

Global epidemiological figures and an update on Variants of Concern: to inform a risk assessment of international travel

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1. Background

Nationally agreed processes have been established to manage travel into Ireland, including isolation advice, testing and contact management, where applicable, with the aim of reducing the importation of SARS-CoV-2 and variants of concern (VOC) and thereby protecting public health. An Expert Advisory Group on Travel (EAGT) has been established to provide advice to the Chief Medical Officer (CMO) with regards to the designation of states as “high risk” for the importation of variants of concern. The initial methodological approach and considerations of the EAGT, in informing the risk-based approach to travel-related recommendations, includes the identification of countries with:

1. A very high absolute incidence of COVID-19 cases (defined as a 14-day incidence rate $\geq 500/100,000$)
2. A high relative incidence (defined as a 14-day incidence greater than 2.5 times the 14-day incidence rate in Ireland)
3. variants of concern reported within the population, the levels of VOC circulating within the country and outbreaks related to VOC.

This report provides the latest international figures pertaining to these three criteria, as well as a brief summary of the global situation (as reported in the weekly WHO Variants of Concern meeting) and of the current situation in Ireland.

2. International COVID-19 incidence

14-day COVID-19 incidence of all countries with incidence over 500/100,000 in the 14 days to 04/04/2021:

Country	14-day notification rate as of 2021-04-04
Curaçao	2452.8
Bonaire, Saint Eustatius and Saba	1334.8
San Marino	1216.1
Hungary	1117.9
Uruguay	1029
Estonia	1007.3
Poland	988.8
Serbia	960.6
Jordan	928.3
Bermuda	915.3
Wallis and Futuna	907
Andorra	900.5
Montenegro	853.4
Aruba	825.2
Czechia	808.7
France	801.9
Bahrain	754.3
Sweden	739.2
Bulgaria	713.2
North Macedonia	710.7

Bosnia and Herzegovina	674.9
Slovenia	673.1
Kosovo	638.8
Cyprus	618.8
Isle of Man	611.5
Lebanon	585.1
Netherlands	571.7
Turkey	569.9
Palestine	555.2
Croatia	551.4
Belgium	550.6
Seychelles	504.4

Table 1. Countries with 14-day incidence over 500/100,000 (source: https://covid19-country-overviews.ecdc.europa.eu/#2_Global [Accessed 13/04/2021])

Additional countries with 14-day incidence >2.5 times that of Ireland (152.1/100,000 on 04/04/2021):

Country	14-day notification rate as of 2021-04-04
Moldova	497.1
Chile	494.4
Austria	491.5
Italy	489.4
Monaco	471.5
Luxembourg	470.2
Ukraine	461
Brazil	454.5
Puerto Rico	440.5
Armenia	435.1
Kuwait	423.1
Romania	399
Maldives	395.5
Lithuania	389.1

Table 2. Countries with 14-day incidence of below 500/100,000 and above 380/100,000 (2.5 times Ireland's 14-day incidence) (source: https://covid19-country-overviews.ecdc.europa.eu/#2_Global [Accessed 13/04/2021])

3. Variants of concern and variants of interest

3.1 Definitions

On 25th February 2021, WHO issued working definitions of variants of interest (VOI) and VOC as follows:

Working Definition of “SARS-CoV-2 Variant of Interest”

A SARS-CoV-2 isolate is a variant of interest (VOI) if it is phenotypically changed compared to a reference isolate or has a genome with mutations that lead to amino acid changes associated with established or suspected phenotypic implications;

AND

has been identified to cause community transmission/multiple COVID-19 cases/clusters, or has been detected in multiple countries;

OR

is otherwise assessed to be a VOI by WHO in consultation with the WHO SARS-CoV-2 Virus Evolution Working Group.

WHO Working Definition of “SARS-CoV-2 Variant of Concern”

A variant of interest is a variant of concern (VOC) if, through a comparative assessment, it has been demonstrated to be associated with

- Increase in transmissibility or detrimental change in COVID-19 epidemiology;
- Increase in virulence or change in clinical disease presentation; or
- Decrease in effectiveness of public health and social measures or available diagnostics, vaccines, therapeutics.

OR

assessed to be a VOC by WHO in consultation with the WHO SARS-CoV-2 Virus Evolution Working Group.

WHO recognises that their definitions are focused on global risk and that countries may designate variants of local concern.

Ireland currently has three designated variants of concern:

- B.1.1.7
- B.1.351
- P.1

Over 95% of all Sars-CoV-2 cases in Ireland are now caused by the B.1.1.7 variant.

Many other “variants of interest”, containing mutations of concern, are being monitored globally. These include:

- B.1.525
- P.3
- B.1.427
- B.1.429
- B.1.526 (predominantly confined to the USA)

3.2 Limitations of global data

The identification and understanding of the extent to which a VOC is established in a country is strictly linked to the area's capacity to identify VOCs. This capacity is dictated by the availability of whole genome sequencing technology in each country. Lower income countries may lack the resources to perform whole genome sequencing, or may rely on facilities in neighbouring countries in order to sequence a low number of samples of interest.

The reporting of data is also reliant on the voluntary submission of sequence data to international open-access data-sharing platforms, such as GISAID. There is a wide variation in the number of sequences submitted by each country, globally. Not all samples sequenced in each country are submitted to GISAID and so the figures reported are determined by which sequences are chosen for submission.

The context in which samples are sequenced in each country also influences the proportion of each Sars-CoV-2 variant reported. Countries in which a random sample of sequences are selected nationwide will provide the most accurate description of the situation, with regards to circulating variants. Countries in which sequencing capacity is limited may restrict resources to the investigation of cases and outbreaks of concern, thus introducing bias into the reporting of the prevalence of each variant.

Nationwide figures may also mask regional variation and it is difficult to appreciate the presence of local clusters or events of concern from data presented by organisations such as the ECDC and WHO, or by platforms such as GISAID. We are therefore heavily reliant on information countries are willing and able to verbally share in global fora, such as the weekly WHO meeting on Sars-CoV-2 variants of concern reports (see section 4). Only a small number of countries are represented at such meetings.

As a result of countries not having the resources or capacity to perform whole genome sequencing, of not sharing data on open-access platforms and of not presenting situational reports at global meetings, there is a paucity of data and knowledge regarding the circulation of VOCs in many countries, which makes a methodological risk assessment very difficult.

Table 3 presents the number of B.1.351 cases reported via the media or the EWRS and the number of sequences submitted to GISAID to 7th April 2021

Country	Total cases reported in media or via IHR/EWRS	Confirmed sequences in GISAID	Cases imported or evidence of local community transmission
Aruba	2	2	Unknown
Angola	7	6	Imported cases
Australia	22	38	Imported cases
Austria	496	167	Community transmission
Bangladesh	1	16	Unknown
Belgium	505	641	Unknown
Botswana	1	24	Unknown
Brazil	1	1	Unknown
Brunei	1	1	Imported cases
Cameroon		1	Unknown
Eswatini		19	
Canada	337	38	Community transmission
China	1		Imported cases
Costa Rica	2	2	Imported cases
Croatia	2	5	
Cuba	1		Imported cases
Czech Republic	20	7	Imported cases
Democratic Republic of the Congo		1	
Denmark	52	12	Unknown
Estonia	16	3	
Finland	225	5	Unknown
France	341	538	Unknown
Gambia	1		Unknown
Germany	2788	512	Unknown
Ghana	1		Unknown

Greece	59		Unknown
Guinea Bissau	1		
Guadeloupe	1	1	Imported cases
Ireland	32	34	Unknown
India	47	13	Unknown
Israel	450	64	Unknown
Italy	37	34	Imported cases
Japan	25	20	Unknown
Kenya	6	35	Unknown
La Reunion	96	18	
Lesotho		15	
Malaysia	9	9	
Luxembourg	299	180	Unknown
Malawi	1	147	Unknown
Malta	1		
Mauritius	3	2	Imported cases
Mayotte	78	369	Unknown
Mozambique	19	56	Unknown
Netherlands	189	333	Unknown
New Zealand	10	23	Local transmission
Oman	6		Unknown
Norway	136	188	Imported cases
Panama	1	1	Imported cases
Portugal	49	48	Unknown
Occupied Palestinian Territories	57		Unknown
Poland	9	10	Unknown
Philippines	163		Unknown
Russia	10	3	
Romania	2	1	Unknown
Qatar	2		Unknown
Slovenia	2	25	
Slovakia	7	7	Unknown
Zimbabwe		202	Unknown
Singapore		71	

South Africa		1411	Community
Uganda	2		Unknown
South Korea	42	5	Unknown
Spain	72	21	Unknown
Sweden	422	295	Imported cases
Switzerland	241	104	Unknown
Taiwan	1		Imported cases
Thailand	3	6	
Turkey	169	50	Unknown
UAE		5	
USA	386	248	Community transmission
Vietnam	1		Imported cases
Zambia	22	31	Unknown
Rwanda	10	11	
United Kingdom		544	
Lithuania	2	3	
Liechtenstein	1		Unknown
Latvia	1		Unknown
Monaco		1	
Namibia	16	9	Unknown
Comoros		6	Unknown
Hong Kong	93		Unknown
Total	8114	6154	

Table 3. the number of B.1.351 cases reported via the media or the EWRS and the number of sequences submitted to GISAID to 7th April 2021 (source: UK Variants and Mutations Taskforce presentation slides 12/04/2021)

Table 4 presents the number of P.1 cases reported via the media or the EWRS and the number of sequences submitted to GISAID to 7th April 2021

Country	Total cases reported in media or via IHR/EWRS	Confirmed sequences in GISAID	Cases imported or evidence of local/community transmission
Brazil	1530	455	Community transmission
Australia	1	4	
Argentina	11		Community transmission
Belgium	156	216	Unknown
Canada	1000	150	Unknown
Colombia	15	25	Unknown
Denmark	12		Unknown
Venezuela	10		Unknown
Faroe Islands	1	1	Imported case
Finland	1		Unknown
France	3	37	
French Guiana		8	
Germany	130	48	Imported cases
India	2		
Ireland	12	12	Imported cases
Italy	62	335	Unknown
Japan	42	25	Imported cases
Uruguay	24		Unknown
Reunion	1		
Luxembourg	3	3	
Mexico	3	5	
Netherlands	30	54	Unknown
Portugal	22	22	Unknown
Peru		24	Unknown
Romania	2	2	Unknown
New Zealand		4	
South Korea	8	1	Unknown
Spain	32	19	Imported case
Sweden	48	14	Unknown

Sint Maarten		1	
Switzerland	13	28	
Taiwan	3		Imported cases
Turkey	4	3	Unknown
Slovenia		1	
Philippines	1		
USA	356	233	Community transmission
Hong Kong	5		Unknown
Dominican Republic	1		Unknown
Vietnam	1		Unknown
Croatia	1		Unknown
Aruba	3	1	Unknown
United Kingdom		36	
Norway	3	1	Unknown
Total	3552	1768	

Table 4. The number of P.1 cases reported via the media or the EWRS and the number of sequences submitted to GISAID to 7th April 2021 (source: UK Variants and Mutations Taskforce presentation slides 12/04/2021)

4. Notes from weekly WHO meeting on variants of concern, 8th April 2021

The World Health Organisation hosts a weekly virtual meeting, to which all countries are invited to give a short account of their up-to-date VOC figures and any other relevant information. Due to the timing of the meeting, nearly all attendees represent European countries (with Israel and South Africa). Some countries present their data on slides.

Country summary

UK:

- B.1.1.7 98-99% of cases
- B.1.351 <0.5% of cases. Some growth in some regions
- B.1.525 Some concerns re recent increases, however prevalence appears to have stabilised
- B.1.1.7 with E484K Regular sporadic cases but no significant/sustained spread

Finland:

Whole genome sequencing (WGS) **10%** of all positive samples:

Increasing prevalence of B.1.351 in the capital region

B.1.525 31 cases (mainly in clusters)

B.1.1.318 17 cases (mainly in clusters)

Surveillance of CoV2 variants in Finland

Week	Number of laboratory confirmed cases	Number of sequenced samples	% of cases with defined virus lineage	% of B.1.1.7 among sequenced samples*	% of B.1.351 among sequenced samples*
2021-W01	1811	205	11.3	15.1	4.9
2021-W02	1753	274	15.6	30.3	0.4
2021-W03	2354	498	21.2	33.3	0.6
2021-W04	2717	591	21.8	37.1	1.2
2021-W05	2603	873	33.5	53.4	3.1
2021-W06	2410	1043	43.3	55.5	4.1
2021-W07	3529	846	24.0	51.2	5.1
2021-W08	3870	450	11.6	46.0	5.6
2021-W09	4447	527	11.9	58.4	5.7
2021-W10	4851	462	9.5	68.4	13.9
2021-W11	4650	196	4.2	48.5	11.2
2021-W12	4128	67	1.6	34.3	20.9
2021-W13	3159	26	0.8	7.7	3.8

* Doesn't reflect the true prevalence of variants since sampling is partially directed

Germany:

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SARS-CoV-2 VOC: sequencing data - random samples * Sequencing of RT-PCR+ve samples (week 12)

Week	B.1.1.7		B.1.351		P.1		Total sequences
	number	%	Number	%	number	%	number
09	1.872	52.7%	65	1,9%	7	0,2%	1.944
10	2.234	64.3%	66	1.9%	2	0.1%	2.302
11	2.299	72.8%	33	1.0%	5	0.2%	2.337
12	1.015	75.7%	25	1.9	0	0	1.040

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VOI/VUM detection by whole genome sequencing weeks 1 - 12 (global data set)

KW 2021	A.23.1	A.27	B.1.1.318	B.1.427	B.1.429	B.1.525	B.1.526	P.2
08	6	93	4	0	0	21	0	0
09	4	53	17	1	3	42	0	0
10	1	76	20	0	1	37	0	0
11	0	64	9	0	0	58	0	0
12	0	29	27	0	0	51	0	0

A.27: changes in Spike: L18F, **L452R**, **N501Y**, A653V, H655Y, D796Y, G1219V
 B.1.525: changes in Spike: Q52R, **E484K**, Q677H, F888L
 B.1.1.318: changes in Spike: T95I, Y144del, **E484K**, P681H, D796H

B.1.1.7 with E484K 48 cases last week

A27; B.1.1.318; B.1.525 all "holding on" in the presence of B.1.1.7

Austria:

Nationwide:

B.1.1.7 68.6% of cases

B.1.351 0.1% of cases

B.1.1.7 with E484K 1.5% of cases

Tyrol:

B.1.351 14 active cases remain

B.1.1.7 with E484K Numbers decreasing

Infections in vaccinated people in Schwarz region:

-16 cases following AstraZeneca vaccine

-“Higher number” following Pfizer vaccine

Israel:

Incidence markedly decreased; now around 300 per day

10m vaccine doses given (population is 10m) – 63% of eligible population vaccinated

Vaccines appear to have 95% efficacy vs B.1.1.7

B.1.1.7 99% of all cases

Rare cases of vaccine escape noted

France:

Incidence, hospitalisations, ICU admissions and deaths all increasing

Prescreening results:

B.1.1.7 82% of cases

B.1.351 or P1 4.2% of cases. Steady

B.1.616 Full WGS of 25 samples (22 in Brittany – 2 hospital clusters and 1 community)

16 cases positive on PCR (12 of these only from lower respiratory tract samples; their NP swabs were negative)

B.1.1.7 with E484K 9 cases

B.1.525 Some additional cases seen this week

Netherlands:

B.1.1.7 approx. 90% of cases

B.1.351 3-4% of cases

P1 1-2%. Prevalence increasing. Some clusters in migrant workers from Poland

Denmark:

WGS over 80% of all cases

B.1.1.7	approx. 90% of cases
B.1.351	59 cases
P1	12 cases (only 3 linked to travel)
B.1.525	Rising numbers
B.1.1.7 with E484K	3 cases
B.1.1.7 with E484G	1 case

Luxembourg:

Sequencing 33% of all cases

B.1.1.7	61% of cases
B.1.351	23% of cases. 1 outbreak in a NH, where all were 2 weeks post-second dose of Pfizer vaccine

5. Variant of Concern COVID-19 cases in Ireland

5.1 Overview

In Ireland, there are two general laboratory techniques used in order to further investigate positive Sars-CoV-2 samples for the presence of VOCs.

1 PCR assays involve the detection of specific mutations and may indicate that the virus is a “probable B.1.351”, “probable P.1” or “probable VOC (either B.1.351 or P.1”, depending on the assay used. These tests can be performed rapidly, with a turn-around time of approximately 2-3 days, and allow a rapid enhanced Public Health response to commence.

All samples identified as requiring further investigation for the presence of a VOC are initially tested via PCR assay. Some laboratories also routinely perform a PCR assay test on all Sars-CoV-2 positive samples.

2 Partial or whole genome sequencing allows a definitive lineage to be assigned and may confirm (or refute) the presence of a VOC. These tests can only be performed reliably on samples with a PCR cycle time below 25. All samples identified as “probable B.1.351/P.1/VOC” are progressed to sequencing, however many do not return results, due to a high CT. For this reason, many samples remain as “probable VOCs”, without having a definitive lineage assigned. Nevertheless, enhanced Public Health measures and investigation will have been implemented upon notification of a “probable” result and so all efforts to trace and contain transmission will have been taken.

Whole genome sequencing is also performed on a stratified national sample of positive Sars-CoV-2 results, for the purposes of surveillance. All confirmed VOCs are notified to regional Departments of Public Health and appropriate action taken. The turn-around time for these results is currently approximately 22 days, and so the opportunity to implement enhanced Public Health measures, beyond those routinely implemented for all COVID-19 cases, is limited, however source investigation may highlight clusters requiring an escalated Public Health response.

5.2 Current situation in Ireland

(Based on NVRL and Eurofins-Biomnis results up to 13th April 2021)

Confirmed cases of Brazilian P1 (new in the last week):	22 (10)
Probable P1 cases (new in the last week):	6 (0)
Confirmed B.1.351 cases (new in the last week):	46 (14)
Probable B.1.351 cases (new in the last week):	6 (0)
“Probable VOC” (either B.1.351 or P1) (new):	37 (14)
Other variants of note (new in the last week):	
Confirmed B.1.525 cases:	16 (1)
Confirmed B.1.526 cases:	5 (0)
Confirmed P.2 cases:	14 (0)
Confirmed B.1.1.7 with E484K mutation:	2 (1)

Links to international travel

Variant	Case is traveller	Case is contact of traveller	No travel link detected	Unknown Source
Confirmed P1	Brazil = 9	Brazil = 2	1	10
Probable P1	Brazil = 5	Brazil = 1	0	0
Confirmed B.1.351	South Africa = 6	South Africa = 3	21	9
	Zambia = 1	Zambia = 1		
	Tanzania = 2	Bangladesh = 2		
	Bangladesh = 1			
Probable B.1.351	South Africa = 5	0	1	0
“Probable VOC” (either B.1.351 or P1)	India = 1	Brazil = 2	8	13
	Brazil = 8			
	South Africa = 2			
	UAE = 1			
	Tanzania = 1			
	Pakistan = 1			

Table 5. Links to recent international travel for each VOC case (information obtained from communication with regional Departments of Public Health, CIDR and CRM)

Cases that are currently under investigation for any link to recent international travel populate the “unknown” column. Cases designated as “probable VOCs” are not recorded as such on CIDR and data must be collated from Depts Public Health, making an investigation into their links to travel very challenging.

5.3 Outbreak report

The information in this section is based on notification data submitted to CIDR, extracted on 12/04/2021 for samples to 03/04/2021, and may not tally with the VOC figures presented above, due to a slight time delay in notification. It must be noted that “probable VOCs” are not notified as VOCs on CIDR and are only recorded as an outbreak if they are linked to one or more “confirmed” VOC.

B.1.351 VOC

Currently, twelve outbreaks (Table 5) have been reported that have more than one B.1.351 associated case. Forty-four confirmed COVID-19 cases were collectively linked to these outbreaks. Sequencing results were available for 33 (of 44), 28 of whom were infected with the B.1.351 variant. Four of the outbreaks were small family clusters associated with travel but no travel associations were identified for the remaining eight outbreaks, most of which were in family/private house settings (table 5).

Of the 18 cases identified as infected with the B.1.351 variant and not currently linked to outbreaks on CIDR, five had recently travelled (Qatar, Bangladesh, country of travel not reported for three), two were contacts of cases who had recently travelled (Zambia, country of travel not reported), five were reported to be contacts of confirmed cases and the remaining six were reported to be community acquired.

P.1 VOC

Nine P1 cases are part of four separate outbreaks (Table 5) involving families/household contacts with a history of travel from Brazil (8 of the cases had travelled and one was a contact of a case who had travelled). Three additional cases were associated with an outbreak in a meat processing plant. The most likely modes of transmission for these three cases are currently reported as “under investigation”, “community transmission” and “close contact of a confirmed case”.

Five further cases are reported to be contacts of confirmed cases. One is linked to an outbreak on CIDR, but is the only linked case and the remaining four cases are not yet linked to outbreaks on CIDR.

Of the remaining two cases, one had recently travelled to Ireland from Brazil and one was linked to a travel-associated case but the country of travel was not reported (Table 5).

Table 5. Description of outbreaks with more than one linked case and at least one case identified as infected with the P.1 (Brazilian variant) and B.1.351 (South African variant), and summary of associated cases, from week 51 (December 13th 2020) to week 13 (April 3rd 2021)

Outbreak Identifier	Outbreak location or mode of transmission	Total number of cases linked to outbreak on CIDR	Whole genome sequencing results					
			Total number of cases with WGS results	B.1.351	Probable B.1.351	B.1.1.7	P.1	Non variant of concern
B.1.351 outbreak 1	Travel related - South Africa	3	2	2				
B.1.351 outbreak 2	Travel related - indirect - South Africa	3	3	3				
B.1.351 outbreak 3	Private house, linked to larger outbreak in residential institution-disability setting, no travel	6	6	6				
B.1.351 outbreak 4	Travel related - South Africa	3	3	1	2			
B.1.351 outbreak 5	Private house, no travel (community, contacts of case)	4	4	2	1			1
B.1.351 outbreak 6	Travel related - Tanzania	2	2	2				
B.1.351 outbreak 7	Private house, no travel (contacts of case)	4	2	1		1		
B.1.351 outbreak 8	Two families, no travel - link to outbreak 9	7	4	4				
B.1.351 outbreak 9	Private house, no travel (community, contacts of case)	4	4	4				
B.1.351 outbreak 10	Private house, no travel (contacts of case)	2	1	1				
B.1.351 outbreak 11	Private house, no travel (community, contacts of case)	4	1	1				
B.1.351 outbreak 12	Private house, no travel (community, contacts of case)	2	1	1				
P.1 Outbreak 1	Travel related - Brazil	3	3				3	
P.1 Outbreak 2	Travel related - Brazil	2	2				2	
P.1 Outbreak 3	Travel related - Brazil	3	3				3	
P.1 Outbreak 4	Travel related - Brazil	3	1				1	
P.1 Outbreak 5	Meat processing plant - no travel	3	3				3	

Note: Travel related cases include imported cases and those cases who acquired their infection from imported cases.

5.4 Regional information

South East:

Two confirmed B.1.351 cases and one “Probable VOC” are associated with an outbreak in a Direct Provision Centre. Mass testing was conducted, with 28 cases reported to the 31st March 2021.

Three P1 cases work at a meat plant in Cahir, where there is an outbreak with 7 COVID-19 cases in total. Sequencing was not possible for the other 4 cases.

CHO7:

Of five P1 cases with links to CHO7, all occurred in Brazilian nationals. Four cases cluster together (2 are from a flight that arrived on 26th Jan; 1 is a close contact of one of these travellers and the 4th lives in the same building as case 3). Phylogenetic analysis indicates that the fifth case, notified on 8th April, is not related to the others – the likely source is a worker at a food processing plant (where a previous outbreak has occurred).

Following the detection of these P1 cases, samples from all cases with Brazilian names resident in [REDACTED] dating back to 1st February, were referred for further investigation by PCR assay – no new VOCs were reported

All positive samples from workers at the food processing plants and four other workplaces, 2 DPCs and 1 school have also been referred for further investigation, both retrospectively and prospectively.

A walk-in testing centre was placed on the [REDACTED] estate in which the three P1 cases reside between the 2nd-6th April. There were just over 1,500 attendees and overall positivity rate was 1.98%.

Kildare ID facility: There was an outbreak at a residential facility for intellectually-disabled individuals in [REDACTED], first notified on 18th Feb. Ultimately this involved **34** cases: 28 primary cases, 5 secondary cases and 1 tertiary case (some in household contacts of staff). To date there are 6 confirmed B.1.351 variant cases associated with this outbreak, the first of whom was identified as a B.1.351 case on the 12th of March.

Midlands:

An extensive investigation was conducted in the [REDACTED] region, following the reporting of several confirmed and probable B.1.351 cases, spread over 3 families.

Retrospective and prospective pcr assays and whole genome sequencing was conducted on all positive samples in the locality and a walk-in testing centre was established. This investigation has now completed and no further VOCs were identified.

Recent flight from Doha (31/03/2021):

This flight is still under investigation. There were 183 passengers and crew on board, with 19 cases detected to date. These cases had travelled from Tanzania, Pakistan and India before transiting in Doha. Two of these cases are Probable VOCs, with further results pending.

5.2 Mandatory hotel quarantine

On the 26th of March, all incoming international travellers whose journey either originated in, or transited through, a “designated state” (i.e. deemed at high risk of VOC importation) were required to self-isolate in Mandatory Hotel Quarantine facilities upon arrival. To date, 17 COVID-19 cases have been detected in incoming travellers from designated states, staying in Mandatory Hotel Quarantine. One case has also occurred in a member of staff at one of the quarantine facilities. These cases have all been sent for sequencing, with results pending.