

Operational strategy for rapid detection and characterization of emergent viral pathogens using third next-generation sequencing technologies

INTRODUCTION

Global human health is challenged by emerging viral threats. Studies of these outbreaks have highlighted the impact of real-time sequencing of viral genomes for a better concerted public health response. Notably, the World Health Organization has recognized the need to deploy genomic surveillance approaches, especially in low and middle-resource settings.

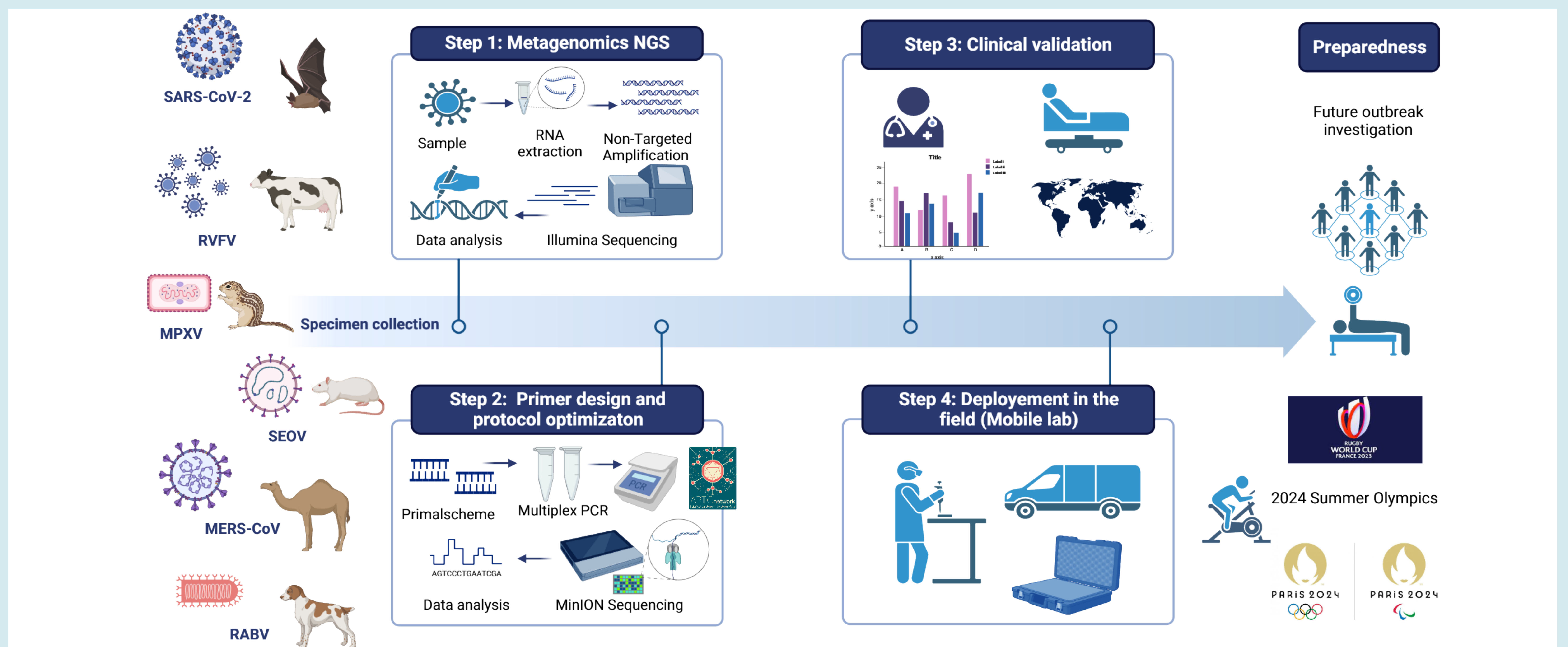
The setup of more robust sequencing/bioinformatics pipelines with low turnaround times could provide crucial insights into the understanding of outbreaks and enhanced monitoring of pathogen transmission, spread, and evolution. Thanks to its features (portability, short time of sequencing run, real-time data analysis), MinION devices, have opened the way towards the implementation of **field-applicable rapid next-generation sequencing**.

OBJECTIVES

As part of its 24/7 duty, the **Laboratory for Urgent Response to Biological Threats** is involved in the diagnosis and molecular characterization of pathogens during outbreaks.

In this context, our unit has set up a generic workflow from human and/or animal samples to data analysis for pathogen identification and characterization by combining metagenomics and amplicon-based approaches.

METHODOLOGY



APPLICATIONS & RESULTS

For the last four years, we have used the amplicon-based approach to directly generate viral genomic sequences from clinical samples, partly by optimizing the sequencing libraries. We worked on different epidemic-prone viruses, such as **Rift Valley Fever virus**, **MERS-CoV**, **SARS-CoV-2** and more recently **Monkeypox**, **Rabies** and **Orthohantaviruses**.

In parallel, specific bioinformatics pipelines have been adapted from the ARTIC network project for user-friendly and rapid analysis. The next step would be to develop ultra-high multiplex syndromic panels for broad spectrum targeting of emerging pathogens.

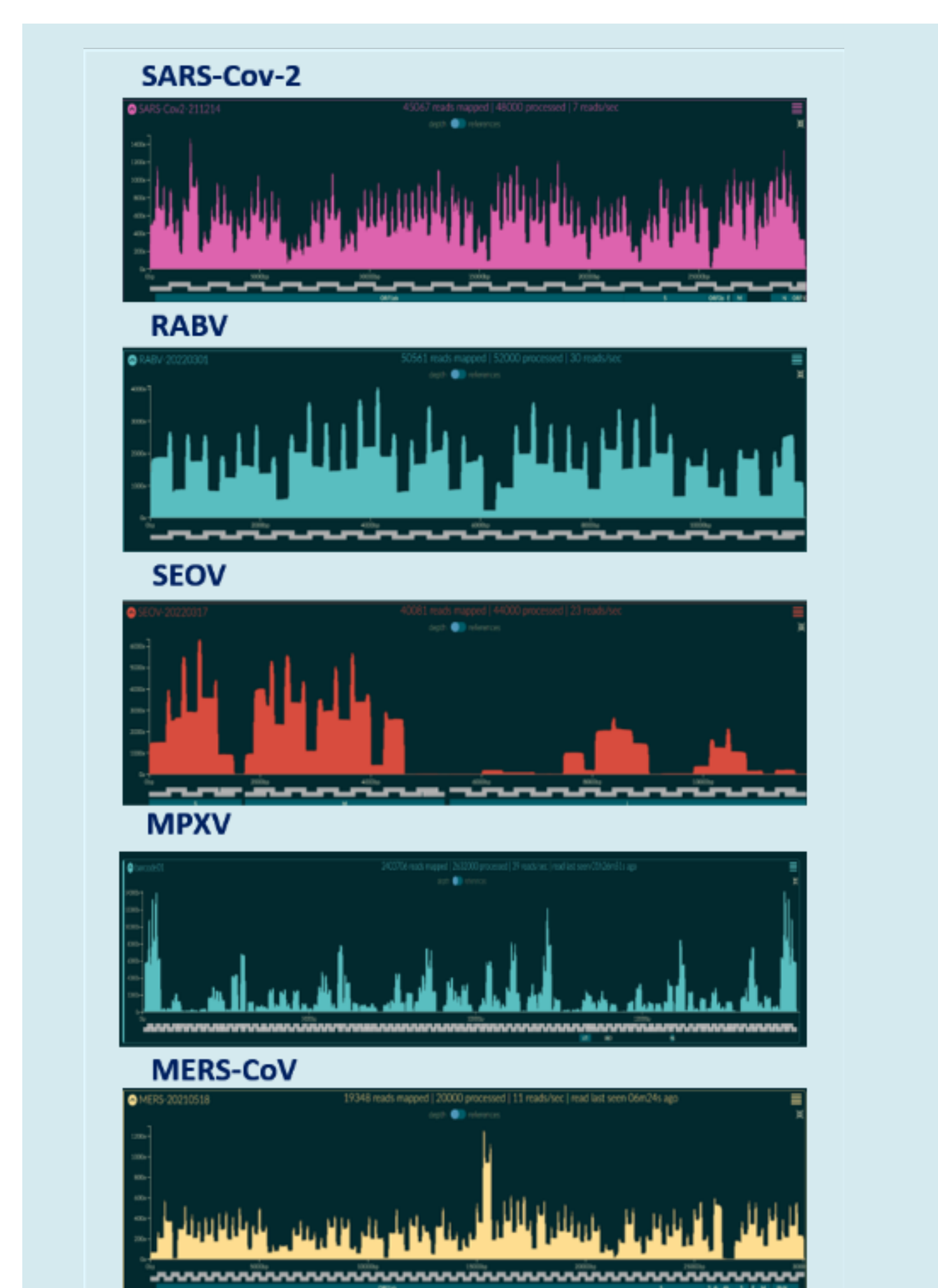


Figure 1. Real-time full genome sequencing visualization with RAMPART. Read depth and coverage for SARS-CoV-2, MPXV, SEOV, MERS-CoV and RABV.

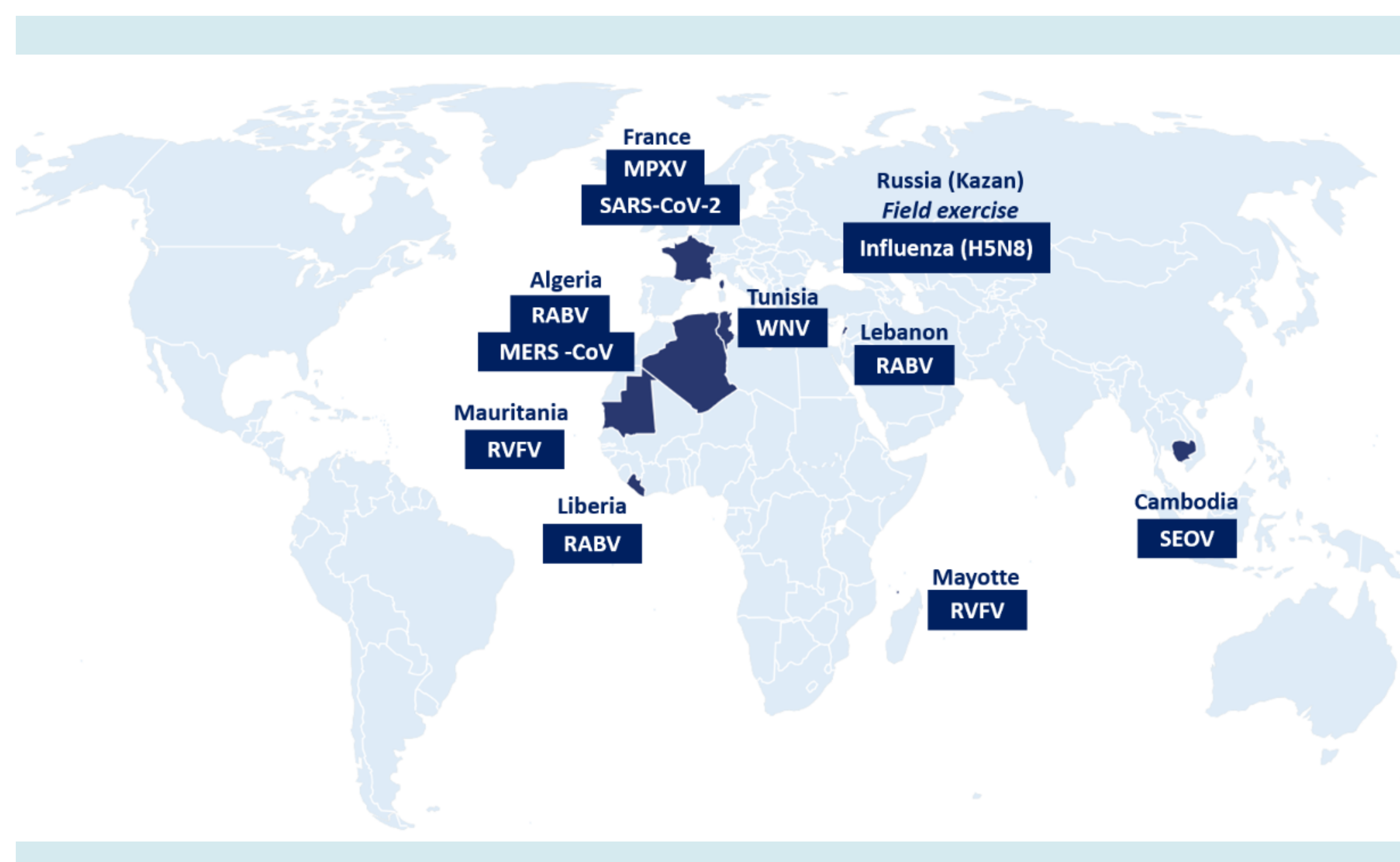


Figure 2. An illustration of public health emergencies in which the amplicon-based sequencing approach was implemented for real-time surveillance of pathogens.

CONCLUSIONS

Within the framework of our studies, nanopore sequencing approaches have proven to be an essential tool for real-time surveillance of pathogens in the context of epidemics and has in particular opened the way towards point-of-care sequencing in low- and middle-income countries.

In addition, in preparation of mass-gathering events such as the **2024 Summer Olympics** in France, this approach could provide information on the causative agent of case clusters, facilitating timely implementation of containment and control measurements.

ACKNOWLEDGEMENTS

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