a R9.4 flow cell. The percent-alignment of reads to reference genomes ranged from 92-96% (Table 3). The number of reads were somewhat different among

the tested organisms and probably due to an error in quantification of the input library prior to pooling. Future barcoding pooling protocols should include a TapeStation or Bioanalyzer (Agilent) quantification in terms of fragment length for more accurate calculation of the nM concentration prior to pooling. Metrichor's cloud base-calling WIMP application correctly identified each organisms in the library pool (Figure 3F). All of the URD organisms listed in Table 3 were reevaluated using our Kraken/Bracken pipeline to verify Metrichor's identification and visualized with KRONA (Figure 3A-E).

1D Rapid libraries

H. influenzae and Coronavirus 229E libraries were prepared using ONT's rapid 1D library preparation kit. These data show that rapid 1D kit is a suitable replacement kit for previously used ONT's 2D kits. Sequencing runs were ran 17.5 hours and the total base yield for an isolate of *H. influenzae* was 44.9 million with a quality score centered on 6 (Figure 4). *H. influenzae* was correctly identified using the cloud based Metrichor's WIMP application (Figure 4A) and the read alignment was verified with our Kraken/Bracken pipeline and visualized with KRONA (Figure 4B). Coronavirus

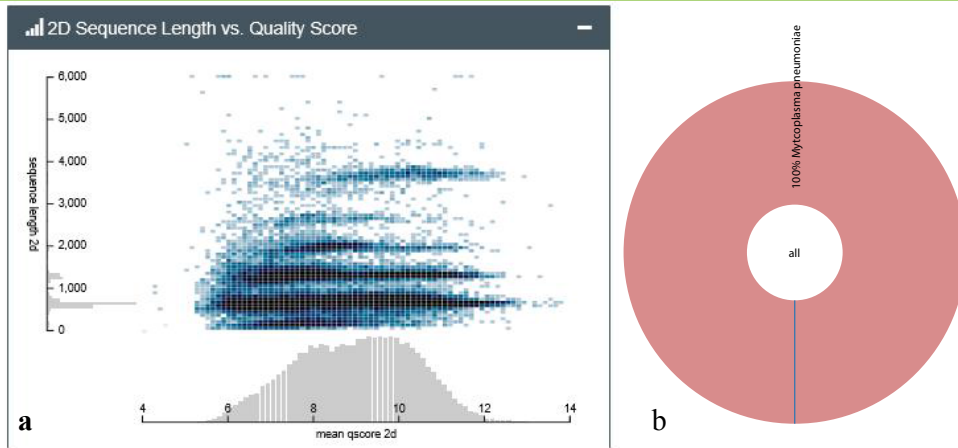


Figure 2: *M. pneumoniae* 2D library identification using Metrichor and Kraken/Bracken. (A) 2D sequence (template + complement strands) as a function of quality score. (B) Bracken was used to align the reads and top hit abundance reads were visualized with KRONA.



Figure 3: Multiplexing libraries of URD organisms. (A-E) Barcoded URD reads were aligned with Bracken and visualized with KRONA. (F) Number of reads for each barcode after analysis with the Metrichor application 2D base calling.

229E was also successfully identified using Metrichor's WIMP application (S1). The coverage was calculated for both the H. influenzae and Coronavirus 229E with the formula $C=LN/G$, where C = coverage, L = average sequence read length, average Length N = number of reads, and G = the genome size. H. influenzae and Coronavirus 229E genome coverage was approximately 186X and 170X, respectively.

Discussion

Sequencing of URD viruses and bacteria was accomplished on the MinION nanopore sequencer using both whole genome and amplicon sequencing. Having the ability to sequence amplicons and whole genomes in a mobile, small-footprint platform is attractive when collecting and analyzing samples in the field, and these qualities are also desirable as sequencing methods move toward environmental and surveillance applications. These methods, data, and results represent a practical and novel application for utilizing MinION nanopore sequencing technology. The data in this study were generated with both R7.3 and 9.4 chemistry flow cells, which accurately identified a panel of URD organisms. As the MinION technology improves, sequencing will generally become cheaper, faster, and more accurate as demonstrated in this study where there was improvements in the error rate as new flow cells and kits were released resulting in improved alignment percentages >92% (Tables 2 and 3).

Base-calling analysis for the MinION nanopore sequencer is an area of active development, as well as flow cell configurations, protocols for kits, and associated kit chemistries. The best quality sequence data are termed 2D reads, while 1D reads are from the template strand. Data quality has improved and was demonstrated in this study with each improvement in kit chemistry and flow cell type. This study shows that the platform can be applied for rapid microbial detection with 3-hour run time, providing sufficient data to generate a reliable identification. As sequencing yield, quality, and turnaround times continue to improve, it is anticipated that nanopore sequencing will challenge mainstays such as PCR for identification of unknown samples.

Comparison of the nanopore and short-read sequencing data (Illumina MiSeq) showed that there was agreement in major taxonomic units identified. Therefore, the methodologies described in this study demonstrate that both whole genome sequencing and targeted sequencing can be used for rapid, accurate, and efficient detection of microbial and viral diversity in clinical samples. The use of WGS is also beneficial when studying viral genetic rearrangements and genetic drift in viruses [43,23]. In addition, these data also support the utilization of targeted sequencing over deep sequencing for field applications where surveillance is needed.

Although long reads generated from the nanopore sequencer were found to have relatively higher error rates when compared with benchtop sequencing reads. However, MinION sequencing has been shown to have significant advantages, such as portability, low cost, and real-time detection. Nevertheless, sequencing of low titer samples,

such as nasal washes, with amplicon sequencing are more desirable over culturing and will provide a rapid method for identification of organisms in clinical samples. This study demonstrated that a low number of long reads are sufficient for accurate identification of small genomes and new flow cells and chemistries (Spot-On 9.4) showed improvements in the number of errors in sequencing data (Table 2 and 3).

The rapid 1D kit is a single stranded library composed of template strands was used to evaluate rapid processing metagenomic samples. The use of rapid 1D library demonstrates it is functionally a game changer when rapid identification of pathogens is needed for tracking acute infections or during surveillance. This approach is especially beneficial when identification is difficult using conventional cell culture techniques or in some cases when targeted methods are not available. Establishing a system for rapid microorganism identification via metagenomic sequencing seems pertinent, especially for field applications [44-48].

Conclusion

Having the ability to sequence in a mobile, small-footprint platform is attractive when collecting and analyzing samples in the field, and these qualities are also desirable as sequencing methodologies moves towards a smaller footprint sequencer (SmidgION). Portable MinION and SmidgION sequencing technologies would have significant advantages for its direct use in field applications, which allows for rapid sample-to-answer capabilities and negating the need to ship samples back to the laboratory.

Acknowledgement

This work was supported by the Defense Health Program and the Chief Scientist Office at Wright Patterson Air Force Base, 711th Human Performance Wing, Ohio. The authors acknowledge the contribution of Mr. Craig Strapple for performing the bioinformatics analyses.

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