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Preliminary risk analysis of the spread of new COVID-19 variants from the UK, South Africa and Brazil

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The novel SARS-CoV-2 variants have raised serious concerns about a new wave of the pandemic, particularly concerning the recent new strains (lineages B.1.1.7, B.1.351, and P.1) found in the UK, South Africa, and Brazil [1-3]. We used de-identified and aggregated worldwide population movement data from billions of geotagged tweets and SafeGraph data in October – December 2020, derived by the ODT Flow Explorer [4], to explore the main destinations of international travellers departing from the UK, South Africa, and Brazil into other regions, and to assess the risk of new variants spreading across the world during the period from late 2020 to early 2021. It is important to note that the biases within these data are not well characterised and that they likely skew towards richer and younger populations, with children, the elderly and the poorest not well represented. Ongoing work within WorldPop is focussed on comparisons of multiple datasets to better understand and quantify such biases.

Spread of lineage B.1.1.7 from the UK

A new variant B.1.1.7 of SARS-CoV-2, also designated a Variant of Concern (VOC) 202012/01 by Public Health England, was detected in November 2020 and thought to have originated in the south-east of England in September or earlier [5]. It is estimated that the new strain increases the reproduction number by 56% (95% credible interval 50-74%) over previous strains of SARS-CoV-2 [6-8]. The new variant has increased infectiousness across all age groups, not just among the younger population, with a surge of cases across the UK being seen [6, 7]. This new

lineage might be also associated with an increase in mortality [9], but more evidence is needed to confirm that this variant would result in greater or lesser severity of disease than pre-existing variants.

Since mid-December 2020, restrictions have been placed by many countries across the globe on incoming travel from the UK to slow down the pace of this variant spreading. However, previous travel before the restrictions were implemented, as well as the high prevalence of this variant among current UK infections, may well have seeded the virus internationally [10]. As of 24 January 2021, a total of 62 countries, territories or areas have identified infections with the variant (**Figure 1**) [11]. Most were found in travellers returning from the UK, which coincides strongly with the main destinations of international travellers from the UK, in October – December 2020 (**Figure 2 and Table 1**). For the time being, multiple countries in Europe, America, and East Asia outside the original focus have reported local cases of this new variants [11].

Spread of lineage B.1.351 from South Africa

On December 18, 2020, the South African government announced that it had also seen the emergence of a new strain, known as 501.V2 or lineage B.1.351, sharing one of the mutations seen in B.1.1.7 found in the UK [12]. This variant was first identified in Nelson Mandela Bay, South Africa, in samples dating back to the beginning of October 2020, and cases have since been detected outside of South Africa [10]. This variant also has the N501Y mutation and several other mutations, but emerged completely independently of the UK strain and is not related to it. It has been found in up to 90 percent of the samples whose genetic sequences have been analysed in South Africa since mid-November. Besides South Africa, 25 other countries have also reported the variant [13]. However, most locations outside southern and eastern Africa have not reported sustained transmission and many cases were returning from South Africa (**Figure 3 and Table 2**).

Spread of lineage P.1 from Brazil

An emerging SARS-CoV-2 lineage, P.1, has been detected in in Manaus, Amazonas state, north Brazil in December 2020 [14]. This new variant is an alias of lineage B.1.1.28.1 and contains a unique constellation of lineage defining mutations

such as E484K, K417T, and N501Y with biological importance [15]. The P.1. and B.1.1.7 lineages share the spike N501Y mutation, while the P.1. and B.1.351 lineages share three mutation positions in common in the spike protein (K417N/T, E484K, N501Y) [15]. It was identified in 42% (13 out of 31) RT-PCR positive samples collected during 15 – 23 December 2020, indicating local transmission and possibly recent increase in the frequency of a new lineage from the Amazon region [3, 14]. According to the recent international mobility data, the main destinations of international travellers leaving Brazil were the USA, Argentina, Paraguay, Uruguay, France, Mexico, and the UK (**Figure 4 and Table 3**). However, as of 24 January 2021, only 6 countries outside of Brazil reported the infection of this novel variant, detected in travellers returning from Brazil [16, 17].

Given limited capacities in diagnosis and healthcare in many countries and the small fraction of infections that have been sequenced, the new variants could already be in other countries without having been detected. We are closely monitoring the rapidly changing situation, and further analyses will be conducted to update analyses on the risk of international spread and onward transmission of these new strains.

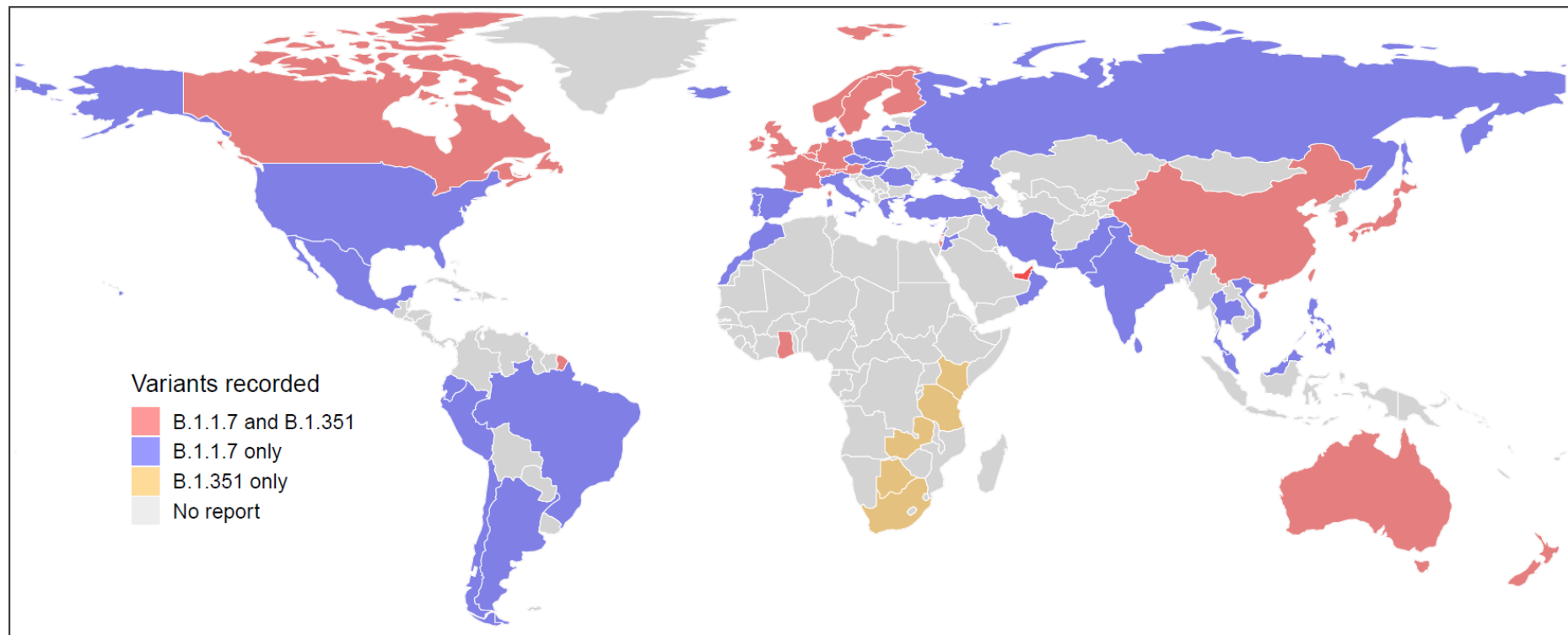


Figure 1. Reports of new SARS-CoV-2 variants, lineage B.1.1.7 and B.1.351, in different countries, territories or areas, as of 24 January 2021. A new variant, P.1 lineage, was also identified in 7 countries, including Brazil, Japan, South Korea, Faroe Islands, Italy, Germany, and the UK. The global records of new variants mapped here are based on the reports published at <https://cov-lineages.org/> [11, 13, 16].

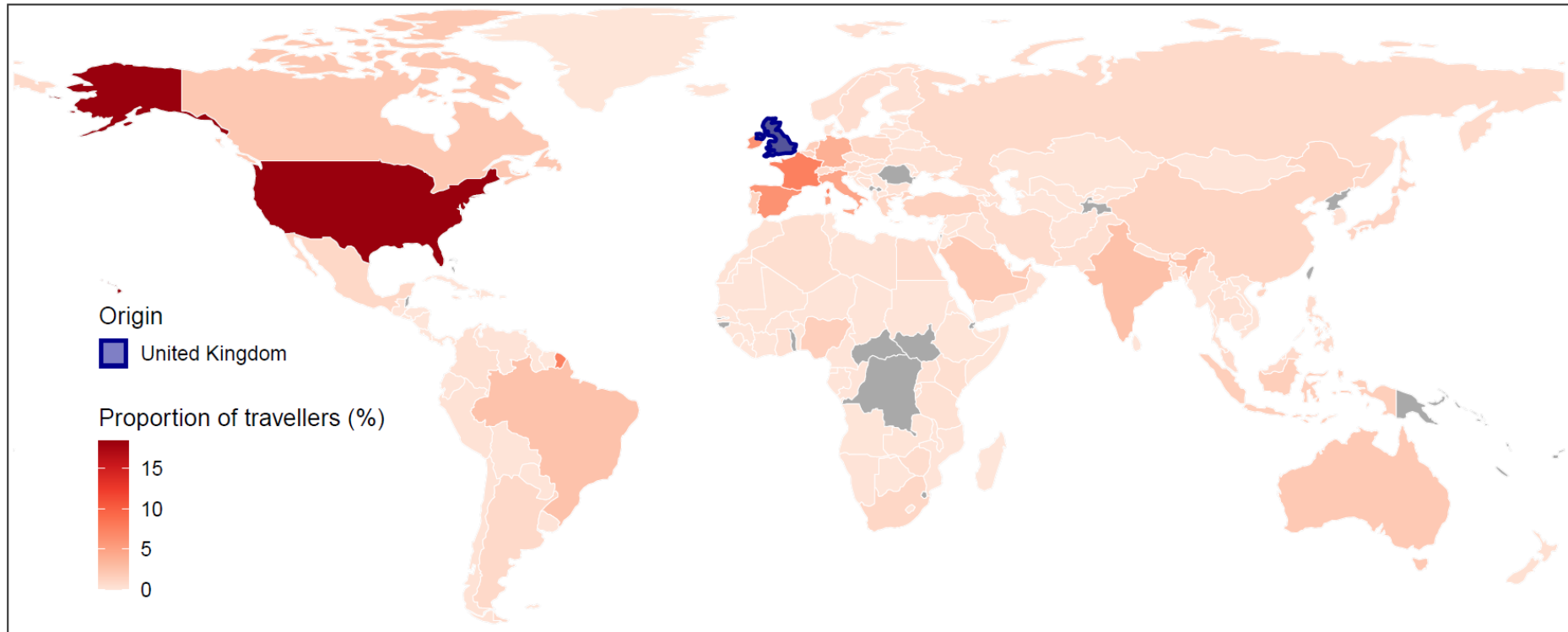


Figure 2. Main destinations of international travellers departing from the UK in October – December 2020. The mobility data are based on the population movement flows derived by the ODT Flow Explorer [4]. The areas with no data are filled in grey.

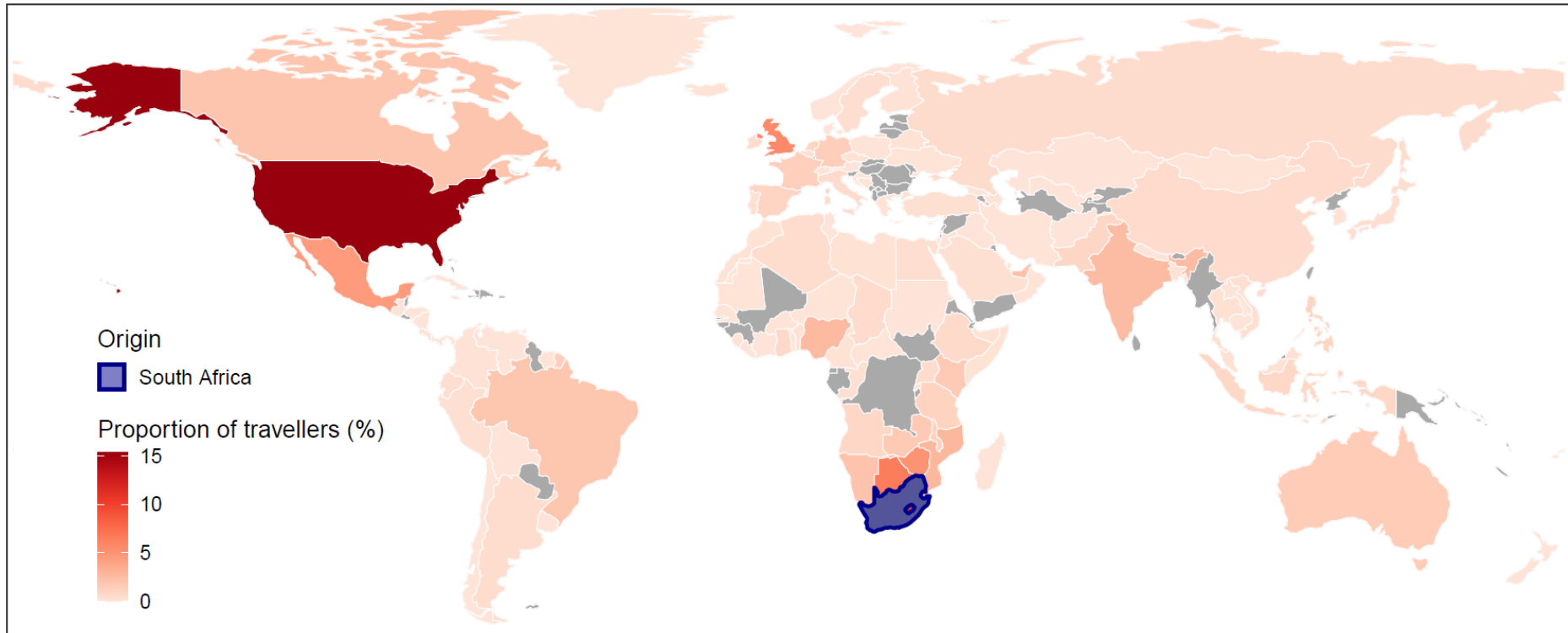


Figure 3. Main destinations of international travellers departing from South Africa in October – December 2020. The mobility data are based on the population movement flows derived by the ODT Flow Explorer [4]. The areas with no data are filled in grey.

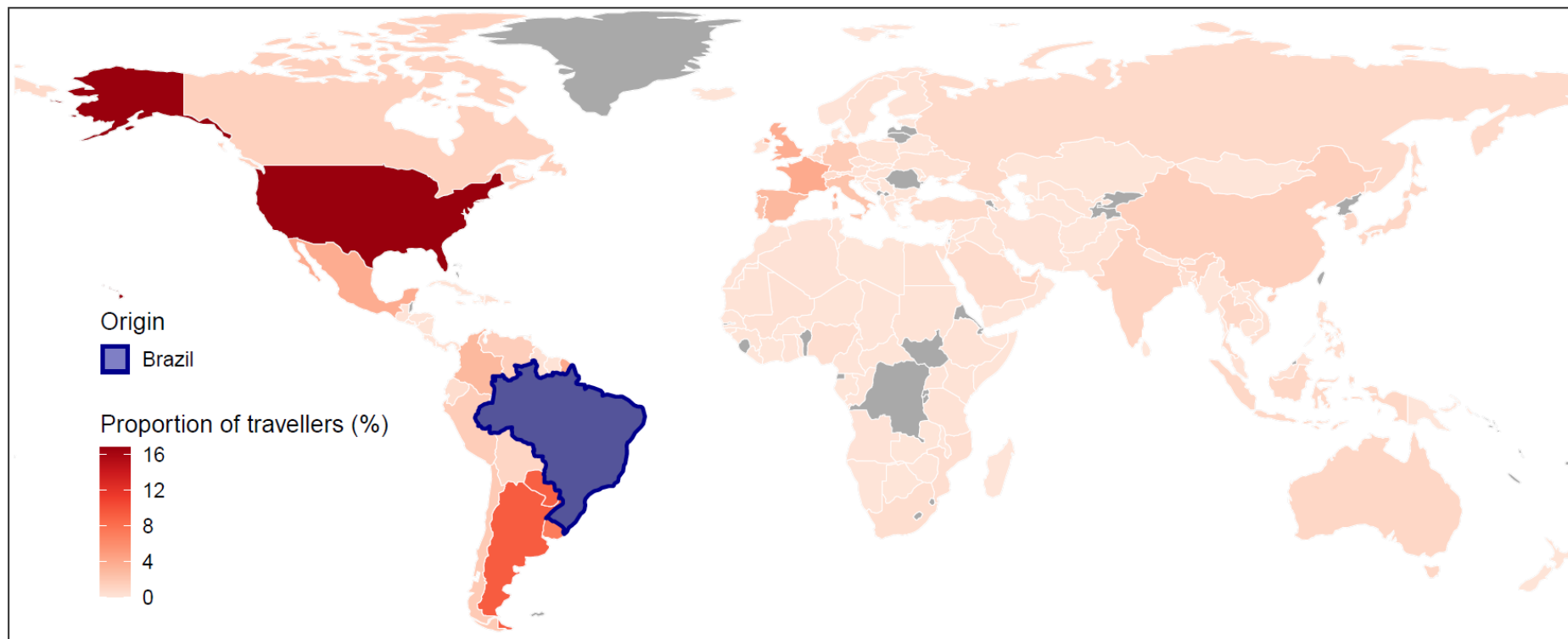


Figure 4. Main destinations of international travellers departing from Brazil in October – December 2020. The mobility data are based on the population movement flows derived by the ODT Flow Explorer [4]. The areas with no data are filled in grey.

Table 1. Top 30 ranked countries or regions receiving international travellers from the UK in October – December 2020.

Rank	Destination	Percentage (%) of international travellers	B.1.1.7 reported
1	United States of America	18.38	Yes
2	France	7.55	Yes
3	Ireland	6.21	Yes
4	Spain	6.10	Yes
5	Italy	4.69	Yes
6	Germany	3.88	Yes
7	India	2.63	Yes
8	Brazil	2.53	Yes
9	Canada	2.10	Yes
10	Australia	2.02	Yes
11	Saudi Arabia	1.89	-
12	United Arab Emirates	1.79	Yes
13	Netherlands	1.67	Yes
14	Indonesia	1.63	-
15	Nigeria	1.58	-
16	Turkey	1.40	Yes
17	Portugal	1.34	Yes
18	Belgium	1.32	Yes
19	Japan	1.21	Yes
20	China	1.19	Yes
21	Greece	1.19	Yes
22	Kuwait	1.01	-
23	South Africa	1.01	-
24	Poland	0.98	Yes
25	Mexico	0.97	Yes
26	Argentina	0.87	Yes
27	Austria	0.87	Yes
28	Switzerland	0.82	Yes
29	Russia	0.82	Yes
30	Malaysia	0.78	Yes

Note: The mobility data are based on the population movement flows derived by the ODT Flow Explorer [4]. The records of B.1.1.7 are based on the reports published at <https://cov-lineages.org/> [11].

Table 2. Top 30 ranked countries or regions receiving international travellers from South Africa in October – December 2020.

Rank	Destination	Percentage (%) of international travellers	B.1.351 reported
1	United States of America	15.32	-
2	Lesotho	9.85	-
3	Botswana	6.48	Yes
4	United Kingdom	5.63	Yes
5	Zimbabwe	5.06	-
6	Mexico	4.53	-
7	Mozambique	2.74	-
8	Nigeria	2.63	-
9	India	2.47	-
10	United Arab Emirates	2.21	Yes
11	Namibia	2.05	-
12	eSwatini	2.00	-
13	Canada	1.95	Yes
14	Brazil	1.90	-
15	Kenya	1.63	Yes
16	Zambia	1.63	Yes
17	Australia	1.53	Yes
18	Germany	1.42	Yes
19	France	1.32	Yes
20	Malawi	1.16	-
21	Philippines	1.11	-
22	United Republic of Tanzania	1.11	Yes
23	Spain	1.05	-
24	Netherlands	1.00	Yes
25	Pakistan	0.90	-
26	Angola	0.84	-
27	Indonesia	0.79	-
28	Ghana	0.74	Yes
29	Ethiopia	0.68	-
30	China	0.58	Yes

Note: The mobility data are based on the population movement flows derived by the ODT Flow Explorer [4]. The records of B.1.351 are based on the reports published at <https://cov-lineages.org/> [13].

Table 3. Top 30 ranked countries or regions receiving international travellers from Brazil in October – December 2020.

Rank	Destination	Percentage (%) of international travellers	P.1 reported
1	United States of America	16.80	-
2	Argentina	9.32	-
3	Paraguay	9.07	-
4	Uruguay	7.17	-
5	France	3.96	-
6	Mexico	3.81	-
7	United Kingdom	3.77	Yes
8	Colombia	2.95	-
9	Spain	2.94	-
10	Portugal	2.35	-
11	Italy	2.23	Yes
12	Chile	1.79	-
13	Germany	1.67	Yes
14	Peru	1.57	-
15	Venezuela	1.51	-
16	China	1.39	-
17	Canada	1.32	-
18	India	1.13	-
19	United Arab Emirates	1.12	-
20	Bolivia	0.99	-
21	Japan	0.96	Yes
22	Australia	0.95	-
23	South Korea	0.95	Yes
24	Indonesia	0.87	-
25	Thailand	0.79	-
26	Russia	0.72	-
27	Netherlands	0.71	-
28	Turkey	0.68	-
29	Saudi Arabia	0.61	-
30	Switzerland	0.59	-

Note: The mobility data are based on the population movement flows derived by the ODT Flow Explorer [4]. The records of P.1 were based on the reports published at <https://cov-lineages.org/> [16].

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Reference

1. Kupferschmidt K: Viral mutations may cause another 'very, very bad' COVID-19 wave, scientists warn. *Science* 2021.
2. SARS-CoV-2 Variant – United Kingdom of Great Britain and Northern Ireland [<https://www.who.int/csr/don/21-december-2020-sars-cov2-variant-united-kingdom/en/>]
3. Emerging SARS-CoV-2 Variants [<https://www.cdc.gov/coronavirus/2019-ncov/more/science-and-research/scientific-brief-emerging-variants.html>]
4. Li Z, et al: ODT Flow Explorer: Extract, Query, and Visualize Human Mobility. *arXiv* 2020:2011.12958.
5. Investigation of novel SARS-CoV-2 variant: Variant of Concern 202012/01 [<https://www.gov.uk/government/publications/investigation-of-novel-sars-cov-2-variant-variant-of-concern-20201201>]
6. Davies NG, et al: Estimated transmissibility and severity of novel SARS-CoV-2 Variant of Concern 202012/01 in England. *medRxiv* 2020:2020.2012.2024.20248822.
7. Volz E, et al: Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from linking epidemiological and genetic data. *medRxiv* 2021:2020.2012.2030.20249034.
8. Covid-19: New variant 'raises R number by up to 0.7' [<https://www.bbc.co.uk/news/health-55507012>]
9. Coronavirus: UK variant 'may be more deadly' [<https://www.bbc.co.uk/news/health-55768627>]
10. Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 [<https://virological.org/t/tracking-the-international-spread-of-sars-cov-2-lineages-b-1-1-7-and-b-1-351-501y-v2/592>]
11. SARS-CoV-2 lineages: B.1.1.7 report [https://cov-lineages.org/global_report_B.1.1.7.html]
12. Tegally H, et al: Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa. *medRxiv* 2020:2020.2012.2021.20248640.
13. SARS-CoV-2 lineages: B.1.351 report [https://cov-lineages.org/global_report_B.1.351.html]
14. Genomic characterisation of an emergent SARS-CoV-2 lineage in Manaus: preliminary findings [<https://virological.org/t/genomic-characterisation-of-an-emergent-sars-cov-2-lineage-in-manaus-preliminary-findings/586>]
15. Phylogenetic relationship of SARS-CoV-2 sequences from Amazonas with emerging Brazilian variants harboring mutations E484K and N501Y in the Spike protein [<https://virological.org/t/phylogenetic-relationship-of-sars-cov-2-sequences-from-amazonas-with-emerging-brazilian-variants-harboring-mutations-e484k-and-n501y-in-the-spike-protein/585>]
16. SARS-CoV-2 lineages: P.1 report [https://cov-lineages.org/global_report_P.1.html]
17. Brief report: New Variant Strain of SARS-CoV-2 Identified in Travelers from Brazil [<https://www.niid.go.jp/niid/en/2019-ncov-e/10108-covid19-33-en.html>]