Mercury Lab: Bringing the Laboratory to the Sample

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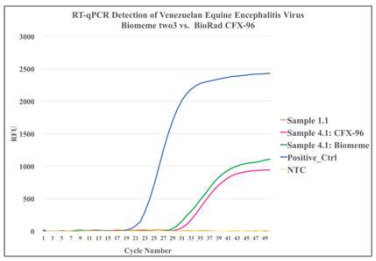
Introduction

Recently developed molecular analysis platforms offer the promise of bringing comprehensive detection, diagnostics, and biosurveillance of emerging infectious diseases to extremely remote and austere locations, completely detached from a traditional brick and mortar laboratory. For example, Biomeme's two3 qPCR machine and the MinION from Oxford Nanopore Technologies (ONT) (Figure 1) offer target amplification and long-read sequencing capability, respectively, in an ultra-compact form factor that is amenable to transport and use by a single operator. Additionally, Biomeme offers nucleic acid extraction kits that can be adapted to different matrices, do not require pipettes, and can be completed in approximately ten minutes. We tested a combination of these technologies in an arbovirus surveillance project monitoring *Culex cedecei* mosquitoes captured at several sites near Everglades National Park. This work is the first demonstration, to our knowledge, of direct, non-PCR-based, metatranscriptomic detection of an RNA virus from mosquitoes using nanopore sequencing. Additionally, this work shows the feasibility of a portable workflow for field-forward, genomics-based biosurveillance. The work has led to understanding critical components & a prototype mobile laboratory described here as Mercury Lab. Clinical & environmental samples can be tested on this mobile laboratory platform with bioinformatics support through MRIGlobal's PanGIA.

Results

Mapping of Illumina MiSeq reads and MinION nanopore reads to Everglades Virus strain EVG3-95. In the region where nanopore reads mapped, 6 out of 9 high-quality variants of 100% frequency detected by Illumina sequencing were also detected by nanopore sequencing. The ratio in parentheses below each variant is the ratio of Illumina reads containing the variant to Illumina read coverage at the specific location. The number of asterisks after the parentheses indicates how many nanopore reads also contained the same variant.



Comparison of Biomeme two3 performance with that of the Bio-Rad CFX-96, a "Gold Standard" q-PCR machine. Biomeme reported a Cq value of 33.92 for EVEV(+) sample well. CFX-96 reported a Cq value of 30.63.

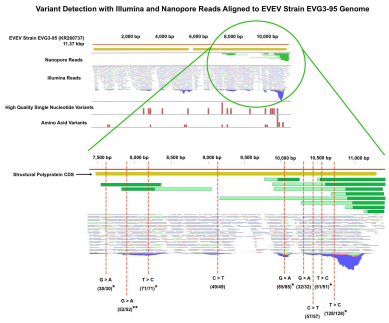
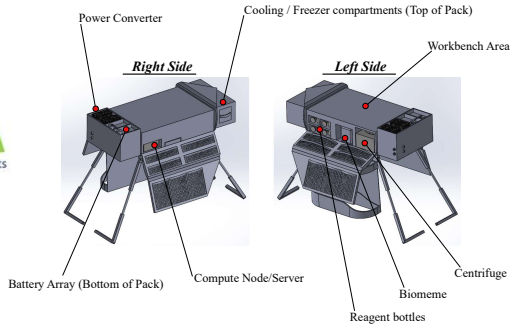


Figure 1

Concept

- Fully-integrated, self-contained laboratory environment for fielding of hand-held genomics devices by a single operator
- Integrated 4ºC and -20ºC storage for samples, reagents, and consumable hardware (e.g., MinION flowcells).
- Integrated power for ~18 hours of nominal use in genomics-focused configuration
- Integrated computing with Intel NUC (32GB RAM, 2TB storage) for complex bioinformatics and cloud-based reach-back support
- Open platform for use of other mobile Point-of-Care or Point-of-Need devices

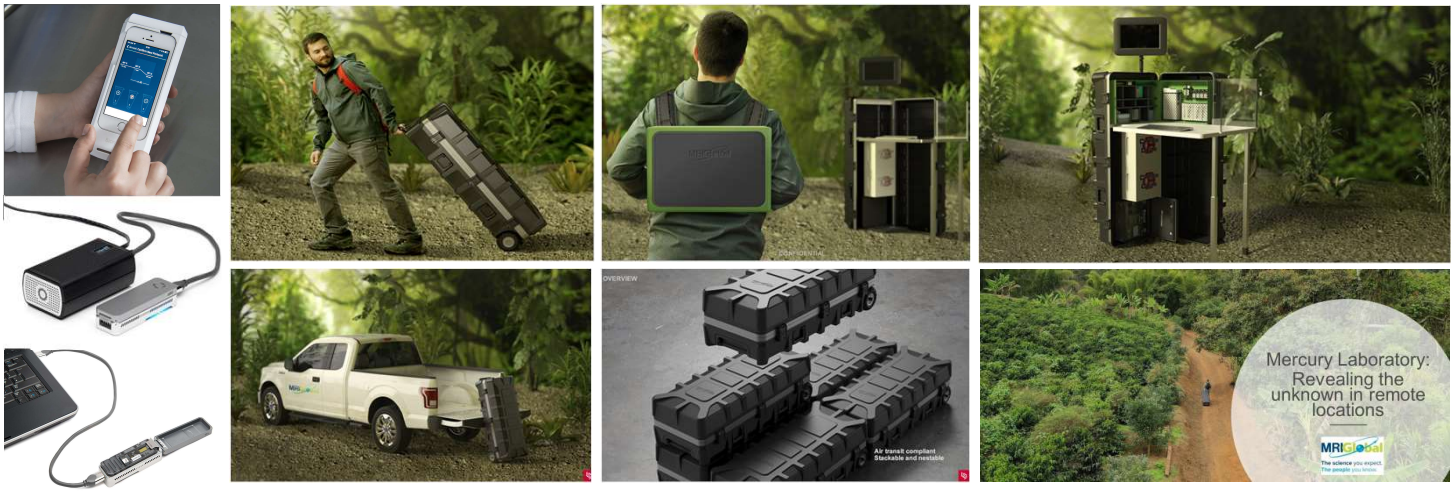
PANGIA
Pangenomics for Infectious Agents



Operational Laboratory for Clinical & Environmental Samples

Figure 1: Extracting total RNA from mosquito pools in the field (A) and readying for analysis on the Biomeme two3 Thermocycler (B). Resulting amplicons can be sequenced on the MinION from ONT (C) for strain-typing of any detected viral pathogen. Alternatively, total RNA can be converted to cDNA and sequenced on the MinION for direct meta-transcriptomic detection of mosquito-born arbovirus. The direct meta-transcriptomic approach was used in this study.

Prototype



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