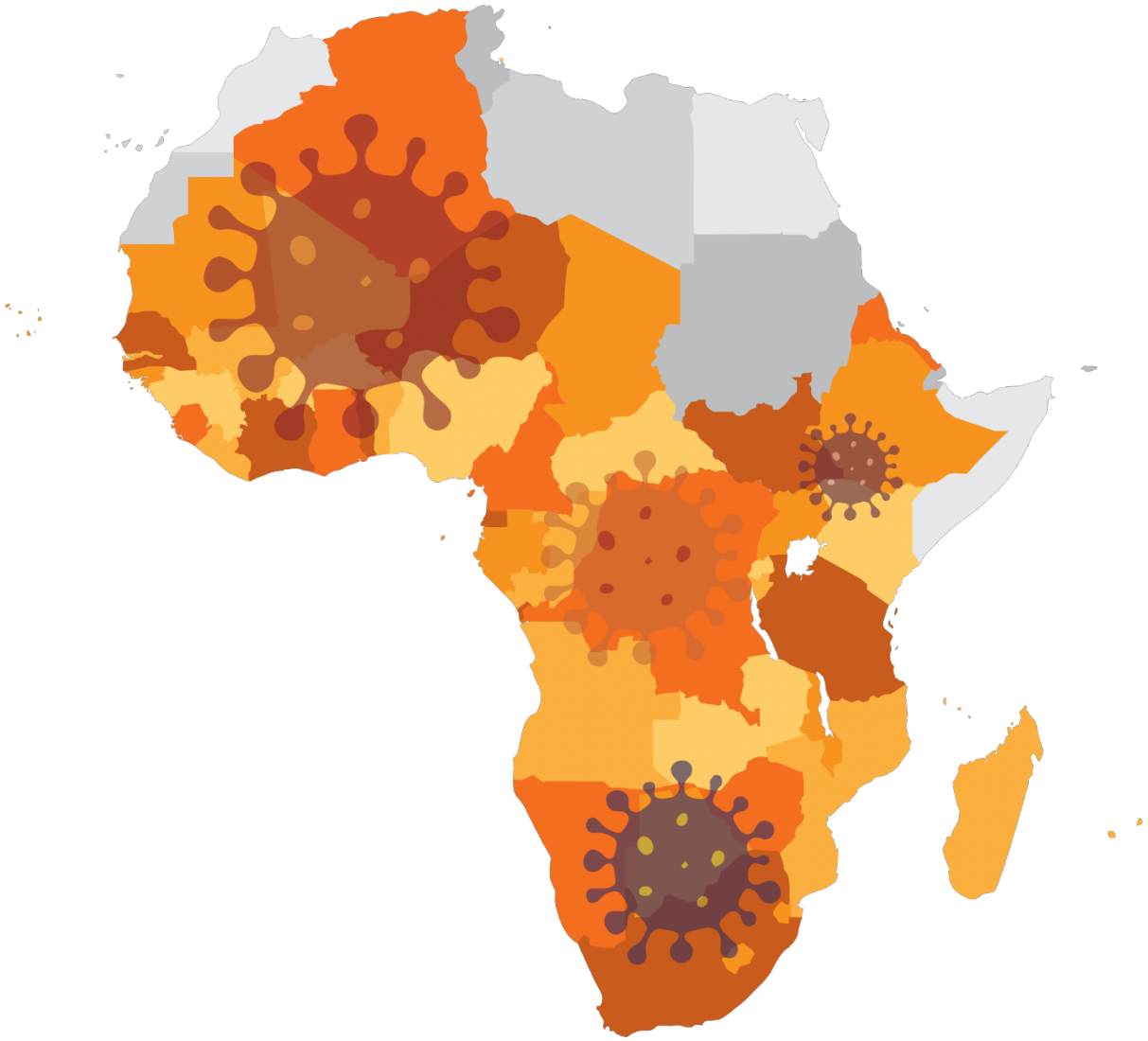
SARS-CoV-2 genomes report for WHO Africa Region

26/05/2021

Produced by the TIBA COVID-19 Pandemic Response Unit



NIHR Global Health Research Unit Tackling Infections to Benefit Africa at the University of Edinburgh

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Summary

- 36 countries from WHO Africa region (AFRO) have deposited 13359 SARS-CoV-2 sequences to publicly available databases, with the biggest contributor being South Africa (47% of sequences).
- Sequences uploaded to GISAID by TIBA partners: Kenya (n=856), Ghana (n=438), Rwanda (n=288), Botswana (n=218).
- 248 transmissible lineages have been identified from WHO AFRO countries, and 67 of these lineages are composed of SARS-CoV-2 genomes mainly from Africa (>50% sequences deposited from Africa).
- Variants of Concern (VOC) reported by WHO AFRO countries include B.1.1.7 (first identified in United Kingdom), B.1.351 (first identified in South Africa), B.1.429 (first identified in USA) and B.1.617.2 (first identified in India).
- Variants of Concern P.1 (first identified in Brazil) and B.1.427 (first identified in USA) have not been found so far.
- B.1.351 is the most prevalent lineage in WHO AFRO countries and has spread to 22 WHO AFRO countries, mostly in southern Africa. This variant accounts for 28% (n=3778) of all African SARS-CoV-2 genomes to date and 64% in the past 4 weeks.
- B.1.1.7, the most widespread lineage globally, has been identified in 19 WHO AFRO countries, mostly in West Africa.
- B.1.617.2 has recently been identified in 4 WHO AFRO countries: South Africa (n=14), Democratic Republic of the Congo (n=6), Uganda (n=4) and Botswana (n=1).

Background

By using SARS-CoV-2 genome sequences and the corresponding metadata downloaded from GISAID on 30th November 2020, we stated 23 countries from WHO Africa region (AFRO) have deposited a total of 3995 SARS-CoV-2 sequences to publicly available databases, with the majority of the genomes being from South Africa (56%). There were 84 different transmissible lineages (266 lineages globally) have been identified from WHO Africa countries with 86% genomes belonging to the B.1 sub-lineage and its descendants. We also found multiple separate introductions of SARS-CoV-2 infections into Africa, approximate 43% of these from Europe. By 30th November 2020, no sequences from 24 WHO AFRO countries and, furthermore, some of the countries with sequence data had submitted a total of less than 10 sequences to date. We have concluded that there is still need for sequencing of virus from other African countries and for the sequences to be deposited in publicly available databases [1].

Variant of concern (VOC) defines a variant for which there is evidence of an increase in transmissibility, more severe disease, significant reduction in neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or diagnostic detection failures (https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html#Concern). Currently identified VOCs include B.1.1.7 (first identified in United Kingdom), B.1.351 (first identified in South Africa), P.1 (first identified in Brazil), B.1.429 and B.1.427 (first identified in California), B.1.617.2 (first identified in India).

A SARS-CoV-2 variant is designated a Variant Under Investigation (VUI) if considered to have concerning epidemiological, immunological or pathogenic properties, are raised for formal investigation.

Currently, 8 lineages are on the VUI list, including P.2, A.23.1, B.1.525, B1.1.318, B1.324.1, P.3, B.1.617 and B.1.617.3. Following a risk assessment with the relevant expert committee, they may be designated Variant of Concern (VOC) (https://www.gov.uk/government/publications/covid-19-variants-genomically-confirmed-case-numbers/).

In this report, we describe the most recent state of genome sequences available publicly from WHO AFRO countries. We focus especially on the prevalence of variants belong to VOC and VUI.

Data sources and methods

Data comprising all SARS-CoV-2 genome sequences and the corresponding metadata from WHO Africa region (AFRO) on the GISAID sequence data repository were downloaded on 26th May 2021 (https://www.gisaid.org). Spatiotemporal phylogenetic analysis was conducted using complete genomes from African countries and other continents. Over-representative sequences have been subsampled.

SARS-Cov-2 in WHO AFRO countries

As of 26th May 2021, 13359 SARS-CoV-2 genomes had been submitted to GISAID from 36 countries in WHO Africa Region (out of 47). These represent ~0.8% of publicly available sequences globally. The biggest contributor is South Africa (47% of genomes) (Figure 1A and B, Table S1).

Currently, 1284 lineages contributing to active spread globally have been identified by the PANGOLIN phylogenetic classification (PANGOLIN version date 12th May 2021) [2]. As of 26th May 2021, 248 of these transmissible lineages have been identified in the sequences from WHO AFRO countries, and 67 lineages are composed of SARS-CoV-2 genomes mainly from Africa (>50% of all sequences). 28 of these are found in South Africa (Figure 1C and Table S2).

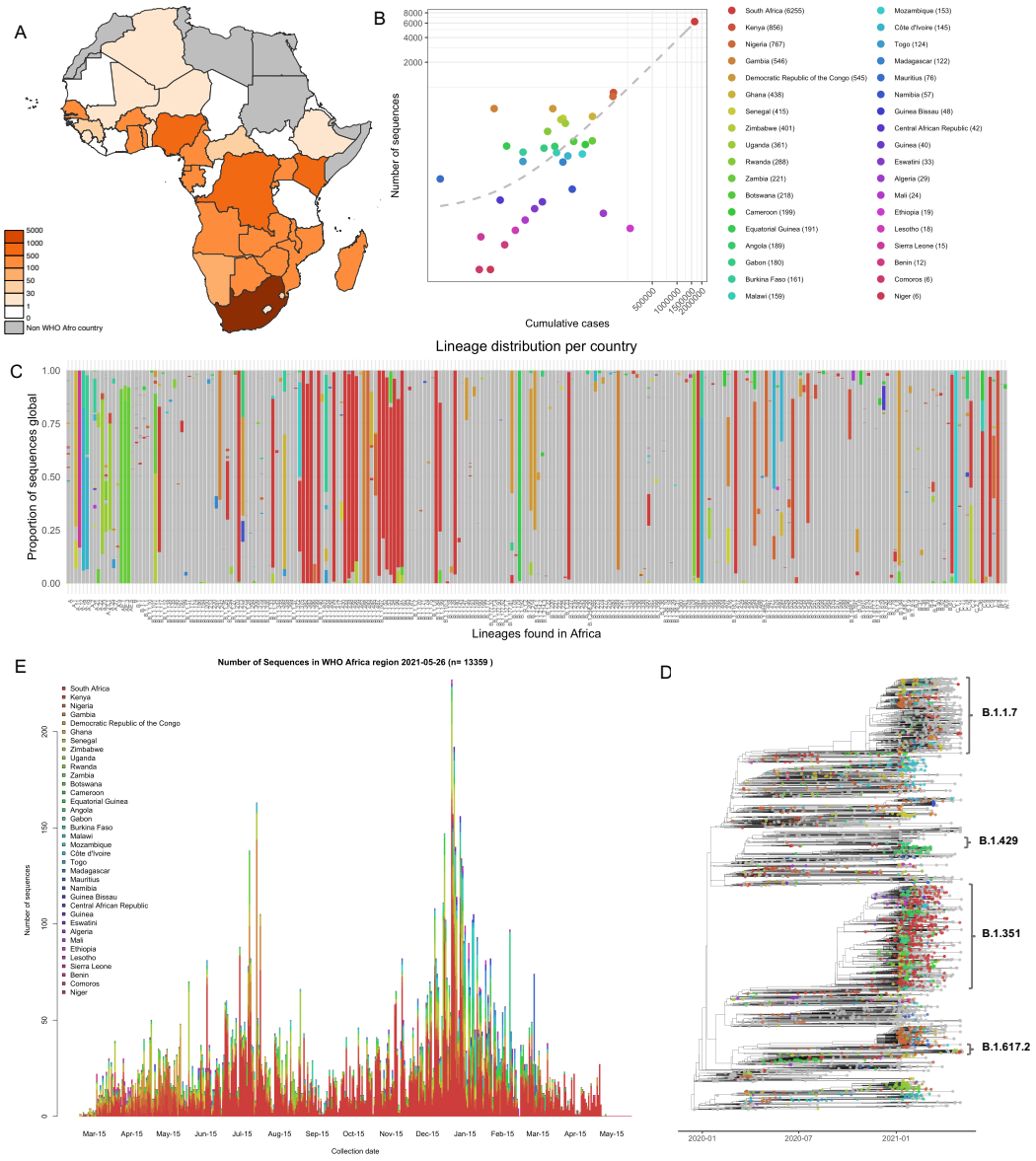


Figure 1 Summary of sequence data for WHO AFRO countries. (A) SARS-CoV-2 genomes available on GISAID by country. (B) Comparison of cumulative reported cases and number of sequences available per country, with coordinates of axes log transformed. (C) Global lineages in African countries compare to other regions (in grey). (D) Genomes from individual countries highlighted on approximate time-scaled global subsampled tree (n=3340), with tips colored by the sampling locations, with VOC lineages labelled. (E) SARS-CoV-2 genomes available on GISAID by collection date. Colours for WHO AFRO countries are consistent in (B) to (E), other regions are in grey.

Prevalence of VOC and VUI in WHO AFRO countries

To date, 4 VOC (B.1.1.7, B.1.351, B.1.429, B.1.617.2) have been identified from 31 different WHO AFRO countries, including: South Africa, Zimbabwe, Malawi, Ghana, Nigeria, Kenya, Botswana, Mozambique, Gambia, Equatorial Guinea, Gabon, Guinea Bissau, Angola, Democratic Republic of the Congo, Zambia, Eswatini, Cameroon, Togo, Senegal, Madagascar, Côte d'Ivoire, Lesotho, Rwanda, Guinea, Namibia, Comoros, Mauritius, Uganda, Ethiopia, Central African Republic, Burkina Faso, while P.1 and B.1.427 have not been identified so far (Figure 1D and Table 1).

Table 1 Prevalence of VOC and VUI globally and within WHO AFRO countries

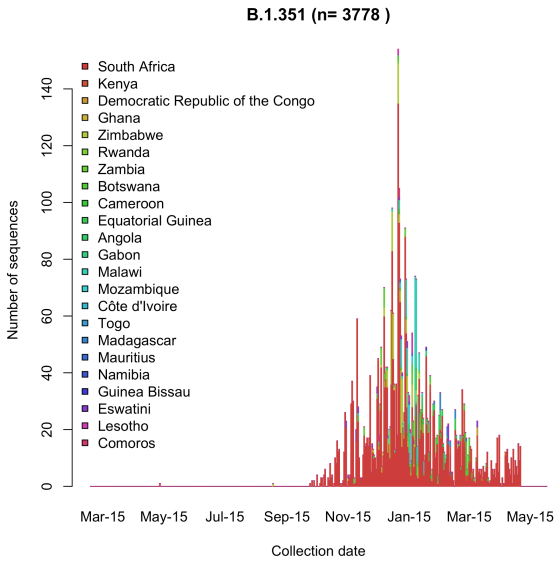
Pango.lineage	*SeqNum AFRO*	*Proportion AFRO (%)*	*SeqNum global*	*Proportion global (%)*	*SeqNum in recent4wk*
VOC					
B.1.351	3778	28.28	19838	1.15	75
B.1.1.7	610	4.57	732318	42.58	8
B.1.617.2	25	0.19	10467	0.61	18
B.1.429	3	0.02	29859	1.74	-
VUI					
B.1.525	261	1.95	5180	0.30	-
A.23.1	259	1.94	1031	0.06	-
B.1.1.318	46	0.34	1860	0.11	-

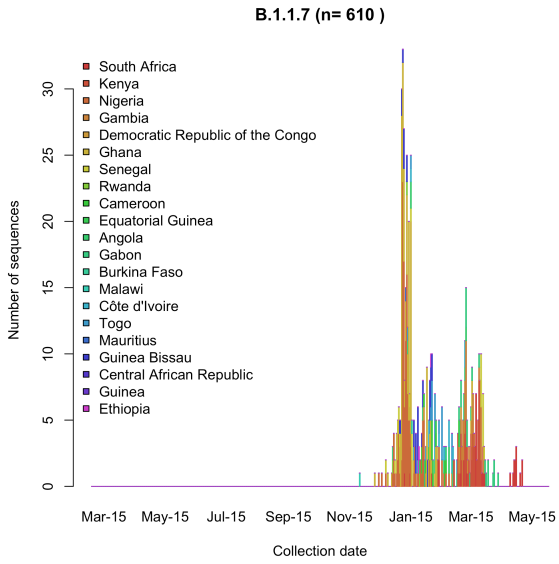
The most prevalent lineage globally is B.1.1.7, first isolated in UK in September 2020 and reported from 138 countries globally. To date, 610 sequences were isolated from WHO AFRO countries, accounting for 1% of total B.1.1.7 sequences globally. Within WHO AFRO, this lineage was first identified in Malawi on 25th of November 2020 and was subsequently identified in 19 countries, mostly in Nigeria (23%) and Ghana (22%). The number of sequences within Africa peaked in mid-January 2021. This variant was most recently on 5th May 2021 from South Africa (Figure 2,3).

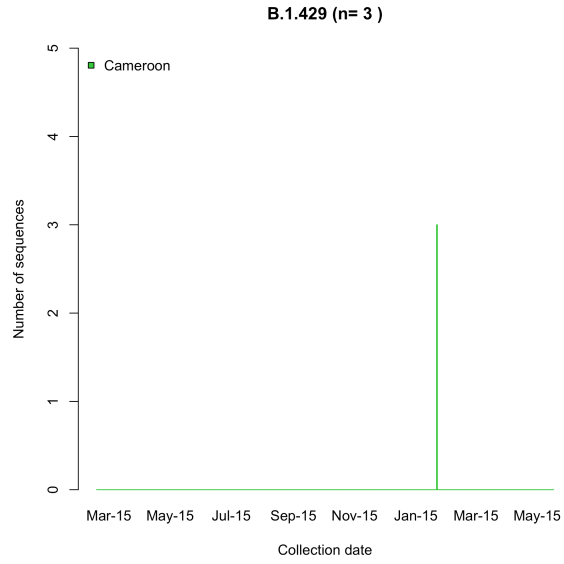
Our analyses show that B.1.351 is the most prevalent lineage in WHO AFRO countries, and ~28% (n=3778) of all African SARS-CoV-2 genomes up to date and 64% in the past 4 weeks. This variant is also known as the South Africa variant or variant 501Y.V2 and was first isolated in South Africa in October 2020. This variant has spread to 96 countries globally and accounts for 1% of all publicly available sequences. Within WHO AFRO, this lineage has mostly been identified from South Africa (79%, n=2967) but also in another 21 countries. The number of sequences within Africa peaked in mid-January 2021. This variant was identified most recently on 11th May 2021 from South Africa (Figure 2,3).

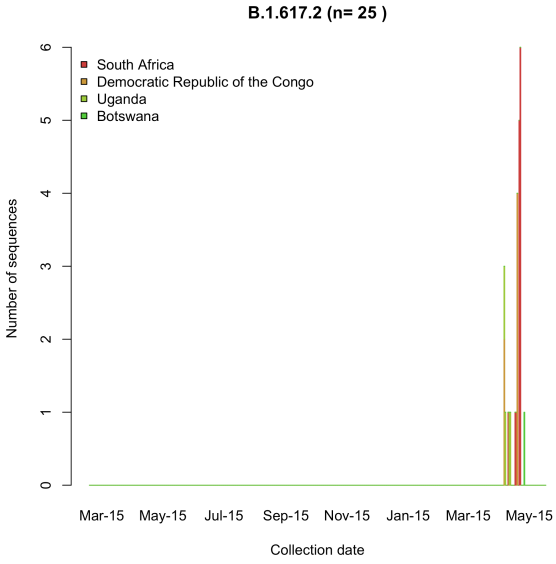
In comparison, B.1.429 (first identified in California in US) has only been identified sporadically (n=3) in one WHO AFRO country – Cameroon, in February 2021 (Figure 2,3).

B.1.617.2 was first detected in India in December 2020 and has spread to 51countries globally. The variant has recently been identified in 4 WHO AFRO countries: South Africa (n=14), Democratic Republic of the Congo (n=6), Uganda (n=4) and Botswana (n=1) between 20th April to 10th of May 2021 (Figure 2,3).


B.1.351 (n= 3778)
South Africa
Kenya
Democratic Republic of the Congo
Ghana
Zimbabwe
Rwanda
Zambia
Botswana
Cameroon
Equatorial Guinea
Angola
Gabon
Malawi
Mozambique
Côte d'Ivoire
Togo
Madagascar
Mauritius
Namibia
Guinea Bissau
Eswatini
Lesotho
Comoros
Number of sequences
0
20
40
60
80
100
120
140
Mar-15
May-15
Jul-15
Sep-15
Nov-15
Jan-15
Mar-15
May-15
Collection date


B.1.1.7 (n= 610)
South Africa
Kenya
Nigeria
Gambia
Democratic Republic of the Congo
Ghana
Senegal
Rwanda
Cameroon
Equatorial Guinea
Angola
Gabon
Burkina Faso
Malawi
Côte d'Ivoire
Togo
Mauritius
Guinea Bissau
Central African Republic
Guinea
Ethiopia
Number of sequences
0
5
10
15
20
25
30
Mar-15
May-15
Jul-15
Sep-15
Nov-15
Jan-15
Mar-15
May-15
Collection date


B.1.429 (n= 3)
Cameroon
Number of sequences
0
1
2
3
4
5
Mar-15
May-15
Jul-15
Sep-15
Nov-15
Jan-15
Mar-15
May-15
Collection date


B.1.617.2 (n= 25)
South Africa
Democratic Republic of the Congo
Uganda
Botswana
Number of sequences
0
1
2
3
4
5
6
Mar-15
May-15
Jul-15
Sep-15
Nov-15
Jan-15
Mar-15
May-15
Collection date

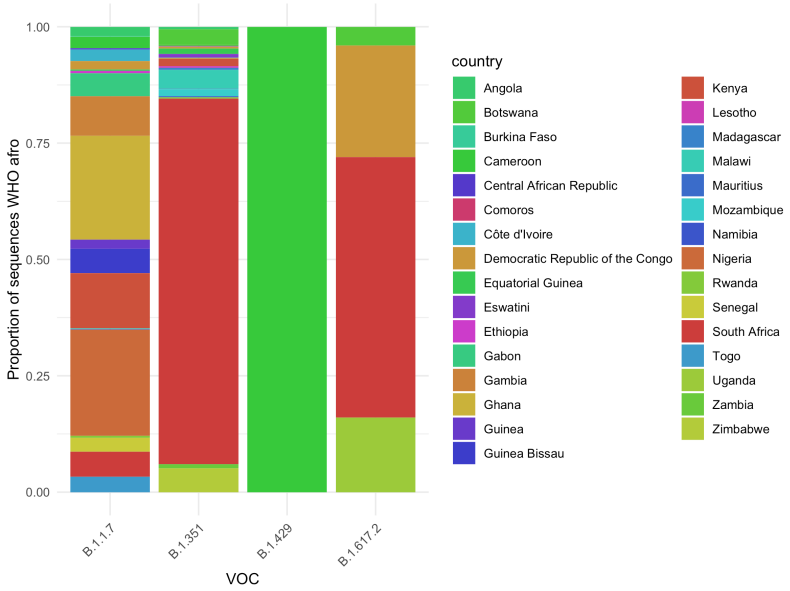

Proportion of sequences WHO afro
0.00
0.25
0.50
0.75
1.00
B.1.1.7
B.1.351
B.1.429
B.1.617.2
VOC
country
Angola
Botswana
Burkina Faso
Cameroon
Central African Republic
Comoros
Côte d'Ivoire
Democratic Republic of the Congo
Equatorial Guinea
Eswatini
Ethiopia
Gabon
Gambia
Ghana
Guinea
Guinea Bissau
Kenya
Lesotho
Madagascar
Malawi
Mauritius
Mozambique
Namibia
Nigeria
Rwanda
Senegal
South Africa
Togo
Uganda
Zambia
Zimbabwe

Figure 2 Proportion of VOC lineages in WHO AFRO countries and genomes available on GISAID by collection date. Colours for WHO AFRO countries are consistent with Figure 1.

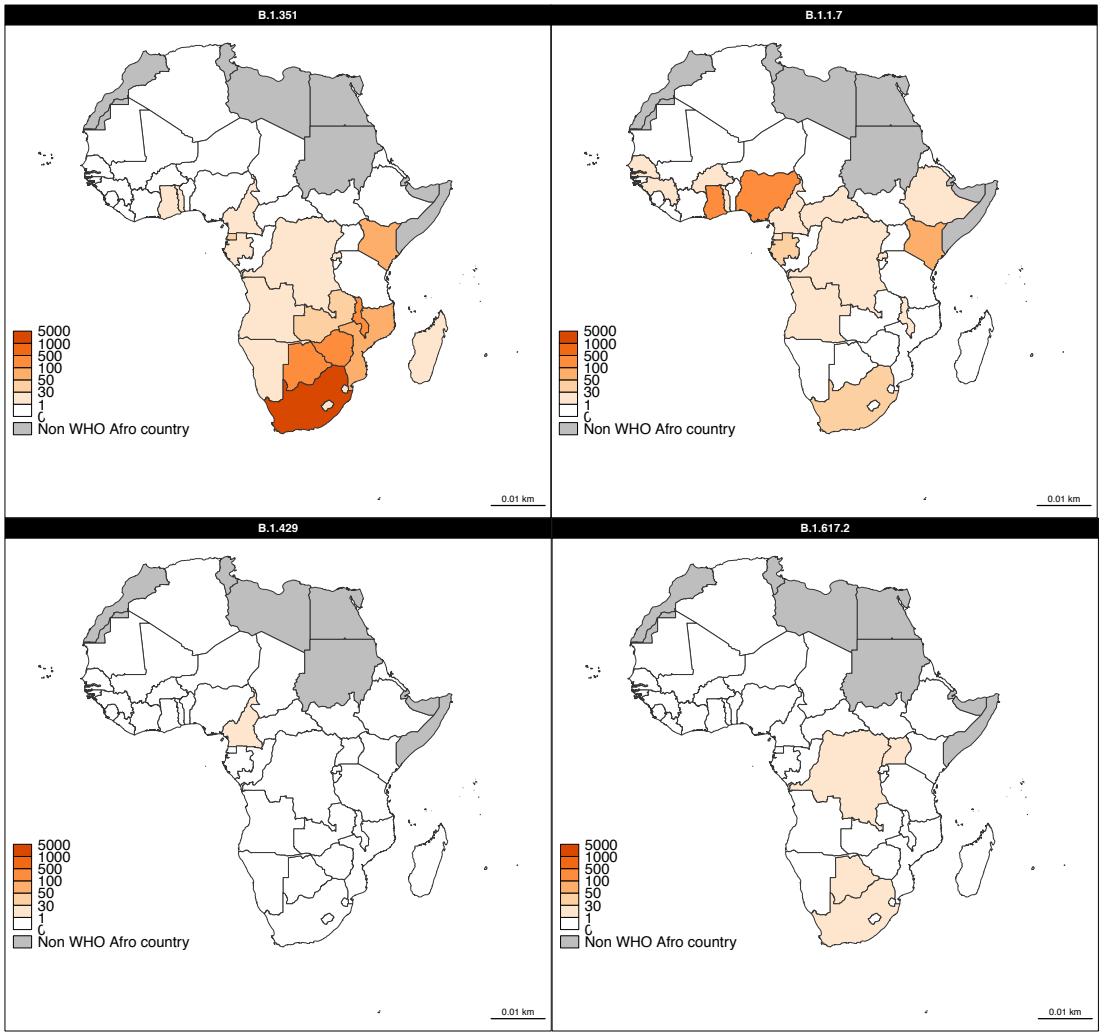


Figure 3 Map of VOC lineages in WHO AFRO countries

Three VUIs (A.23.1, B.1.525 and B.1.318) have been identified from 18 different WHO AFRO countries, including Angola, Botswana, Cameroon, Côte d'Ivoire, Democratic Republic of the Congo, Gabon, Gambia, Ghana, Guinea, Kenya, Mauritius, Niger, Nigeria, Rwanda, South Africa, Togo, Uganda, Zimbabwe, while the other VUIs (P.2, B1.324.1, P.3, B.1.617, B.1.617.3) have not been identified so far (Table 1, Table S1 and Table S2).

VUI A.23.1 was first isolated in Uganda and dominated the Uganda epidemic between October 2020 and January 2021. This variant has spread to 41 countries globally. Within WHO AFRO, this lineage has been reported from 11 countries, mostly from Uganda (53%, n=136) and Rwanda (35%, n=91). The number of sequences within Africa peaked in early-January 2021 and decreased since then. This variant was last reported from Kenya on 17th of March 2021 (Figure 4,5).

VUI B.1.525 was first detected by genome sequence in mid-December in Nigeria but was also quickly found in cases in the United Kingdom and spread to 60 countries globally. Within WHO AFRO, this lineage has been reported from 12 countries, mostly from Nigeria (73 %, n=160). This variant was last reported in South Africa on 16th of April 2021 (Figure 4,5).

B.1.1.318 had been declared as a VUI and contains the E484K mutation, which is a feature of the South African and Brazilian variants. This VUI has been found in 37 countries globally, mainly in UK and US. Within WHO AFRO, this lineage has been identified in 6 countries (n=28), mostly from Nigeria (50%). This lineage was first identified in Nigeria on 7th of January 2021 and last reported from Gabon on 16th of April 2021(Figure 4,5).

In the 4 weeks between 28 April to 26 May 2020, 116 genomes belonging to 7 lineages (B.1, B.1.1.7, B.1.351, B.1.1.67 , B.1.617.2, B.1.1, B.1.551) have been identified from WHO AFRO countries (Table 1 and Table S2). Three of them (B.1.1.7, B.1.351, B.1.617.2) are VOC. B.1.351 accounted for 64% of the 116 genomes; B.1.617.2 accounted for 15%; and B.1.1.7 accounted for 7%.

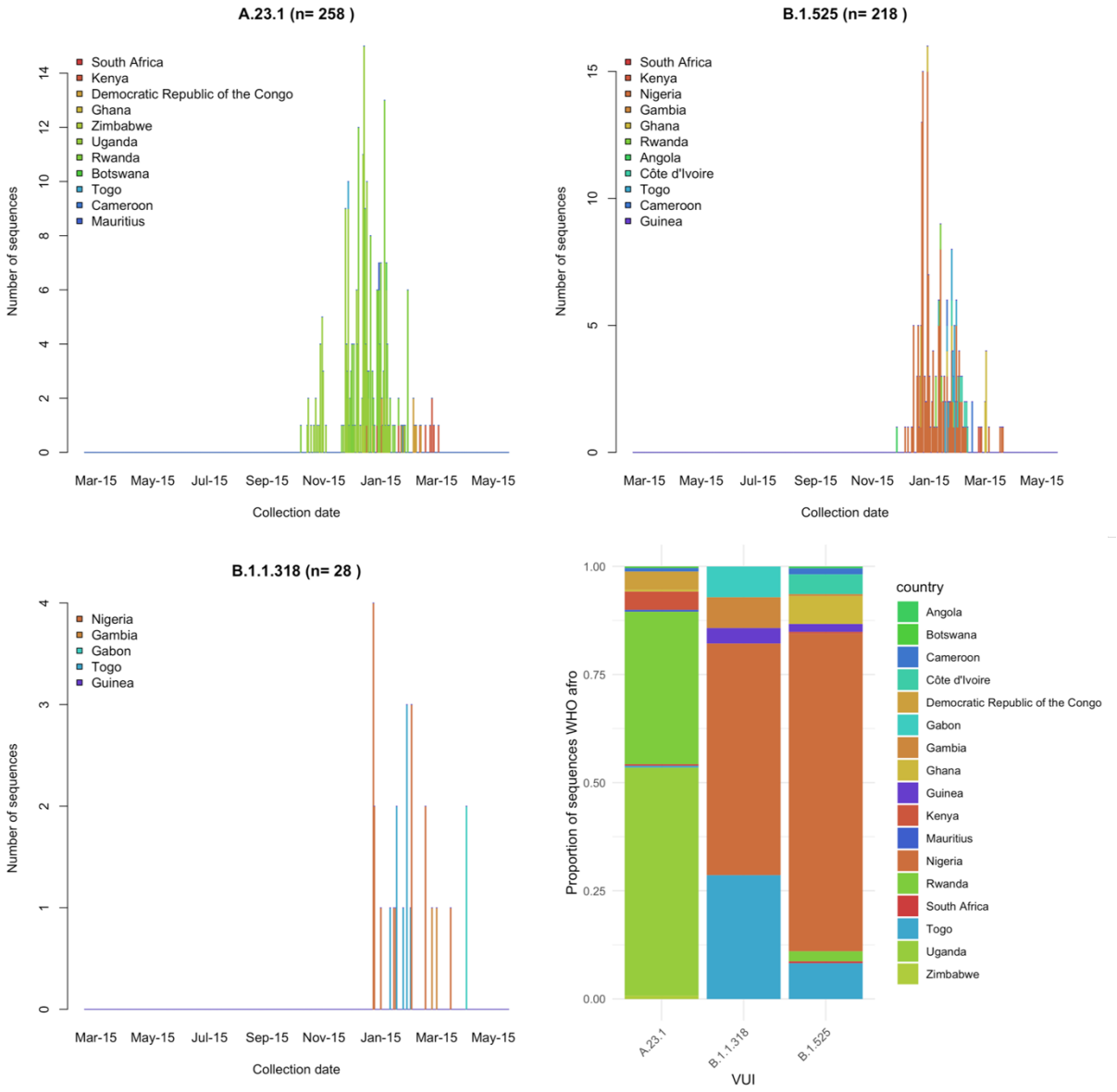


Figure 4 Proportion of VUI lineages in WHO AFRO countries and genomes available on GISAID by collection date. Colours for WHO AFRO countries are consistent with Figure 1.

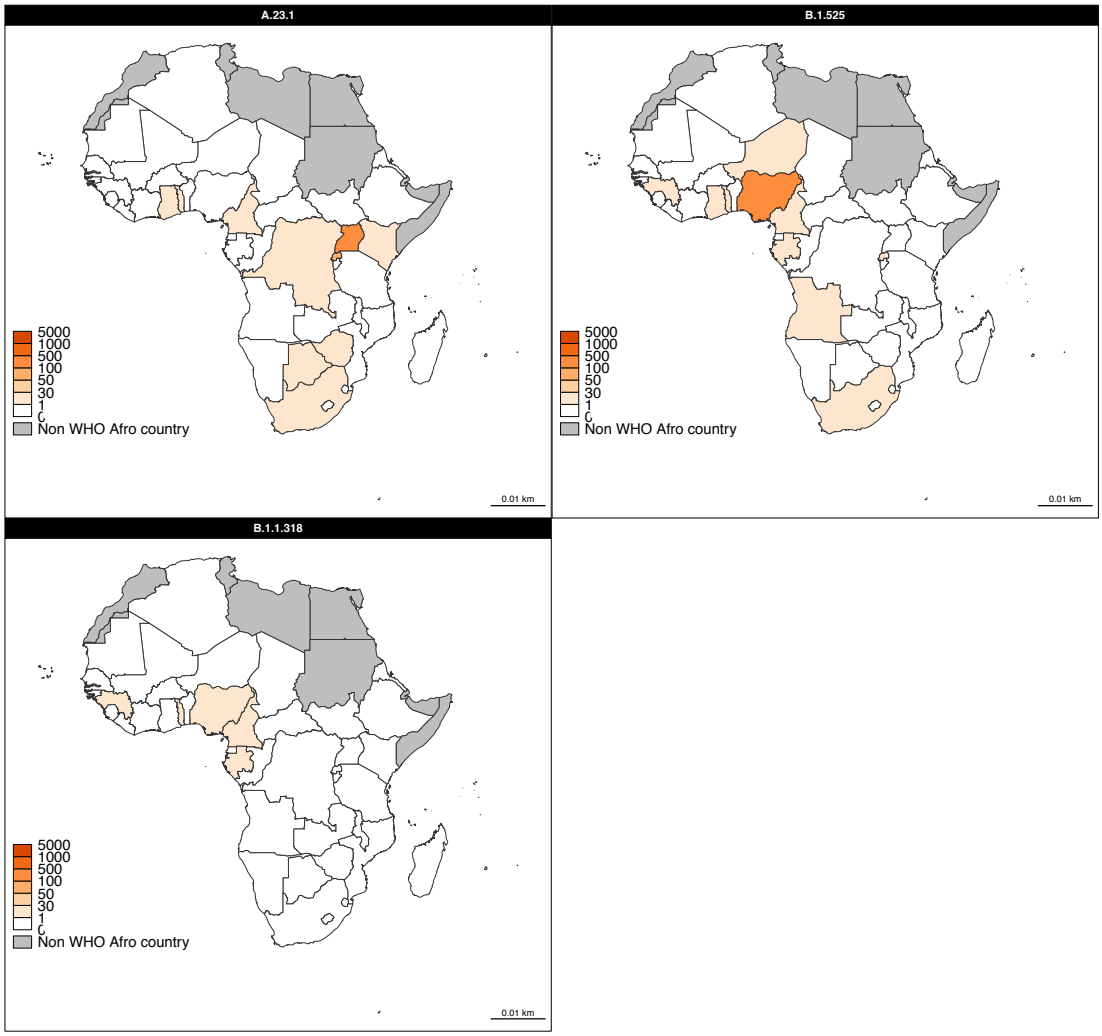


Figure 5 Map of VUI lineages in WHO AFRO countries

Appendix

Table S1 Number of sequences in each WHO AFRO country

country	SeqNum	pecent	B.1.1.7	B.1.351	B.1.525	A.23.1	B.1.617.2	B.1.1.318	B.1.429
South Africa	6255	46.82	33	2967	2	1	14	-	-
Kenya	856	6.41	72	61	-	11	-	-	-
Nigeria	767	5.74	139	-	190	-	-	23	-
Gambia	546	4.09	52	-	1	-	-	2	-
Democratic Republic of the Congo	545	4.08	11	14	-	12	6	-	-
Ghana	438	3.28	136	4	14	1	-	-	-
Senegal	415	3.11	18	-	-	-	-	-	-
Zimbabwe	401	3.00	-	195	-	2	-	-	-
Uganda	361	2.70	-	-	-	136	4	-	-
Rwanda	288	2.16	3	11	5	91	-	-	-
Zambia	221	1.65	-	31	-	-	-	-	-
Botswana	218	1.63	-	126	-	1	1	-	-
Cameroon	199	1.49	15	9	3	2	-	2	3
Equatorial Guinea	191	1.43	2	46	-	-	-	-	-
Angola	189	1.41	12	20	1	-	-	-	-
Gabon	180	1.35	30	3	1	-	-	10	-
Burkina Faso	161	1.21	1	-	-	-	-	-	-
Malawi	159	1.19	1	152	-	-	-	-	-
Mozambique	153	1.15	-	58	-	-	-	-	-
Côte d'Ivoire	145	1.09	15	1	10	-	-	-	-
Togo	124	0.93	20	1	23	1	-	8	-
Madagascar	122	0.91	-	17	-	-	-	-	-
Mauritius	76	0.57	1	3	-	1	-	-	-
Namibia	57	0.43	-	9	-	-	-	-	-
Guinea Bissau	48	0.36	32	1	-	-	-	-	-
Central African Republic	42	0.31	2	-	-	-	-	-	-
Guinea	40	0.30	12	-	5	-	-	1	-
Eswatini	33	0.25	-	29	-	-	-	-	-
Algeria	29	0.22	-	-	-	-	-	-	-
Mali	24	0.18	-	-	-	-	-	-	-
Ethiopia	19	0.14	3	-	-	-	-	-	-
Lesotho	18	0.13	-	14	-	-	-	-	-
Sierra Leone	15	0.11	-	-	-	-	-	-	-
Benin	12	0.09	-	-	-	-	-	-	-
Comoros	6	0.04	-	6	-	-	-	-	-
Niger	6	0.04	-	-	6	-	-	-	-

Table S2 1 Prevalence of Pango-lineages globally and within WHO AFRO countries

Pango.lineage	*SeqNum AFRO*	*Proportion AFRO (%)*	*SeqNum global*	*Proportion global (%)*	*SeqNum in recent4wk*	*Note*
B.1.351	3778	28.28	19838	1.15	75	VOC
B.1	1925	14.41	78000	4.54	12	
B.1.1	1060	7.93	47037	2.73	1	
B.1.1.7	610	4.57	732318	42.58	8	VOC
B.1.1.448	414	3.10	419	0.02	-	
C.1	345	2.58	354	0.02	-	
B.1.416	300	2.25	606	0.04	-	
B.1.1.54	283	2.12	302	0.02	-	
B.1.525	261	1.95	5180	0.30	-	VUI
A.23.1	259	1.94	1031	0.06	-	VUI
A	181	1.35	3239	0.19	-	
B.1.237	168	1.26	172	0.01	-	
C.16	141	1.06	814	0.05	-	
B.1.380	140	1.05	145	0.01	-	
B.1.1.273	139	1.04	139	0.01	-	
None	132	0.99	27702	1.61	-	
B.1.1.412	128	0.96	130	0.01	-	
B.1.192	109	0.82	110	0.01	-	
B.1.1.1	92	0.69	2501	0.15	-	
B.1.1.375	85	0.64	108	0.01	-	
A.19	82	0.61	91	0.01	-	
A.23	78	0.58	103	0.01	-	
B.1.381	78	0.58	78	0.00	-	
L.3	76	0.57	238	0.01	-	
B.1.1.420	73	0.55	732	0.04	-	
B.1.1.111	60	0.45	64	0.00	-	
B.1.1.34	58	0.43	68	0.00	-	
B.1.1.117	57	0.43	82	0.00	-	
B.1.1.466	57	0.43	57	0.00	-	
B.1.1.57	57	0.43	67	0.00	-	
A.21	56	0.42	242	0.01	-	
B.1.549	55	0.41	78	0.00	-	
B	54	0.40	5478	0.32	-	
B.1.214	53	0.40	82	0.00	-	
B.1.140	47	0.35	49	0.00	-	
B.1.1.318	46	0.34	1860	0.11	-	VUI
B.1.620	46	0.34	332	0.02	-	
B.1.1.52	45	0.34	57	0.00	-	
B.1.530	45	0.34	60	0.00	-	
B.1.214.2	43	0.32	1116	0.06	-	
AE.1	42	0.31	46	0.00	-	

B.1.1.487	42	0.31	141	0.01	-		
B.1.128	39	0.29	1281	0.07	-		
B.1.1.459	38	0.28	39	0.00	-		
C.2	38	0.28	49	0.00	-		
A.27	36	0.27	455	0.03	-		
B.1.8	35	0.26	672	0.04	-		
B.1.84	35	0.26	36	0.00	-		
B.1.1.404	34	0.25	49	0.00	-		
B.1.1.275	32	0.24	41	0.00	-		
B.1.393	31	0.23	200	0.01	-		
C.9	31	0.23	33	0.00	-		
N.8	30	0.22	30	0.00	-		
B.1.149	29	0.22	146	0.01	-		
B.1.1.40	28	0.21	28	0.00	-		
B.1.1.507	28	0.21	29	0.00	-		
B.1.1.53	28	0.21	31	0.00	-		
B.1.214.1	27	0.20	36	0.00	-		
B.1.1.254	26	0.19	87	0.01	-		
B.1.1.62	26	0.19	26	0.00	-		
B.1.462	26	0.19	34	0.00	-		
B.1.1.485	25	0.19	91	0.01	-		
B.1.1.56	25	0.19	26	0.00	-		
B.1.617.2	25	0.19	10467	0.61		18	VOC
B.1.619	24	0.18	637	0.04	-		
AE.5	23	0.17	25	0.00	-		
B.1.1.359	23	0.17	30	0.00	-		
A.25	22	0.16	40	0.00	-		
B.1.1.99	22	0.16	33	0.00	-		
B.1.1.306	21	0.16	1805	0.10	-		
B.1.160	21	0.16	22544	1.31	-		
B.1.417	21	0.16	22	0.00	-		
B.6	21	0.16	1071	0.06	-		
B.1.1.382	20	0.15	20	0.00	-		
B.1.1.456	18	0.13	19	0.00	-		
B.40	18	0.13	2945	0.17	-		
B.1.177	17	0.13	70493	4.10	-		
B.1.178	17	0.13	26	0.00	-		
B.1.2	17	0.13	85687	4.98	-		
R.1	17	0.13	5683	0.33	-		
A.18	16	0.12	17	0.00	-		
B.1.1.241	16	0.12	271	0.02	-		
B.1.1.383	15	0.11	16	0.00	-		
B.1.292	15	0.11	16	0.00	-		

B.1.1.242	14	0.10	23	0.00	-	
B.1.1.386	14	0.10	14	0.00	-	
B.1.356	14	0.10	533	0.03	-	
A.11	13	0.10	15	0.00	-	
AE.3	13	0.10	14	0.00	-	
B.1.544	13	0.10	130	0.01	-	
B.1.612	13	0.10	834	0.05	-	
B.1.1.10	12	0.09	803	0.05	-	
C.1.1	12	0.09	12	0.00	-	
B.1.1.372	11	0.08	1292	0.08	-	
B.1.1.84	11	0.08	11	0.00	-	
B.1.467	11	0.08	22	0.00	-	
B.4.7	10	0.07	105	0.01	-	
B.1.388	9	0.07	9	0.00	-	
B.1.480	9	0.07	304	0.02	-	
C.11	9	0.07	552	0.03	-	
B.1.596.1	8	0.06	34	0.00	-	
B.1.1.28	7	0.05	2883	0.17	-	
B.1.1.369	7	0.05	2235	0.13	-	
B.1.153	7	0.05	424	0.02	-	
B.1.258	7	0.05	12476	0.73	-	
B.1.6	7	0.05	55	0.00	-	
C.6	7	0.05	7	0.00	-	
B.1.1.27	6	0.04	166	0.01	-	
B.1.1.484	6	0.04	6	0.00	-	
B.1.336	6	0.04	315	0.02	-	
B.1.476	6	0.04	9	0.00	-	
B.1.610	6	0.04	1732	0.10	-	
A.12	5	0.04	6	0.00	-	
B.1.1.220	5	0.04	391	0.02	-	
B.1.1.444	5	0.04	5	0.00	-	
B.1.214.3	5	0.04	104	0.01	-	
B.1.36.10	5	0.04	991	0.06	-	
B.1.36.29	5	0.04	1144	0.07	-	
B.1.588	5	0.04	1125	0.07	-	
B.1.9.5	5	0.04	150	0.01	-	
C.8	5	0.04	197	0.01	-	
A.2	4	0.03	1502	0.09	-	
B.1.1.67	4	0.03	237	0.01		1
B.1.446	4	0.03	345	0.02	-	
B.1.482	4	0.03	9	0.00	-	
B.1.596	4	0.03	11147	0.65	-	
B.1.597	4	0.03	84	0.00	-	

B.1.1.166	3	0.02	55	0.00	-	
B.1.147	3	0.02	1196	0.07	-	
B.1.159	3	0.02	66	0.00	-	
B.1.22	3	0.02	804	0.05	-	
B.1.221	3	0.02	12759	0.74	-	
B.1.36	3	0.02	4669	0.27	-	
B.1.36.31	3	0.02	497	0.03	-	
B.1.429	3	0.02	29859	1.74	-	VOC
B.31	3	0.02	257	0.01	-	
B.39	3	0.02	409	0.02	-	
A.22	2	0.01	15	0.00	-	
A.9	2	0.01	96	0.01	-	
B.1.1.135	2	0.01	176	0.01	-	
B.1.1.270	2	0.01	99	0.01	-	
B.1.1.74	2	0.01	259	0.02	-	
B.1.177.4	2	0.01	4486	0.26	-	
B.1.177.52	2	0.01	521	0.03	-	
B.1.179	2	0.01	258	0.02	-	
B.1.240	2	0.01	3051	0.18	-	
B.1.273	2	0.01	20	0.00	-	
B.1.338	2	0.01	118	0.01	-	
B.1.378	2	0.01	124	0.01	-	
B.1.407	2	0.01	27	0.00	-	
B.1.450	2	0.01	84	0.00	-	
B.1.545	2	0.01	59	0.00	-	
B.1.577	2	0.01	1655	0.10	-	
B.1.601	2	0.01	30	0.00	-	
B.1.88.1	2	0.01	203	0.01	-	
B.1.9	2	0.01	160	0.01	-	
B.3	2	0.01	1158	0.07	-	
C.14	2	0.01	178	0.01	-	
C.2.1	2	0.01	125	0.01	-	
C.36	2	0.01	1420	0.08	-	
W.1	2	0.01	93	0.01	-	
A.1	1	0.01	3234	0.19	-	
B.1.1.101	1	0.01	97	0.01	-	
B.1.1.12	1	0.01	122	0.01	-	
B.1.1.134	1	0.01	99	0.01	-	
B.1.1.145	1	0.01	24	0.00	-	
B.1.1.161	1	0.01	267	0.02	-	
B.1.1.17	1	0.01	56	0.00	-	
B.1.1.171	1	0.01	236	0.01	-	
B.1.1.174	1	0.01	239	0.01	-	

B.1.1.186	1	0.01	250	0.01	-
B.1.1.194	1	0.01	176	0.01	-
B.1.1.200	1	0.01	134	0.01	-
B.1.1.213	1	0.01	48	0.00	-
B.1.1.25	1	0.01	1395	0.08	-
B.1.1.294	1	0.01	656	0.04	-
B.1.1.315	1	0.01	99	0.01	-
B.1.1.326	1	0.01	508	0.03	-
B.1.1.33	1	0.01	1944	0.11	-
B.1.1.344	1	0.01	80	0.00	-
B.1.1.349	1	0.01	58	0.00	-
B.1.1.37	1	0.01	4979	0.29	-
B.1.1.399	1	0.01	11	0.00	-
B.1.1.403	1	0.01	27	0.00	-
B.1.1.406	1	0.01	131	0.01	-
B.1.1.417	1	0.01	330	0.02	-
B.1.1.462	1	0.01	108	0.01	-
B.1.1.63	1	0.01	1960	0.11	-
B.1.1.70	1	0.01	2624	0.15	-
B.1.1.71	1	0.01	151	0.01	-
B.1.1.75	1	0.01	96	0.01	-
B.1.1.8	1	0.01	281	0.02	-
B.1.110.3	1	0.01	616	0.04	-
B.1.118	1	0.01	116	0.01	-
B.1.143	1	0.01	47	0.00	-
B.1.166	1	0.01	121	0.01	-
B.1.177.32	1	0.01	553	0.03	-
B.1.177.50	1	0.01	621	0.04	-
B.1.177.7	1	0.01	5891	0.34	-
B.1.177.81	1	0.01	4237	0.25	-
B.1.206	1	0.01	948	0.06	-
B.1.220	1	0.01	88	0.01	-
B.1.222	1	0.01	573	0.03	-
B.1.225	1	0.01	68	0.00	-
B.1.23	1	0.01	162	0.01	-
B.1.239	1	0.01	485	0.03	-
B.1.243	1	0.01	10382	0.60	-
B.1.258.20	1	0.01	57	0.00	-
B.1.265	1	0.01	615	0.04	-
B.1.274	1	0.01	83	0.00	-
B.1.277	1	0.01	32	0.00	-
B.1.279	1	0.01	1834	0.11	-
B.1.280	1	0.01	110	0.01	-

B.1.289	1	0.01	308	0.02	-	
B.1.311	1	0.01	2722	0.16	-	
B.1.313	1	0.01	135	0.01	-	
B.1.324	1	0.01	510	0.03	-	
B.1.326	1	0.01	62	0.00	-	
B.1.350	1	0.01	328	0.02	-	
B.1.355	1	0.01	78	0.00	-	
B.1.36.18	1	0.01	1740	0.10	-	
B.1.360	1	0.01	88	0.01	-	
B.1.361	1	0.01	665	0.04	-	
B.1.379	1	0.01	57	0.00	-	
B.1.391	1	0.01	854	0.05	-	
B.1.395	1	0.01	134	0.01	-	
B.1.398	1	0.01	285	0.02	-	
B.1.404	1	0.01	585	0.03	-	
B.1.416.1	1	0.01	540	0.03	-	
B.1.459	1	0.01	194	0.01	-	
B.1.466	1	0.01	37	0.00	-	
B.1.466.1	1	0.01	99	0.01	-	
B.1.471	1	0.01	345	0.02	-	
B.1.524	1	0.01	433	0.03	-	
B.1.535	1	0.01	35	0.00	-	
B.1.551	1	0.01	620	0.04		1
B.1.553	1	0.01	15	0.00	-	
B.1.558	1	0.01	175	0.01	-	
B.1.563	1	0.01	56	0.00	-	
B.1.564	1	0.01	1646	0.10	-	
B.1.575	1	0.01	2676	0.16	-	
B.1.580	1	0.01	74	0.00	-	
B.1.617.1	1	0.01	2622	0.15	-	
B.1.76	1	0.01	79	0.00	-	
B.1.78	1	0.01	76	0.00	-	
B.38	1	0.01	38	0.00	-	
B.4	1	0.01	401	0.02	-	
B.52	1	0.01	85	0.00	-	
B.61	1	0.01	163	0.01	-	

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