Title: Summary of COVID-19 virus variants in Ireland

This report summarises whole genome sequencing and epidemiological data for COVID-19 cases that have been sequenced in Ireland between week 41 2020 (4th October 2020) and week 8 2021 (27th February 2021).

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Introduction

All medical practitioners, including clinical directors of diagnostic laboratories, are required to notify the Medical Officer of Health (MOH)/Director of Public Health (DPH) of any confirmed, probable or possible cases of COVID-19 that they identify. Laboratory, clinical and epidemiological data, on notified COVID-19 cases, are recorded on Health Protection Surveillance Centre's (HPSC) Computerised Infectious Disease Reporting System (CIDR).

Whole genome sequencing (WGS) is carried out by the National Virus Reference Laboratory (NVRL) on a proportion of confirmed COVID-19 cases. NVRL use a sampling frame, developed by Prof. Phillip Nolan (chair of the NPHET Epidemiological Modelling Advisory Group), for selecting cases to sequence from community sources. Hospitals will be asked to refer a proportion of their samples, as decided by the National WGS Steering Group, from confirmed cases for sequencing so that variants that may cause more severe disease can be identified. Specimens from the sentinel GP Surveillance programme will also be sequenced. If sentinel GPs send less than 50 samples for testing in a given week, NVRL will sequence all of them. If more than 50 sentinel samples are referred, they will sequence a random selection based on a random selection tool.

This report summarises whole genome sequencing and epidemiological data for COVID-19 cases that have been sequenced in Ireland between week 41 2020 (4th October 2020) and week 8 2021 (27th February 2021). WGS sequencing data were provided by NVRL. Epidemiological data on these cases were extracted from CIDR on 11/03/2021. CIDR is a dynamic system and case details may be updated at any time. Therefore, the data described here may differ from previously reported data and data reported for the same time period in the future.

Overview

Table 1 shows whole genome sequencing results since week 51 2020 (week starting December 13th) by most likely mode of transmission. Cases of three variants of concern (VOC) have been identified in Ireland to date; UK VOC (B.1.1.7), South African VOC (B.1.351), Brazilian VOC (P.1). Four variants of interest have also been identified; P.2 (a different variant from Brazil), B.1.525 (variant from Nigeria) B.1.526 (variant from New York) and A.27.

The first case of the UK VOC (B.1.1.7) was identified in Ireland in week 51 2020 (figures 1 & 2). Transmission of this variant is now widespread in Ireland. Of cases sequenced in week 8 2021, 87% were found to be infected with the B.1.1.7 variant. See table 1, figure 1, figure 2 & table 2 for more details. The South African VOC (B.1.351) was first identified in Ireland in a case with a specimen date in week 52 2020 (week starting December 19th). A total of 21 COVID-19 cases have been confirmed to have been infected with this variant in Ireland to date. To date the Brazilian VOC (P.1) has been confirmed in seven cases of COVID-19. See table 1, figure 1, figure 2, table 3 & table 4 for more details.

Table 1. **Whole genome sequencing results for COVID-19 cases sampled from week 51 (December 13th 2020) to Week 8 (February 27th 2021)**

		Most likely mode of transmission*					
Virus variant	**Number of cases**	**Close contact with a confirmed case**	**Travel related***	**Community transmission**	**Healthcare setting acquired: staff**	**Healthcare setting acquired: patient**	**Under investigation**
Confirmed B.1.351 (South African variant)	**21**	**5**	**11**	**4**	**1**		
Probable B.1.351	6	1	5				
Possible B.1.351	1		1				
Confirmed P.1 (Brazilian variant)	**7**	**2**	**5**				
Probable P.1	**2**	**1**	**1**				
Possible P.1	2		2				
Confirmed B.1.1.7 (UK Variant)	**2148**	**1142**	**16**	**502**	**128**	**127**	**233**
Other variants of interest							
P.2	10	4	5	1			
B.1.525	8	5	2	1			
B.1.526	5	5					
A.27	2		2				
Other - not variants of concern or interest	624	245	11	115	65	85	103
Total	**2836**	**1410**	**61**	**623**	**194**	**212**	**336**

*travel related includes imported cases and those cases who acquired their infection from imported cases. **source of infection is not known for these two cases

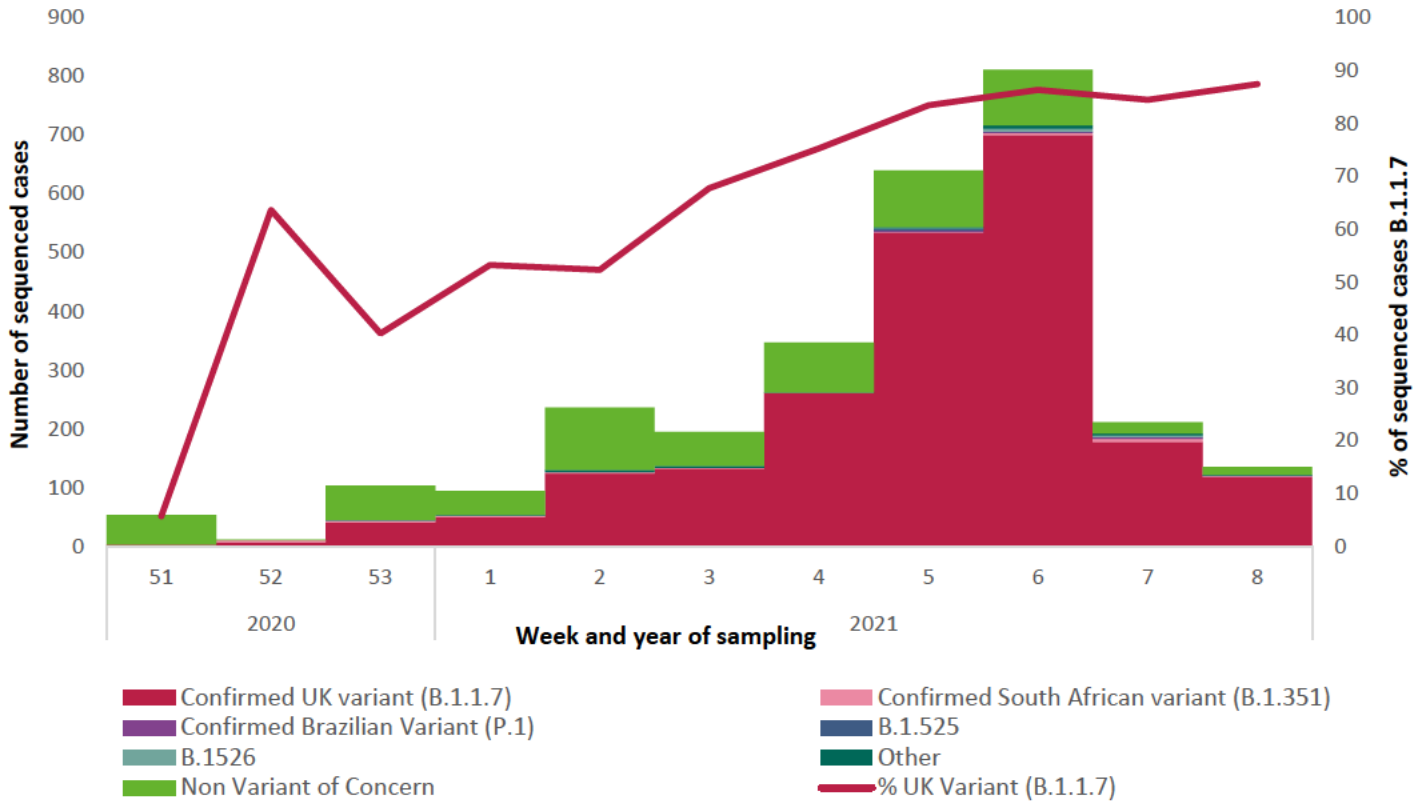

Figure 1. **Whole genome sequencing results and percentage of sequenced specimens* that were found to be the UK variant (B.1.1.7), specimen collection dates from week 51 (13th December 2020) to week 8 (27th February 2021)**

*The proportion of cases attributed to lineage B.1.1.7 is based on S gene target failure (SGTF) data from the Thermo Fisher TaqPath assay. To date, all those SGTF samples that have undergone WGS have been identified as lineage B.1.1.7. Other includes probable or possible variants of concern and other variants of interest.

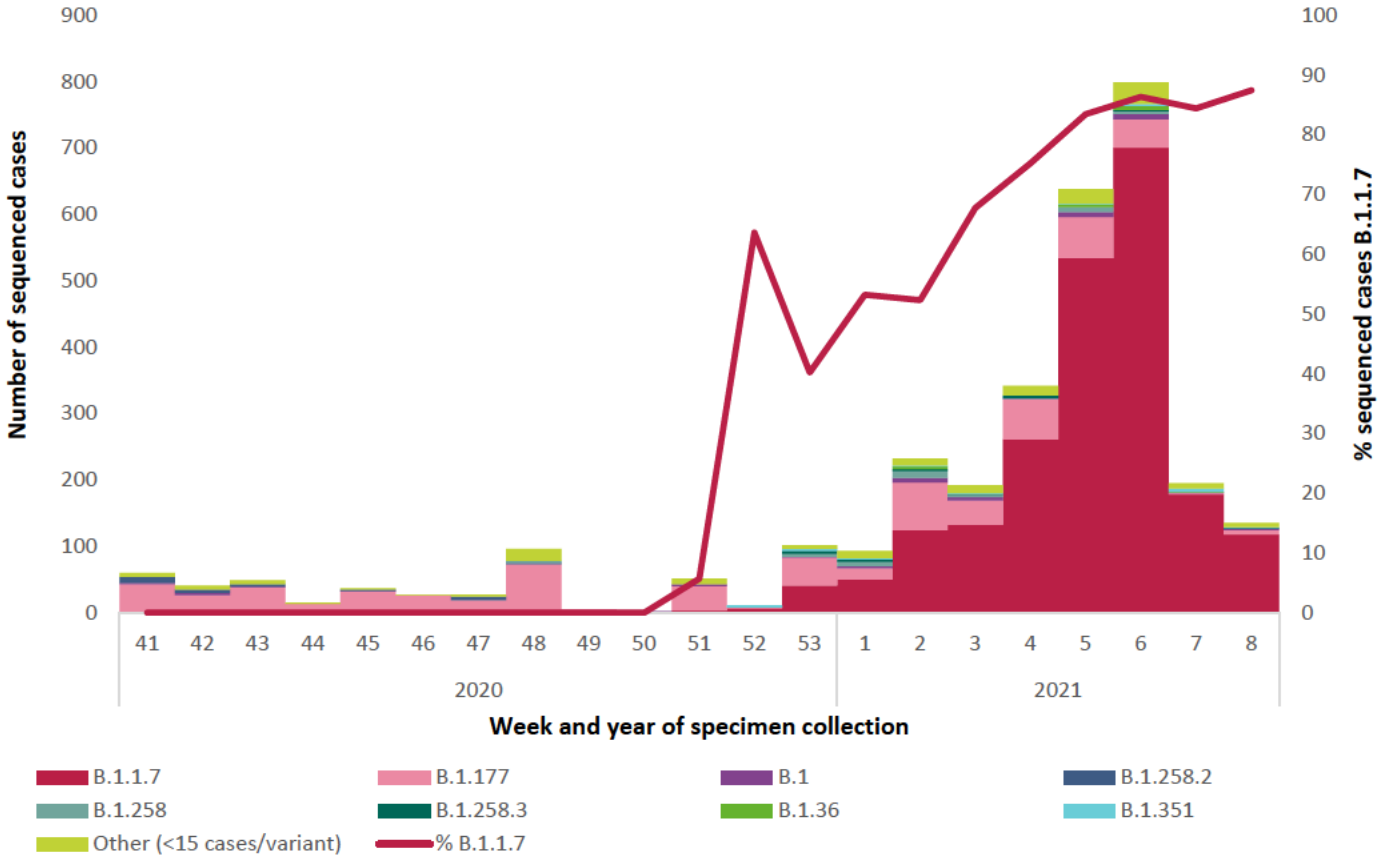

Figure 2. Whole genome sequencing results and percentage of sequenced specimens* that were found to be the UK variant (B.1.1.7), specimen collection dates from week 41 (Oct 4th 2020) to week 7 (27th February 2021)

*Variants with less than 15 cases in total during this time period are included in the 'Other' category. This includes P.1.

Comparison of B.1.1.7 (the UK variant) and Non variants of concern

The age profile of cases sequenced from week 51 to date and found to be have the UK variant (B.1.1.7) was slightly younger (median: 40 years, mean: 38 years) than those found not to be infected with variants of concern in the same time period (median: 44 years, mean: 43 years), but the overall age distributions were quite similar (table 2 & figure 3).

Hospital admission rates and case fatality ratios were slightly lower for cases with the B.1.1.7 variant compared to cases who were not infected with variants of concern. This varied slightly by age group, with a higher percentage of cases aged 45-64 years with the B.1.1.7 variant hospitalised compared to non-variants of concern and a slightly lower percentage of cases in the ≥65 years age group hospitalised (table 2). However, the number of cases who were hospitalised is very low and these differences were small and were not statistically significant.

The percentage of cases with the B.1.1.7 variant who were admitted to ICU was similar to that for cases who were not infected with variants of concern (table 2 & figure 4).

Table 2. Summary of sequenced cases infected with B.1.1.7 (UK variant) compared to non-variants of concern, specimen collection dates from week 51 (13th December 2020) to week 8 (27th February 2021)

	B.1.1.7 (UK Variant)		Non variants of concern	
Characteristic	**Num**	**%**	**Num**	**%**
Age group				
≤18 yrs	319	14.9	83	13.3
19-34 yrs	615	28.6	146	23.4
35-44 yrs	383	17.8	96	15.4
45-64 yrs	562	26.2	177	28.4
65-74 yrs	114	5.3	35	5.6
75-84 yrs	82	3.8	49	8
85+ yrs	70	3.3	31	5
Unknown	3	0.1	7	1
Sex				
Male	1027	48	284	46
Female	1117	52	331	53
Unknown	4	0	9	1
Clinical				
Hospitalised	**65**	**3.0**	**25**	**4.0**
<19 yrs	*0*	*0.0*	*0*	*0.0*
19-44 yrs	*14*	*1.4*	*3*	*1.2*
45-64 yrs	*19*	*3.4*	*4*	*2.3*
65+ yrs	*32*	*12.0*	*18*	*15.7*
Admitted to ICU	12	0.6	3	0.5
Died	24	1.1	15	2.4
CHO area				
[redacted]	[redacted]	[redacted]	[redacted]	[redacted]
[redacted]	[redacted]	[redacted]	[redacted]	[redacted]
[redacted]	[redacted]	[redacted]	[redacted]	[redacted]
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[redacted]	[redacted]	[redacted]	[redacted]	[redacted]
[redacted]	[redacted]	[redacted]	[redacted]	[redacted]
Unknown	49	2	21	3
Total	**2148**		**624**	

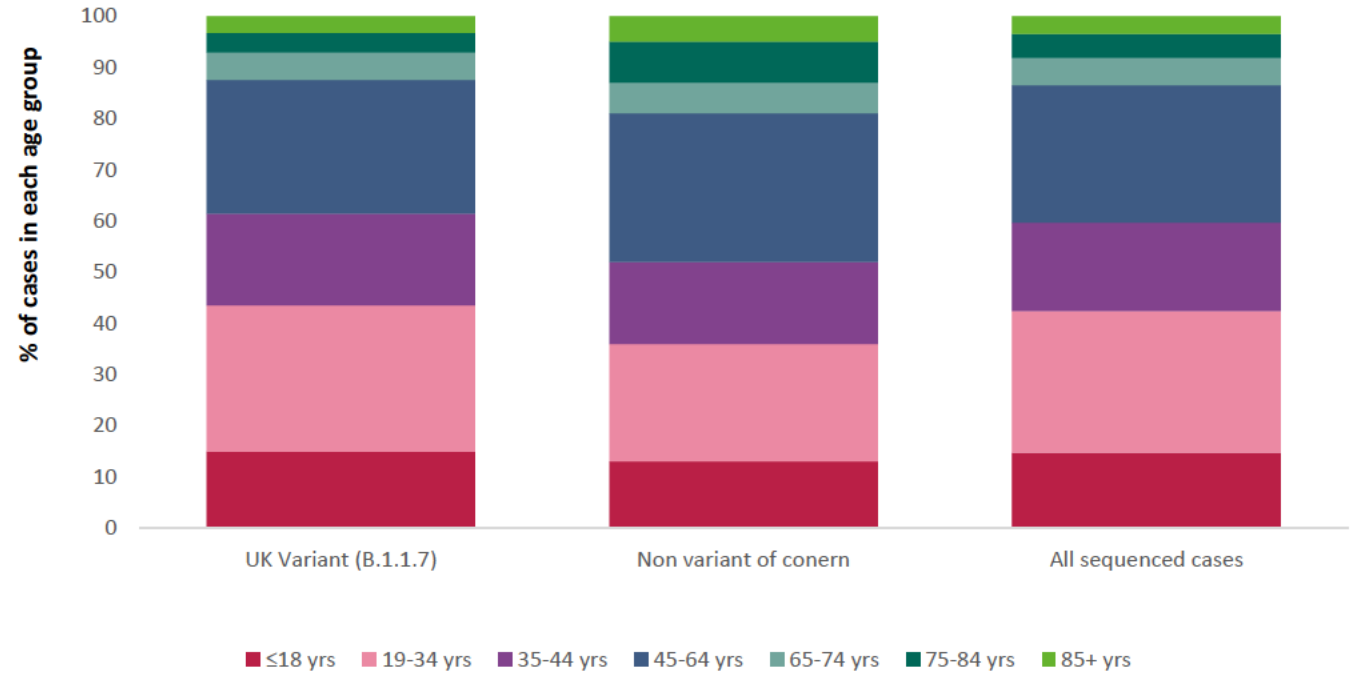

Figure 3. Age profile of sequenced specimens that were found to be the UK variant (B.1.1.7) compared to cases found not to be infected with variants of concern, specimen collection dates from week 51 (13th December 2020) to week 8 (27th February 2021)

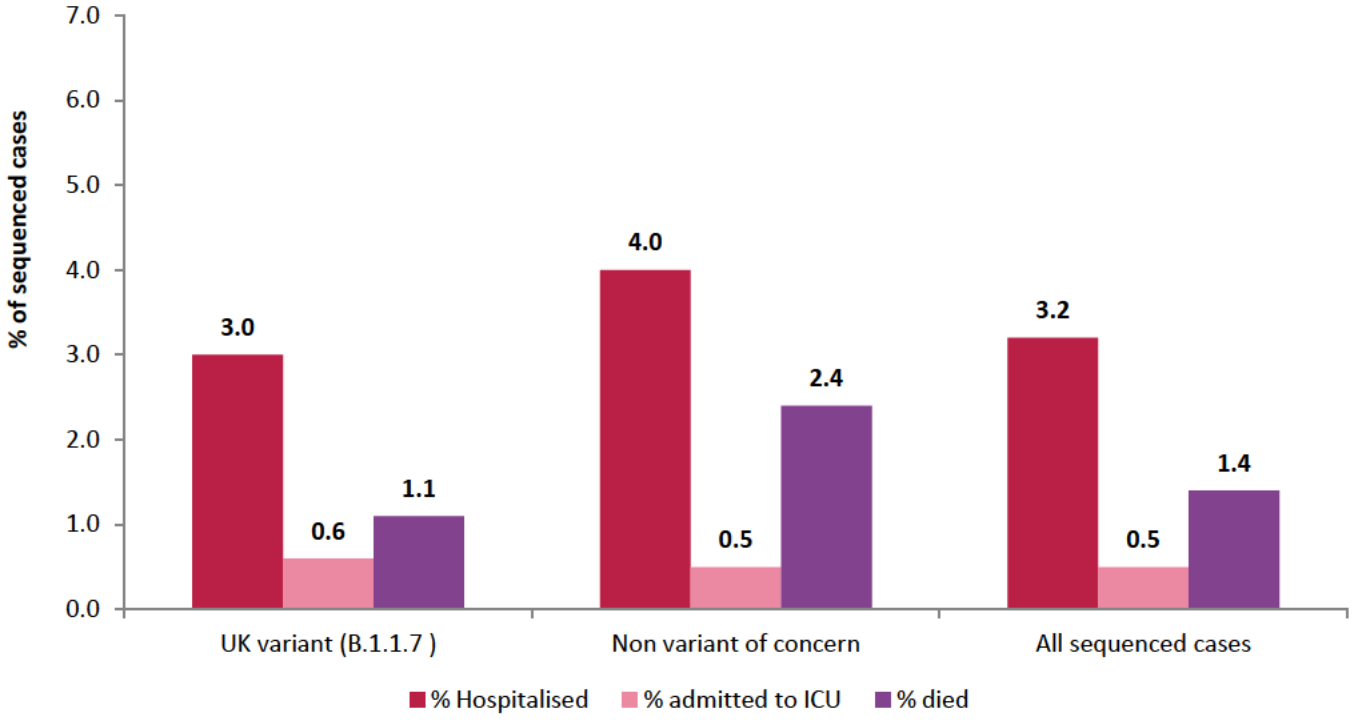

Figure 4. Percentage of sequenced cases hospitalised, admitted to ICU and who died, UK variant (B.1.1.7) compared to cases found not to be infected with variants of concern and all sequenced cases, specimens from week 51 (13th December 2020) to week 8 (27th February 2021)

Focus on the emerging variants of concern and variants of interest (excluding variant B.1.1.7)

The South African VOC (B.1.351) was first identified in Ireland in a case with a specimen date in week 52 2020 (week starting December 19th). A total of 21 COVID-19 cases have been confirmed to have been infected with this variant in Ireland to date. Of these, 11 were related to travel, five were contacts of a known cases, one was reported to be a healthcare worker who acquired the infection in a work setting and four cases are currently classified as community transmission. Seventeen of these cases are associated with twelve outbreaks, most of which are family clusters linked to travel. Four of the outbreaks have no further linked cases. No links have been identified between the remaining four cases (table 4). To date the Brazilian VOC (P.1) has been confirmed in seven cases of COVID-19. Five were part of two separate outbreaks involving families who had travelled from Brazil. The remaining two cases were reported to be contacts of confirmed cases, but are not currently linked to an outbreak on CIDR.

Table 3. Summary of sequenced cases infected with the B.1.351, P.1, B.1.525 and B.1.526 variants, specimen collection dates from week 51 (13th December 2020) to week 8 (27th February 2021)

	B.1.351 (South African variant)		P.1 (Brazilian variant)		B.1.525		B.1.526	
Characteristic	**Num**	**%**	**Num**	**%**	**Num**	**%**	**Num**	**%**
Age group								
≤18 yrs	1	5	1	14	2	25	5	100.0
19-34 yrs	6	28.6	4	57.1	4	50.0	0	0
35-44 yrs	3	14.3	0	0.0	1	12.5	0	0
45-64 yrs	9	42.9	2	28.6	1	12.5	0	0
65-74 yrs	1	4.8	0	0	0	0	0	0
75-84 yrs	1	5	0	0	0	0	0	0
85+ yrs	0	0	0	0	0	0	0	0
Unknown								
Sex								
Male	8	38	3	43	4	50	3	60
Female	13	62	4	57	4	50	2	40
Unknown	0	0	0	0	0	0	0	0
Clinical								
Hospitalised	2	10	0	0	0	0	0	0
Admitted to ICU	0	0	0	0	0	0	0	0
Died	0	0	0	0	0	0	0	0
CHO area								
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Unknown	0	0	0	0	0	0	0	0
Total	**21**		**7**		**8**		**5**	

Table 4. Description of cases infected with P.1 (Brazilian variant), B.1.351 (South African variant), P.1.526 and P.1.525, and summary of associated cases, from week 51 (13th December 2020) to week 8 (27th February 2021)

Outbreak Identifier	Outbreak location or mode of transmission	Total num cases linked to outbreak on CIDR	[redacted]	Whole genome sequencing results							
				Total num of cases with WGS results	B.1.351	Probable B.1.351	B.1.1.7	Non variant of concern	B.1.525	B.1.526	P.1
B.1.351 outbreak 1	HCW Residential institution, disability setting, no travel	**26**		**1**	**1**						
B.1.351 outbreak 2	Travel related	1		1	1						
B.1.351 outbreak 3	Travel related	3		1	1						
B.1.351 outbreak 4	Travel related - South Africa	3		3	3						
B.1.351 outbreak 5	Indirect travel link to Zambia	1		1	1						
B.1.351 outbreak 6	Private house	1		1	1						
B.1.351 outbreak 7	Travel related - South Africa	3		3	1	2					
B.1.351 outbreak 8	Travel related - Tanzania	2		2	2						
B.1.351 outbreak 9	Travel related	3		2	2						
B.1.351 outbreak 10	Travel related	1		1	1						
B.1.351 outbreak 11	Private house, no travel	4		4	2	1		1			
B.1.351 outbreak 12	Private house, no travel	4		2	1		1				
B.1.351. No outbreak. Case 1	Healthcare acquired: staff, no travel	0		1	1						
B.1.351. No outbreak. Case 2	Travel related	0		1	1						
B.1.351. No outbreak. Case 3	Community transmission	0		1	1						
B.1.351. No outbreak. Case 4	Close contact with known case	0		1	1						
B.1.525. Outbreak 1	Travel related - probably Nigeria	4		4					4		
B.1.525. Household cluster, OB not yet created on CIDR	Travel related - Brazil	0		3					3		
B.1.525. No outbreak. Case 1	Community transmission	0		1					1		
B.1.526. Outbreak 1	Contact with cases who had travelled from US	7		7				2		5	
P.1 Outbreak 1	Travel related - Brazil	3		3							3
P.1 Outbreak 2	Travel related - Brazil	2		2							2
P.1 No outbreak. Case 1	Close contact with confirmed case	0		1							1
P.1 No outbreak. Case 2	Close contact with confirmed case	0		1							1

National SARS-CoV-2 Surveillance & Whole Genome Sequencing Programme Steering Group

The National SARS-CoV-2 Surveillance & Whole Genome Sequencing Programme Steering Group was established in March 2021. The group is a multi-disciplinary expert group tasked with overseeing the design and development of a comprehensive and sustainable national WGS surveillance programme. The group has met on two occasions and draft terms of reference have been developed.

The group is currently working on the description of an appropriate frame work for sampling of cases. This includes agreement on the appropriate mix of samples for the 'routine (proactive) pathway' and also consideration of broad guidance regarding sequencing in outbreak situations and other components of the 'reactive pathway'.

Other areas of focus for the Steering Group include; liaising with the regional hospital laboratory network to consider integration of existing WGS capacity into the programme, establishing a process for incorporating previously sequenced cases into CIDR retrospectively, ensuring the efficient use of sequencing capacity to serve public health objectives.

The Steering Group currently meets on a weekly basis.