



Cairo, 21 October 2021– In order to control a disease like COVID-19, scientist need to better understand the evolution of the virus, as well as how it mutates into different strains.

Throughout the course of the pandemic, genome sequencing is vital in detecting, identifying, and understanding the evolution and genomic diversity of COVID-19. Genomic surveillance plays a key role in tracking transmission, developing vaccines, diagnostics, and therapeutics, as well as monitoring the mutation of the virus.

To date, 14 out of 22 countries in WHO’s Region for the Eastern Mediterranean use genome sequencing to detect and monitor variants of concern circulating locally. The other eight countries are receiving support from WHO to sequence abroad.

“As COVID-19 continues to evolve, the Regional response in the area of genome sequencing plays a key role on our efforts to better understand the virus. The progress made by countries since the start of the pandemic with the use of genome sequencing is significant but can still be strengthened and further expanded.” said Dr Ahmed Al-Mandhari, WHO Regional Director for the Eastern Mediterranean. “Not only will this help us learn more about the current virus and known strains, but also help us be better prepared to prevent and control future strains.”

WHO’s Regional Office for the Eastern Mediterranean is working closely with governments to boost genomic surveillance capacity to track and monitor the virus’s behavior, as well as the evolving strains.

In addition, WHO provides constant support to eight countries to continue sequencing abroad while working with concerned authorities to enhance local capacities to conduct local sequencing.

However, genome sequencing still faces several challenges in the Region. These include lack of trained health workforce, limited resources to sustain sequencing, availability of reagents and other essential supplies, in addition to logistical difficulties in shipping specimens to international or regional reference laboratories.

“As more countries implement sequencing programs, there will be further opportunities to better understand the virus, how it develops and most importantly how it came into our lives,” Dr. Al-Mandhari added.

WHO emphasizes that the rapid sharing of virus genome sequence data, together with the relevant epidemiological and clinical metadata, maximizes the impact of genomic sequencing in the public health response. WHO encourages all countries to share data generated by genome sequencing with the global community as rapidly as possible, to ensure access to critical information for improving public health.

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