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WHO event addressing public health priorities

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Summary report on the Subregional training on SARS-CoV-2 sequencing and molecular phylogenetics for national influenza centres in the Eastern Mediterranean Region. https://applications.emro.who.int/docs/WHOEMCSR516E-eng.pdf?ua=1.

## Introduction

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection spreads rapidly, acquiring new mutations and thus increasing human-to-human transmission (1). These variations in genetic material occur over time, causing the emergence of new variants with different and sometimes more infective features (2). Therefore, laboratory preparedness for genomic sequencing is indispensable for the identification and monitoring of the new variants, to guide public health response and strategies to reduce the burden of COVID-19 (3).

Since the onset of the COVID-19 pandemic, the WHO Regional Office for the Eastern Mediterranean (WHO/EMRO) has been working with its 22 countries and territories to scale-up technical capacity for genomic sequencing of SARS-CoV-2 through training, mentoring and the provision of supplies (4).

In December 2021, WHO/EMRO held a 5-day training on the implementation of next generation sequencing (NGS) for 8 countries – Afghanistan, Iraq, Lebanon, Libya, Somalia, Sudan, Syria Arab Republic and Yemen – in preparation for NGS implementation by the national influenza centres of these countries. The objective was to strengthen the capacity of the countries to set up and install the MinION Mk1C system for NGS, manage the MinION Mk1C data, perform sequence analysis, and share sequence data through the established platforms (5).

## Key discussions

The training was conducted using materials developed by WHO/EMRO in partnership with the Sheikh Khalifa Medical City, United Arab Emirates. It focused on 6 key areas: overview of molecular biology and the SARS-CoV-2 genome; sequencing platforms, including Illumina, Ion Torrent and Oxford Nanopore Technologies; laboratory work, including sample preparation, multiplex PCR, library preparation, rapid barcoding, and MinION setup and sequencing; SARS-CoV-2 variants; data analysis and phylogeny, including the construction of phylogenetic trees using FigTree and MEGA software, and nomenclature systems for SARS-CoV-2 clades/lineages using Nextstrain and Pangolin; and how to report sequencing data to public genome repositories.

The training helped participants to understand the basic concepts of NGS, how to set up and install the MinION Mk1C system, manage the data collected from the system, and share sequencing data through the sequence-sharing platforms. Using feedback from the participants, facilitators addressed key gaps and concerns in using NGS at the country level and made recommendations based on identified needs.

## Recommendations

Participants requested WHO/EMRO to provide further technical support to enhance genomic sequencing capacities in the participating countries, including the analysis and interpretation of sequence data.

## References

1. World Health Organization. Genomic sequencing of SARS-CoV-2: a guide to implementation for maximum impact on public health. Geneva: World Health Organization; 2021. https://www.who.int/publications/i/item/9789240018440.

2. Osman IO, Levasseur A, Brechard L, Abdillahi Hassan I, Salah Abdillahi I, Ali Waberi Z, Delerce J, Bedotto M, Houhamdi L, Fournier P-E, Colson P, Aboubaker MH, Raoult D, Devaux CA (2021) Whole genome sequencing of SARS-CoV-2 strains in COVID-19 patients from

Djibouti shows novel mutations and clades replacing over time. Front Med. 2012; 8:737602. DOI: 10.3389/fmed.2021.737602.

3. Grimaldi A, Panariello F, Annunziata P, et al. Improved SARS-CoV-2 sequencing surveillance allows the identification of new variants and signatures in infected patients. Genome Med 2022;14:90. DOI: https://doi.org/10.1186/s13073-022-01098-8.

4. Al-Mandhari A, Barakat A, Abubakar A, Brennan R. Genomic sequencing for epidemic and pandemic preparedness and response: EMRO's vision and strategic interventions. East Mediterr Health J. 2022;28(12):851–852. DOI: https://doi.org/10.26719/2022.28.12.851.

5. Oxford Nanopore Technologies. MinION brochure. Oxford: Oxford Nanopore Technologies. https://nanoporetech.com/resource-centre/minion-brochure.

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