

Detection of SARS-CoV-2 Variant 501Y.V2 (variant of concern) in Comoros Islands

Background

The 501Y.V2 variant (also known as Lineage B.1.351) has been reported extensively in South Africa (447 genomes publicly available), Botswana (6 genomes publicly available), Ghana and Kenya (2 genomes publicly available) and 11 other countries across the globe.

Summary

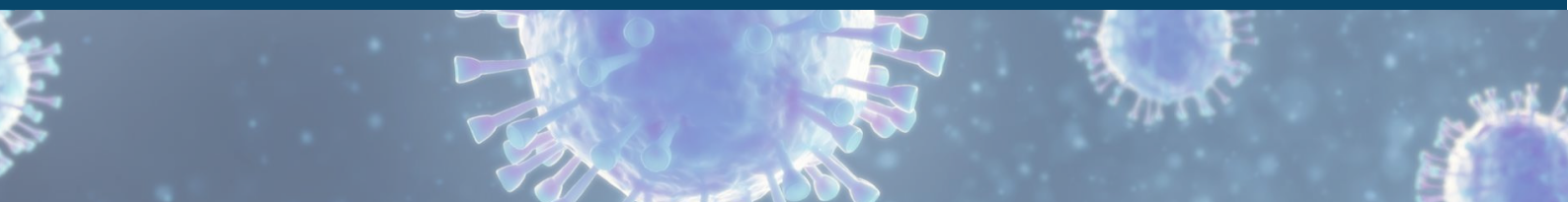
- We received 11 samples from Comoros Islands for sequencing, 6 of which met our inhouse RT-PCR criteria for genome sequencing
- Our sequencing and bioinformatics analysis confirmed that the 6 samples belong to the lineage B.1.351 (Variant 501Y.V2).

Findings from sequence data

We processed 11 samples and obtained near complete genomes for all the samples that passed QC. All the six Comoros sequences had 6/9 defining 501Y.V2 mutations that are characteristic of this lineage as tabulated (Table 1). The sequences fell into a single lineage B.1.351 (clade 20H/501Y.V2). Phylogenetic clustering placed the sequenced genomes with the 501Y.V2 cluster (Figure 1).

Table 1: Summary of mutations in the six sequences.

Gene	Amino Acid Change	P180124 (Ngazidja)	P180125 (Ngazidja)	P180128 (Ngazidja)	P180130 (Mohéli)	P180132 (Mohéli)	P180134 (Mohéli)
Envelope (E)	P71L	observed	observed	observed	observed	observed	observed
Nucleocapsid (N)	T205I	observed	observed	observed	observed	observed	observed
ORF1a	T265I	observed	observed	observed	observed	observed	observed
	K1655N	Amplicon drop off to be re-sequenced					
	K3353R	observed	observed	observed	observed	observed	observed
ORF1b	P314L	observed					
ORF3a	Q57H	observed	observed	observed	observed	observed	observed
	S171L	observed	observed	observed	observed	observed	observed
ORF14							
Spike (S)	D80A	observed	observed	observed	observed	observed	observed
	D215G	observed	observed	observed	observed	observed	observed
	K417N	observed	observed	observed	observed	observed	observed
	E484K	Amplicon drop off to be re-sequenced					
	N501Y	Amplicon drop off to be re-sequenced					
	D614G	observed	observed	observed	observed	observed	observed
	A701V	observed	observed	observed	observed	observed	Observed



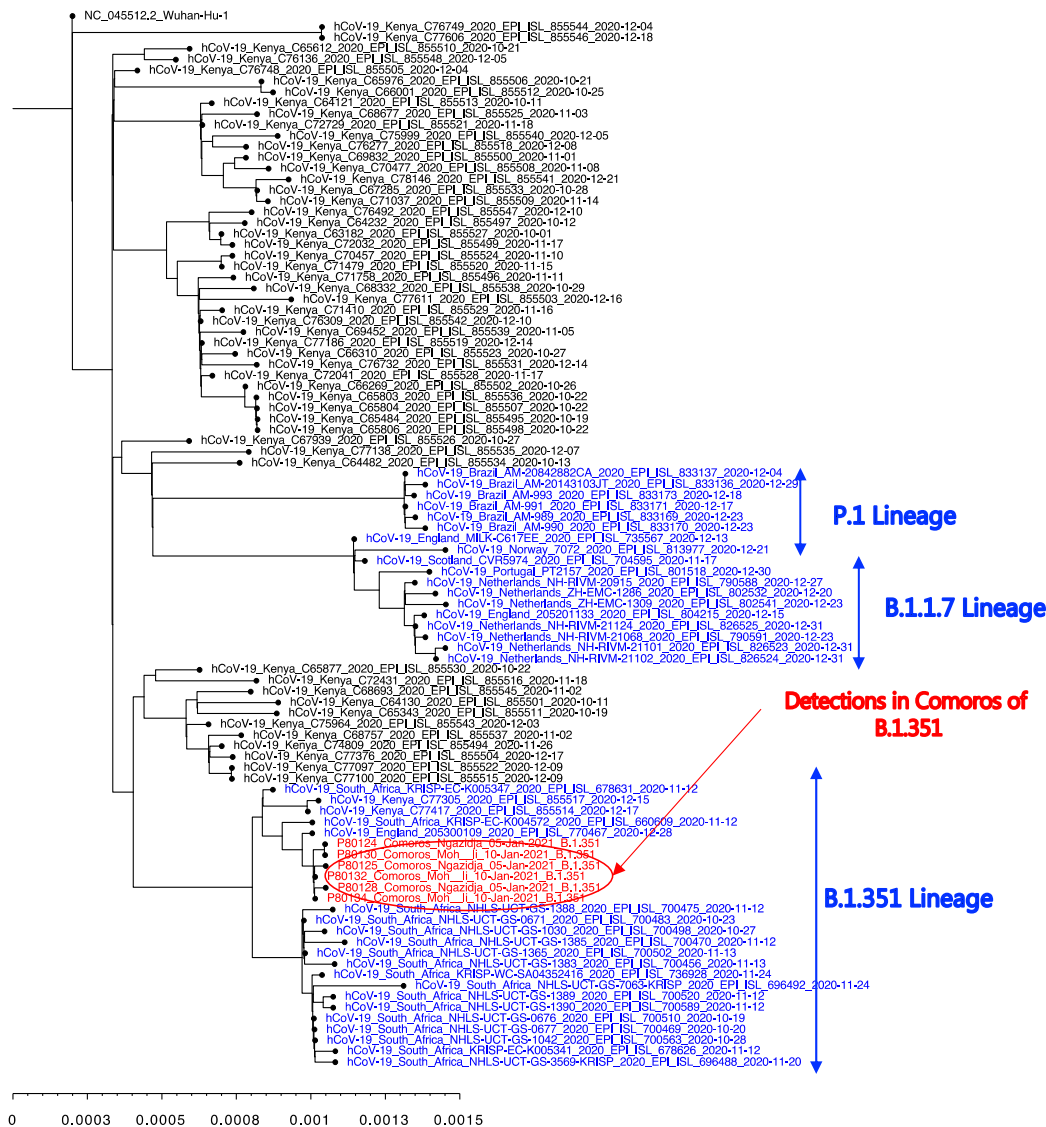


Figure 1: A phylogenetic tree showing the placement of the six samples from Comoros (coloured in red) relative to other SARS-CoV-2 sequences from the South African region and Kenya in relation coloured in grey . Sequences of the three variants of concern identified globally are indicated in blue.

Recommendation

Continued genomic surveillance of the affected islands to establish the extent of spread and transmission of this variant in the Comoros.

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