Use of MinION sequencing for contact tracing of Ebola and Marburg virus diseases in outbreak situations

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MinION sequencing

Overview

Devices

Analysis

MinION

MK1C
MinION sequencing
Molecular epidemiology

Amplicon-based
Targeted
Specific target known and “conserved”
Ex: Ebola virus, SARS-CoV-2

Metagenomic
Non-targeted
Specific target unknown no amplicon avail./target too diverse
Ex. Marburg virus, Lassa virus

Phylogeny
Complete virus genomes

Origin of the virus
Linkage with others? New?
Chains of transmission
The **European Mobile Laboratory: EMLab**

Diagnostic lab to deploy anywhere needed

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**University of Birmingham, UK**
Nick Loman, Joshua Quick

**EMLab**
Joseph Ako Bore, Raymond Koundouno
EVD 2014-2016
Real-time sequencing

Mother’s breast milk to child

Sexual transmission

Ebola Virus Persistence in Breast Milk After No Reported Illness: A Likely Source of Virus Transmission From Mother to Child

Clinical Infectious Diseases

https://doi.org/10.1093/cid/ciw601

Resurgence of Ebola Virus Disease in Guinea Linked to a Survivor With Virus Persistence in Seminal Fluid for More Than 500 Days

Emerging Infectious Diseases
EVD Guinea 2021
Real-time amplicon-based sequencing

Arrival 5 March & Set-up 6 March 2021 – morning

https://artic.network/
• Resurgence of an EBOV related to the one from 2014-2016
  • 6.4-fold (95%/ HPD3.3-fold – 10.1-fold) vs Koropara 5.5-fold
• No new introduction from the animal world
• Long latency/persistence
• Epi investigations not conclusive
• Caution ag. Stigmatization

CERFIG-IPD-LFHVG

nature

Research of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks
Marburg virus disease Guinea 2021

New introduction
Link to Angola/Sierra Leone

data from the image is not legible due to the image quality.
Key Tool to support field epidemiology and outbreak response
Results shared in real-time with MoH → further reporting
Reassures about outbreak origin/adequate communication
Link with laboratory
  • Sample quality for the sequencing lab
Sequence quality
  • Nucleotide level (SNP) for chains of transmissions
  • Full length: approx. 20,000 bp
  • Public health versus chains of transmissions!
Sets the ground for future research grounds with discoveries about virus evolution, persistence, ... continuous improvements needed!
Conclusions and perspectives
Filovirus MinION sequencing

2015: amplicon-based
-1 sample per MinION
-max 2 samples per day
-Lab-prep 24hr
-Up to 20 tubes for 1 sample
-Sequencing few hr: 20,000 reads
-Remote analysis
-Full-length genome recovery
-Consensus: nucleotide level
-Remote phylogeny

2017: Metagenomic development
-Up to 5 samples per MinION
-10 samples per day
-Lab-prep 48hr
-1 tube per sample
-Sequencing 24-48 hr: 10 Million reads
-Pipeline development
-Analysis on site 72 hr
-Genome recovery variable
-Consensus: nucleotide level
-On site/remote phylogeny

2021: amplicon-based
-12-96 samples per MinION
-Lab-prep 24hr
-2 tubes per sample
-Sequencing 24-48 hr: 10 Million reads
-Pipeline development
-Analysis on site 24hr
-Full-length genome recovery: 85-98%
-Consensus: nucleotide level
-On site/remote phylogeny

Collaborative network
https://labs.epi2me.io/
Conclusions and perspectives

• Sequencing is not the new RT-PCR...

• Strong technical lab expertise: continuous protocol development
  • Amplicon-based and metagenomic (knowledge of pathogen, sequence, protocol available; EBOV needs improvements! MARV to be setup? Specific expertise – various types of samples)

• Bioinformatics/pipeline development/analysis/quality assurance/phylogeny (ARTIC/Epi2me/in-house)

• IT: Computers/large data/backup/offline access

• In-country capacity building!

• Logistics! Electricity...

• Our experience:
  • team of 6 people for protocol setup/optimization and troubleshooting, need of network/collaborative work/harmonized pipeline

• Framework for data sharing

• Ethics! Nagoya! Funding! Expertise! Network!
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