Emerging SARS-CoV-2 Variants

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Sciences

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National Research
Institute of Tuberculosis
and Lung Disease
(NRITLD)

GISAID Clade and lineage nomenclature

- GISAID introduced a nomenclature system for major clades:
  - based on marker mutations within 6 high-level phylogenetic groupings from the early split of S and L, to the further evolution of L into V and G and later of G into GH and GR
  - more detailed lineages assigned by the Phylogenetic Assignment of Named Global Outbreak LINeages (PANGOLIN) tool
- Using specific combinations of 9 genetic markers, 95% of the hCOV-19 data in GISAID can be classified in 6 size-balanced clades:
  - starting with S and L (initiated also by other research groups Tang et al, 2020), S continued at moderate levels and L split into initially equal G and V versions with G reaching 50% in March 2020 and splitting further into GR and GH.
- The list of the 9 marker variants is as follows:
  - **S**: C8782T,T28144C includes NS8-L84S
  - **L**: C241,C3037,A23403,C8782,G11083,G25563,G26144,T28144,G28882 (WIV04-reference sequence)
  - **V**: G11083T,G26144T NSP6-L37F + NS3-G251V
  - **G**: C241T,C3037T,A23403G includes S-D614G
  - **GH**: C241T,C3037T,A23403G,G25563T includes S-D614G + NS3-Q57H
  - **GR**: C241T,C3037T,A23403G,G28882A includes S-D614G + N-G204R

Clade and lineage nomenclature

- Another effort, by Hodcroft et al, uses a Year-Letter nomenclature to facilitate discussion of large-scale diversity patterns of hCoV-19 and label clades that persist for at least several months and have significant geographic spread. Each clade name consists of the year when the clade emerged and a capital letter starting with A for each year.
- Clades are defined by signature mutations. New major clades are named once the frequency of a clade exceeds 20% in a representative global sample and that clade differs in at least two positions from its parent clade, currently using the clades 19A, 19B, 20A, 20B, and 20C.

Rough correspondence of different clade nomenclature systems in format: Rambaut et al (GISAID) Hodcroft et al

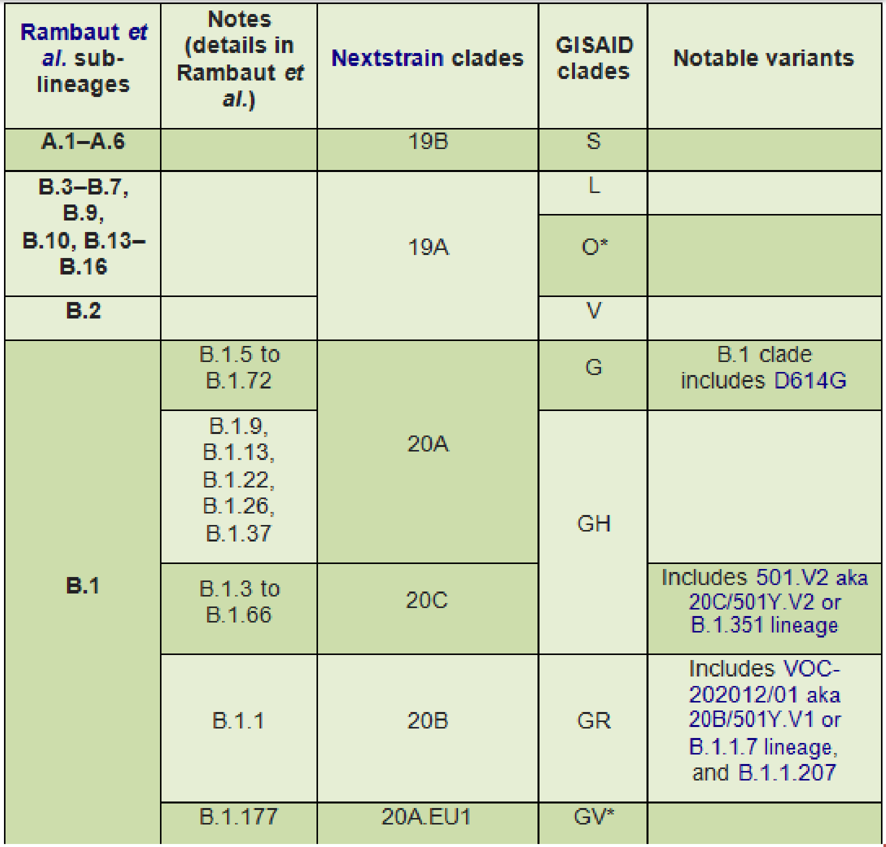
GISAID - Clade and lineage nomenclature aids in genomic epidemiology of active hCoV-19 viruses

Nomenclature of SARS-CoV-2

Clades

- While there are many thousands of variants of SARS-CoV-2, there are also much larger groupings called clades. Several different clade nomenclatures for SARS-CoV-2 have been proposed.
- As of December 2020, GISAID—referring to SARS-CoV-2 as hCoV-19—identified seven clades (O, S, L, V, G, GH, and GR).
- Also as of December 2020 , Nextstrain identified five (19A, 19B, 20A, 20B, and 20C).
- In an article in the November 2020 issue of *International Journal of Infectious Diseases*, Guan et al. identified five global clades (G_{614}, S_{84}, V_{251}, I_{378} and D_{392}).
- Rambaut et al. proposed the term "lineage" in a 2020 article in *Nature Microbiology*; as of December 2020, there have been five major lineages (A, B, B.1, B.1.1, and B.1.177) identified.

SARS-CoV-2 Corresponding Nomenclatures



Rambaut *et al.* sub-lineages	Notes (details in Rambaut *et al.*)	Nextstrain clades	GISAID clades	Notable variants
A.1–A.6		19B	S	
B.3–B.7, B.9, B.10, B.13–B.16		19A	L	
			O*	
B.2			V	
B.1	B.1.5 to B.1.72	20A	G	B.1 clade includes D614G
	B.1.9, B.1.13, B.1.22, B.1.26, B.1.37		GH	
	B.1.3 to B.1.66	20C		Includes 501.V2 aka 20C/501Y.V2 or B.1.351 lineage
	B.1.1	20B	GR	Includes VOC-202012/01 aka 20B/501Y.V1 or B.1.1.7 lineage, and B.1.1.207
	B.1.177	20A.EU1	GV*	

*NOTE: in another source, GISAID name a set of 7 clades without the 'O' clade but including a 'GV' clade.

doi:10.5802/crbiol.29/ doi:10.2807/1560-7917.ES.2020.25.32.2001410/ *www.gisaid.org*. / doi:10.2471/BLT.20.253591/ doi:10.1016/j.ijid.2020.08.052/ doi:10.1016/j.ijid.2020.08.052/ cov-lineages.org

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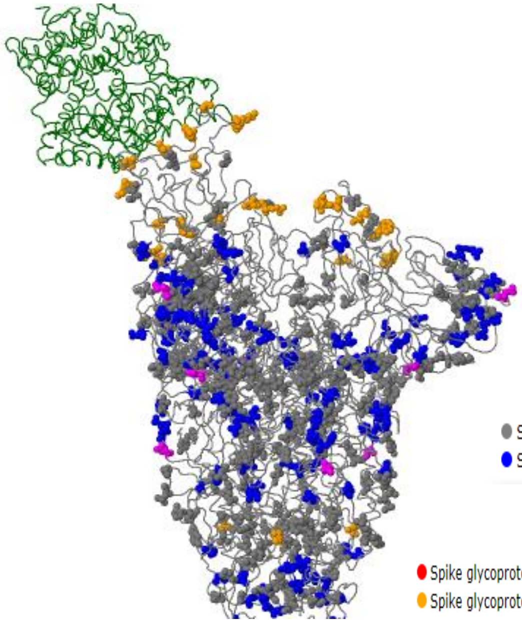
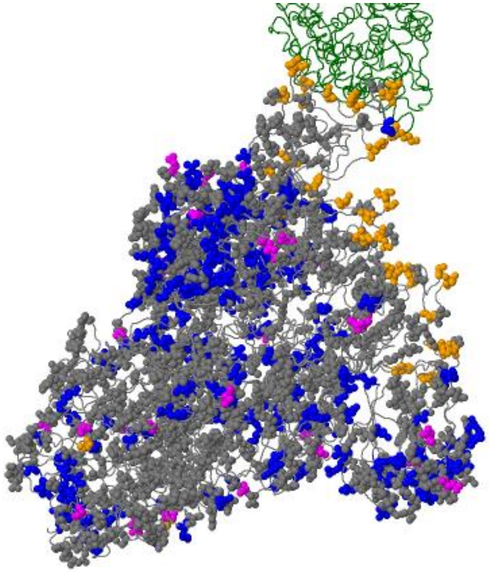
GISAID hCoV-19 Spike Glycoprotein Mutation Surveillance Dashboard



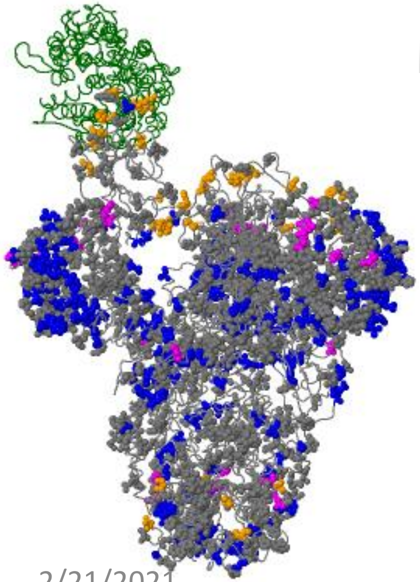
N501T K417N Y453F
N501Y E484K E484D
N439K S494P S477R
G446V S477N
in GH clade (B.1.*)

● Spike glycoprotein variation occurring 100 times or less
● Spike glycoprotein variation occurring greater than 100 times



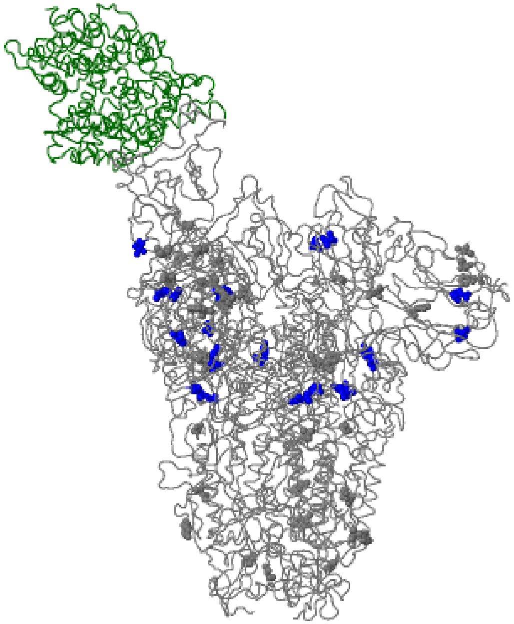
N501S E484Q
T478I S477G
N439K A475V
F456L F490S
S477R S477I
S477N S494A
N501Y V445I
E484K T478K
S494P
in G & GV clades
(B.1 & B.1.177)

● Spike glycoprotein variation near host receptor with effect history
● Spike glycoprotein variation near host receptor, or other functional annotation
● Insertion/deletion
● Spike glycoprotein variation altering potential N-glycosylation sites



S477G A475V F490S
G446V S477R S477I
S477N G502V K417T
N501Y G446S G447V
E484K K458N T478K
S494P
in GR clade (B.1.1.1)

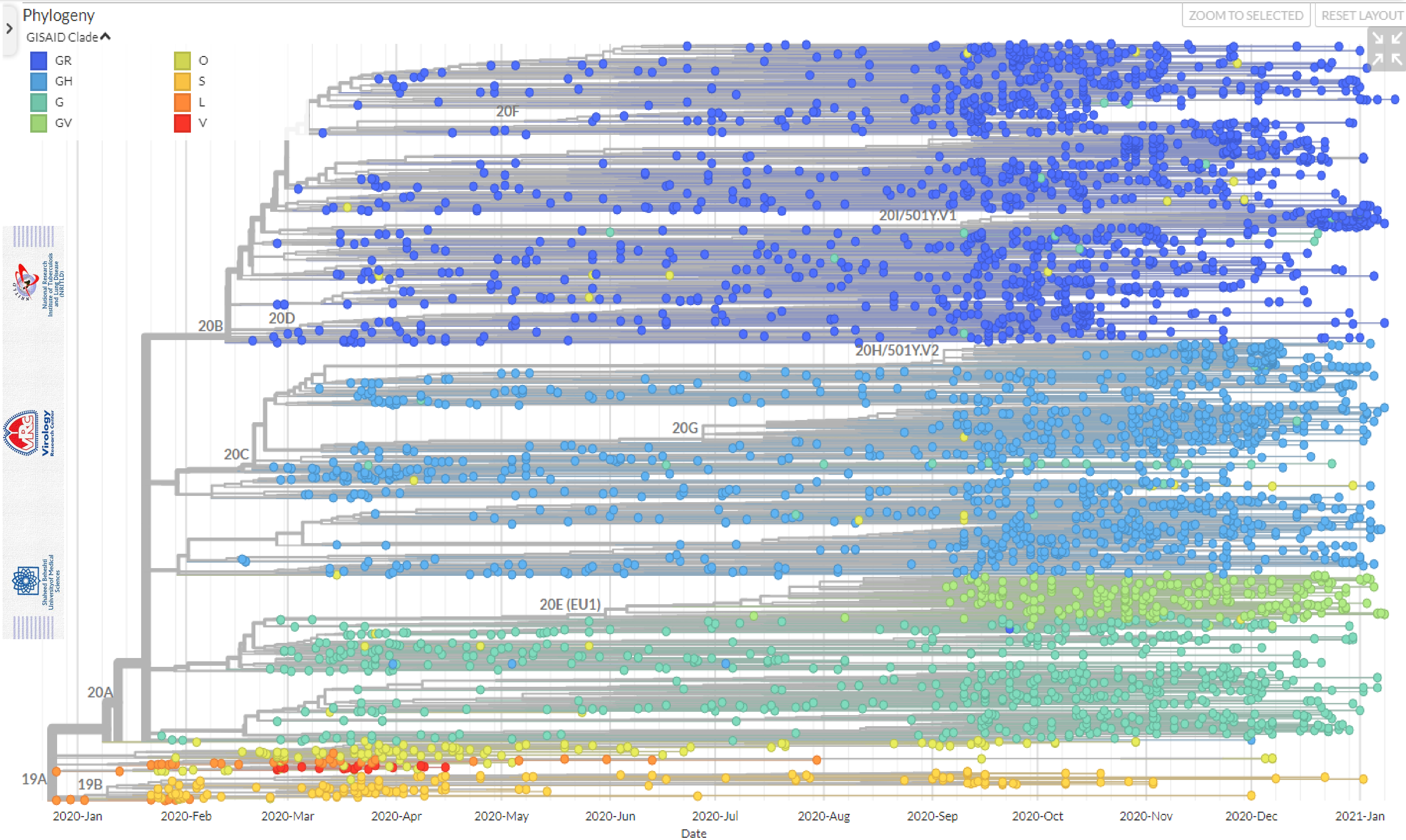
https://www.gisaid.org/hcov
mutation-dashboard/



E484K K417N
N501Y S477N
in nonG clade
(A, B & B.2)

Genomic epidemiology of hCoV-19

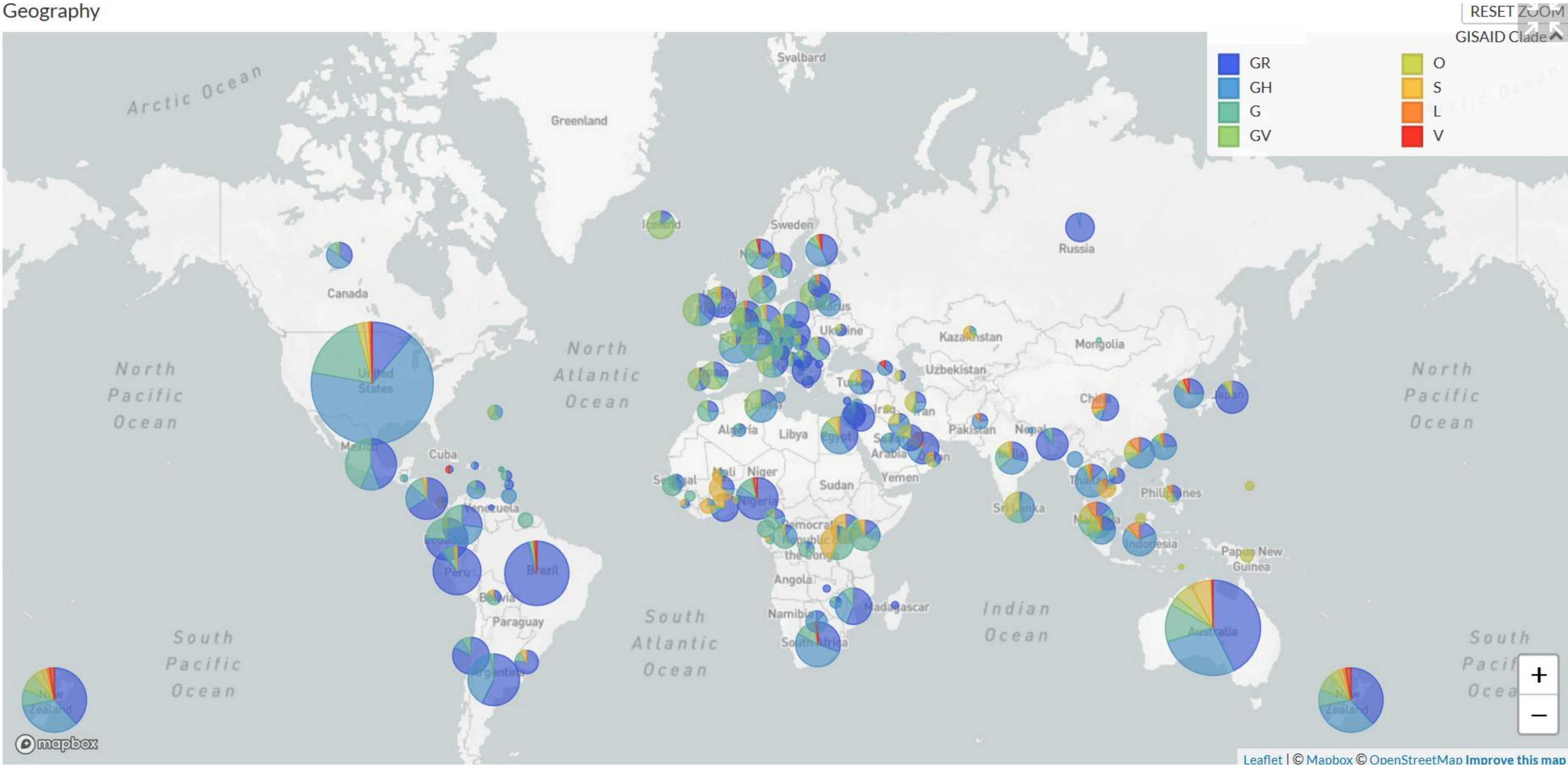
Phylogenetic tree in Newick format with branch lengths in units of years



https://nextstrain.org/ncov/global?c=GISAID_clade&onlyPanels&p=full&sidebar=closed

Genomic epidemiology of hCoV-19

Geography



https://nextstrain.org/ncov/global?c=GISAID_clade&onlyPanels&p=full&sidebar=closed

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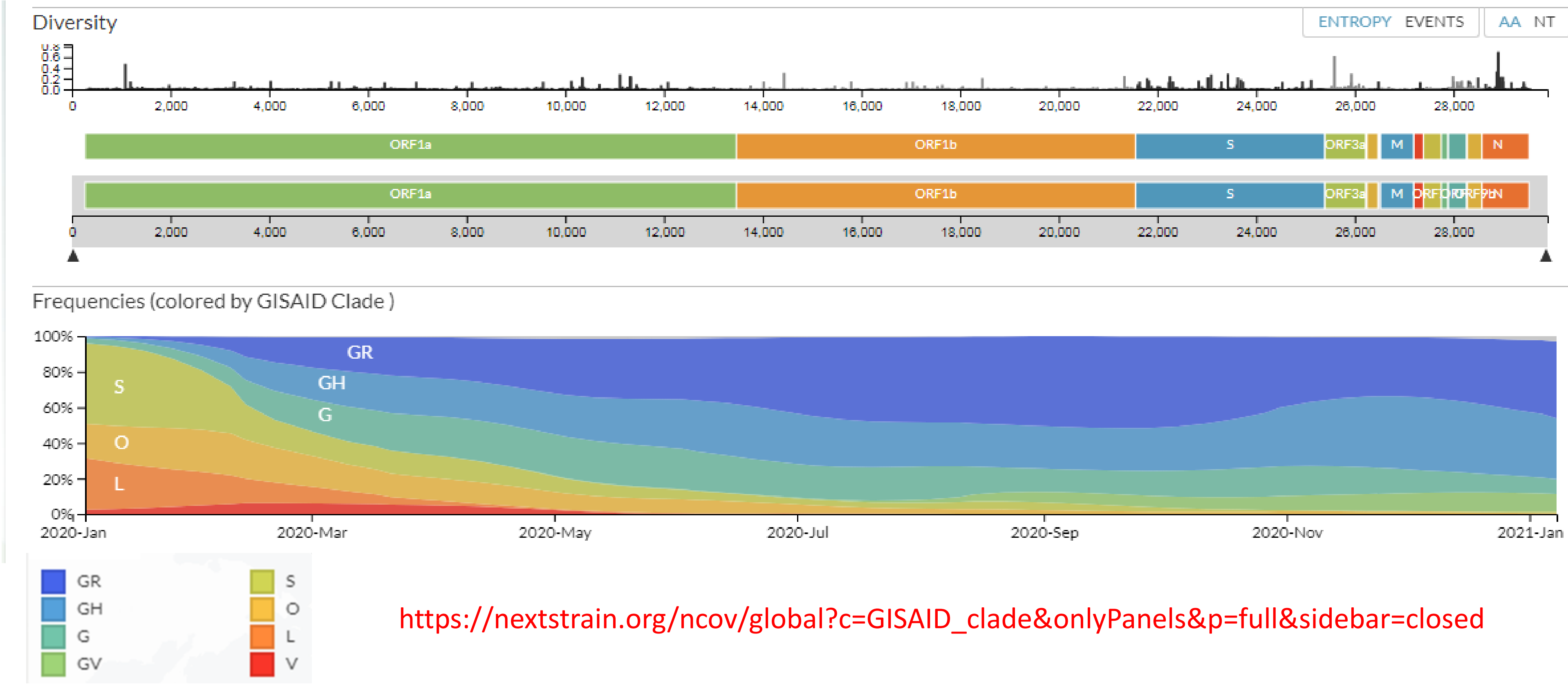
Genomic epidemiology of hCoV-19

Genome Diversity & Clade Frequencies



https://nextstrain.org/ncov/global?c=GISAID_clade&onlyPanels&p=full&sidebar=closed

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Confusion reigns over naming of new COVID variants

- ‘the UK variant’, ‘the South African variant’, ‘the Brazil variant’ — and there will be more variants.”
  - Terms such as ‘variant’, ‘lineage’ and ‘strain’ add to the confusion, because they have no unambiguous definitions and are sometimes used interchangeably.
- UK variant
  - Variant Under Investigation 202012/01 (VUI 202012/01)
  - Variant of Concern 202012/01 (VOC 202012/01)
  - ‘the Kent variant’ (southeast England)
  - ***B.1.1.7 lineage (a.k.a. 20I/501Y.V1 Variant of Concern (VOC) 202012/01)***
  - N501Y
    - **501st amino acid site of the virus’s spike protein that changes the residue there from an asparagine to a tyrosine**
- South African variant; a worrying variant
  - 501Y.V2; it is now also called ***B.1.351 lineage (a.k.a. 20H/501Y.V2)***
  - N501Y, E484K and K417N
- Brazil variant
  - 484K.V2 → E484K
    - circulating in several states from the South, Northeast, and North Brazilian regions
  - ***P.1 lineage (a.k.a. 20J/501Y.V3) ;*** first reported in Japan in four travelers from Brazil

Nature 589, 339 (2021), doi: https://doi.org/10.1038/d41586-021-00097-w

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New Emerging SARS-CoV-2 Variants

The British variant

- In the UK, a new variant strain of SARS-CoV-2
  - known as 20B/501Y.V1 (The CDC), VOC 202012/01 (Public Health England (PHE), or B.1.1.7 lineage (COVID-19 Genomics UK (COG-UK) Consortium)
- Emerged with an unusually large number of mutations.
- This variant has since been detected in numerous countries around the world

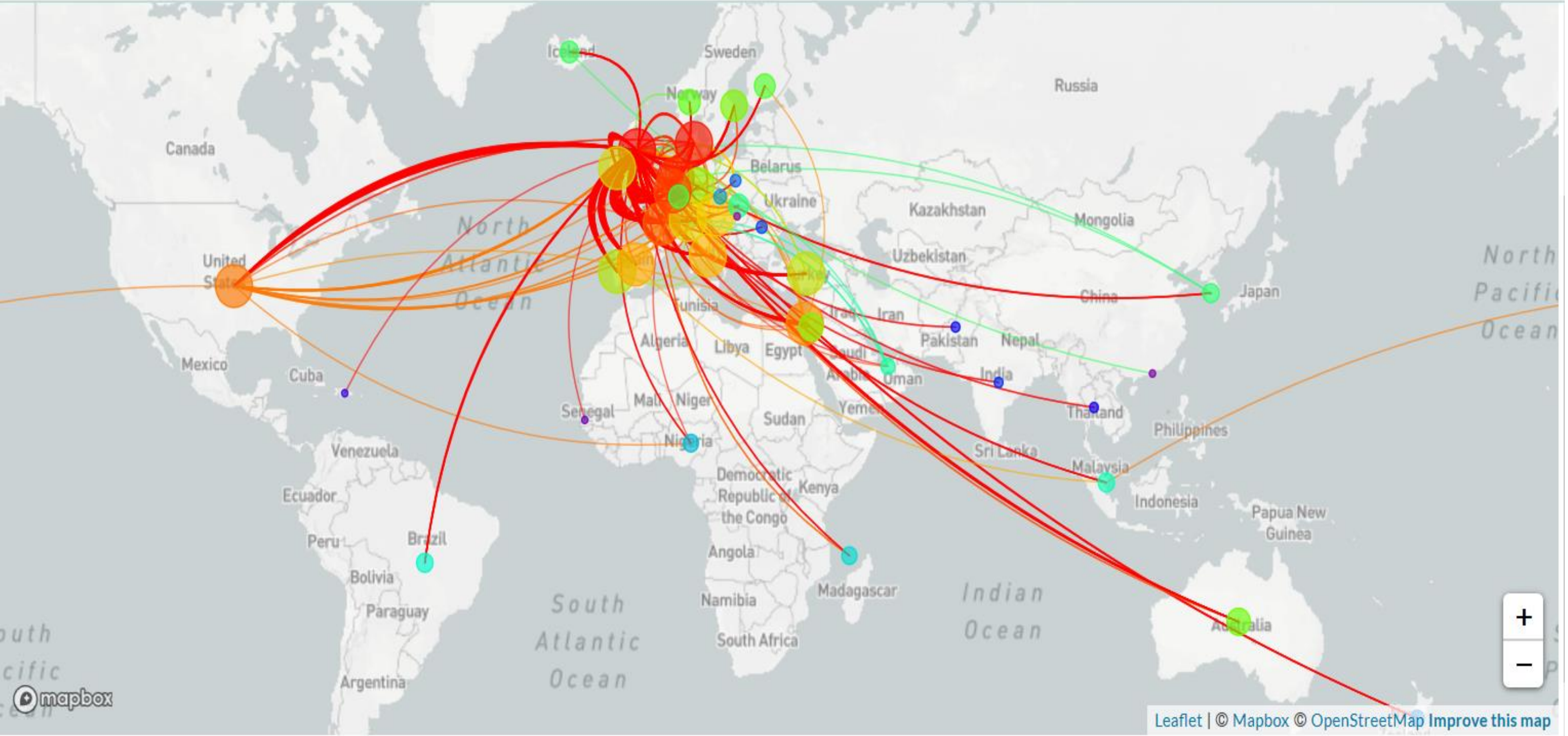
S.A. Variant

- In South Africa, another variant of SARS-CoV-2
  - known as 20C/501Y.V2 or B.1.351 lineage)
- Emerged independently of the B.1.1.7 lineage.
- This variant shares some mutations with the B.1.1.7 lineage.
- Cases attributed to this variant have been detected outside of South Africa.

GISAID

Phylodynamics of pandemic coronavirus variant VUI202012/01

3,988 of 3,988 genomes collected between October 2020 and January 2021
last updated 2021-02-09



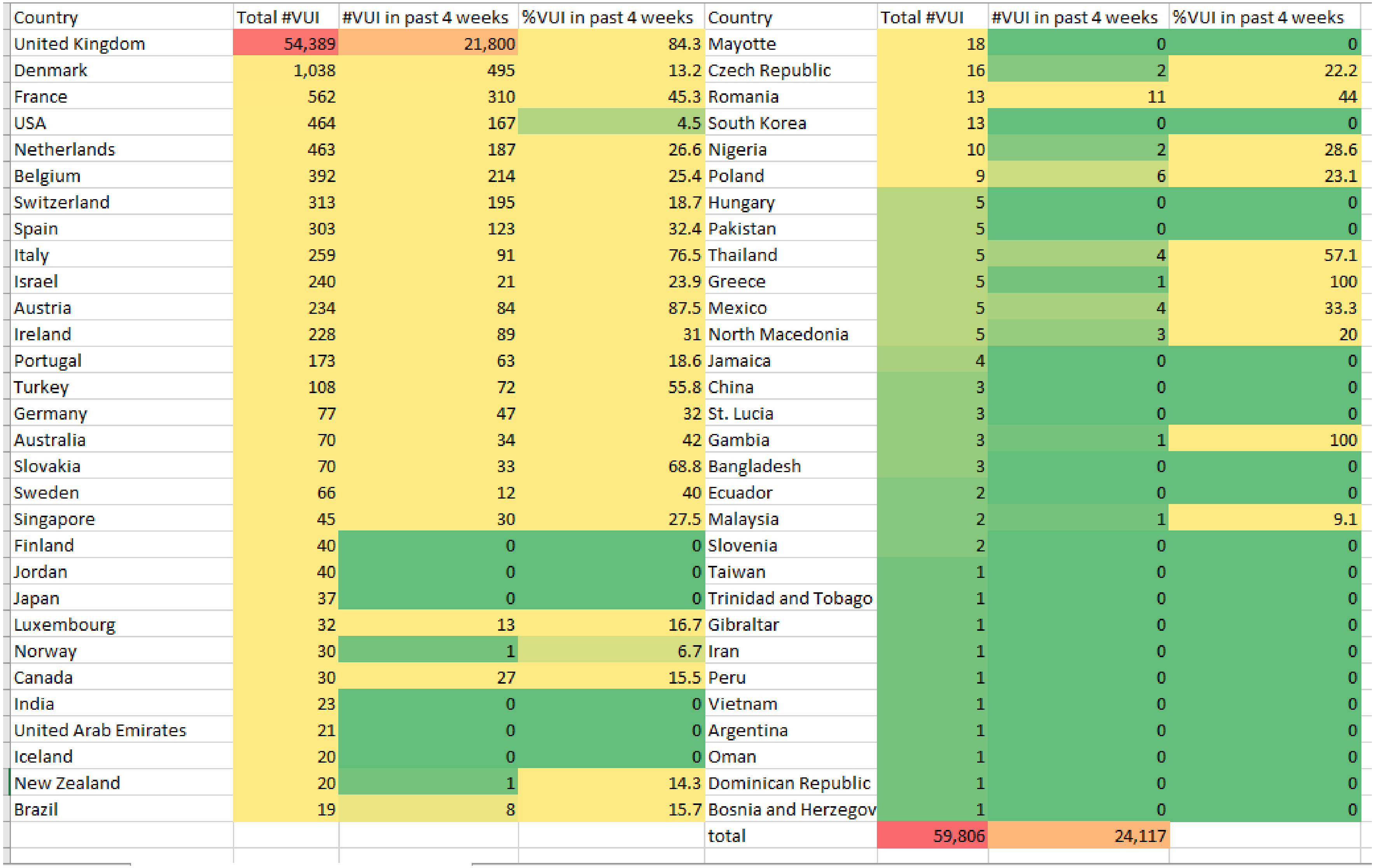
Transmissions

Most recent reported occurrences in different countries VUI202012/01

Country	Strain Name	Collection Date	Country	Strain Name	Collection Date
Australia	hCoV-19/Australia/QLD1545/2021	2/5/2021	Gambia	hCoV-19/Gambia/3930/2021	1/15/2021
Italy	hCoV-19/Italy/ABR-IZSGC-66415/202	2/4/2021	Israel	hCoV-19/Israel/CVL-2567/2021	1/15/2021
United Kingdom	hCoV-19/England/SHEF-10C8326/202	2/4/2021	Norway	hCoV-19/Norway/0428/2021	1/14/2021
Singapore	hCoV-19/Singapore/142/2021	2/3/2021	New Zealand	hCoV-19/New Zealand/21CV0110/202	1/14/2021
Slovakia	hCoV-19/Slovakia/UKBA-1214/2021	2/2/2021	Trinidad and Tobago	hCoV-19/Trinidad and Tobago/TT2627	1/12/2021
USA	hCoV-19/USA/MI-UM-10038131441/2	2/2/2021	Mayotte	hCoV-19/Mayotte/IPP00637/2021	1/11/2021
Romania	hCoV-19/Romania/Valcea418423/20	1/31/2021	Hungary	hCoV-19/Hungary/UD-V147/2021	1/9/2021
Spain	hCoV-19/Spain/IB-IBV-99016832/202	1/29/2021	Iran	hCoV-19/Iran/N193/2021	1/8/2021
Thailand	hCoV-19/Thailand/CU-SI2104499-NT/	1/29/2021	Pakistan	hCoV-19/Pakistan/NIH-5185B/2021	1/8/2021
Switzerland	hCoV-19/Switzerland/GE-33105744/2	1/28/2021	Jordan	hCoV-19/Jordan/PHBC6/2021	1/7/2021
Canada	hCoV-19/Canada/ON-S2512/2021	1/27/2021	Slovenia	hCoV-19/Slovenia/NK7961/2021	1/7/2021
France	hCoV-19/France/IDF-IPP02081/2021	1/27/2021	Bangladesh	hCoV-19/Bangladesh/G039392/2021	1/6/2021
Belgium	hCoV-19/Belgium/ULG-11667/2021	1/27/2021	Iceland	hCoV-19/Iceland/4061/2021	1/5/2021
Germany	hCoV-19/Germany/BW-FR0481/2021	1/27/2021	Ecuador	hCoV-19/Ecuador/INSPI-179112/2021	1/5/2021
Denmark	hCoV-19/Denmark/DCGC-35581/202	1/25/2021	Finland	hCoV-19/Finland/HEL4-18/2021	1/4/2021
Portugal	hCoV-19/Portugal/PT2618/2021	1/25/2021	China	hCoV-19/Hong Kong/VM21000371/202	1/3/2021
Netherlands	hCoV-19/Netherlands/NH-RIVM-110	1/25/2021	Japan	hCoV-19/Japan/IC-0664/2021	2021-01-00
Poland	hCoV-19/Poland/NIPH-NIH-49/2021	1/25/2021	India	hCoV-19/India/KA-NIMH-SEQ-49/202	12/31/2020
Malaysia	hCoV-19/Malaysia/IMR-WC61542/20	1/24/2021	Peru	hCoV-19/Peru/LIM-INS-173/2020	12/31/2020
North Macedonia	hCoV-19/North Macedonia/5022/202	1/23/2021	South Korea	hCoV-19/South Korea/KDCA0838/202	12/30/2020
Turkey	hCoV-19/Turkey/HSGM-1505/2021	1/22/2021	United Arab Emirates	hCoV-19/United Arab Emirates/4260/	12/29/2020
Brazil	hCoV-19/Brazil/SP-1051/2021	1/22/2021	Dominican Republic	hCoV-19/Dominican Republic/CDC-9K	12/27/2020
Ireland	hCoV-19/Ireland/D-NVRL-84IRL1347	1/21/2021	St. Lucia	hCoV-19/St Lucia/LCA47894/2020	12/26/2020
Luxembourg	hCoV-19/Luxembourg/LNS3416774/2	1/19/2021	Taiwan	hCoV-19/Taiwan/CGMH-CGU-44/2020	12/26/2020
Sweden	hCoV-19/Sweden/21-50442/2021	1/19/2021	Bosnia and Herzegovina	hCoV-19/Bosnia and Herzegovina/VFS	12/25/2020
Nigeria	hCoV-19/Nigeria/CV650/2021	1/19/2021	Oman	hCoV-19/Oman/182621/2020	12/22/2020
Mexico	hCoV-19/Mexico/NLE-InDRE_240/20	1/18/2021	Jamaica	hCoV-19/Jamaica/JAM47542/2020	12/21/2020
Greece	hCoV-19/Greece/3459/2021	1/18/2021	Argentina	hCoV-19/Argentina/PAIS-E0126/2020	12/21/2020
Czech Republic	hCoV-19/Czech Republic/Tilia-12/20	1/18/2021	Gibraltar	hCoV-19/Gibraltar/205000662/2020	2020-12-00
Austria	hCoV-19/Austria/CeMM3102/2021	1/15/2021	Vietnam	hCoV-19/Vietnam/PIHCM-1565/2020	2020-12-00
60 countries			Samples with missing day value are assigned '00'		

https://www.gisaid.org/hcov19-variants/

Country Submission Count VUI202012/01



Country	Total #VUI	#VUI in past 4 weeks	%VUI in past 4 weeks	Country	Total #VUI	#VUI in past 4 weeks	%VUI in past 4 weeks
United Kingdom	54,389	21,800	84.3	Mayotte	18	0	0
Denmark	1,038	495	13.2	Czech Republic	16	2	22.2
France	562	310	45.3	Romania	13	11	44
USA	464	167	4.5	South Korea	13	0	0
Netherlands	463	187	26.6	Nigeria	10	2	28.6
Belgium	392	214	25.4	Poland	9	6	23.1
Switzerland	313	195	18.7	Hungary	5	0	0
Spain	303	123	32.4	Pakistan	5	0	0
Italy	259	91	76.5	Thailand	5	4	57.1
Israel	240	21	23.9	Greece	5	1	100
Austria	234	84	87.5	Mexico	5	4	33.3
Ireland	228	89	31	North Macedonia	5	3	20
Portugal	173	63	18.6	Jamaica	4	0	0
Turkey	108	72	55.8	China	3	0	0
Germany	77	47	32	St. Lucia	3	0	0
Australia	70	34	42	Gambia	3	1	100
Slovakia	70	33	68.8	Bangladesh	3	0	0
Sweden	66	12	40	Ecuador	2	0	0
Singapore	45	30	27.5	Malaysia	2	1	9.1
Finland	40	0	0	Slovenia	2	0	0
Jordan	40	0	0	Taiwan	1	0	0
Japan	37	0	0	Trinidad and Tobago	1	0	0
Luxembourg	32	13	16.7	Gibraltar	1	0	0
Norway	30	1	6.7	Iran	1	0	0
Canada	30	27	15.5	Peru	1	0	0
India	23	0	0	Vietnam	1	0	0
United Arab Emirates	21	0	0	Argentina	1	0	0
Iceland	20	0	0	Oman	1	0	0
New Zealand	20	1	14.3	Dominican Republic	1	0	0
Brazil	19	8	15.7	Bosnia and Herzegov	1	0	0
				total	59,806	24,117	

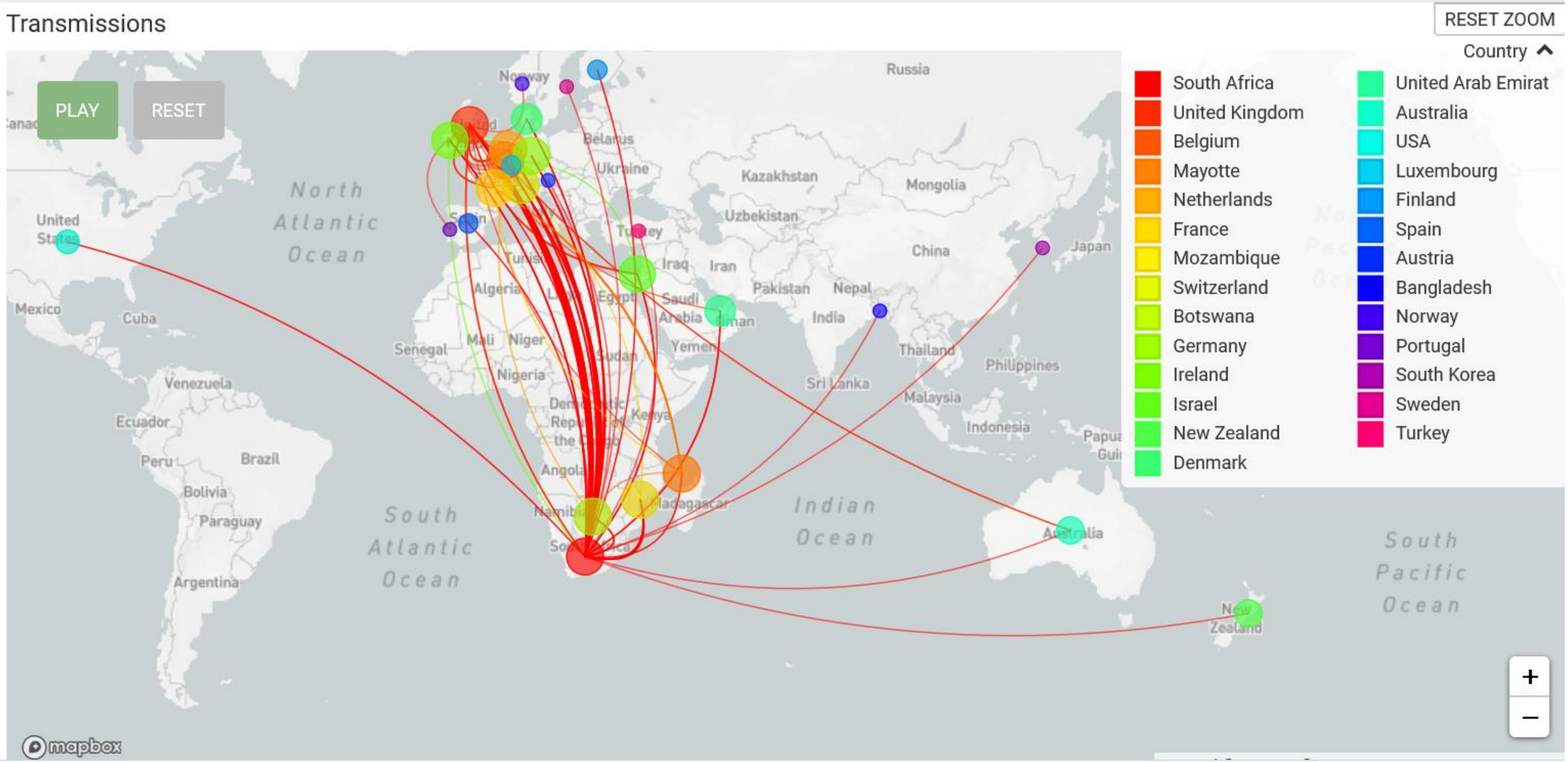
https://www.gisaid.org/hcov19-variants/

GISAID

Phylodynamics of pandemic coronavirus variant 501Y.V2

843 of 843 genomes collected between October 2020 and January 2021

last updated 2021-02-09



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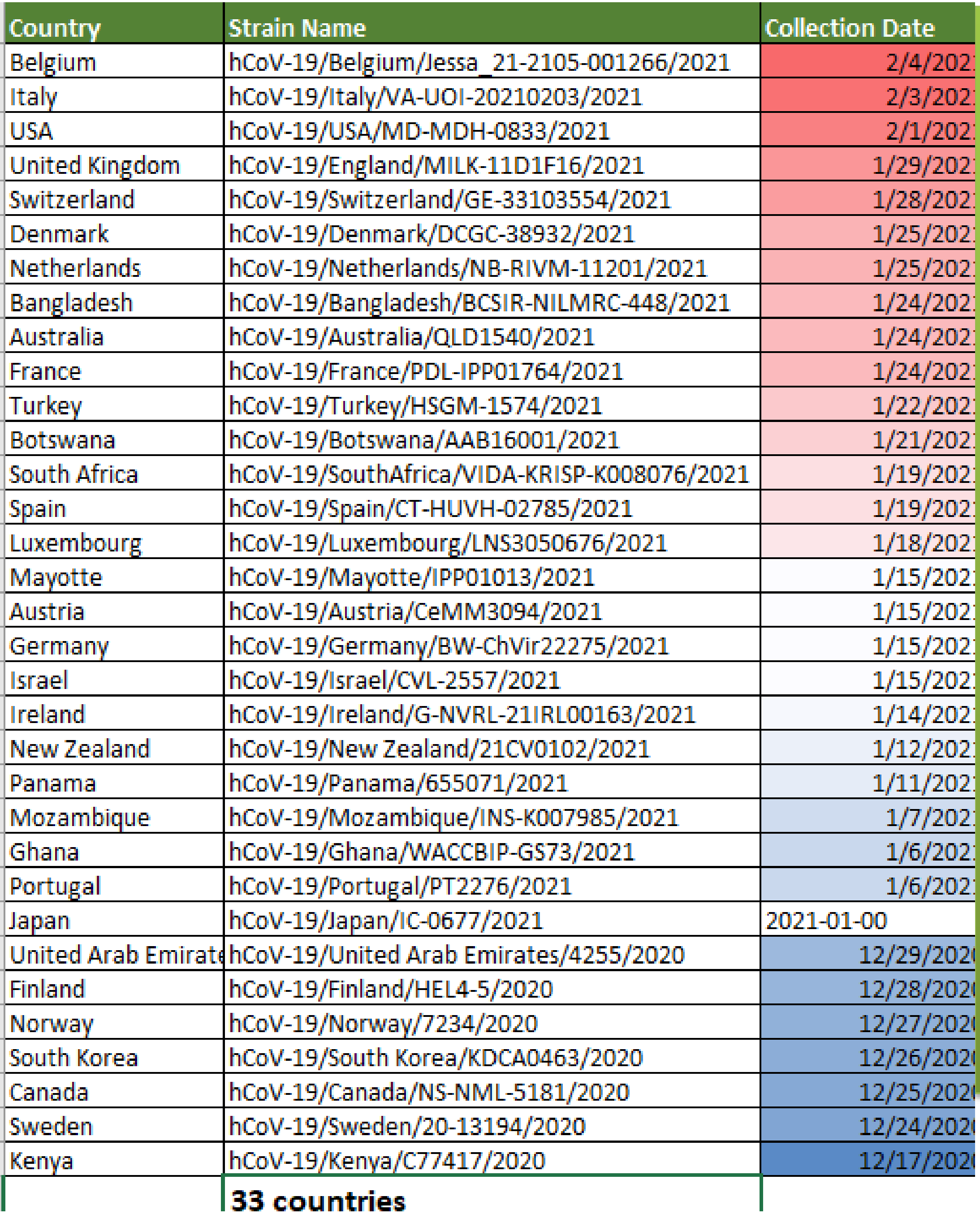

Country	Strain Name	Collection Date
Belgium	hCoV-19/Belgium/Jessa_21-2105-001266/2021	2/4/202
Italy	hCoV-19/Italy/VA-UOI-20210203/2021	2/3/202
USA	hCoV-19/USA/MD-MDH-0833/2021	2/1/202
United Kingdom	hCoV-19/England/MILK-11D1F16/2021	1/29/202
Switzerland	hCoV-19/Switzerland/GE-33103554/2021	1/28/202
Denmark	hCoV-19/Denmark/DCGC-38932/2021	1/25/202
Netherlands	hCoV-19/Netherlands/NB-RIVM-11201/2021	1/25/202
Bangladesh	hCoV-19/Bangladesh/BCSIR-NILMRC-448/2021	1/24/202
Australia	hCoV-19/Australia/QLD1540/2021	1/24/202
France	hCoV-19/France/PDL-IPP01764/2021	1/24/202
Turkey	hCoV-19/Turkey/HSGM-1574/2021	1/22/202
Botswana	hCoV-19/Botswana/AAB16001/2021	1/21/202
South Africa	hCoV-19/SouthAfrica/VIDA-KRISP-K008076/2021	1/19/202
Spain	hCoV-19/Spain/CT-HUVH-02785/2021	1/19/202
Luxembourg	hCoV-19/Luxembourg/LNS3050676/2021	1/18/202
Mayotte	hCoV-19/Mayotte/IPP01013/2021	1/15/202
Austria	hCoV-19/Austria/CeMM3094/2021	1/15/202
Germany	hCoV-19/Germany/BW-ChVir22275/2021	1/15/202
Israel	hCoV-19/Israel/CVL-2557/2021	1/15/202
Ireland	hCoV-19/Ireland/G-NVRL-21IRL00163/2021	1/14/202
New Zealand	hCoV-19/New Zealand/21CV0102/2021	1/12/202
Panama	hCoV-19/Panama/655071/2021	1/11/202
Mozambique	hCoV-19/Mozambique/INS-K007985/2021	1/7/202
Ghana	hCoV-19/Ghana/WACCBIP-GS73/2021	1/6/202
Portugal	hCoV-19/Portugal/PT2276/2021	1/6/202
Japan	hCoV-19/Japan/IC-0677/2021	2021-01-00
United Arab Emirate	hCoV-19/United Arab Emirates/4255/2020	12/29/202
Finland	hCoV-19/Finland/HEL4-5/2020	12/28/202
Norway	hCoV-19/Norway/7234/2020	12/27/202
South Korea	hCoV-19/South Korea/KDCA0463/2020	12/26/202
Canada	hCoV-19/Canada/NS-NML-5181/2020	12/25/202
Sweden	hCoV-19/Sweden/20-13194/2020	12/24/202
Kenya	hCoV-19/Kenya/C77417/2020	12/17/202
	33 countries	

GISAID

Most recent reported occurrences in different countries 501Y.V2

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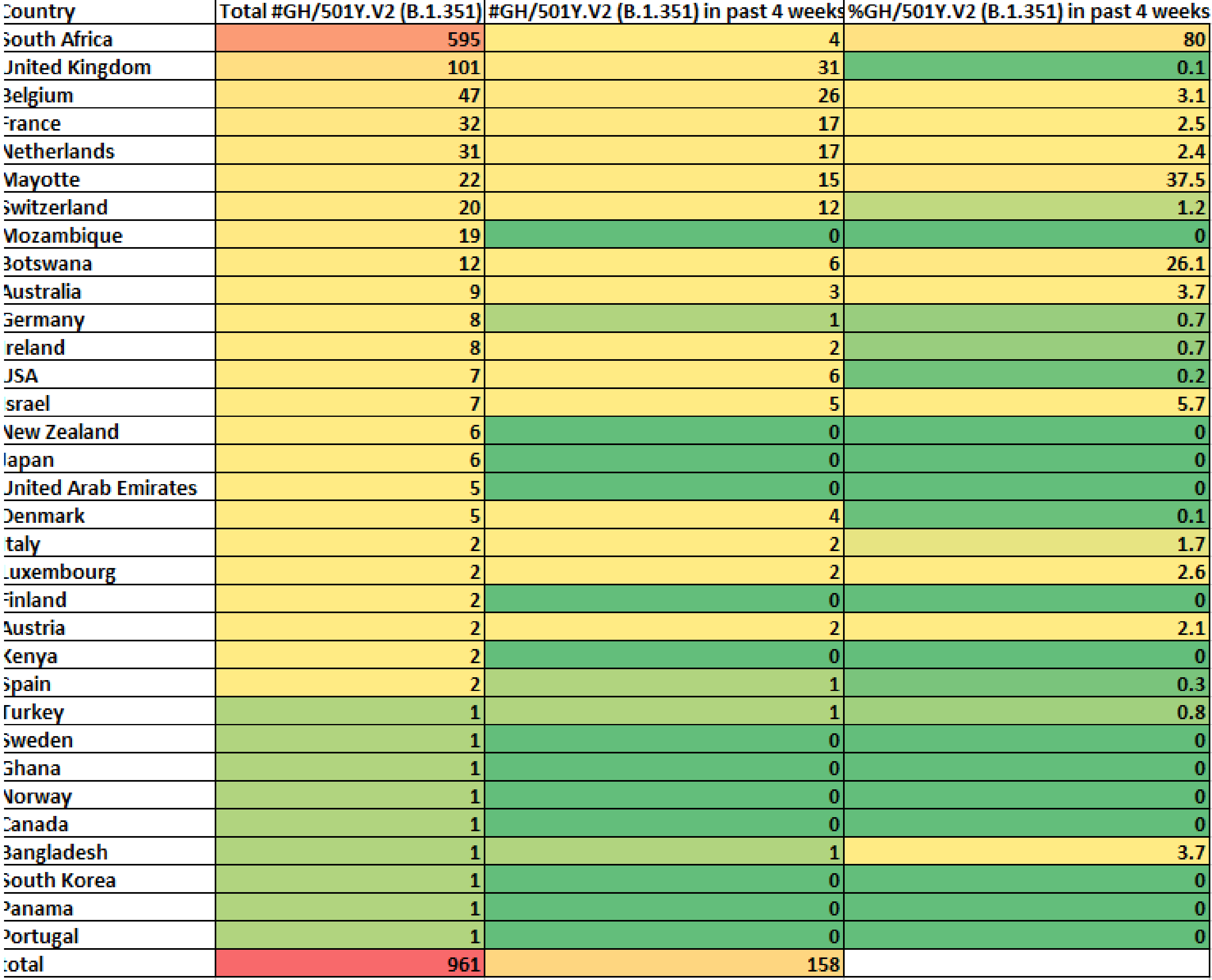
https://www.gisaid.org/hcov19-variants/

Country Submission Count 501Y.V2



Country	Total #GH/501Y.V2 (B.1.351)	#GH/501Y.V2 (B.1.351) in past 4 weeks	%GH/501Y.V2 (B.1.351) in past 4 weeks
South Africa	595	4	80
United Kingdom	101	31	0.1
Belgium	47	26	3.1
France	32	17	2.5
Netherlands	31	17	2.4
Mayotte	22	15	37.5
Switzerland	20	12	1.2
Mozambique	19	0	0
Botswana	12	6	26.1
Australia	9	3	3.7
Germany	8	1	0.7
Ireland	8	2	0.7
USA	7	6	0.2
Israel	7	5	5.7
New Zealand	6	0	0
Japan	6	0	0
United Arab Emirates	5	0	0
Denmark	5	4	0.1
Italy	2	2	1.7
Luxembourg	2	2	2.6
Finland	2	0	0
Austria	2	2	2.1
Kenya	2	0	0
Spain	2	1	0.3
Turkey	1	1	0.8
Sweden	1	0	0
Ghana	1	0	0
Norway	1	0	0
Canada	1	0	0
Bangladesh	1	1	3.7
South Korea	1	0	0
Panama	1	0	0
Portugal	1	0	0
Total	961	158	

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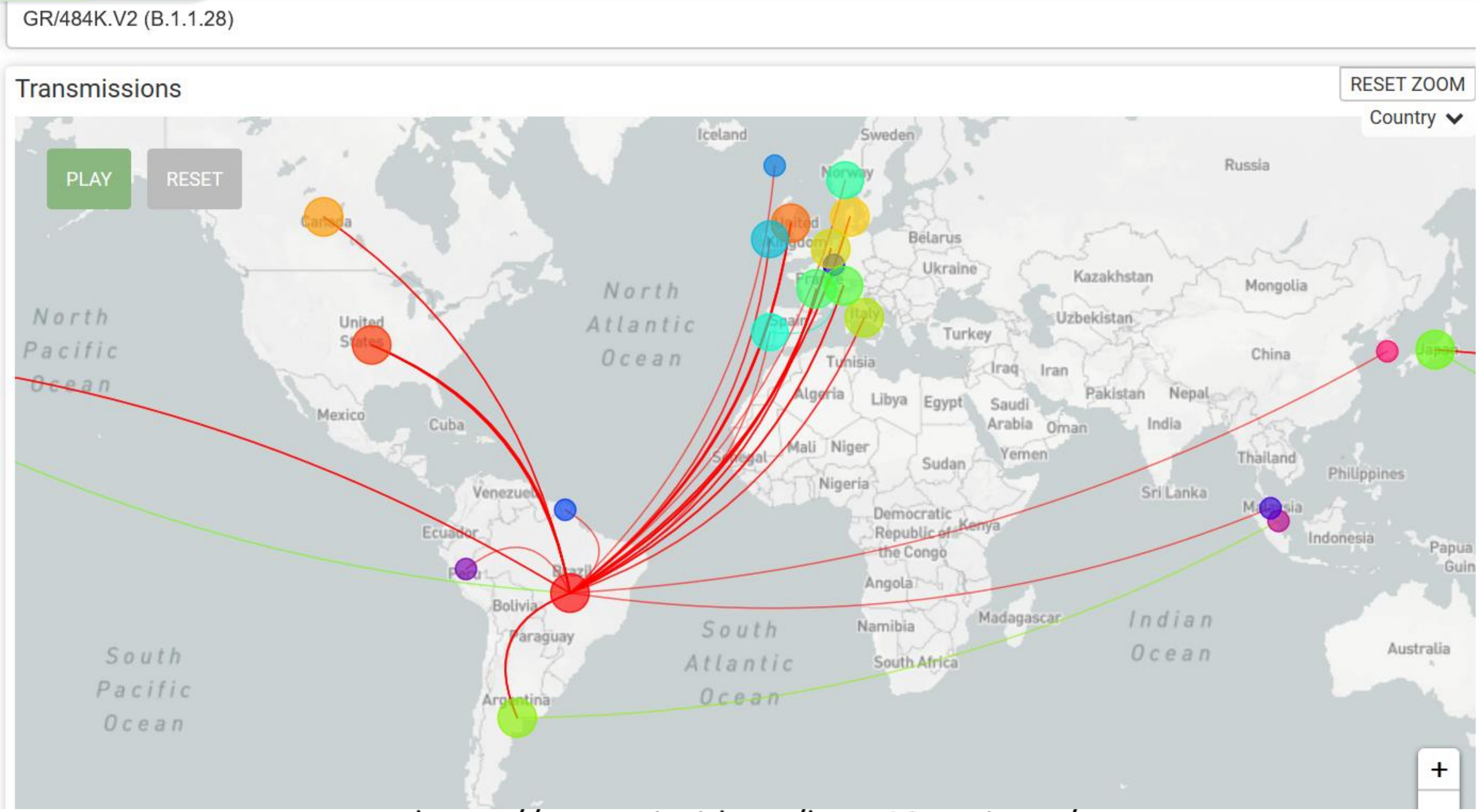
https://www.gisaid.org/hcov19-variants/

Phylodynamics of pandemic coronavirus variant 484K.V2
376 of 376 genomes collected between April 2020 and January 2021
last updated 2021-02-09


GR/484K.V2 (B.1.1.28)

Transmissions

https://www.gisaid.org/hcov19-variants/

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Virology Research Center

National Research Institute of Tuberculosis and Lung Disease (NRITLD)

Tracking of Variants
484K.V2

Most recent reported occurrences in different countries

Country	Strain Name	Collection Date
United Kingdom	hCoV-19/England/SHEF-10D7430/2021	2/3/2021
Peru	hCoV-19/Peru/LIM-INS-175/2021	1/28/2021
Ireland	hCoV-19/Ireland/C-NVRL-84IRL69373/2021	1/28/2021
USA	hCoV-19/USA/WI-GMF-51897/2021	1/26/2021
Brazil	hCoV-19/Brazil/RR-1087/2021	1/25/2021
France	hCoV-19/France/ARA-0011082/2021	1/25/2021
Netherlands	hCoV-19/Netherlands/NH-RIVM-10916/2021	1/25/2021
Colombia	hCoV-19/Colombia/AMA-INS-VG-631/2021	1/23/2021
French Guiana	hCoV-19/French Guiana/IPP01950/2021	1/22/2021
Switzerland	hCoV-19/Switzerland/BE-620-3486/2021	1/19/2021
Denmark	hCoV-19/Denmark/DCGC-36886/2021	1/18/2021
Italy	hCoV-19/Italy/ABR-IZSGC-TE30964/2021	1/18/2021
Luxembourg	hCoV-19/Luxembourg/LNS0817333/2021	1/17/2021
Portugal	hCoV-19/Portugal/PT2443/2021	1/16/2021
Faroe Islands	hCoV-19/Faroe Islands/HFS-193/2021	1/12/2021
South Korea	hCoV-19/South Korea/KDCA0464/2021	1/10/2021
Japan	hCoV-19/Japan/IC-0562/2021	1/2/2021
Canada	hCoV-19/Canada/LTRI-1617/2020	12/24/2020
Argentina	hCoV-19/Argentina/PAIS-E0103/2020	12/22/2020
Norway	hCoV-19/Norway/7025/2020	12/17/2020
Malaysia	hCoV-19/Malaysia/IMR_WC348412/2020	12/15/2020
Singapore	hCoV-19/Singapore/1486/2020	12/14/2020
	22 countries	

Country Submission Count

Country	Total #GR/484K.V2 (B.1.1.28)	#GR/484K.V2 (B.1.1.28) in past 4 weeks	%GR/484K.V2 (B.1.1.28) in past 4 weeks
Brazil	254	40	78.4
USA	43	10	0.3
United Kingdom	25	8	0
Canada	13	0	0
Japan	9	0	0
French Guiana	8	6	18.2
Netherlands	8	7	1
Denmark	8	2	0.1
Colombia	7	5	23.8
Italy	5	3	2.5
Switzerland	5	4	0.4
France	5	4	0.6
Argentina	5	0	0
Ireland	5	4	1.4
Norway	3	0	0
Portugal	3	1	0.3
Faroe Islands	1	0	0
Luxembourg	1	1	1.3
Singapore	1	0	0
Peru	1	1	50
South Korea	1	0	0
Malaysia	1	0	0
total	412	96	

https://www.gisaid.org/hcov19-variants/

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B.1.1.7 lineage 20I/501Y.V1/ VOC-202012/01)

- This variant has a mutation in RBD of the spike protein ; N501Y
- This variant also has several other mutations, including:
  - 69/70 deletion: occurred spontaneously many times and likely leads to a conformational change in the spike protein
  - P681H: near the S1/S2 furin cleavage site, a site with high variability in coronaviruses.
  - ORF8 stop codon (Q27stop): mutation in ORF8, the function of which is unknown.
- This variant is estimated to have first emerged in the UK during September 2020.
- This variant is associated with increased transmissibility
- Currently there is evidence to suggest that the variant has impact on the severity of disease and death but not vaccine efficacy.

Emerging SARS-CoV-2 Variants | CDC

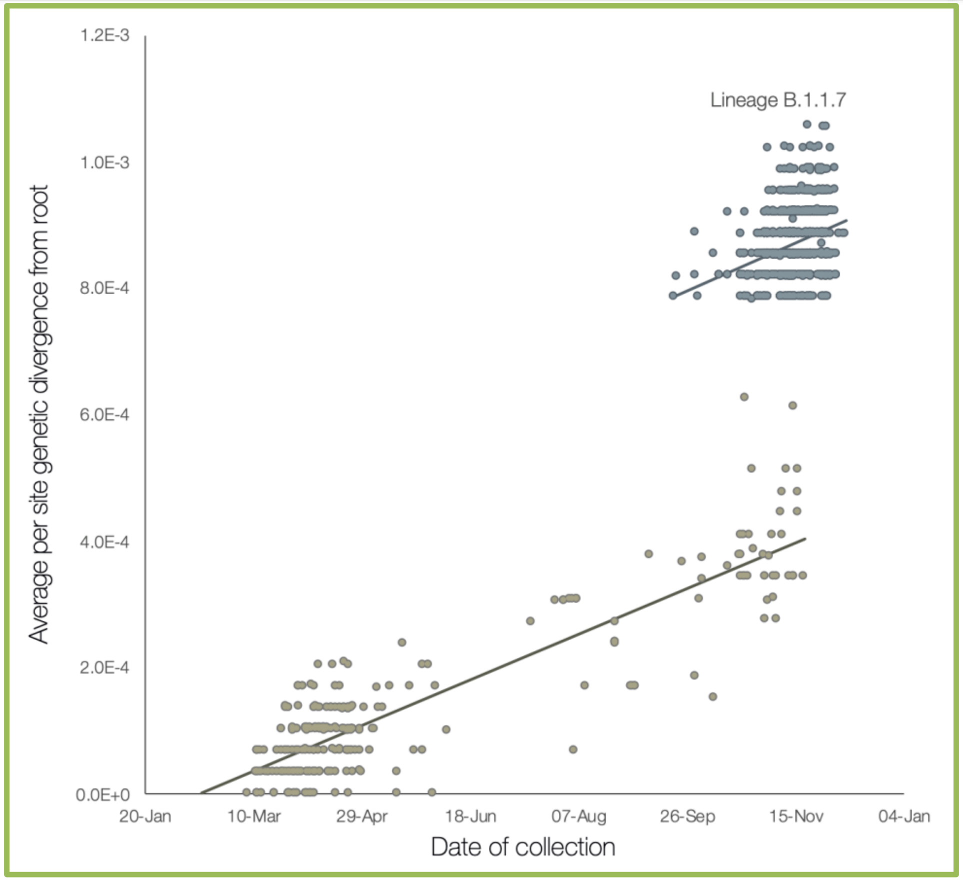
SARS-CoV-2 Variants

Name (Pangolin)	Name (Nextstrain)	First Detected	Countries Reporting Cases	Key Mutations	Transmissibility Rate
B.1.1.7	20I/501Y.V1	United Kingdom	70	•69/70 deletion •144Y deletion •N501Y •A570D •D614G •P681H	~50% increase
P.1	20J/501Y.V3	Japan/ Brazil	>4	•E484K •K417N/T •N501Y •D614G	Not determined
B.1.351	20H/501.V2	South Africa	>30	•K417N •E484K •N501Y •D614G	Not determined

https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html

characterization of VUI202012/01 SARS-CoV-2 variant

lineage B.1.1.7 is more divergent from the phylogenetic root of the pandemic



Non-synonymous mutations and deletions inferred to occur on the branch leading to lineage B.1.1.7 lineage

gene	nucleotide	amino acid
ORF1ab	C3267T	T1001I
	C5388A	A1708D
	T6954C	I2230T
	11288-11296 deletion	SGF 3675-3677 deletion
spike	21765-21770 deletion	HV 69-70 deletion
	21991-21993 deletion	Y144 deletion
	A23063T	N501Y
	C23271A	A570D
	C23604A	P681H
	C23709T	T716I
	T24506G	S982A
	G24914C	D1118H
Orf8	C27972T	Q27stop
	G28048T	R52I
	A28111G	Y73C
N	28280 GAT->CTA	D3L
	C28977T	S235F

501.V2 variant

- first detected in the Nelson Mandela Bay , metropolitan area of the Eastern Cape province of South Africa and reported on 18 December 2020.
  - driving the second wave
  - the variant spreads faster than other earlier variants of the virus
- the variant can attach more easily to human cells because of three mutations in the receptor-binding domain (RBD) in the spike glycoprotein
  - N501Y, K417N, and E484K
  - E484K and N501Y, are within the receptor-binding motif (RBM) of the receptor-binding domain (RBD)
- 501Y.V1 & 501Y.V1; Phylogenetically unlinked
  - N501Y mutation has also been detected in the 501Y.V1
  - Two mutations found in 501Y.V2, E484K and K417N, are not found in 501Y.V1
  - Also, 501.V2 does not have the 69-70del mutation found in the other variant
- Vaccine evasion; "a big question mark“
  - “vaccine might not have the full efficacy“
  - the variant's multiple spike mutations "could lead to some escape from immune protection“
  - Pfizer researchers conducted tests involving 20 blood assays to be capable of affording protection against one of the 501.V2 variant mutations (N501Y, shared with variant B1.1.7)
  - Further investigation was to be undertaken to ascertain the level of protection involved
    - Oxford vaccine & Johnson&Johnson vaccine

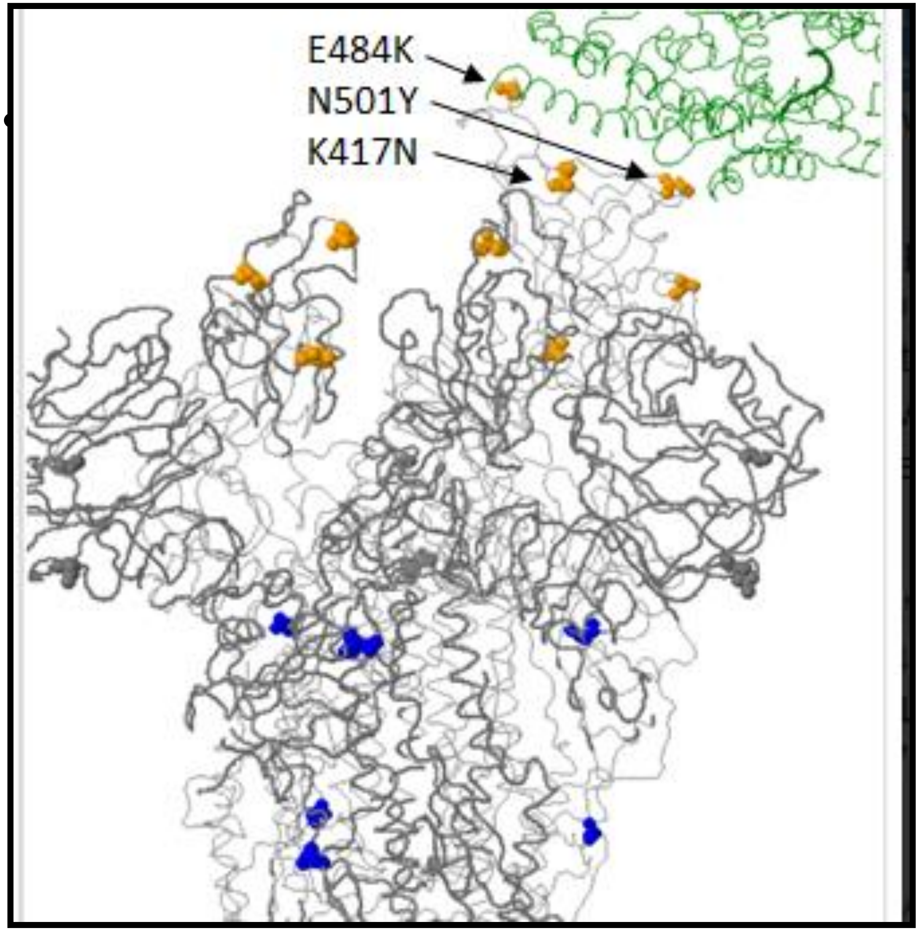
Gene	Nucleotide	Amino acid
ORF1ab	C1059T	T265I
	G5230T	K1655N
	C8660T	H2799Y
	C8964T	S2900L
	A10323G	K3353R
	G13843T	D4527Y
	C14408T^1	P4715L
	C17999T	T5912I
Spike	C21614T	L18F
	A21801C	D80A
	A22206G	D215G
	G22299T	R246I
	G22813T	***K417N***
	G23012A	***E484K***
	A23063T	***N501Y***
	A23403G^1	D614G
	G23664T	A701V
ORF3a	G25563T	Q57H
	C25904T	S171L
E	C26456T	P71L
N	C28887T	T205I

Footnote: ^{1}Presented in parent lineage B.1.
Source: Tegally et al. (2020)

Novel variant 501Y.V2 with triple spike receptor binding site substitutions

GISAID

- The 301 recent virus genomes
  - 182 from clade GH
  - 71 from clade GR
  - 45 from clade G
  - one from clade GV
  - and two from other clades.
- Of the 182 genomes from clade GH
  - 89% have three mutations in the spike receptor binding site (K417N, E484K, and N501Y)
  - 27% of the 182 have a nine-nucleotide deletion in NSP6 in addition to the three mutations
    - Nsp6 limits autophagosome expansion and interferes with autophagosome delivery of viral factors to lysosomes for destruction.



https://www.gisaid.org/references/gisaid-in-the-news/novel-variant-combination-in-spike-receptor-binding-site/

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P.1 lineage (20J/501Y.V3)

- The P.1 variant is a branch off the B.1.1.28 lineage that was first reported by the National Institute of Infectious Diseases (NIID) in Japan in four travelers from Brazil, sampled during routine screening at Haneda airport outside Tokyo.
- The P.1 lineage contains 17 unique amino acid changes and 3 deletions.
  - This variant contains three mutations in the spike protein receptor binding domain: K417T, E484K, and N501Y.
  - identified 5 lineage-defining SNPs: C100U (5’UTR), T10667G (NSP5_L205V), C11824T (NSP6), G23012A (Spike_E484K), and G28628T (N_A119S)
- There is evidence to suggest that some of the mutations in the P.1 variant may affect its transmissibility and antigenic profile, which may affect the ability of antibodies generated through a previous natural infection or through vaccination to recognize and neutralize the virus.
  - A recent study reported on a cluster of cases in Manaus, the largest city in the Amazon region, in which the P.1 variant was identified in 42% of the specimens sequenced from late December. In this region, it is estimated that approximately 75% of the population had been infected with SARS-CoV2 as of October 2020. However, since mid-December the region has observed a surge in cases. The emergence of this variant raises concerns of a potential increase in transmissibility or propensity for SARS-CoV-2 re-infection of individuals.

Emerging SARS-CoV-2 Variants | CDC

SARS-CoV-2ViralVariants—Tackling a Moving Target

- **‘Finnish’ Covid strain**
  - dubbed Fin-796H
  - **Difficult to detect**
    - “Mutations in this variant make it difficult to detect in at least one of the WHO-recommended PCR tests.
    - “The discovery could have a significant impact on determining the spread of the disease.”
- **New Covid variant in UK**
  - dubbed B.1.525, are spread across England, and a further cases are in Wales.
  - carries a mutation that can make Covid-19 vaccines less effective
- **California variant**
  - a novel SARS-CoV-2 variant in Southern California that accounted for 44% of samples collected and studied in January 2021
  - dubbed CAL.20C; lineage 20C/S:452R
  - derives from lineage (B.1.429 and B.1.427)
  - S13I, W152C, and L452R

- The hybrid virus is the result of recombination of the highly transmissible B.1.1.7 variant discovered in the UK and the B.1.429 variant that originated in California and which may be responsible for a recent wave of cases in Los Angeles because it carries a mutation making it resistant to some antibodies.
- If confirmed, the recombinant would be the first to be detected in this pandemic.
- it does carry a mutation from B.1.1.7, called Δ69/70, which makes the UK virus more transmissible, and another from B.1.429, called L452R, which can confer resistance to antibodies.

"This kind of event could allow the virus to have coupled a more infectious virus with a more resistant virus,"

Exclusive: Two variants have merged into heavily mutated coronavirus

The UK and California variants of coronavirus appear to have combined into a heavily mutated hybrid, sparking concern that we may be entering a new phase of the covid-19 pandemic

HEALTH 16 February 2021

By Graham Lawton

People get tested for covid-19 in Los Angeles

New Variant Lab Diagnosis

- Whole genome or partial sequencing
- Multiplex real time PCR
  - Detection of 69-70 deletion
- Melting Curve study

Thank you

Question:

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