Report on the Detection of Omicron Variant in Namibia, November 2021

Report prepared by University of Namibia, 03.12.2021

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Sample collection and molecular analysis

A total number of 19 samples which tested positive for SARS-Cov-2 by RT-PCR from the NIP, Pathcare and Diagnolab between the 11th-26th November 2021 were selected for sequencing after passing quality control for Next Generation Sequencing. RNA was extracted with standard procedures and reverse transcription of the viral RNA into cDNA was done for all the samples using the LunaScript RT SuperMix Kit (New England BioLabs). The samples were prepared for whole genome sequencing (WGS) using the hCoV-2019/nCoV-2019 Version 3 Amplicon Set (https://artic.network/resources/ncov/ncov-amplicon-v3.pdf). In short, 98 primer pairs were combined in two primer pair pools that create 400bp amplicons using a PCR reaction with 35 cycles that cover the full SARS-CoV-2 genome. After quality checks, amplicons were used for Illumina next generation sequencing (NGS) library preparation and sequenced on a Illumina Iseq 100 sequencer at UNAM Molecular Diagnostic Laboratory. All obtained NGS datasets were sent to RCB for analysis using a standard bioinformatic pipeline. The full diagnostic and analytical workflow is shown in Fig. 1.

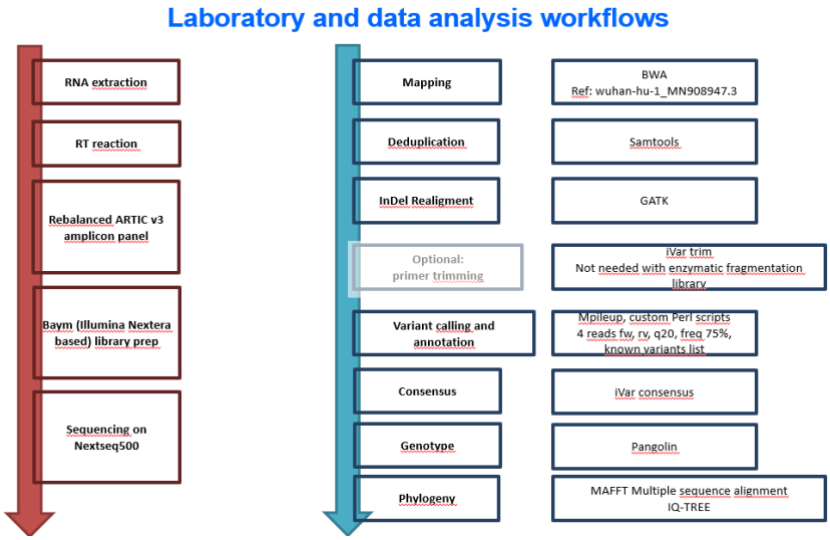

Fig. 1. Laboratory and data analysis workflow.

Sample analysis

The raw sequence data files of a total of 19 sequenced samples were analyzed at RCB using a modified version of the MTBseq pipeline [5]. In addition to the general workflow of the pipeline, the genome of SARS-CoV-2 MN908947.3 Wuhan strain was used as a reference genome for the mapping of the NGS reads. Furthermore, we performed primer trimming and consensus sequence calling with iVar [6] and lineage classification with pangolin v3.1.5 [7]

NGS data analysis and lineage classification

The 19 samples sequenced passed our internal quality control, and were further analyzed for the scope of this report. Of the 19 samples tested between the 11th – 26th November 2021, one was from Oshana, two (2) from South Africa and the remaining 16 were from Khomas. Out of 19 samples, 18 tested samples belong to the Omicron Variant of Concern B.1.1.529 first reported in Botswana and South Africa and the remaining one samples showed AY.91 lineage. Reported symptoms ranged from coughing being frequently experienced (8 people), followed by sore throats and body (muscle) pain/myalgia

Table 2: Detection and Confirmation of Delta B. 1.1.529 Variant in 18 samples by Genomic Sequencing performed at UNAM School of Medicine.

SampleID	Lineage	Run	Region	Gender	Symptoms	Collection date
MDL035780	AY.91	02.12.2021	Khomas	Female	Sore throat, myalgial/body pain	16/11/2021
MDL035783	B.1.1.529	02.12.2021	Khomas	Male	Cough	10/11/2021
MDL035784	B.1.1.529	02.12.2021	Khomas	Female	Cough	10/11/2021
MDL035786	B.1.1.529	02.12.2021	Khomas	Female	N/A	23/11/2021
MDL035788	B.1.1.529	02.12.2021	Khomas	Male	N/A	25/11/2021
MDL035789	B.1.1.529	02.12.2021	Khomas	Male	Cough	25/11/2021
MDL035790	B.1.1.529	02.12.2021	Khomas	Male	Cough	25/11/2021
MDL035797	B.1.1.529	02.12.2021	Khomas	Female	Cough	25/11/2021
MDL035798	B.1.1.529	02.12.2021	Khomas	Male	N/A	24/11/2021
MDL035803	B.1.1.529	02.12.2021	Khomas	Female	none	25/11/2021
MDL035804	B.1.1.529	02.12.2021	Oshana	Female	Chills, fever, cough, myalagia	25/11/2021
MDL035805	B.1.1.529	02.12.2021	South Africa	Female	None	25/11/2021
MDL035806	B.1.1.529	02.12.2021	Khomas	Female	Sore throat, diarrhoea, myalagia, cough	26/11/2021
MDL035807	B.1.1.529	02.12.2021	Khomas	Male	None	26/11/2021
MDL035808	B.1.1.529	02.12.2021	South Africa	Female	None	26/11/2021
MDL035809	B.1.1.529	02.12.2021	Khomas	Male	Sore throat	26/11/2021
MDL035810	B.1.1.529	02.12.2021	Khomas	Male	Sore throat, myalagia, headache	26/11/2021
MDL035811	B.1.1.529	02.12.2021	Khomas	Female	Sore throat, cough	26/11/2021
MDL035812	B.1.1.529	02.12.2021	Khomas	Male	Fever, chillls, myalagia	22/11/2021

A SARS-CoV-2 variant belonging to Pango lineage B.1.1.529, with a high number of S-gene mutations compared to the original virus and designated a variant of concern (VOC) and assigned the label Omicron by the World Health Organization (WHO) [1]. was detected in 18 out of 19 samples analyzed by genomic sequencing. This is the first report of the presence of the Omicron variant in Namibia as early as 10th November 2021. that was detected in the world at the beginning of November 2021. This variant is characterised by 30 changes, three small deletions and one small insertion in the spike protein, of these, 15 are in the receptor binding domain. This variant was first detected in samples collected on 11 November 2021 in Botswana and on 14 November 2021 in South Africa. As of the 3rd December 2021, travel related cases have also been detected in more than 26 countries globally [4]. The Omicron variant is the most divergent variant that has been detected in significant numbers during the pandemic so far, which raises concerns that it may be associated with increased transmissibility, significant reduction in vaccine effectiveness and increased risk for reinfections.

Previous experiences with the Alpha, Beta and Delta variants show that introduction and spread of new variants can happen very rapidly. Given its immune escape potential and possible transmissibility advantage compared to Delta, Omicron may have the capacity to spread rapidly once introduced in a country, making the probability of spread high [2]. However, this assessment is based on substantial uncertainty and will be updated when new information and evidence when available. If infection with the new variant is acquired, it is likely that at least a part of the population will experience severe disease. There is still no severity information for Omicron, however it is likely that that the same populations with higher likelihood of severe outcomes from other SARS-CoV-2 variants (the elderly, those with underlying comorbidities) are likely to have severe outcomes due to Omicron.

On vaccine effectiveness, current available vaccines may offer some level of protection against hospitalisation and death, however in vitro studies evaluating the neutralising capacity of both vaccinee and convalescent sera against Omicron live virus isolates are urgently required to better understand its escape potential against both vaccination and infection-acquired immunity. Genomic surveillance remains of utmost importance for early detection of the presence of this variant, to enable the following of epidemiological trends and guide containment measures. Therefore, utmost priority should be given towards vaccination of individuals initially targeted by COVID-19 vaccination programmes that remain unvaccinated or not yet fully vaccinated.

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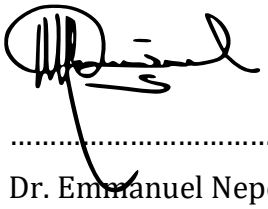

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