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Ref No.: 10/5

Date: 09 March 2021

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Media Release

for
Immediate Release

Outcome of the Genomic Sequencing results for COVID-19 variants in Namibia

On 30th December 2020, the Government of Republic of South Africa announced the discovery of a new SARS-COV-2 variant known as the **501Y.V2** (the Variant of Concern (VoC))**.** Following this announcement, and considering that Namibia shares long borders with South Africa with various Points of Entry and frequent movements of people between the two countries, the Ministry of Health and Social Services, together with the Namibia Institute of Pathology (NIP) resolved to send a specified number of samples of confirmed positive COVID-19 tests (stored samples) to the National Institute for Communicable Diseases (NICD) in South Africa for genomic sequencing. The samples were randomly selected, with assured anonymity. They were packaged and dispatched in line with international best practice.

The samples were drawn from the tested specimens that are stored by the different accredited laboratories that conduct COVID-19 tests in the country. The samples were chosen to represent the different geographic regions of the country in order to determine the extent of the spread of the variant in Namibia. It is through genomic sequencing that the presence or absence of the variant of concern can be determined.

A total of **105 samples** were drawn from the stored samples at three (3) laboratories. Eighty-one (81) from NIP, twelve (12) from Pathcare, and twelve (12) from the University of Namibia. The samples sent for genomic sequencing represent tests conducted between August 2020 and early February 2021.

Today, I would like to share the results of the genomic sequencing process with the Nation.

Conducting genomic sequencing is important to investigate outbreak dynamics, changes in the growth of the epidemic over time, the spread of the virus and its transmission routes. Moreover, virus genome sequencing is helpful in disease surveillance and selection of vaccines that are effective against identified variants. It is not uncommon for viruses to mutate, forming new variants. Available information has shown that the variant of concern identified in South Africa is more transmissible compared to other variants.

What do the results of the genome sequencing show?

Of the one hundred and five (105) samples submitted for analysis, eighty-one **(81) samples were successfully** sequenced and analyzed. The results were released on 06 March 2021. They indicate that there is a diversity of lineages/clades of the virus in Namibia. The Variant of Concern (VoC) first identified in South Africa (20H/501Y.V2/B.1.351) was found in **16 out of 81 samples** from Namibia isolated between October 2020 and February 2021. This was the same time this variant was detected in the South African population. The remnant samples were drawn from all Regions, namely Erongo, Omaheke, Ohangwena, Khomas, Kharas, Oshikoto, Omusati, Otjozondjupa, Oshana, Zambezi Regions. The ages of the persons from whom the samples were drawn range between eleven (11) to fifty-four (54) years.

Based on these results, we now know that the variant identified in South Africa is present in Namibia. The variant was detected in sixteen 16) samples from ten (10) Regions. However, its presence in other regions cannot be ruled out. We should note that this variant has also been detected in neighboring countries including Botswana and Zambia.

In conclusion, Namibia will continue to collaborate with partners and countries in the region and beyond for routine genomic surveillance for COVID-19 variants. In the same vein, the country will expedite plans to set-up local genomic sequencing capacity. Genomic sequencing results will also inform important policy decisions in our COVID-19 response and preparedness, including the selection of vaccines and other medical interventions.

We will keep the nation informed of future developments in the COVID-19 response and related interventions.

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