49th Myanmar Health Research Congress

Lessons Learnt from COVID-19 Pandemic

Genomic Perspective

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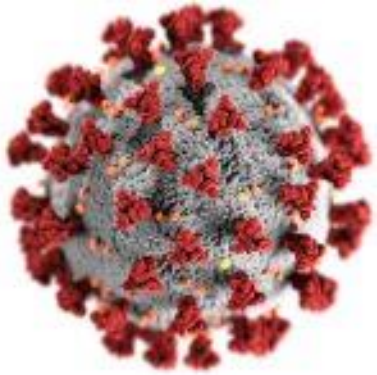
18-Jan-2021

CONTENT

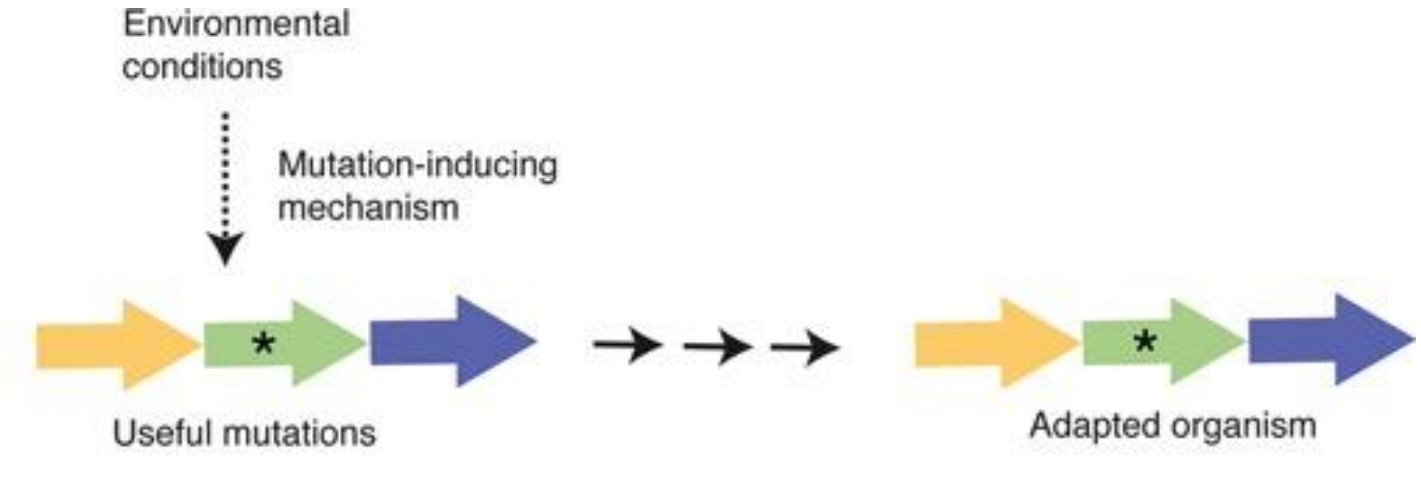


- Genomic Study: Why & How?
- SARS-CoV-2 Genome
- Mutations of SARS-CoV-2
- Findings on SARS-CoV-2 Genomic study in Myanmar
- Further Directions of Genomic study

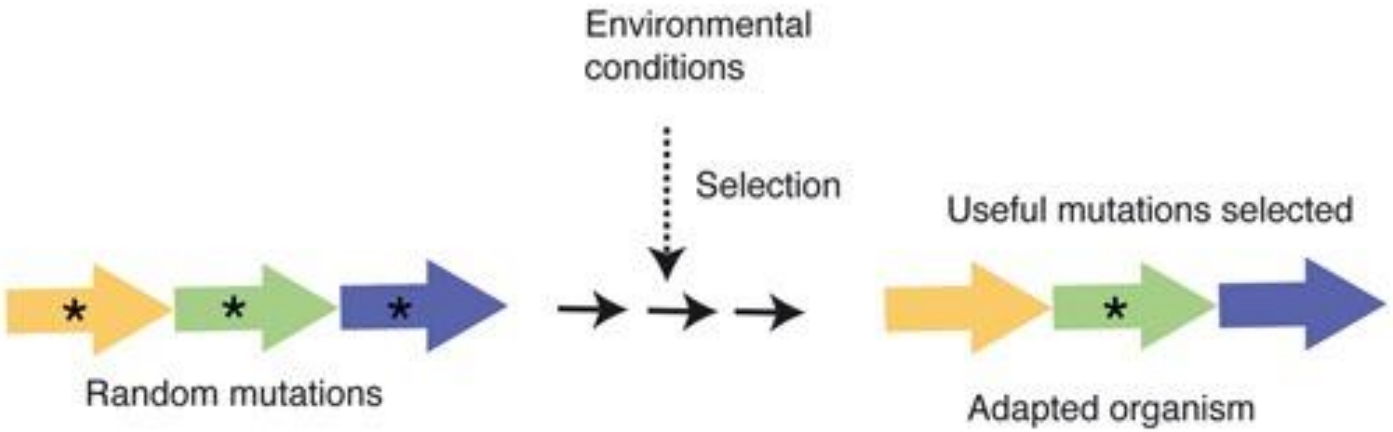
Mutation -- Evolution -- Development

Why we need to know pathogen's Genome?

Jean-Baptiste Lamarck
(1744~1829)



Charles R. Darwin
(1809~1882)



Genomic Character of the SARS-CoV-2

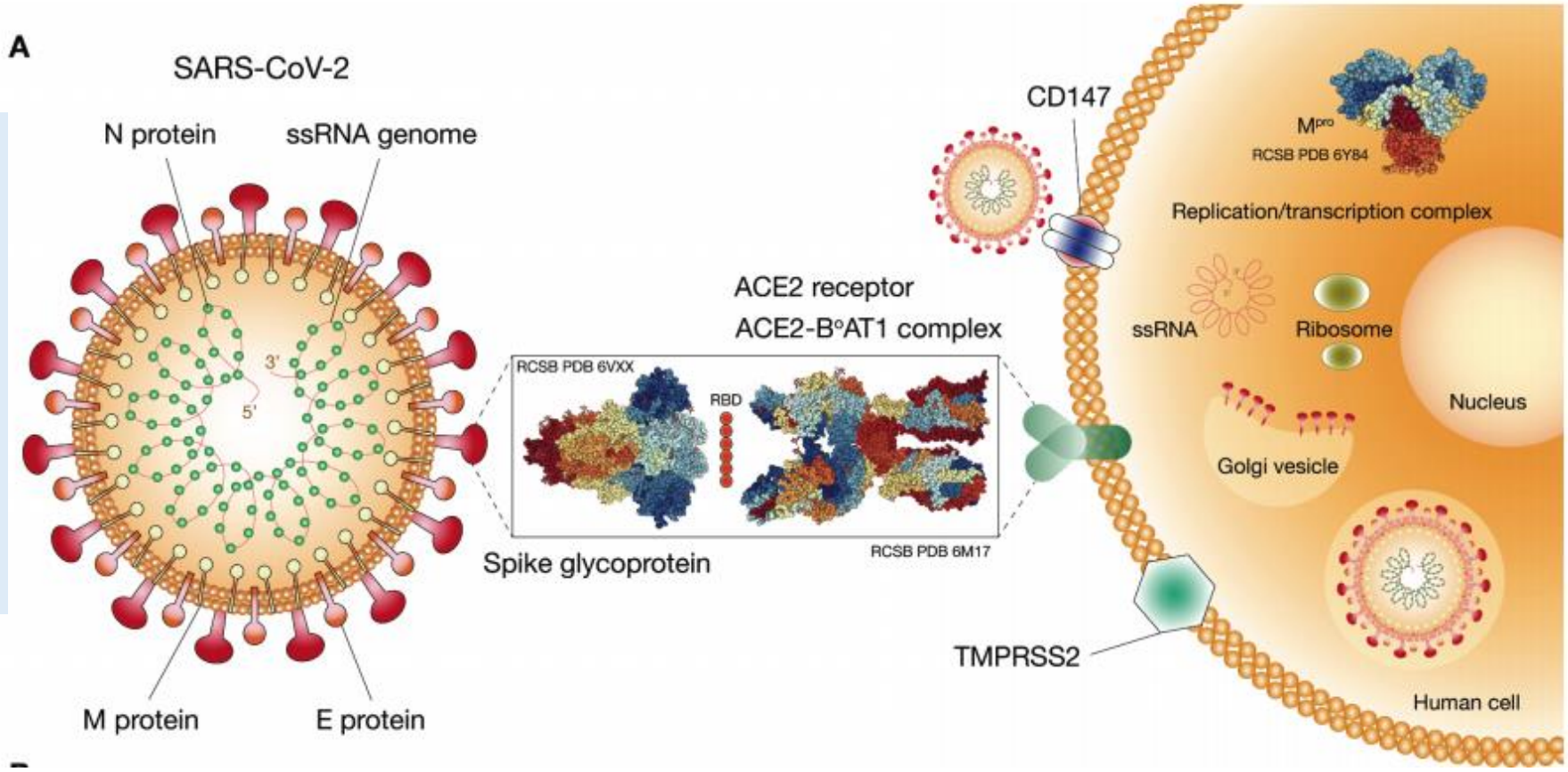
60-140 nm in diameter.

~30 kb genome length.
Largest genomes of any known RNA viruses

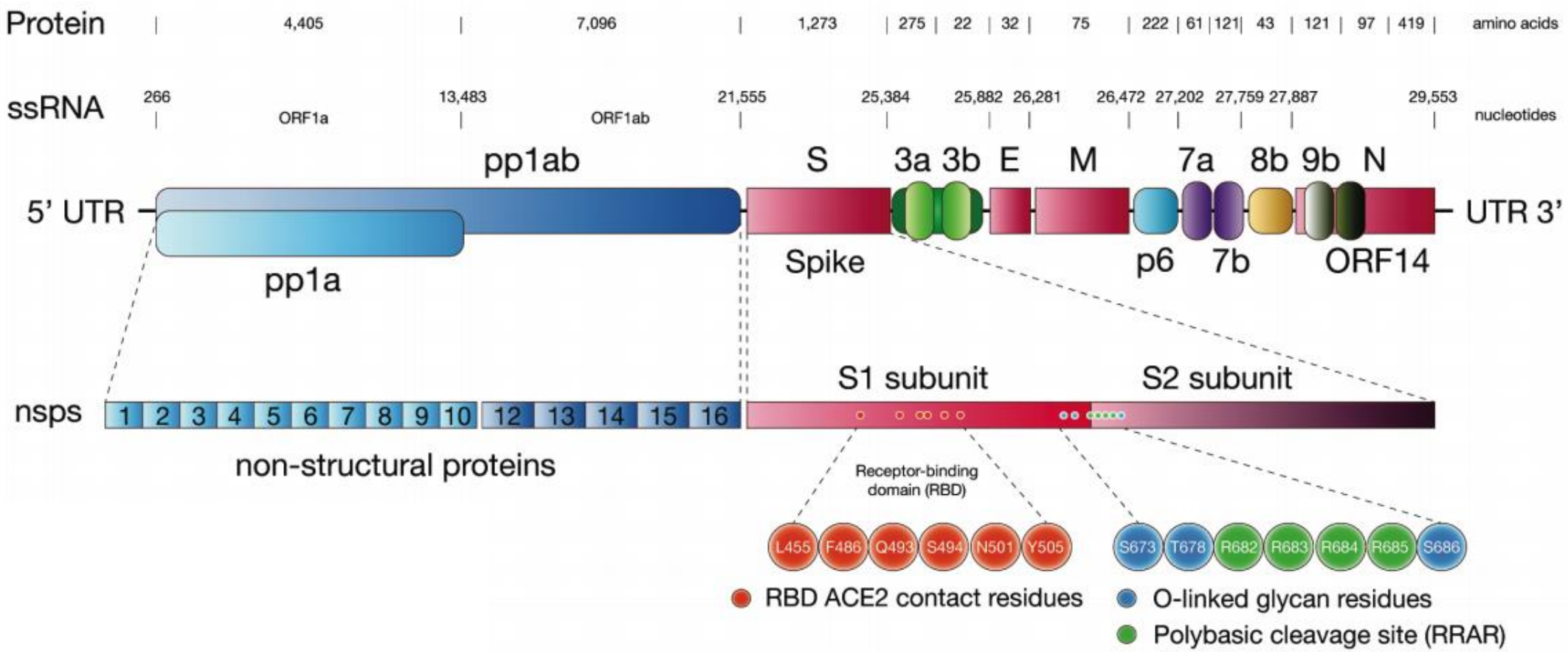
96% similarity to the bat coronavirus

80% similarity with SARS-CoV

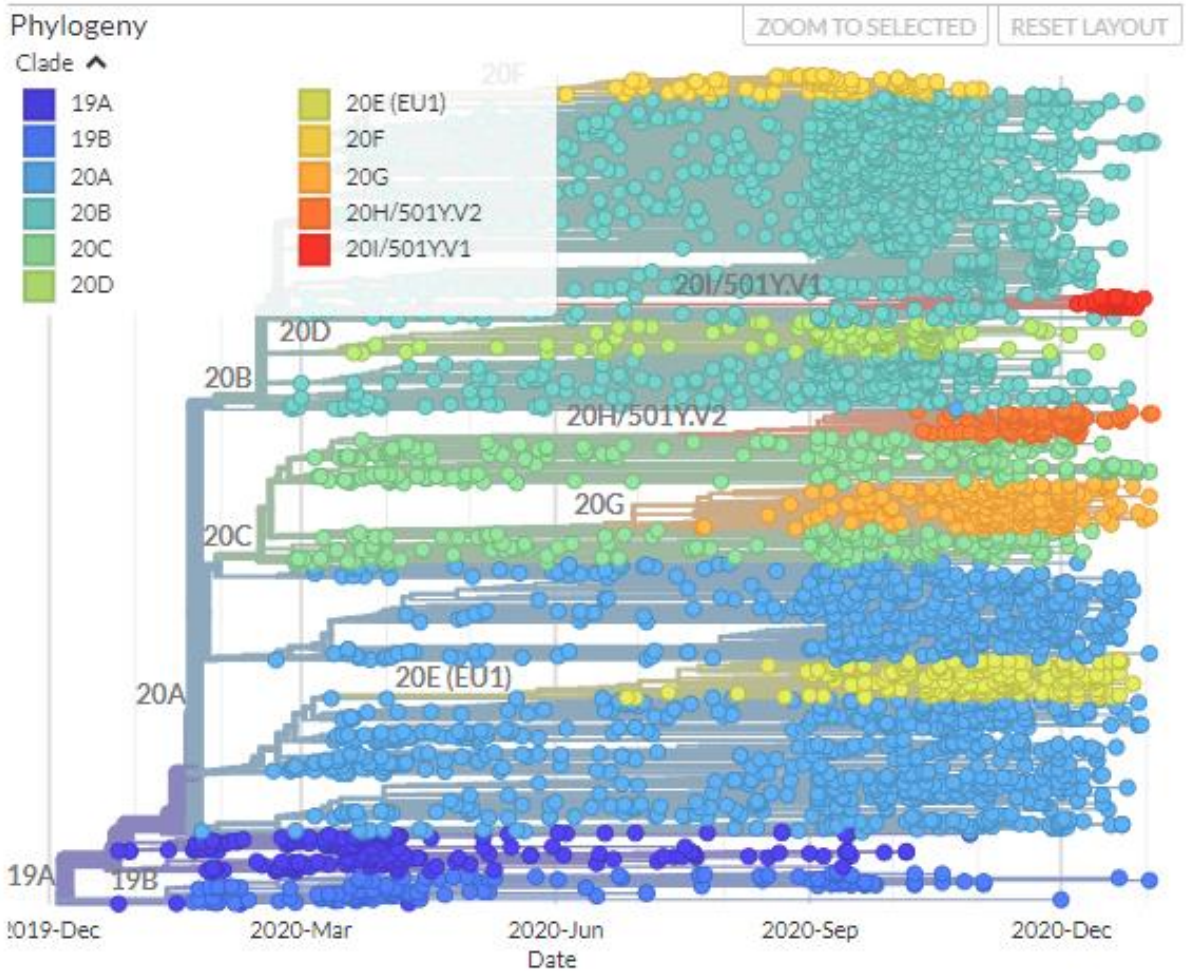
50% identity with MERS-CoV

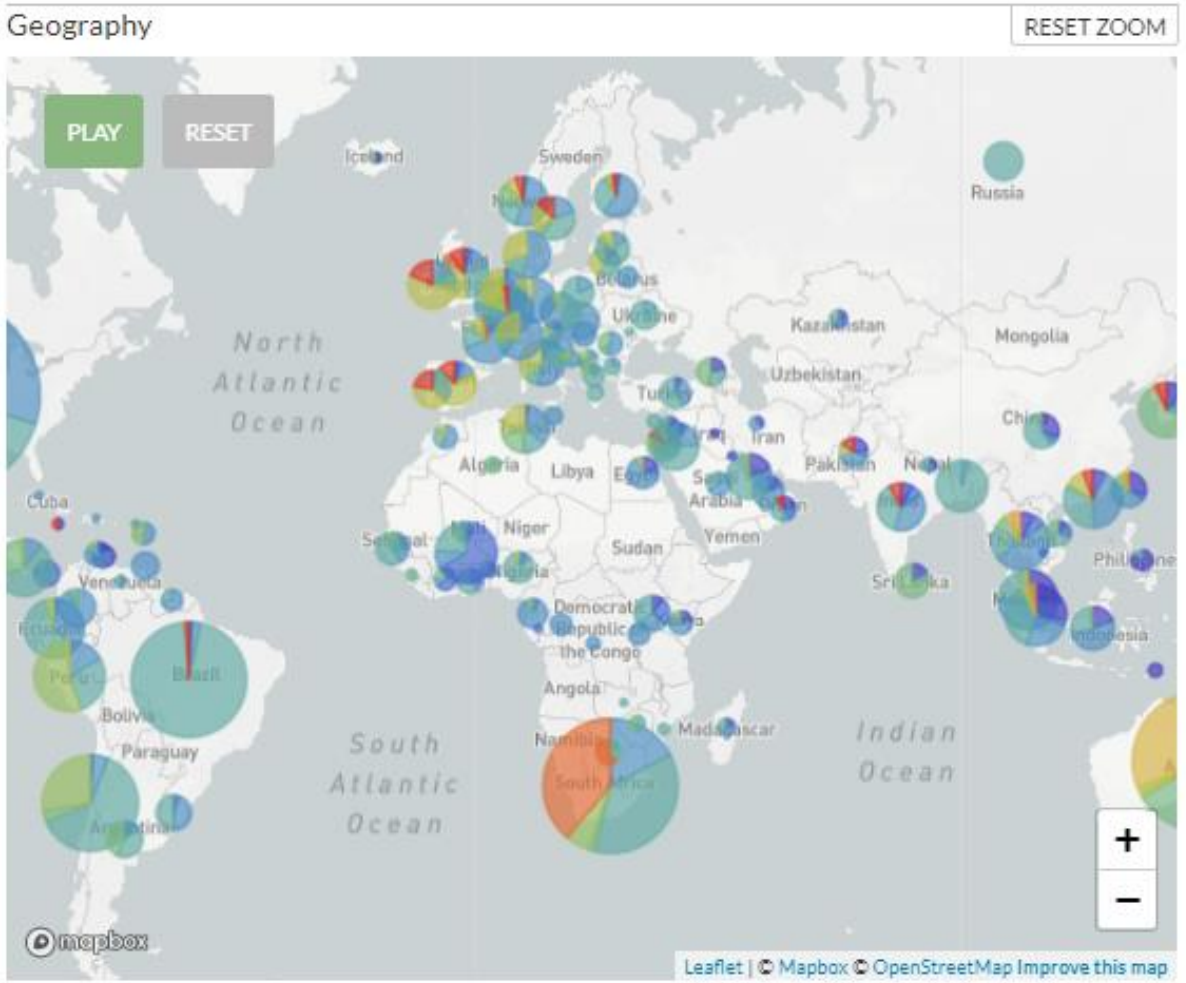


Genomic Character of the SARS-CoV-2



Phylogeny Clade of the SARS-CoV-2

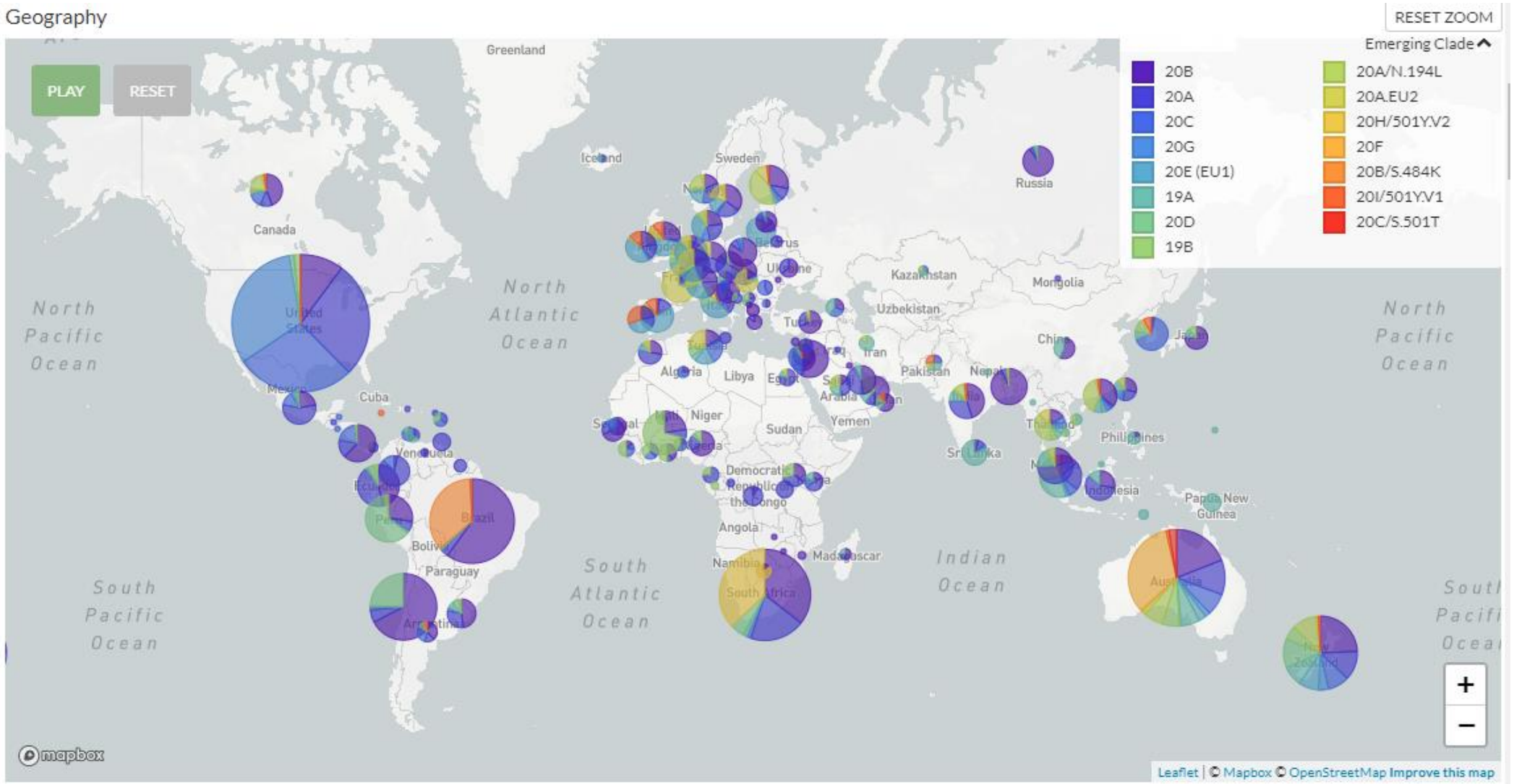




https://nextstrain.org/

As of Jan-10, 2021

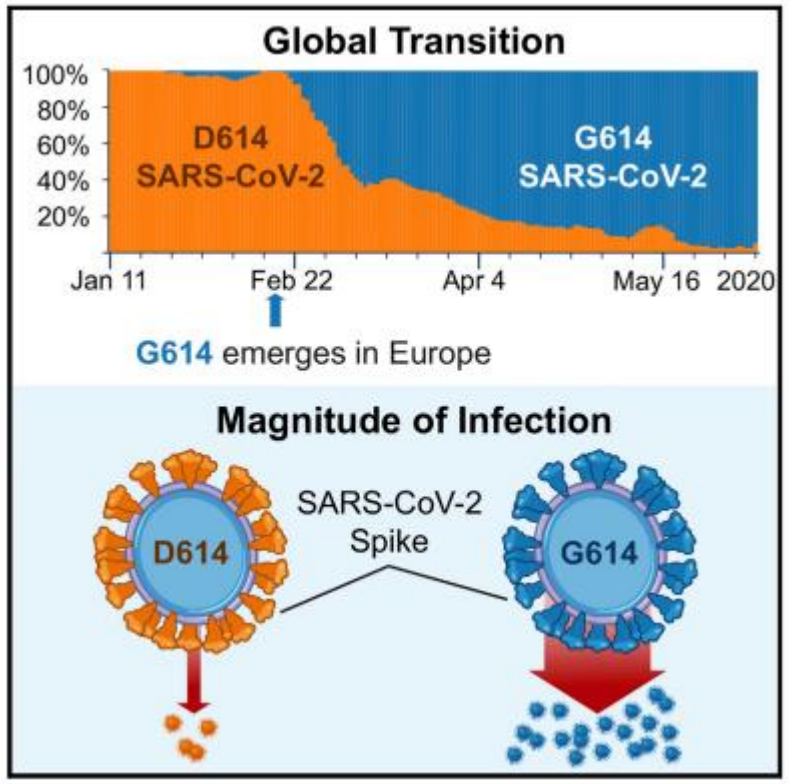
Emerging clade

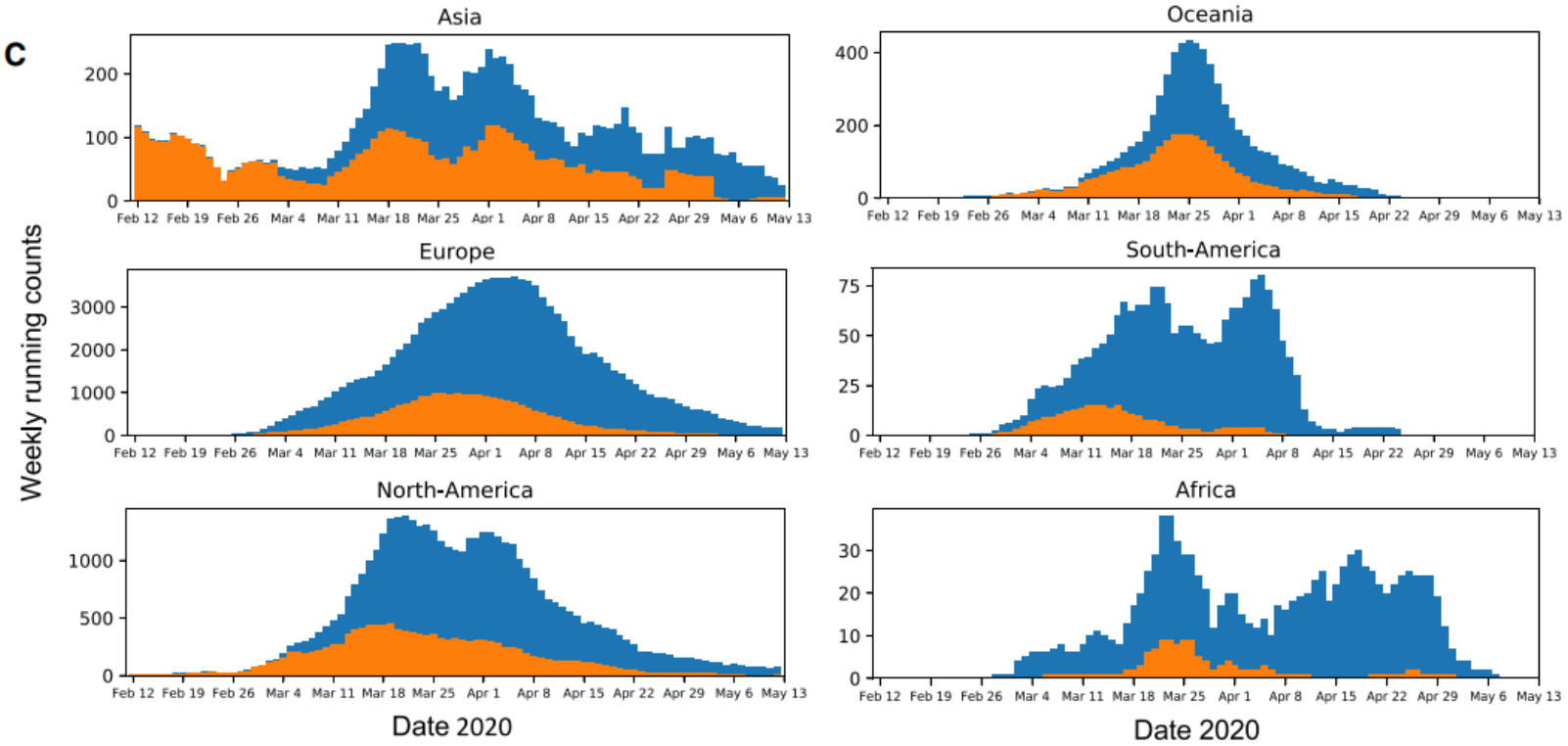


As of Jan-10,2021

https://nextstrain.org/

D614G, a variant replacing the old strain

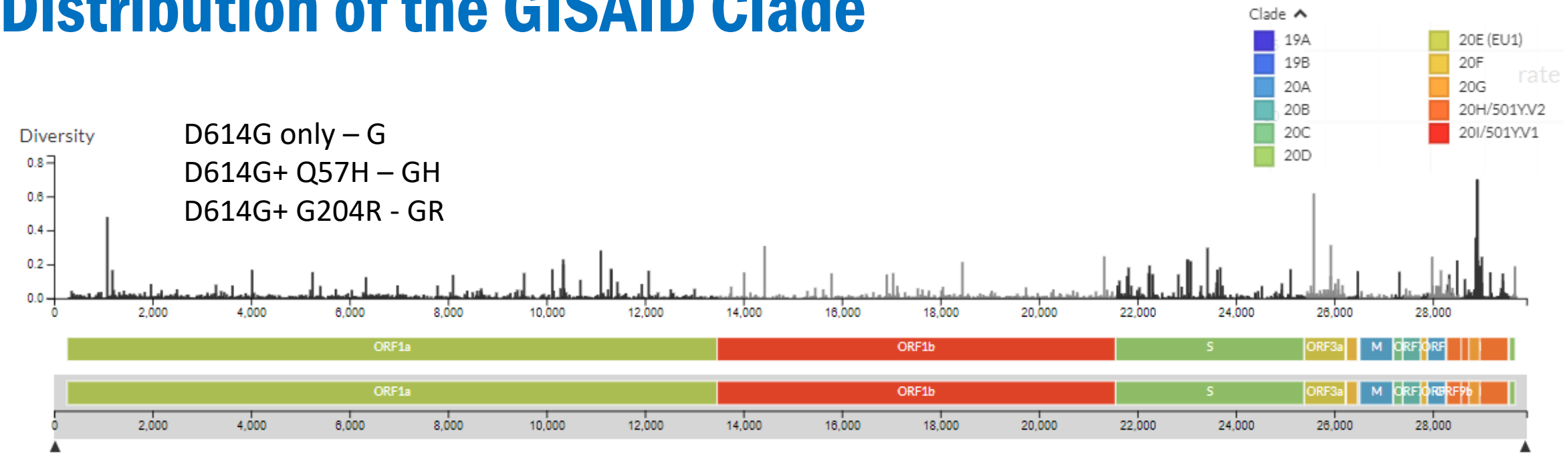




- Link to the surge of the infection in many countries
- It may be responsible for increased infectivity, but no enough evidence for disease severity

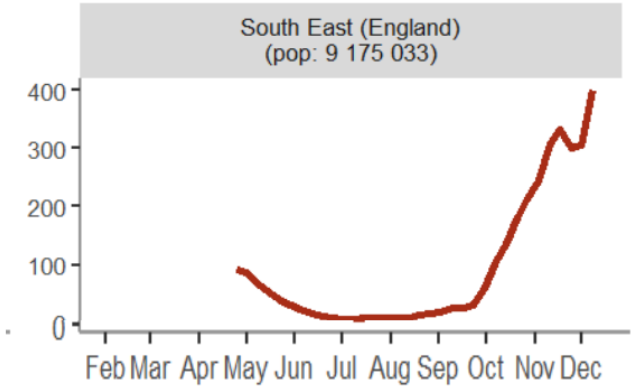
https://doi.org/10.1016/j.cell.2020.06.043

Distribution of the GISAID Clade



https://nextstrain.org/

UK variant: VOC-202012/01 (Lineage B.1.1.7)



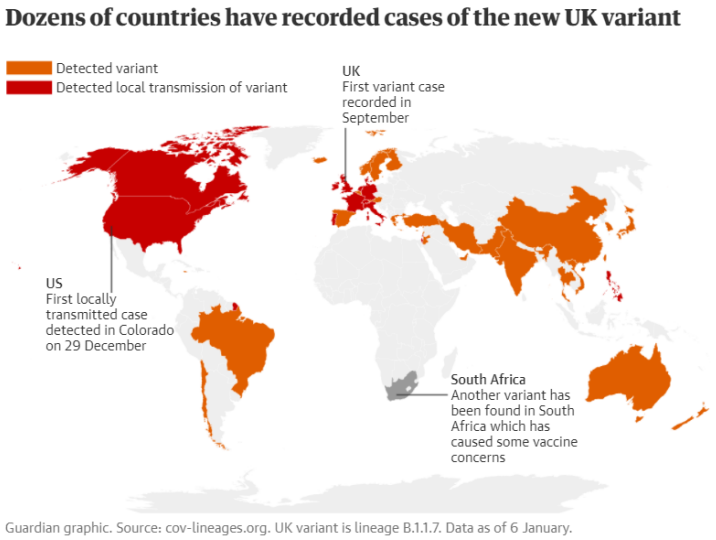
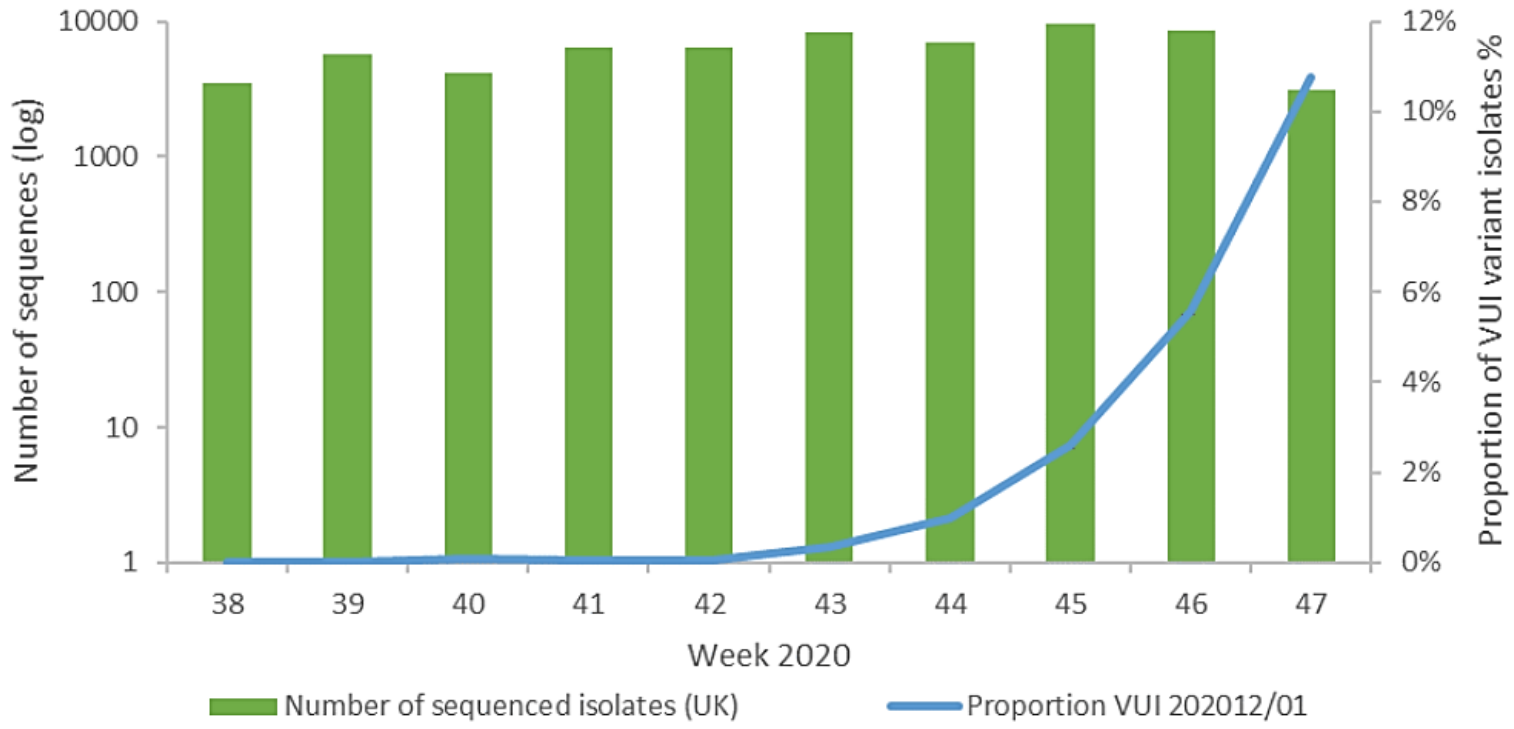
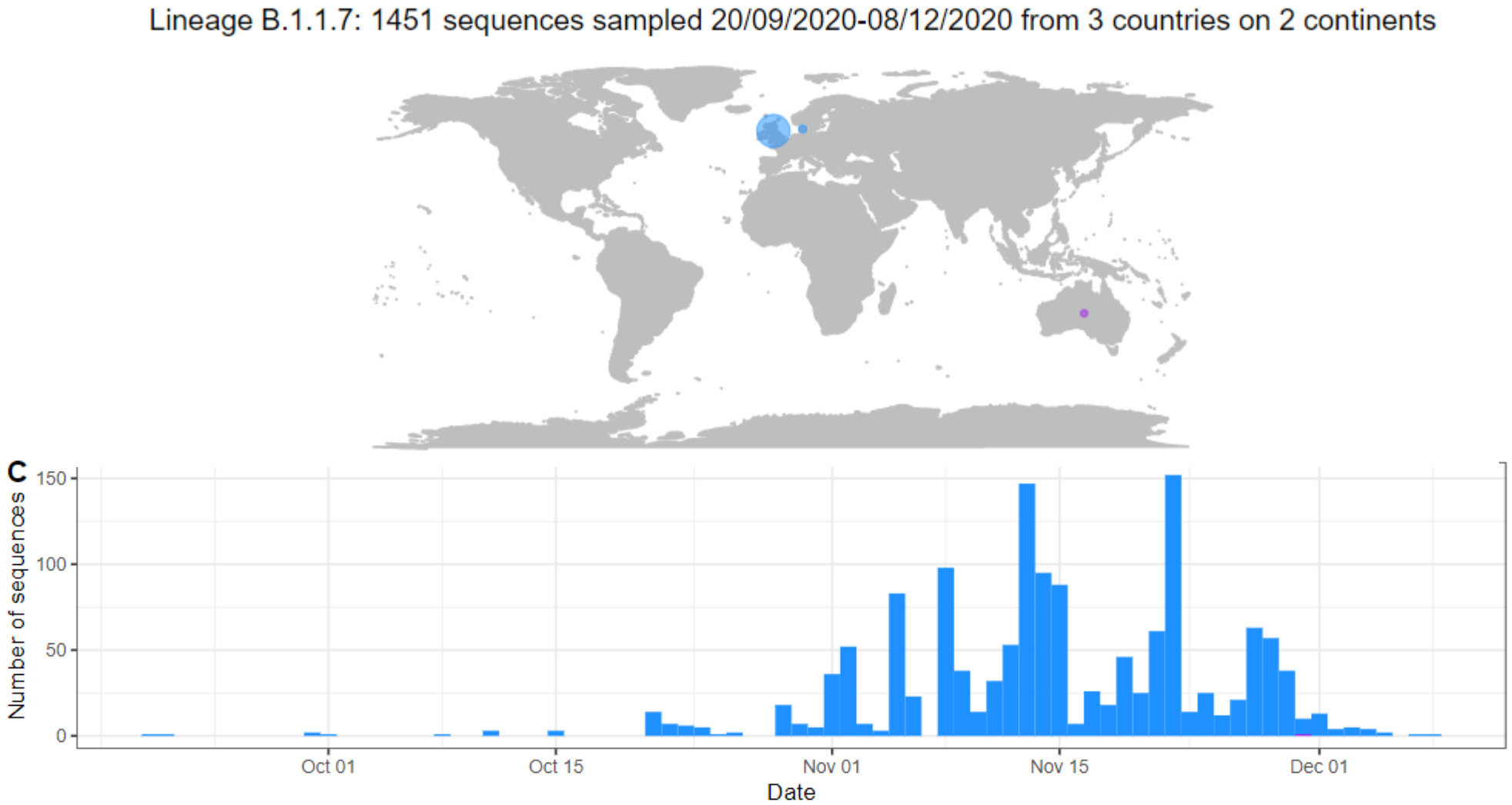


Figure 3. Total number of SARS-CoV-2 sequences from the UK and proportion of VUI 202012/01 variant sequences among all UK sequences in the GISAID EpiCoV database (as of 20 December 2020) by week of sampling, 2020



- Multiple Mutations in Spike of SARS-CoV-2
- Gene deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H

Identification the UK variants

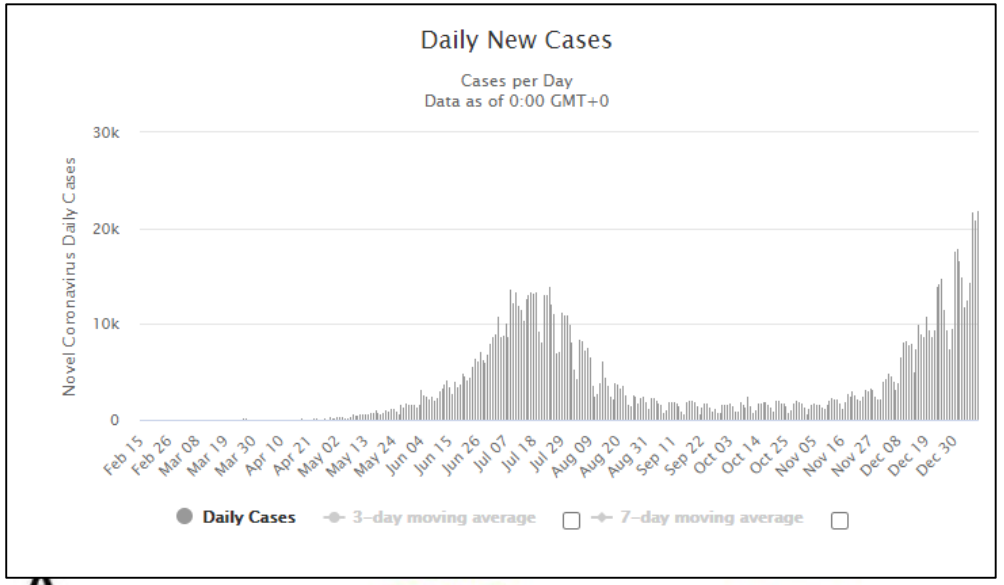


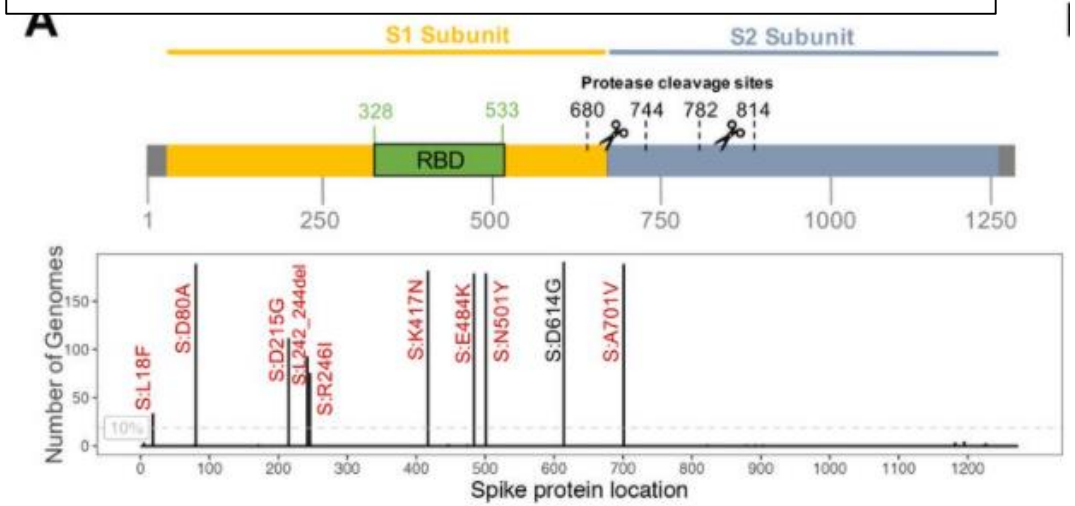
Lineage B.1.1.7 sequence distributions. (A) Map of Lineage B.1.1.7 global sampling locations. Point size is proportional to the number of sequences from the country. (B) Number of Lineage B.1.1.7 sequences collected from each country. (C) Collection day of Lineage B.1.1.7 sequences.

South African variant: 501Y.v2 (Lineage: B.1.351)

B.1.351 report

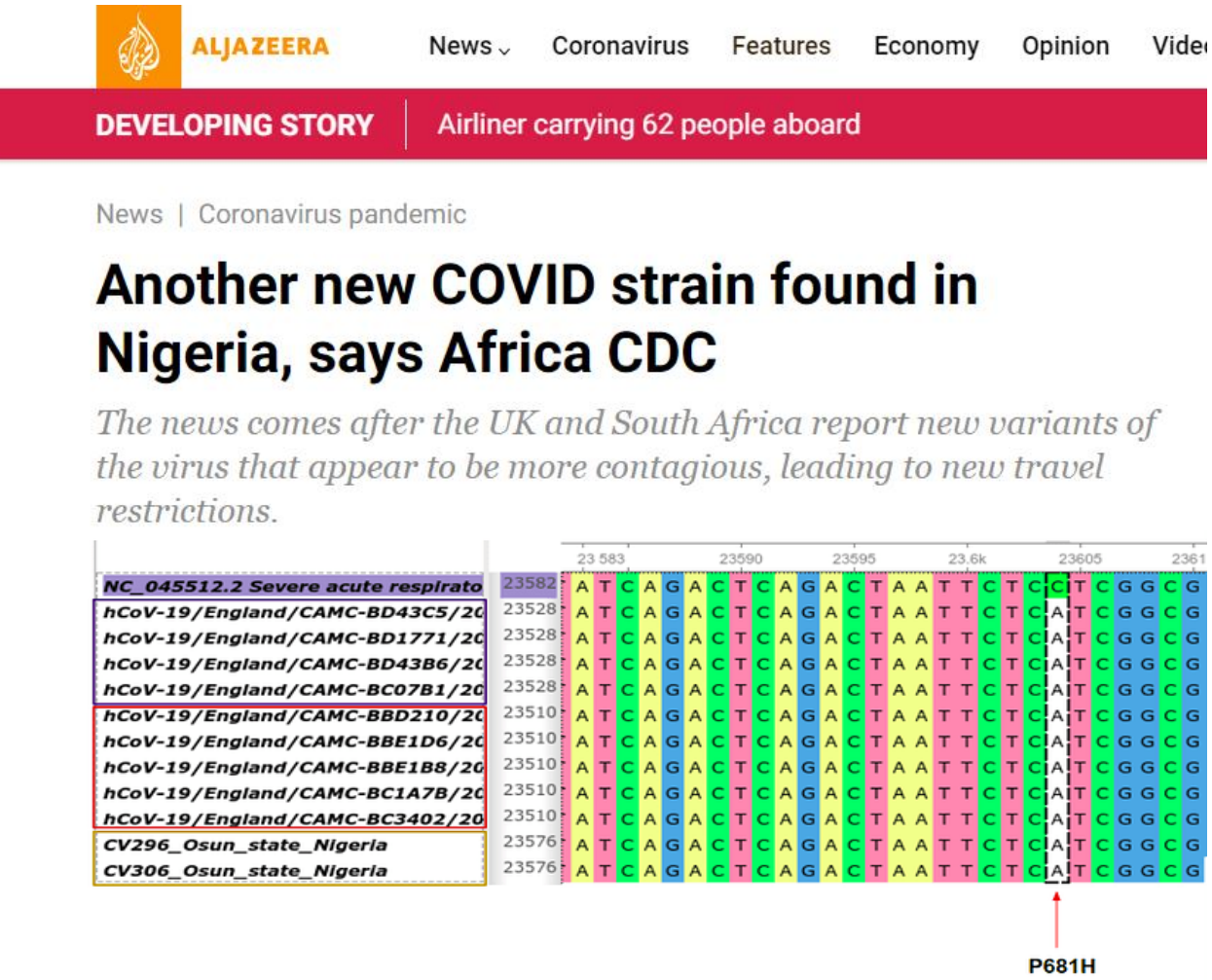
Daily global report for lineage B.1.351

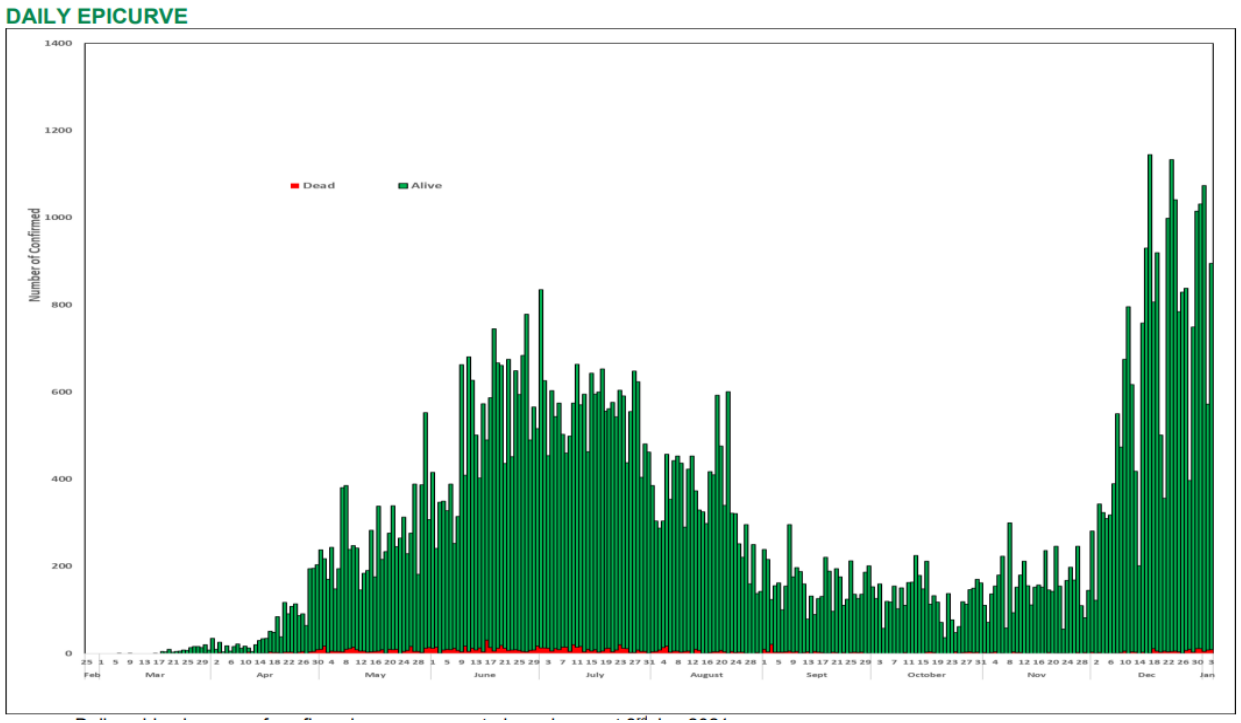




Spike Mutations: N501Y, K417N, and E484K

Nigeria Variant: P681H mutation





P681H is directly adjacent to the furin cleavage site, which may have biological significance.

Cluster 5 (ΔFVI spike)

World Health Organization

Health Topics | Countries | Newsroom

Emergencies preparedness, response

SARS-CoV-2 mink-associated variant strain – Denmark

Disease Outbreak News: Update
3 December 2020

Since June 2020, Danish authorities have reported an extensive spread of SARS-CoV-2, the virus that causes COVID-19, on mink farms in Denmark. On 5 November, the Danish public health authorities reported the detection of a mink-associated SARS-CoV-2 variant with a combination of mutations not previously observed (referred to as "Cluster 5") in 12 human cases in North Jutland, detected from August to September 2020.

Denmark to cull all farmed minks over coronavirus mutation

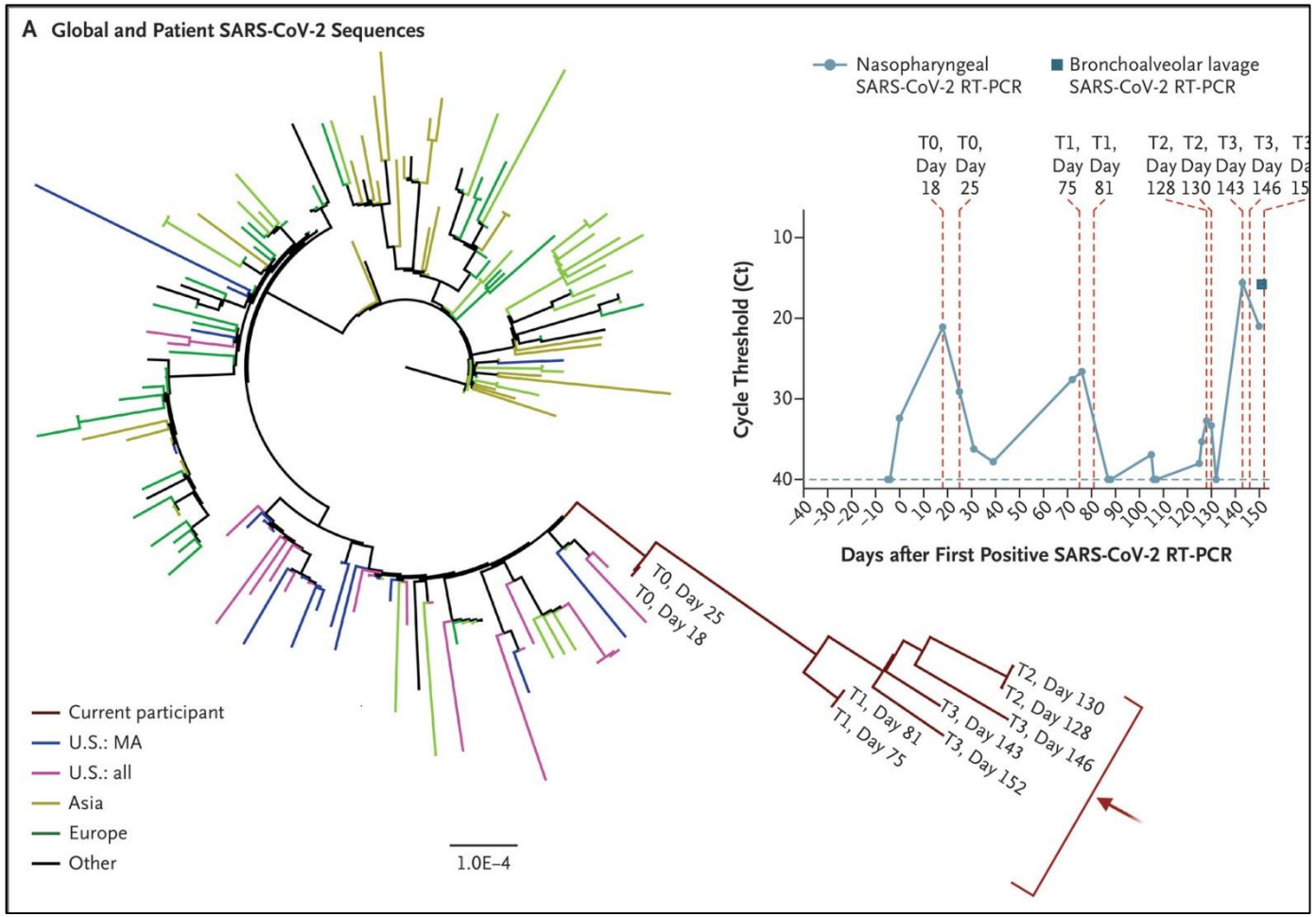
Denmark has said it would cull around 15 million minks after a mutated version of the coronavirus spread to people. The government said the mutation poses a risk to the efficacy of future vaccines.

Deletion 69-70, Y453F, I692V, M1229I

- Seven unique mutations (four amino acid changes) in the spike protein among variants co-circulating in mink and humans.
- There was a **lower capability of antibodies to neutralize the Cluster 5 strain**.

https://www.who.int/csr/don/03-december-2020-mink-associated-sars-cov2-denmark/en/

Mutation after convalescent plasma therapy/ drug treatment

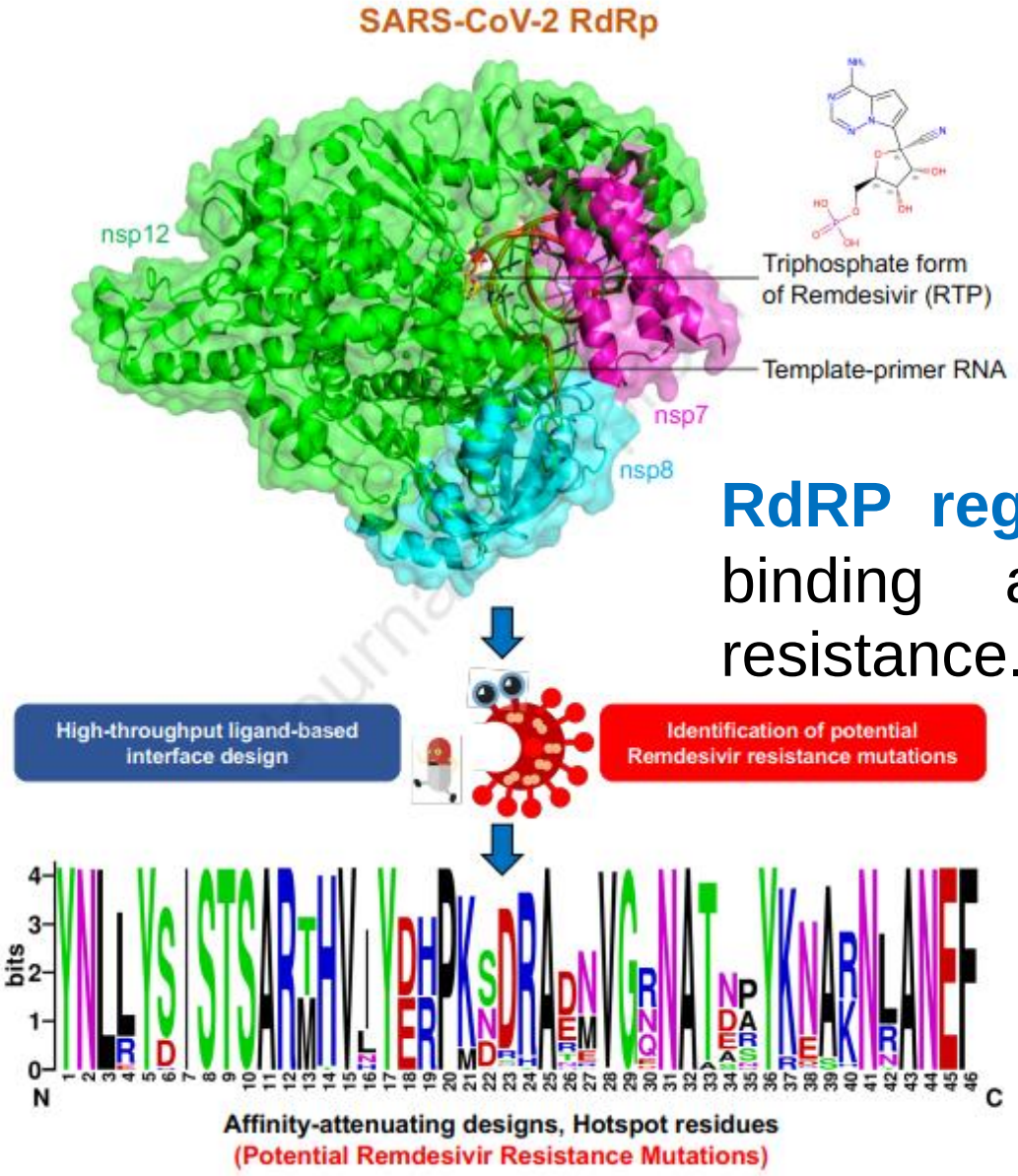


Mutation after a patient received 3 treatments of convalescent plasma starting at day 63.
Something similar in a 65-year-old cancer patient who survived after 105 days with the virus.
N439K (also found in South African variant)—may allow the virus to bypass monoclonal antibody drugs.
Special caution is needed to give treatment in Immunocompromised patients.

DOI: 10.1056/NEJMc2031364

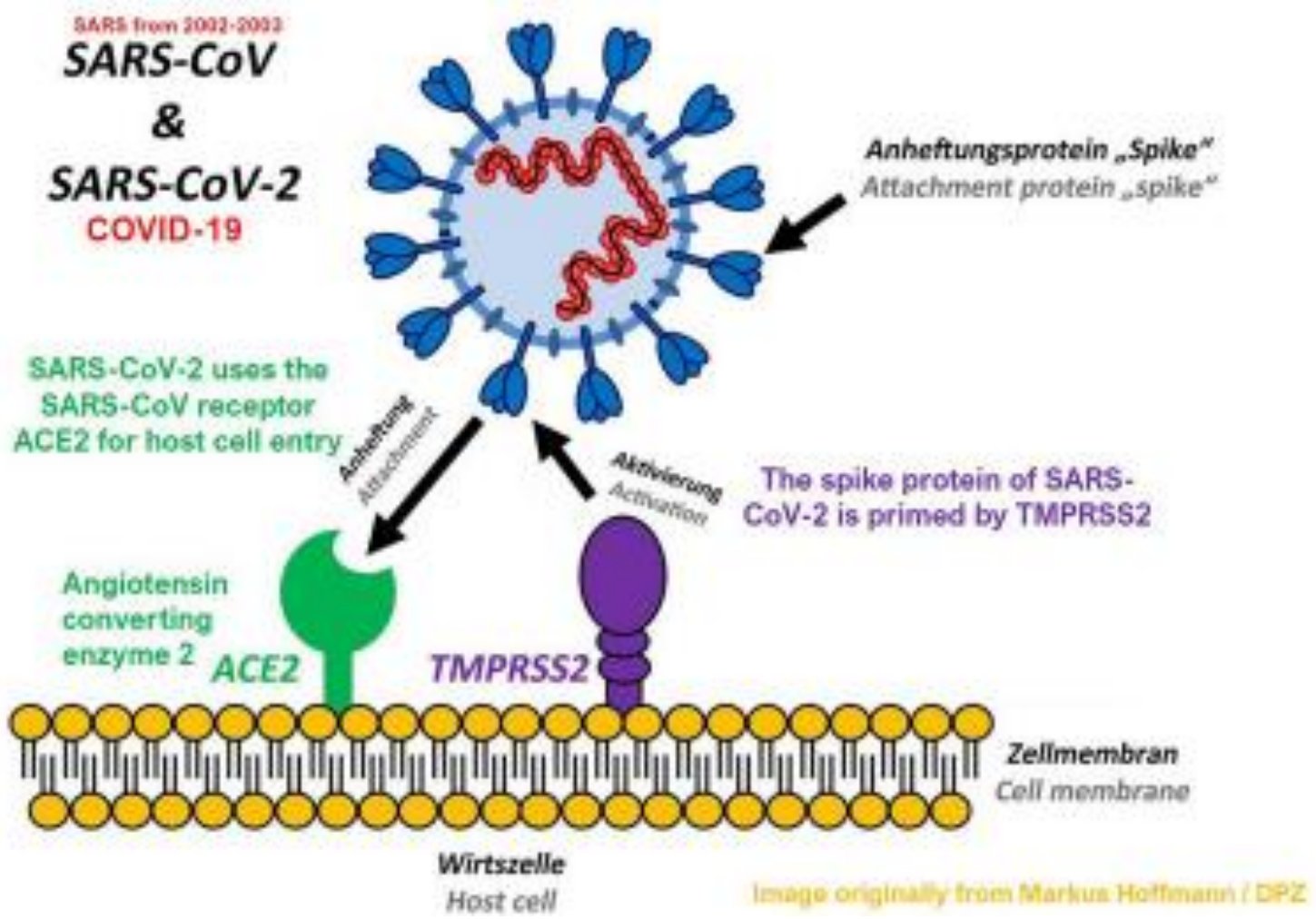
doi: https://doi.org/10.1101/2020.12.05.20241927

Potential drug resistance site in the genome of SARS-CoV-2



RdRP region: Several mutants displayed decreased binding affinity to remdesivir, suggesting drug resistance.

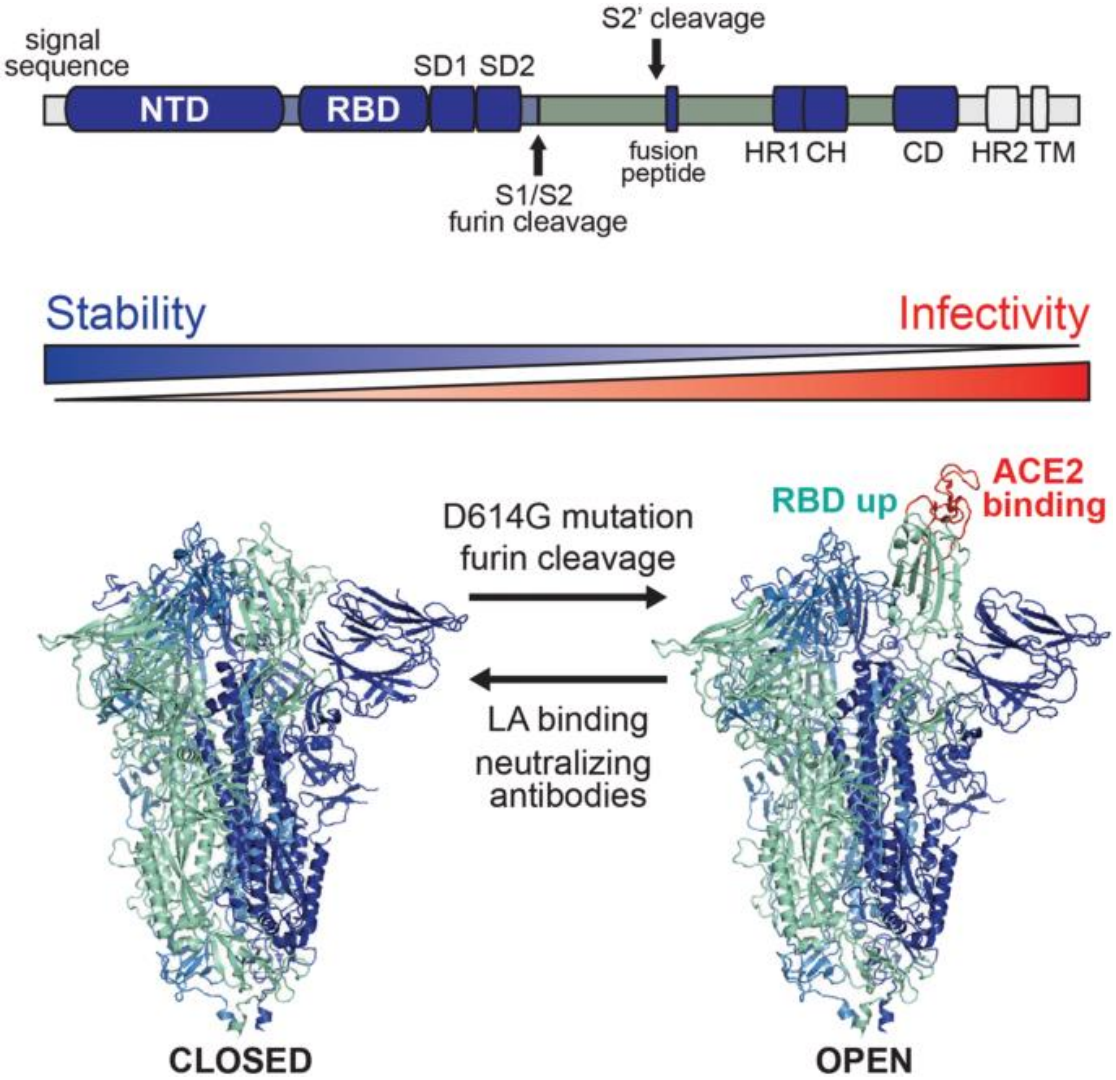
Role of Spike in cell-entry



Mutation rate: 10^{-8} to10^{-6} s/n/c for DNA viruses and from 10^{-6} to 10^{-4} s/n/c for RNA viruses.

DOI: *10.1128/JVI.00694-10*

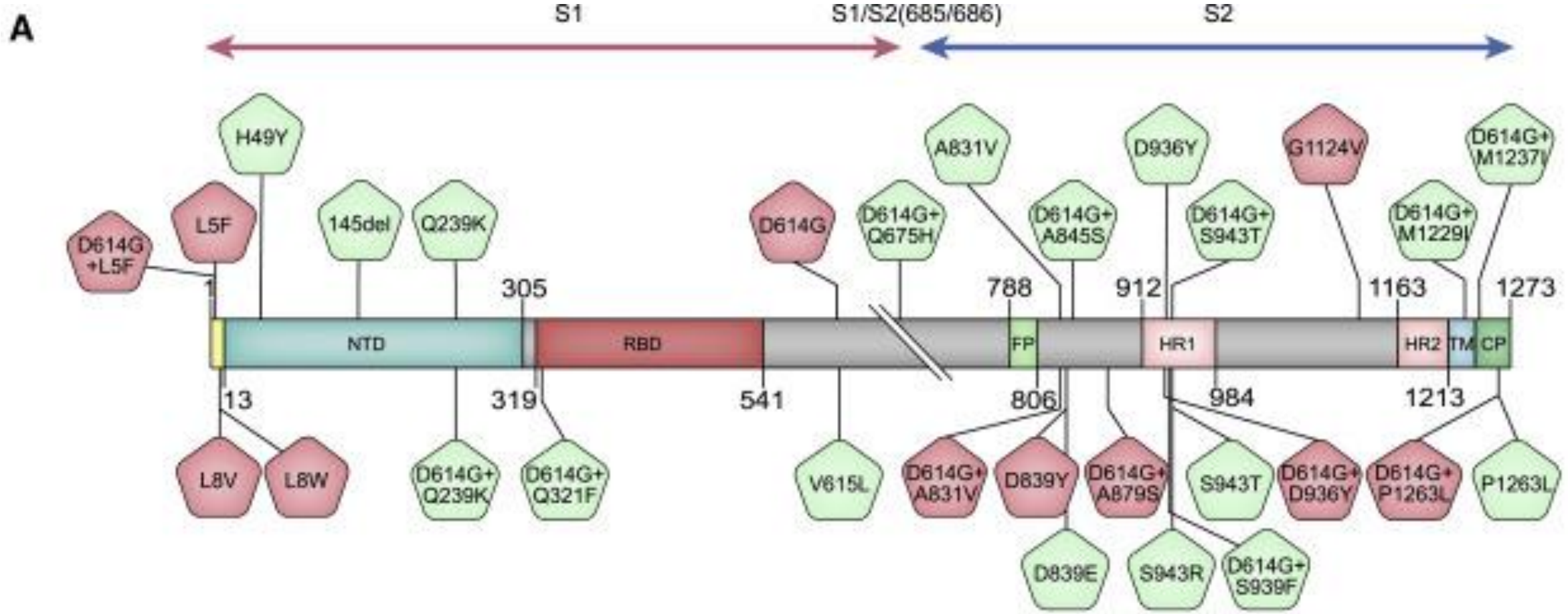
Spike mutation and Infectivity



SARS-CoV-2 S has higher affinity for angiotensin-converting enzyme 2 (ACE2) as compared to SARS-CoV S due to six mutations in the receptor-binding motif (RBM).

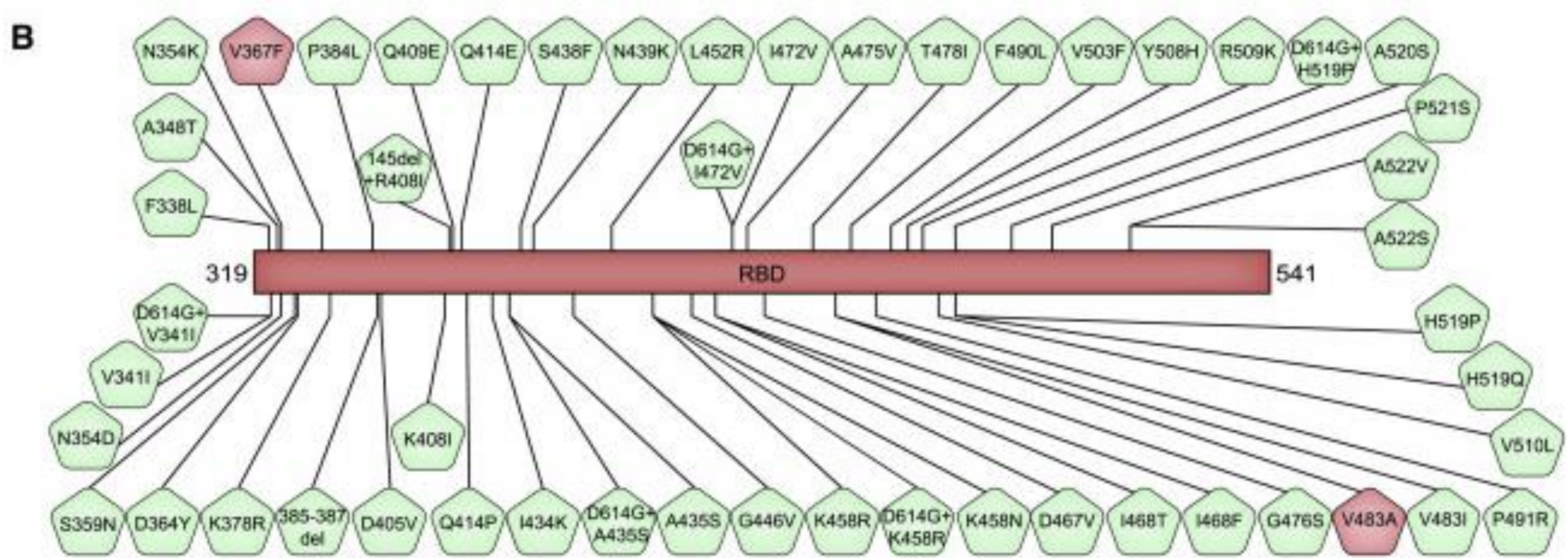
https://doi.org/10.1038/s41422-020-00430-4

Variants and combined variants with D614G across the entire S gene excluding the RBD region



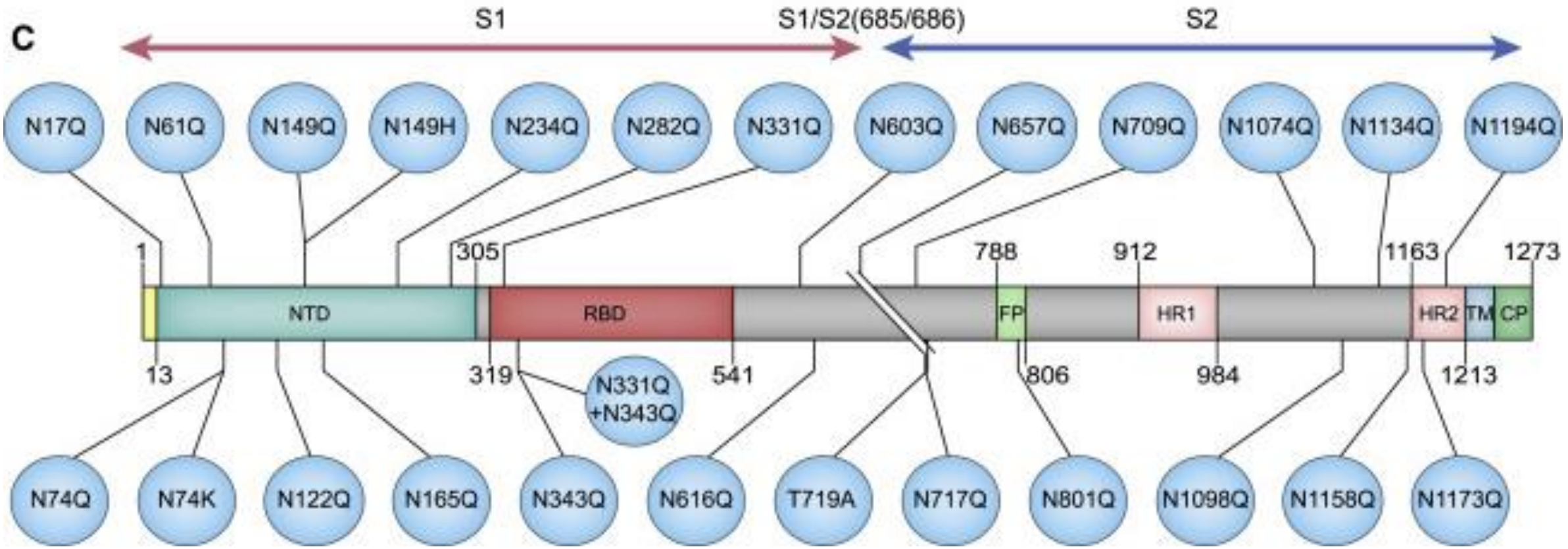
doi.org/10.1016/j.cell.2020.07.012

Variants in RBD



doi.org/10.1016/j.cell.2020.07.012

Mutants at the putative glycosylation sites (22 sites)



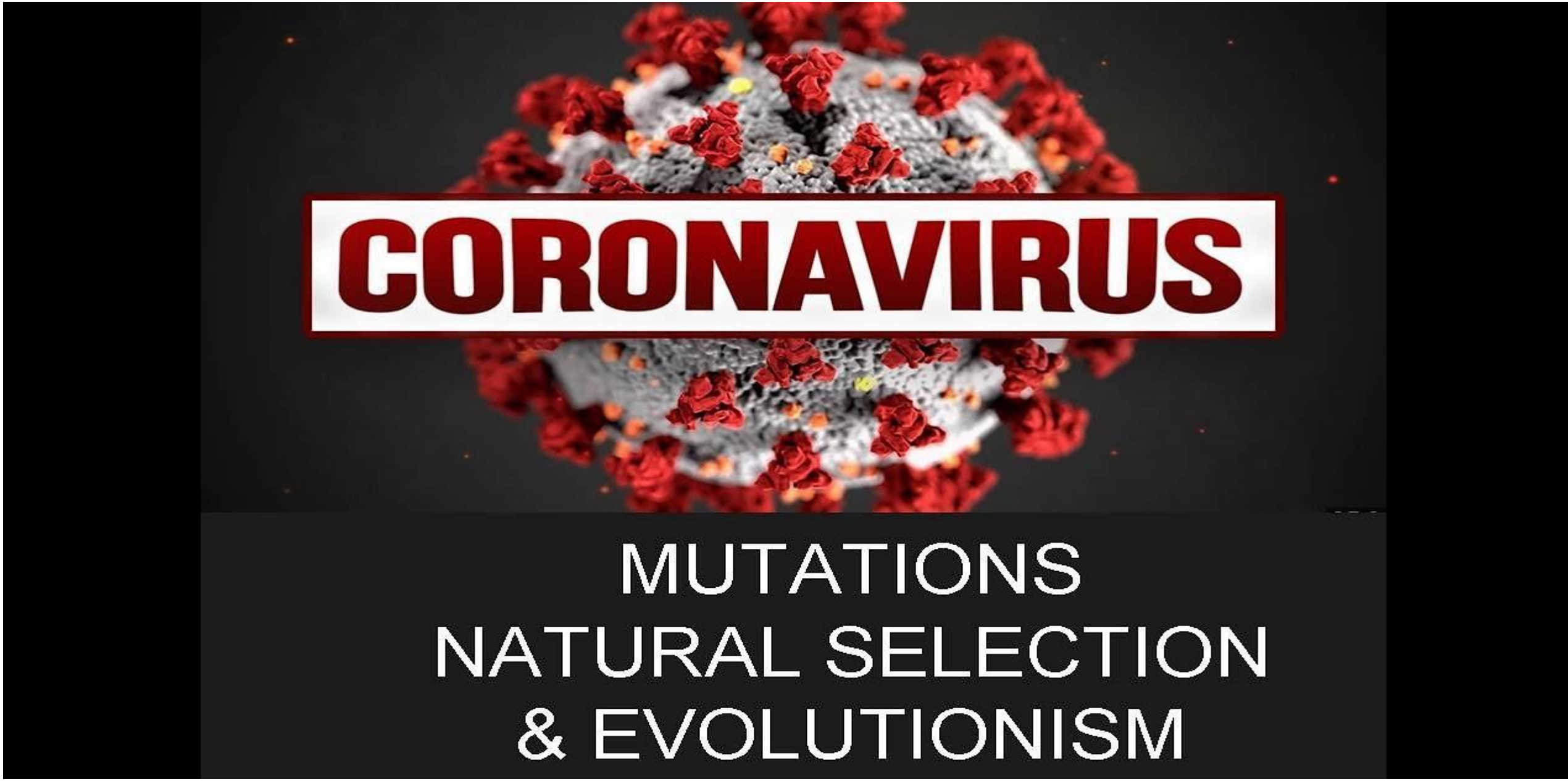
doi.org/10.1016/j.cell.2020.07.012

Known Characters of the some mutations

	Group A	Group B	Group C
Number of variants or mutants	29	51	26
Increased infectivity	D614G, D614G+L5F, D614G+D936Y, D614G+S939F, D614G+S943T	D614G+V341I, D614G+K458R, D614G+I472V[a]	none
Decreased infectivity	Q239K, D839Y, P1263L, D614G+Q675H	V341I, D364Y, 385-387del, D405V, Q414P, I434K, S438F, D467V, P491R, V503F, R509K, V510L, P521S	N122Q, N343Q, N717Q, T719A, N801Q, N1074Q, N331Q+N343Q
Increased sensitivity to neutralizing mAbs	none	V367F, Q409E, Q414E, I468F, I468T, Y508H, A522V	N165Q, N709Q
Decreased sensitivity to neutralizing mAbs	A831V	N439K, L452R, A475V, V483A, F490L, Y508H, D614G+A435S, D614G+I472V[a]	N234Q
Increased sensitivity to convalescent sera	V615L	F338L, V367F, I468F, I468T	N149H, N149Q, N165Q, N331Q, N354D, N709Q, N1173Q
Decreased sensitivity to convalescent sera	Y145del, A831V, D614G+A831V, D614G+A879S, D614G+M1237I	Q414E, N439K, G446V, K458N, I472V, A475V, T478I, V483I, F490L, H519P, D614G+Q321L, D614G+I472V[a]	none

[a]D614G+I472V is the only variant with increased infectivity and decreased sensitivity to neutralizing mAb and convalescent sera. It is of note only one sequence is recorded in GISAID.

https://doi.org/10.1016/j.cell.2020.07.012


CORONAVIRUS
MUTATIONS
NATURAL SELECTION
& EVOLUTIONISM

Severity Vs 382-nucleotide deletion (Δ382)

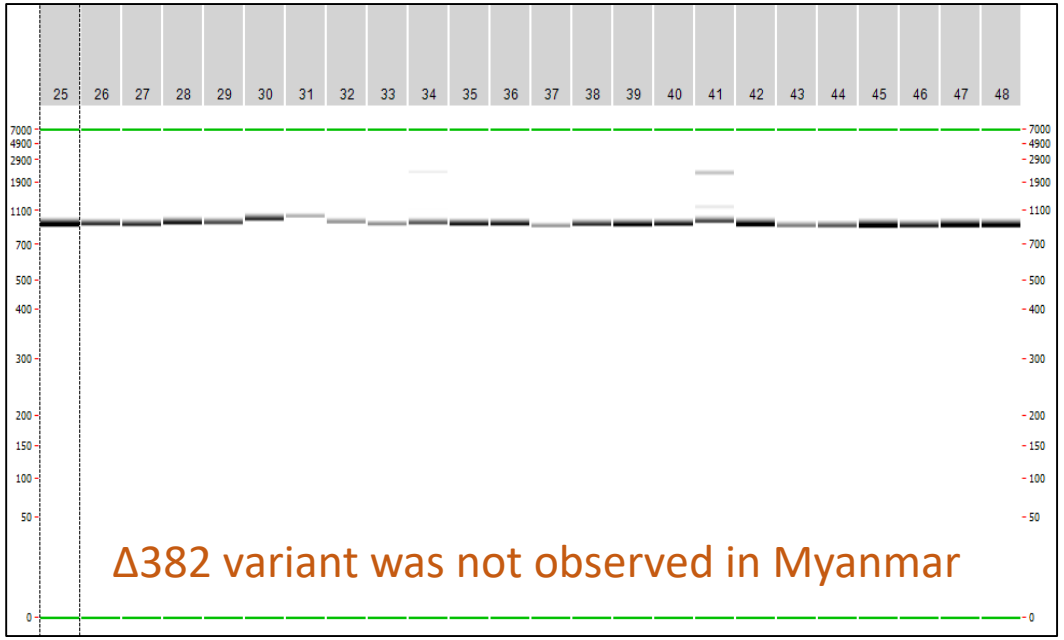
Effects of a major deletion in the SARS-CoV-2 genome on the severity of infection and the inflammatory response: an observational cohort study

Barnaby E Young, Siew-Wai Fong*, Yi-Hao Chan*, Tze-Minn Mak, Li Wei Ang, Danielle E Anderson, Cheryl Yi-Pin Lee, Siti Naqiah Amrun, Bernett Lee, Yun Shan Goh, Yvonne C F Su, Wycliffe E Wei, Shirin Kalimuddin, Louis Yi Ann Chai, Surinder Pada, Seow Yen Tan, Louisa Sun, Purnima Parthasarathy, Yuan Yi Constance Chen, Timothy Barkham, Raymond Tzer Pin Lin, Sebastian Maurer-Stroh, Yee-Sin Leo, Lin-Fa Wang, Laurent Renia, Vernon J Lee, Gavin J D Smith, David Chien Lye, Lisa F P Ng*

Summary

Background Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants with a 382-nucleotide deletion (Δ382) in the open reading frame 8 (ORF8) region of the genome have been detected in Singapore and other countries. We investigated the effect of this deletion on the clinical features of infection.

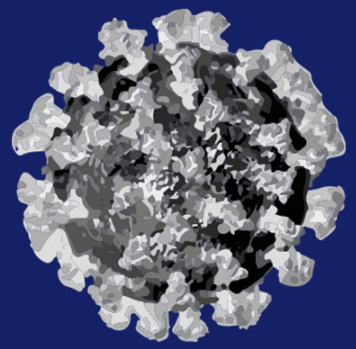
Lancet 2020; 396: 603–11
Published Online
August 18, 2020
https://doi.org/10.1016/
S0140-6736(20)31757-8



ORF8 is a hotspot for coronavirus mutation. The clinical effect of deletions in this region appears to be a milder infection with less systemic release of proinflammatory cytokines and a more effective immune response to SARS-CoV-2.

https://doi.org/10.1016/ S0140-6736(20)31757-8

Host Genetic Factors?



The COVID-19 Host Genetics Initiative

34 studies from **16** countries
~15% of all registered studies (N=220)

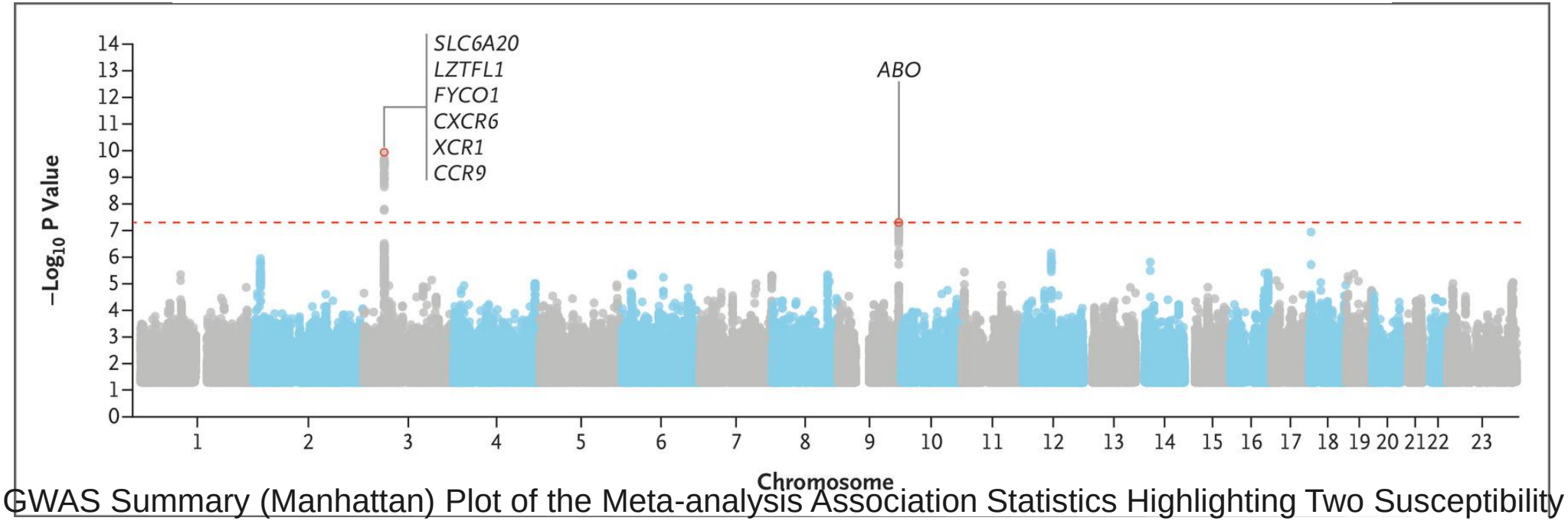
30,937 COVID-19 positive cases among
> 1.7 million individuals

Human Genetic Factors for severity?

ORIGINAL ARTICLE

Genomewide Association Study of Severe Covid-19 with Respiratory Failure

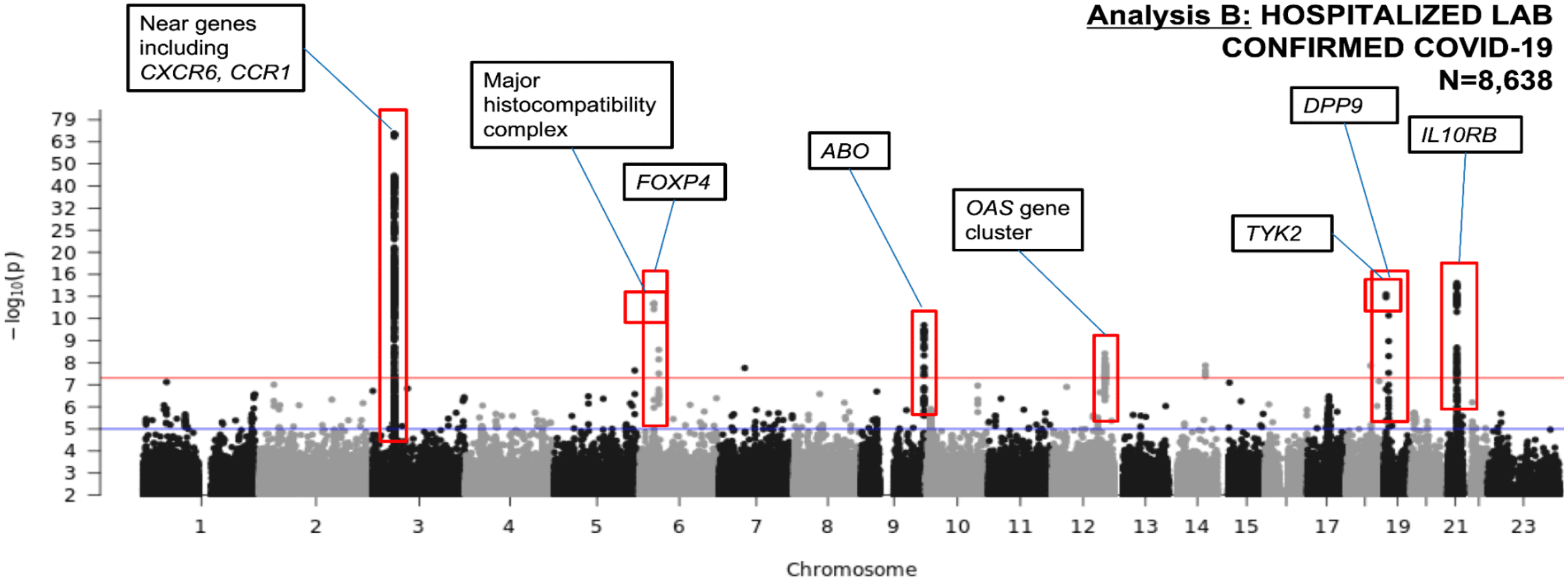
The Severe Covid-19 GWAS Group*



GWAS Summary (Manhattan) Plot of the Meta-analysis Association Statistics Highlighting Two Susceptibility Loci with Genomewide Significance for Severe Covid-19 with Respiratory Failure.

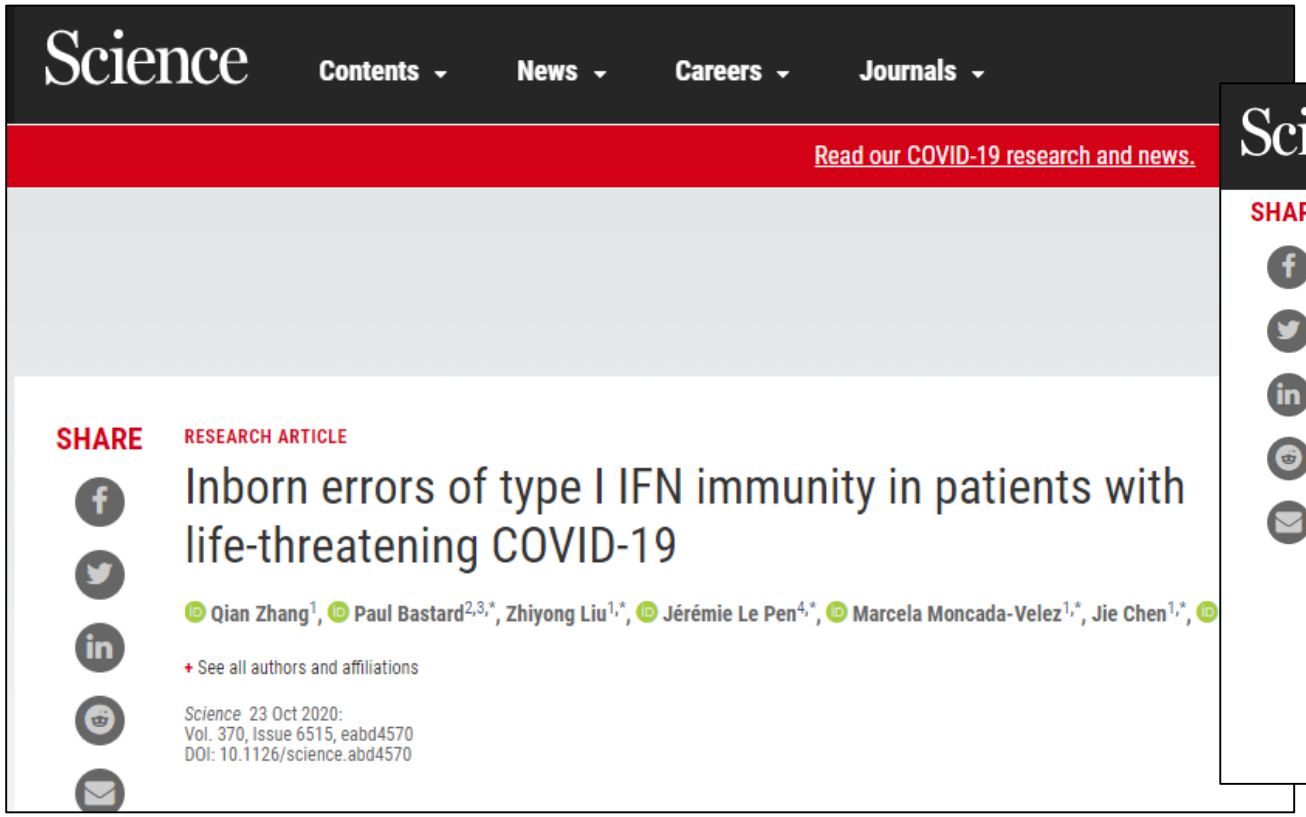
DOI: 10.1056/NEJMoa2020283

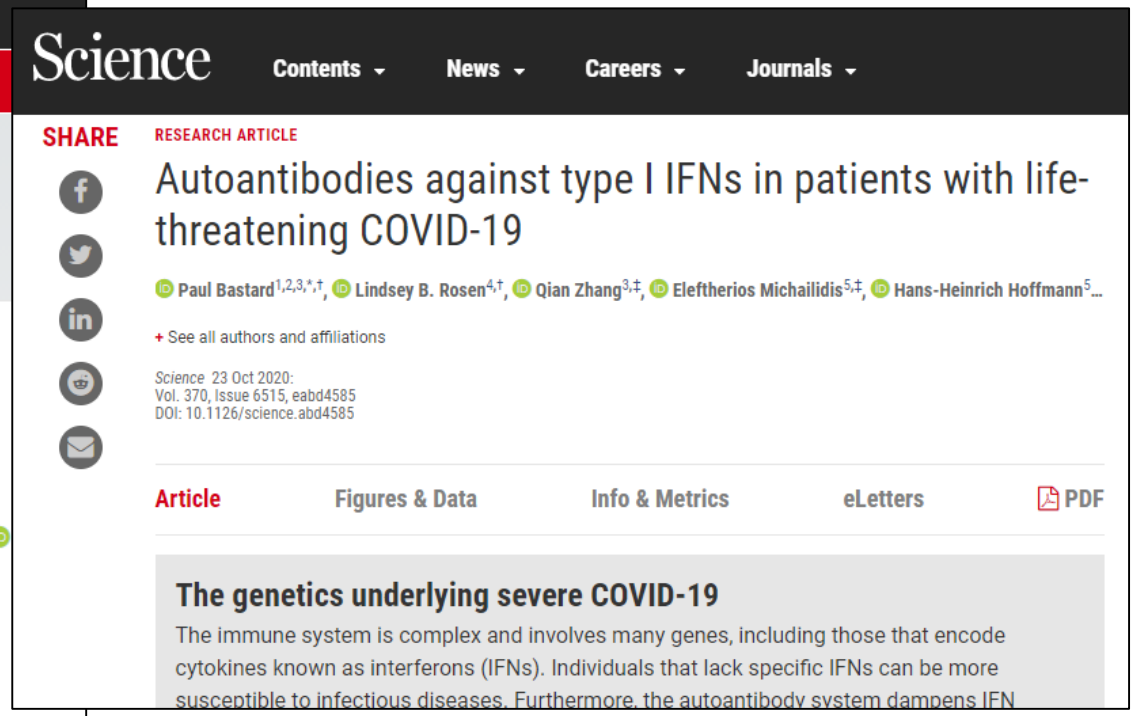
Human Genetic Factors for severity?



Manhattan plot showing the GWAS results for COVID-19 Severity in 8,638 hospitalized COVID-19 cases and 1.7 million controls. The analysis identified independent significant associations as indicated by red boxes around genetic “peaks” rising above the threshold.

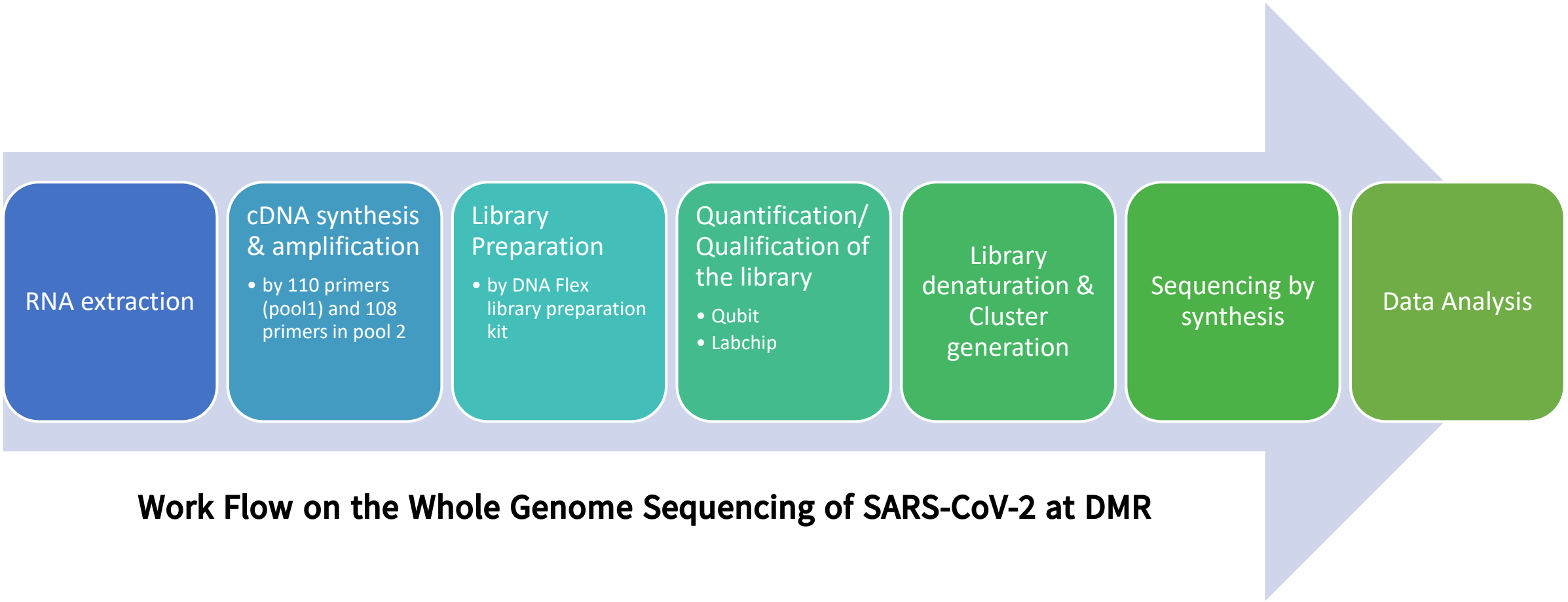
Severity: Why Male, Why old age?





Patients with life-threatening COVID-19 pneumonia had known (AR IRF7 and IFNAR1 deficiencies or AD TLR3, TICAM1, TBK1, and IRF3 deficiencies) or new (AD UNC93B1, IRF7, IFNAR1, and IFNAR2 deficiencies) genetic defects at eight of the 13 candidate loci involved in the TLR3- and IRF7-dependent induction and amplification of type I IFNs. A B cell autoimmune phenocopy of inborn errors of type I IFN immunity accounts for life-threatening COVID-19 pneumonia in at least 2.6% of women and 12.5% of men.

Findings on SARS-CoV-2 Genomic study in Myanmar



Work Flow on the Whole Genome Sequencing of SARS-CoV-2 at DMR

Existing Capacity

- BSL2+ lab
- Capillary electrophoresis
- Conventional PCR
- Real-time PCR
- Sanger's Sequencer
- Next-Generation Sequencer (Miseq)
- Molecular medical scientists

What we have

Spectrophotometer
(DNA quality/quantifier)

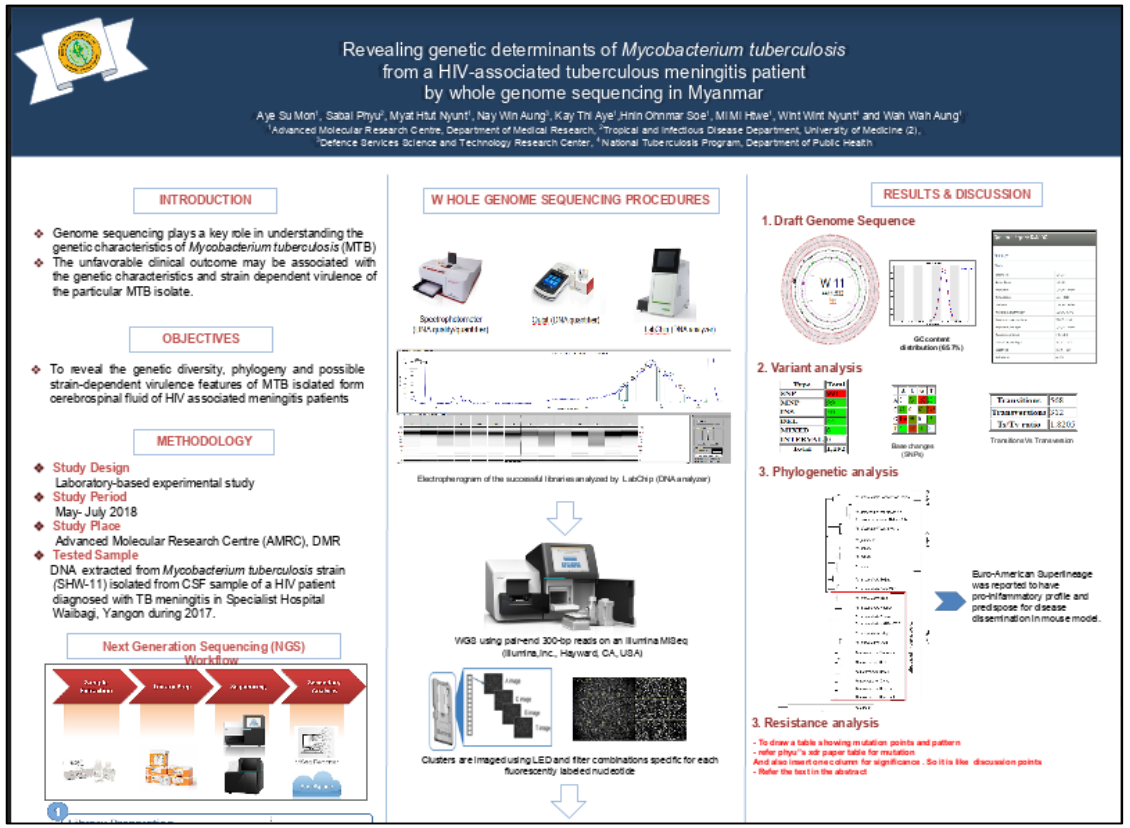
Qubit (DNA quantifier)

LabChip (DNA analyzer)

MiSeq (Cluster generator+ Sequencer)

Dell super computer (+BE Patho)

Established Technology and experiences



Revealing genetic determinants of *Mycobacterium tuberculosis* from a HIV-associated tuberculous meningitis patient by whole genome sequencing in Myanmar

Aye Su Mon[1], Sabai Phyu[2], Myat Htut Nyunt[1], Nay Win Aung[3], Kay Thi Aye[1], Hnin Ohmmar Soe[1], MI MI Htwe[1], Wint Wint Nyunt[4] and Wah Wah Aung[1]
[1]Advanced Molecular Research Centre, Department of Medical Research, [2]Tropical and Infectious Disease Department, University of Medicine (2), [3]Defence Services Science and Technology Research Center, [4]National Tuberculosis Program, Department of Public Health

INTRODUCTION

- Genome sequencing plays a key role in understanding the genetic characteristics of *Mycobacterium tuberculosis* (MTB)
- The unfavorable clinical outcome may be associated with the genetic characteristics and strain dependent virulence of the particular MTB isolate.

OBJECTIVES

- To reveal the genetic diversity, phylogeny and possible strain-dependent virulence features of MTB isolated form cerebrospinal fluid of HIV associated meningitis patients

METHODOLOGY

- Study Design
  Laboratory-based experimental study
- Study Period
  May- July 2018
- Study Place
  Advanced Molecular Research Centre (AMRC), DMR
- Tested Sample
  DNA extracted from *Mycobacterium tuberculosis* strain (SHW-11) isolated from CSF sample of a HIV patient diagnosed with TB meningitis in Specialist Hospital Waibagi, Yangon during 2017.

Next Generation Sequencing (NGS) Workflow

WHOLE GENOME SEQUENCING PROCEDURES

Electropherogram of the successful libraries analyzed by LabChip (DNA analyzer)

WGS using pair-end 300-bp reads on an Illumina MiSeq (Illumina,Inc., Hayward, CA, USA)

Clusters are imaged using LED and filter combinations specific for each fluorescently labeled nucleotide

RESULTS & DISCUSSION

1. Draft Genome Sequence

2. Variant analysis

3. Phylogenetic analysis

Euro-American Superlineage was reported to have pro-inflammatory profile and predispose for disease dissemination in mouse model.

3. Resistance analysis

- To draw a table showing mutation points and pattern
- refer phyu"s xdr paper table for mutation
And also insert one column for significance . So it is like discussion points
- Refer the text in the abstract

Pseudomonas aeruginosa strain:MMK2018 Accession: PR

Pseudomonas aeruginosa strain:MMK2018 Genome sequencing and assembly

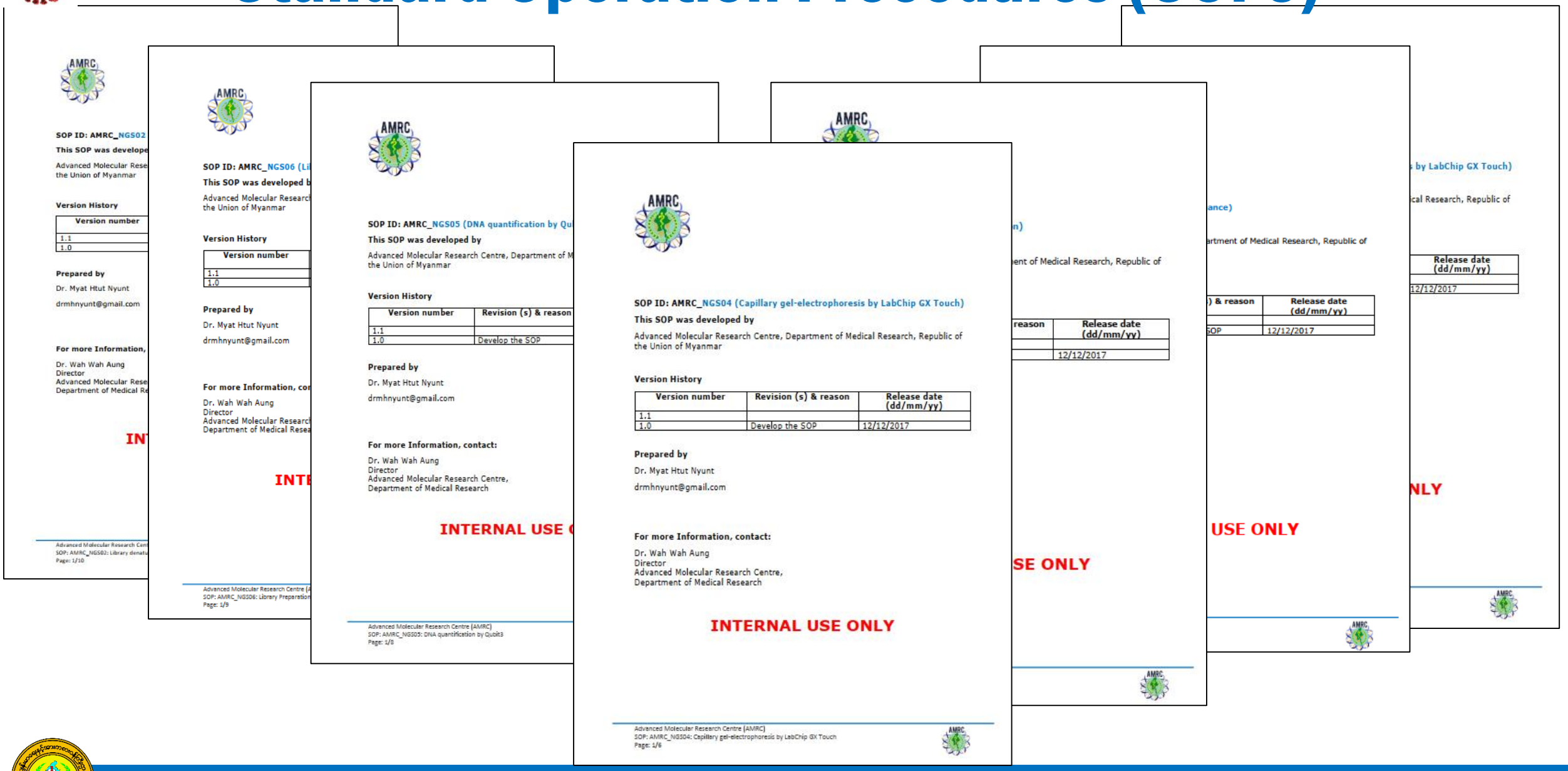
Whole Genome Analysis of the Drug Resistance Pseudomonas aeruginosa Isolate (P38) in Myanmar

Accession	PRJNA530358
Data Type	Genome sequencing and assembly
Scope	Monoisolate
Organism	Pseudomonas aeruginosa [Taxonomy ID: 287] Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas aeruginosa
Submission	Registration date: 7-Apr-2019 Department of Medical Research
Relevance	Medical
Locus Tag Prefix	E5D53

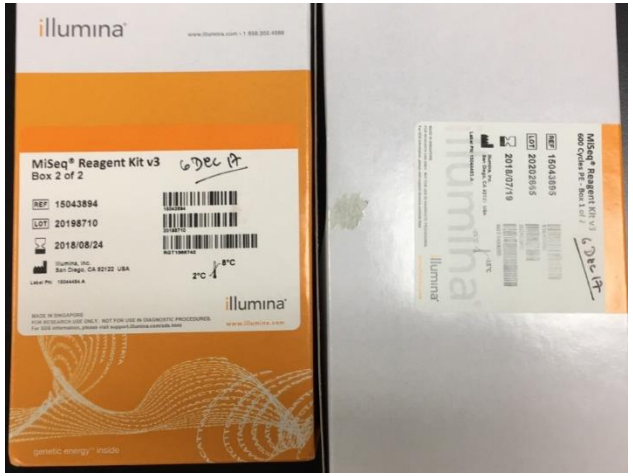
Since 2018, Advanced Molecular Research Center (AMRC), DMR have the facilities and technology for Whole Genome Sequencing.

Successfully sequencing- WGS of Tuberculosis, and multi-drug resistance Pseudomonas aeruginosa.

Standard Operation Procedures (SOPs)



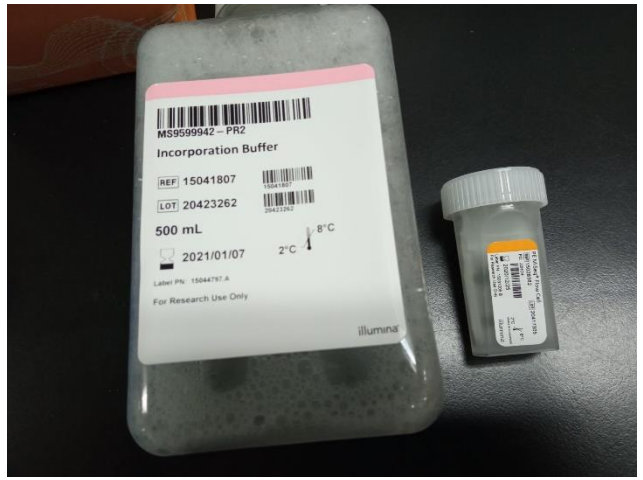
Reagents used



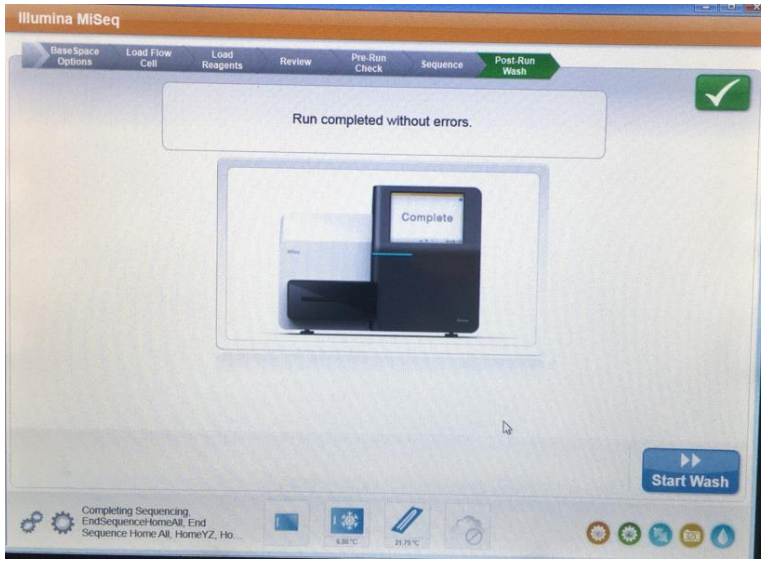
Illumina Seq. V2 Kit

Q5 Hot Start Taq

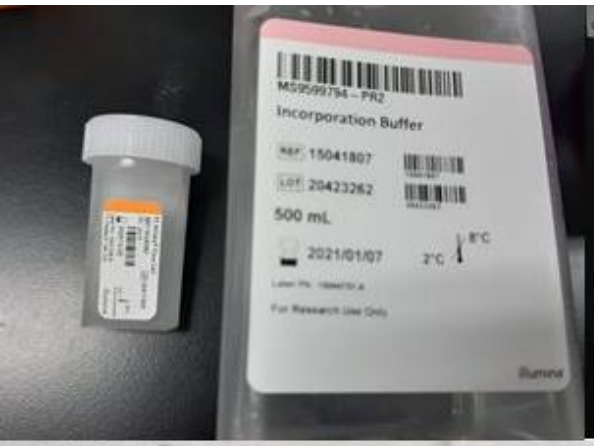
pH check

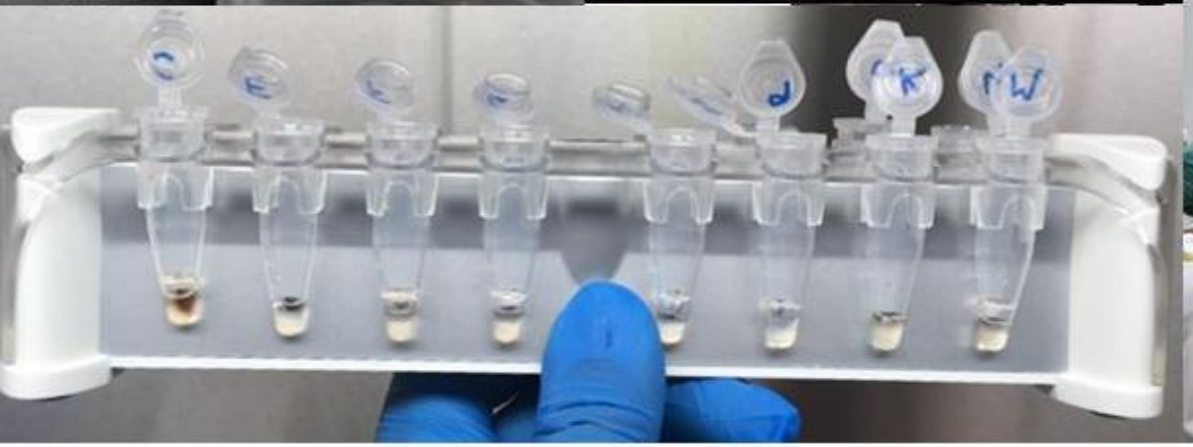


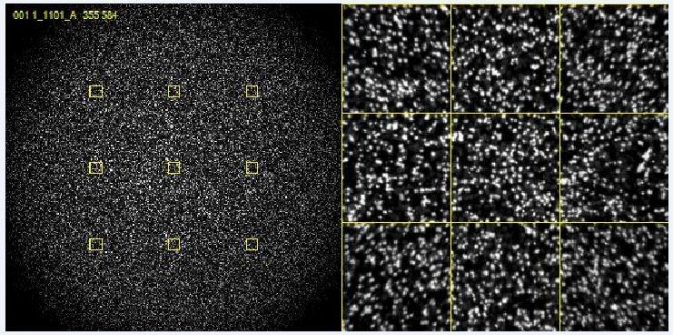
Incorporation Buffer and Flow-cell



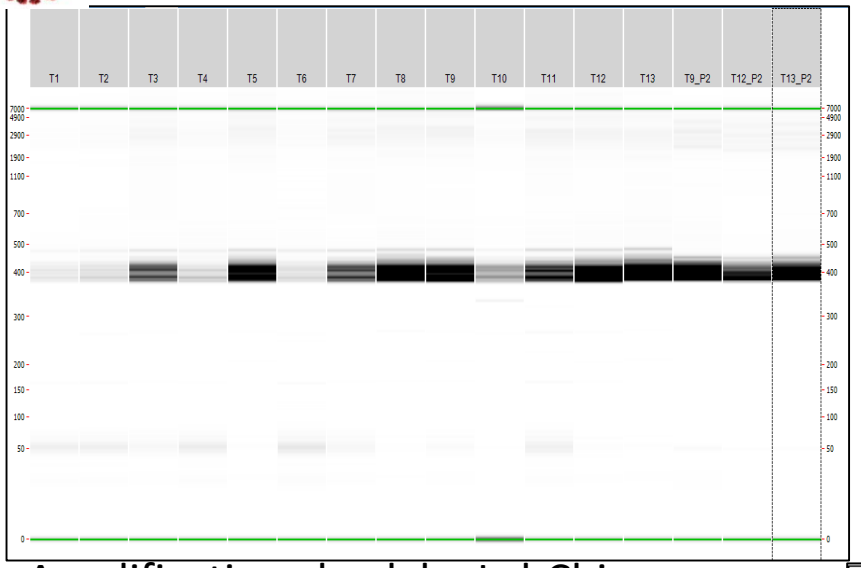
Pictorial Record of the Workflow



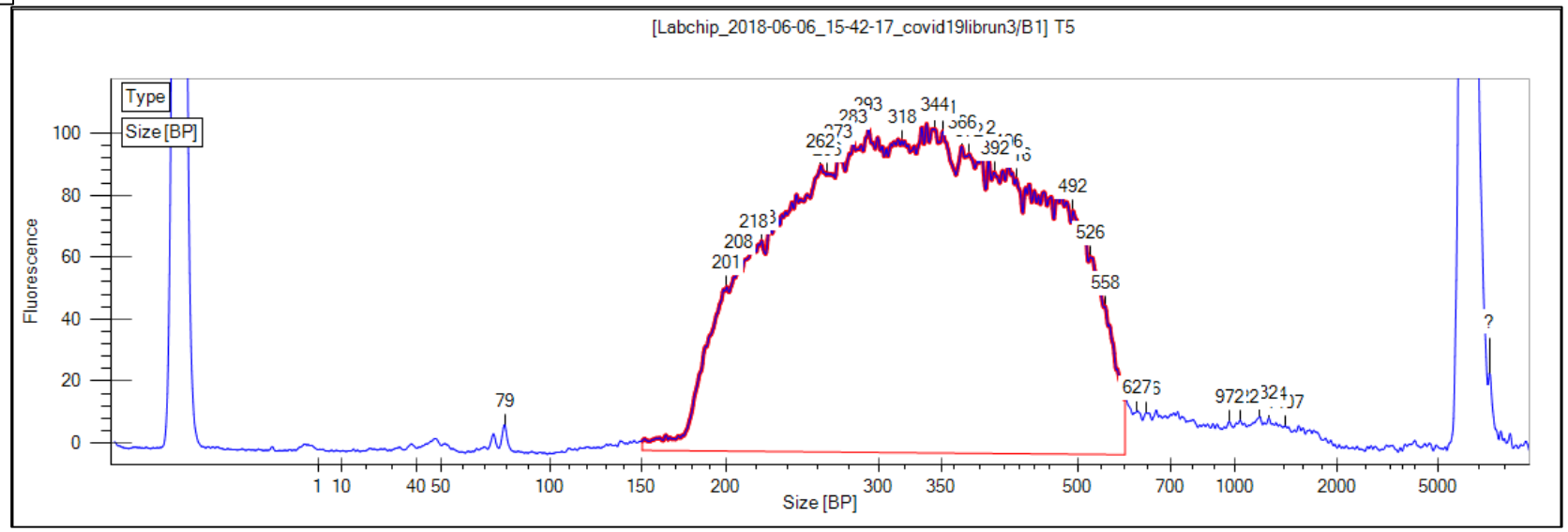




Qualification of the amplification and Library by LabChip

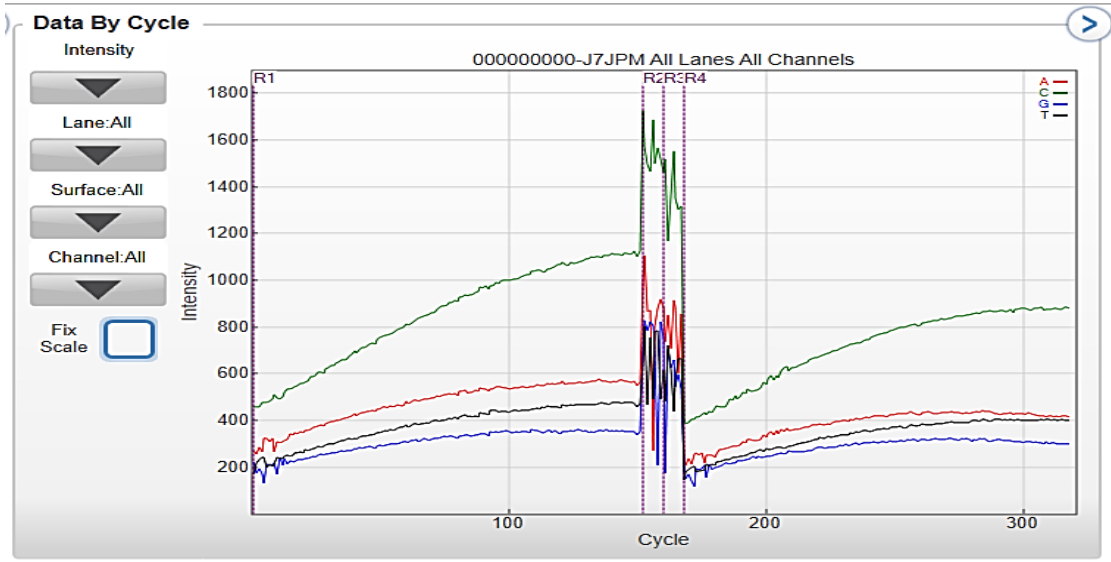


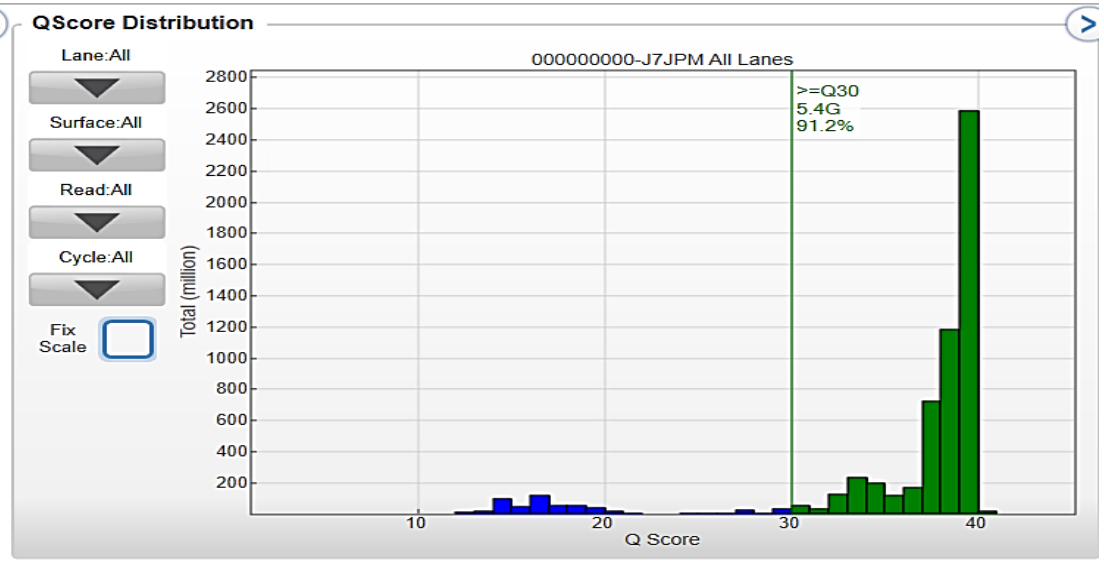
Amplification check by LabChip

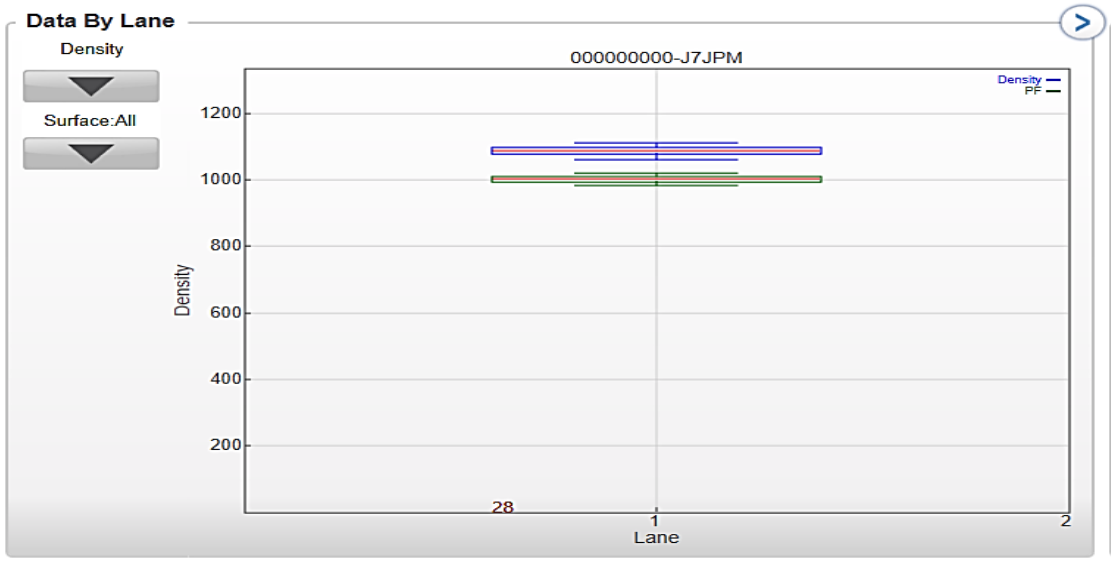


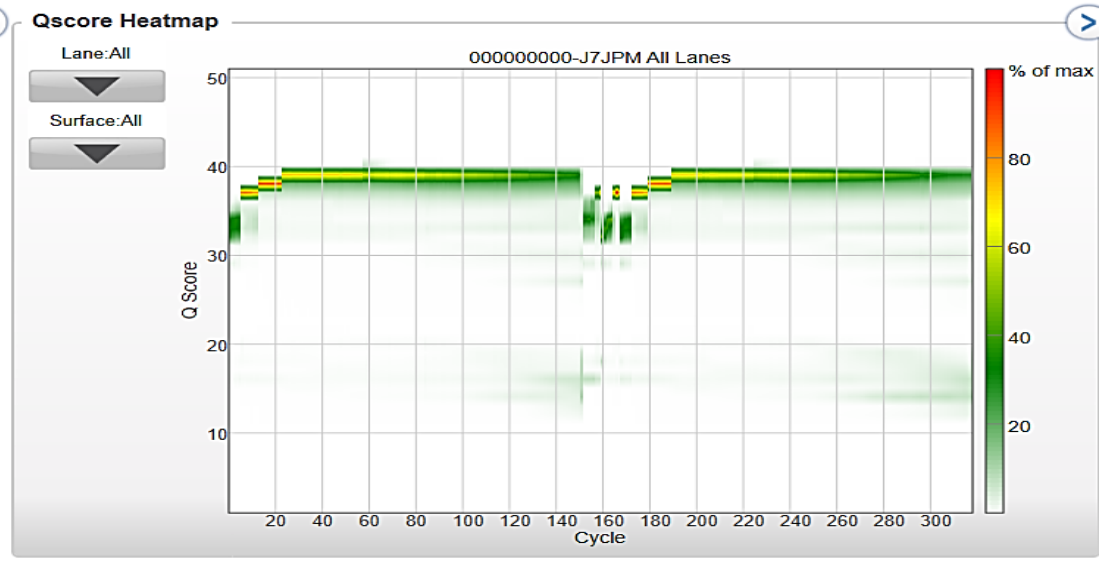
Library qualification check by LabChip

Run Analysis information









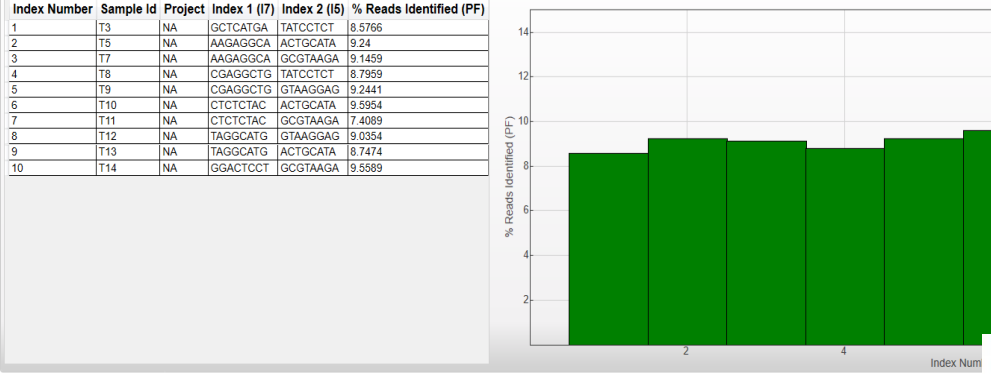
Run Analysis information

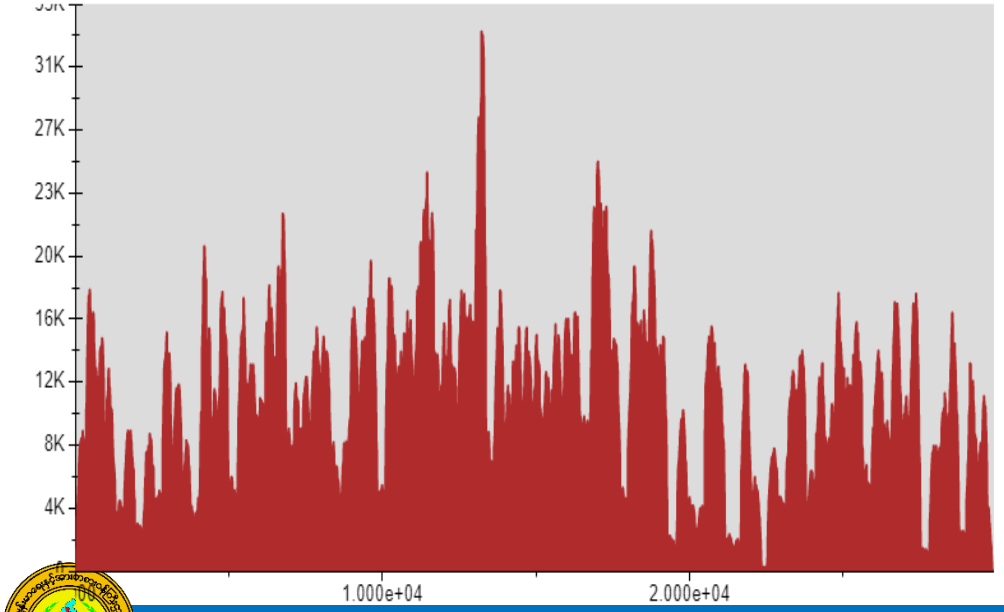
Lane All

Reads mapped to Index Id

Total Reads	PF Reads	% Reads Identified (PF)	CV	Min	Max
20347718	18747503	89.3487	0.0706	7.4089	9.5954

Index Number	Sample Id	Project	Index 1 (I7)	Index 2 (I5)	% Reads Identified (PF)
1	T3	NA	GCTCATGA	TATCCTCT	8.5766
2	T5	NA	AAGAGGCA	ACTGCATA	9.24
3	T7	NA	AAGAGGCA	GCGTAAGA	9.1459
4	T8	NA	CGAGGCTG	TATCCTCT	8.7959
5	T9	NA	CGAGGCTG	GTAAGGAG	9.2441
6	T10	NA	CTCTCTAC	ACTGCATA	9.5954
7	T11	NA	CTCTCTAC	GCGTAAGA	7.4089
8	T12	NA	TAGGCATG	GTAAGGAG	9.0354
9	T13	NA	TAGGCATG	ACTGCATA	8.7474
10	T14	NA	GGACTCCT	GCGTAAGA	9.5589





Sequencing Reads Quality Control

Sample	Raw Reads (pairs)	Raw Bases	Clean Reads (pairs)	Clean Bases
C	1,263,854	286,799,189	1,107,085	232,543,183
E	1,301,550	291,010,242	1,138,170	237,156,562
F	1,344,315	301,370,397	1,173,291	245,108,570
G	1,339,262	298,026,135	1,157,401	240,784,918
H	1,371,296	306,862,413	1,193,052	248,784,080
J	1,424,886	316,216,039	1,243,905	257,990,191
K	1,326,979	296,827,450	1,160,324	241,902,281
M	1,343,785	300,161,894	1,167,858	243,355,035
N	1,368,931	306,128,689	1,192,448	248,132,955
O	1,311,782	297,670,564	1,147,570	240,769,951

All Myanmar samples showed good read data enough to do Genome-wide study.

Sequences quality

NGS details

Assembly

Coverage length	29901 (1 contig(s))
Est. depth of coverage	9779.8
Est. number of reads	2611118
Ambiguities	0

Assignment

Type	Severe acute respiratory syndrome-related coronavirus (Taxonomy ID: 694009)
Reference Genome	NC_045512.3 (Length: 29903bp)
Host(s)	Homo sapiens / Paguma larvata
NT Identity (%)	99.9231
NT Quality	1.99652

Alignment

Alignment score	59698 (NT) + 99486 (AA) = 159184
Concordance (%)	99.8845
Alignment method	Global, seeded, nucleotide + amino acids (AGA)

Genome Region

Sequence starts at position null and ends at position null relative to the null reference sequence for null.

All samples showed

- Depth of coverage >8000
- Number of reads >2,600,000
- NT identity(%) - >99.9

Software used for Bioinformatics Analysis

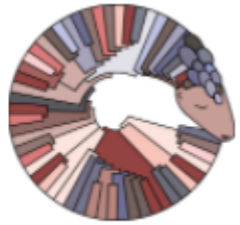
Powered by

GLUE

CoV-GLUE enabled by data from GISAID

Pangolin COVID-19 Lineage Assigner

Phylogenetic Assignment of Named Global Outbreak LINeages



Nextstrain

Nextstrain

Real-time tracking of pathogen evolution

geneious prime

FastTree 2

iTOL INTERACTIVE TREE OF LIFE

Welcome to iTOL v5

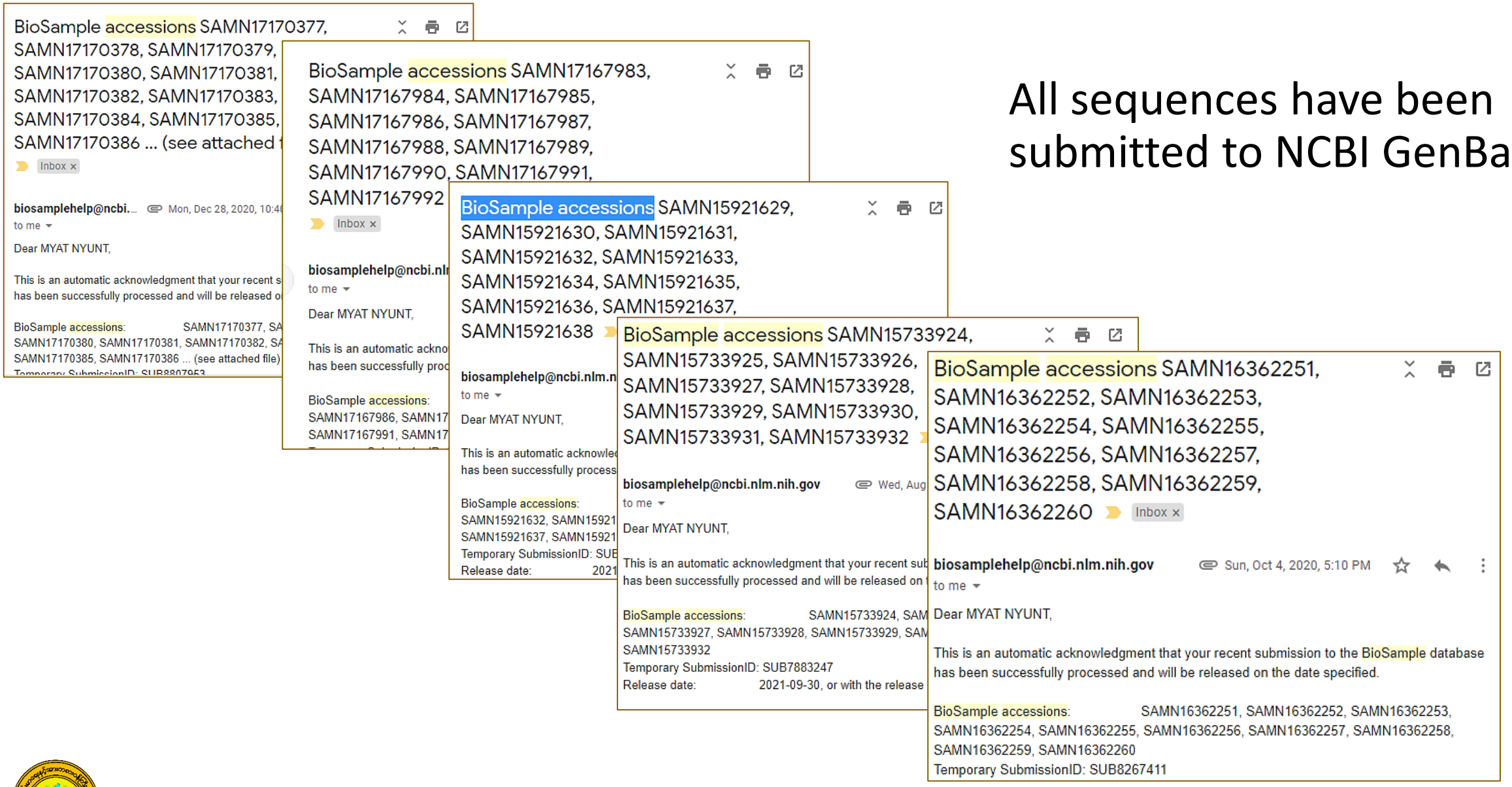
MEGA Molecular Evolutionary Genetics Analysis

Illumina Sequencing Analysis Viewer

ViPR

B. E. Box

NCBI GenBank SRA Accessions



All sequences have been submitted to NCBI GenBank.

Number of samples for WGS (as of 10-Jan-2021)

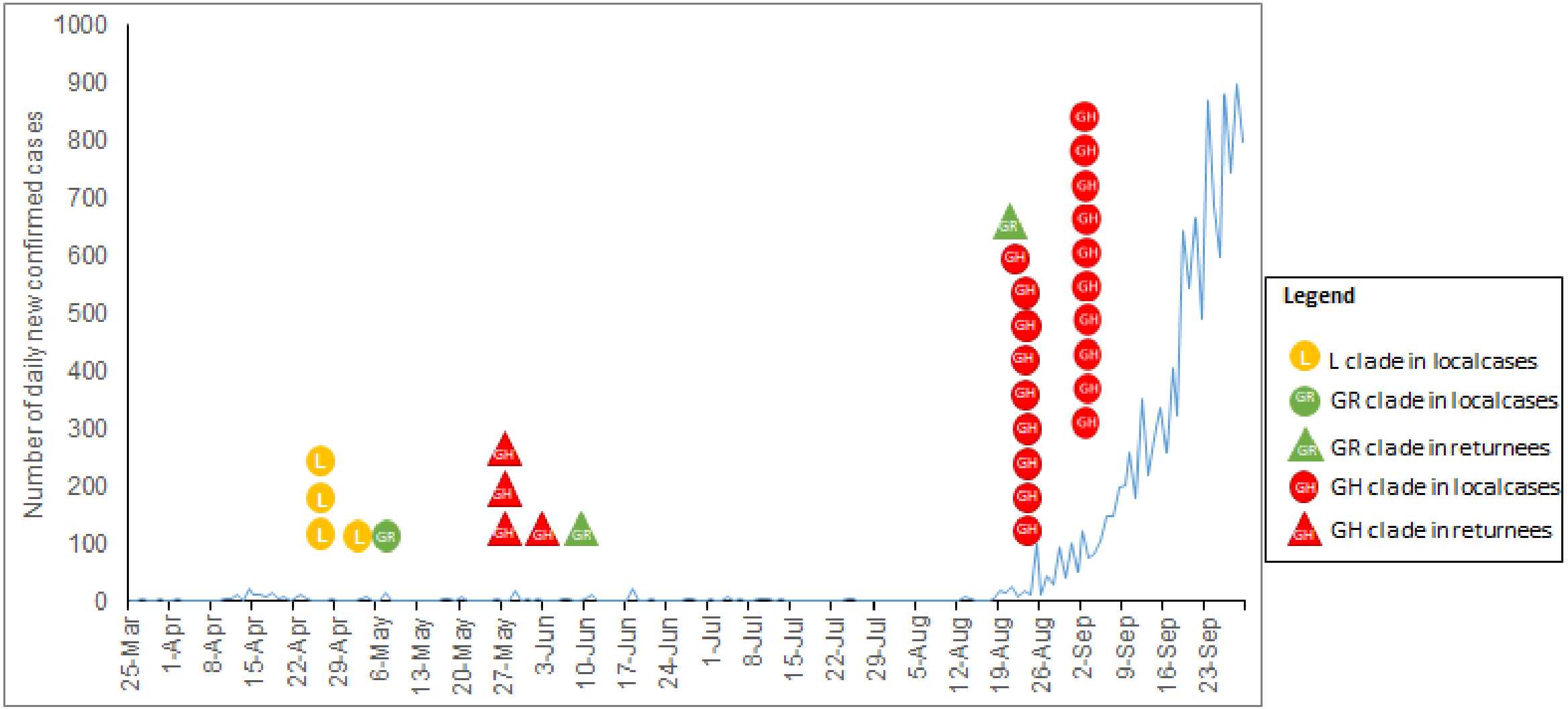
Run time	Total samples test	Sample collection site	Time of sample collection	Remark
1	10	Yangon/Q-site of returnees	April-Jul (2020)	- 4 Returnees from India - 1 Returnee from China - 5 from local infection (Yangon) (First wave)
2	10	Rakhine/Q-site of returnees	August (2020)	- 9 from Rakhine - 1 from Philippines Returnee
3	10	Yangon	September (2020)	- 10 deceased cases from Yangon (Second wave)
4	11	Mandalay/Sagaing	December (2020)	- 1 PyiGyiTakon, 1 PyinOoLwin, 1 NaungCho, 1 ChanAyeThaZan, 1 Sagaing, 1 Tadaoo, 1 MyinGyan, 1 ChanMyaTharSi, 1 AungMyayTharSan, 1 Mattaya, 1 MaharAungMyay
5	11	Yangon/Bago	December (2020)	- 4 Yangon, 2 Bago, 2 Padaung, 2 Tharyarwaddy, 1 Yadeshay
Total	52			

Summary Findings (as of 9-Jan-2021)

ID	Place	Foreign country travel history	Diagnosis date (2020)	Nextstrain clade	GISAID clade	PANGOLIN Lineage
MM1	Yangon	No	24-Apr	19A	L	B.6
MM2	Yangon	No	24-Apr	19A	L	B.6
MM3	Yangon	No	24-Apr	19A	L	B.6
MM4	Yangon	No	3-May	19A	L	B.6
MM5	Yangon	No	7-May	20B	GR	B.1.1
MM6	Yangon	Yes (India)	25-May	20A	GH	B.1.36.1
MM7	Yangon	Yes (China)	2-Jun	20A	GH	B.1.80
MM8	Yangon	Yes (India)	26-May	20A	GH	B.1.36.1
MM9	Yangon	Yes (India)	26-May	20A	GH	B.1.36.1
MM10	Yangon	Yes (India)	30-May	20B	GR	B.1.1
MM11	Sittwe	No	21-Aug	20A	GH	B.1.36
MM12	Sittwe	No	21-Aug	20A	GH	B.1.36
MM13	Sittwe	No	21-Aug	20A	GH	B.1.36
MM14	Sittwe	No	20-Aug	20A	GH	B.1.36
MM15	Sittwe	No	20-Aug	20A	GH	B.1.36
MM16	Sittwe	No	20-Aug	20A	GH	B.1.36
MM17	Sittwe	No	20-Aug	20A	GH	B.1.36
MM18	Sittwe	No	21-Aug	20A	GH	B.1.36
MM19	Sittwe	No	19-Aug	20A	GH	B.1.36
MM20	Yangon	Yes(Philippine)	19-Aug	20B	GR	B.1.1
MM21	Yangon	No	12-Sep	20A	GH	B.1.36
MM22	Yangon	No	13-Sep	20A	GH	B.1.36
MM23	Yangon	No	16-Sep	20A	GH	B.1.36
MM24	Yangon	No	16-Sep	20A	GH	B.1.36
MM25	Yangon	No	14-Sep	20A	GH	B.1.36
MM26	Yangon	No	17-Sep	20A	GH	B.1.36
MM27	Yangon	No	17-Sep	20A	GH	B.1.36
MM28	Yangon	No	17-Sep	20A	GH	B.1.36
MM29	Yangon	No	17-Sep	20A	GH	B.1.36
MM30	Yangon	No	28-Sep	20A	GH	B.1.36

ID	Place	Foreign country travel	Diagnosis date (2020)	Nextstrain clade	GISAID clade	ANGOLIN Lineage
MM31	Pyinoolowin	No	11-Dec	20A	GH	B.1.36
MM32	PyiGyiTakon	No	11-Dec	20A	GH	B.1.36
MM33	NaungCho	No	11-Dec	20A	GH	B.1.36
MM34	Chanayethazan	No	11-Dec	20A	GH	B.1.36
MM35	Sagaing	No	11-Dec	20A	GH	B.1.36
MM36	Tadaoo	No	12-Dec	20A	GH	B.1.36
MM37	MyinGyan	No	12-Dec	20A	GH	B.1.36
MM38	Chanmyatharsi	No	19-Dec	20A	GH	B.1.36
MM39	AungMyayTharzan	No	19-Dec	20A	GH	B.1.36
MM40	SalTawGyi (Mattaya)	No	20-Dec	20A	GH	B.1.36
MM41	MaharAungMyay	No	21-Dec	20A	GH	B.1.36
MM42	Yangon	No	18-Dec	20A	GH	B.1.36
MM43	NOGTH	No	14-Dec	20A	GH	B.1.36
MM44	NOGTH	No	14-Dec	20A	GH	B.1.36
MM45	Tharyarwaddy	No	15-Dec	20A	GH	B.1.36
MM46	Tharyarwaddy	No	15-Dec	20A	GH	B.1.36
MM47	Pandaung	No	15-Dec	20A	GH	B.1.36
MM48	Pandaung	No	15-Dec	20A	GH	B.1.36
MM49	Bago	No	17-Dec	20A	GH	B.1.36
MM50	Bago	No	17-Dec	20A	GH	B.1.36
MM51	Yedashay	No	13-Dec	20A	GH	B.1.36
MM52	YGH (DMR)	No	24-Nov	20A	GH	B.1.36

COVID-19 pandemic wave and clades detected in Myanmar



Phylogenetic analysis of 30 genome of SARS-CoV2 detected in Myanmar

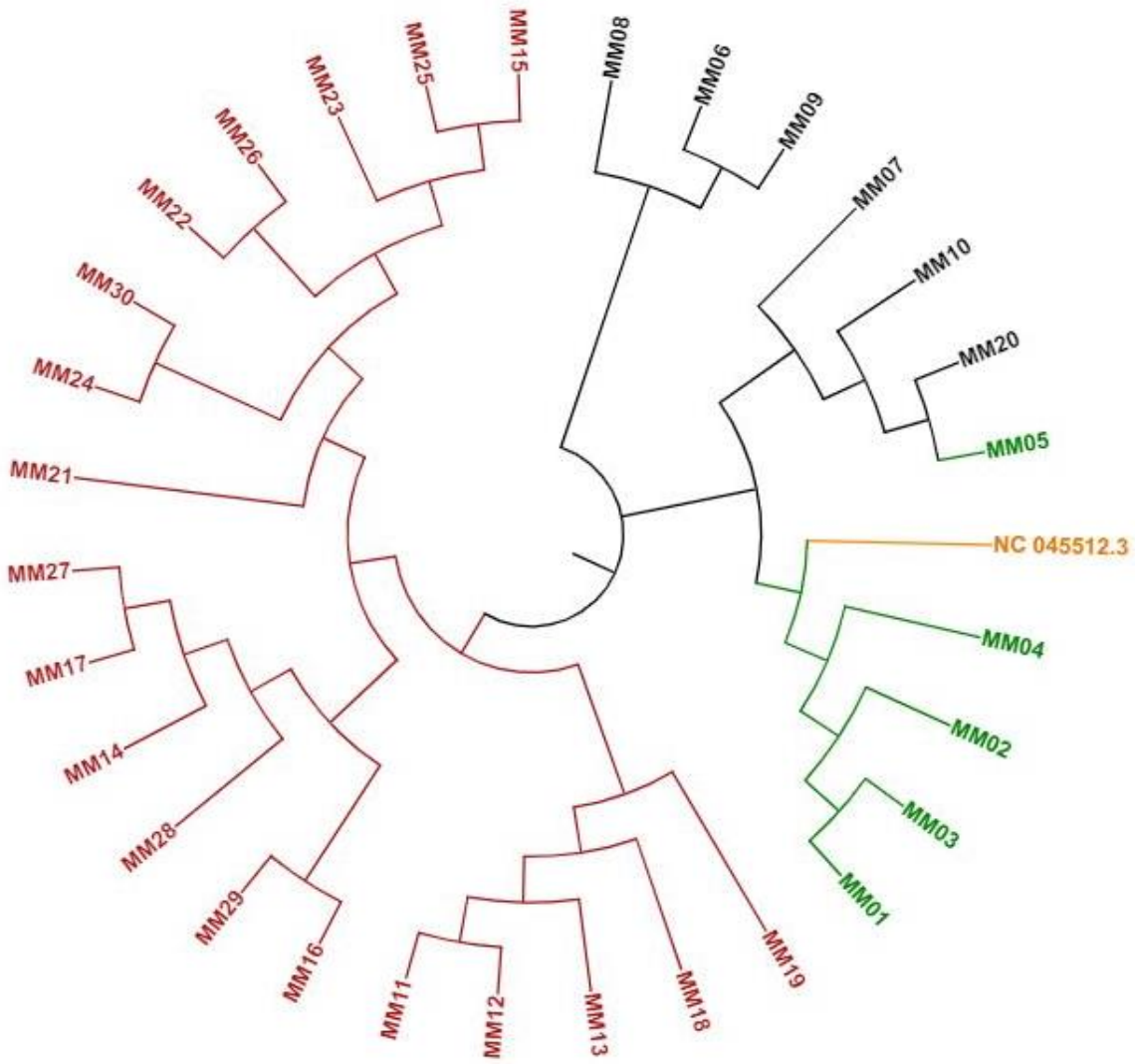
RESEARCH ARTICLE

Surge of Severe Acute Respiratory Syndrome Coronavirus 2 Infections Linked to Single Introduction of a Virus Strain in Myanmar, 2020

Myat Htut Nyunt, Hnin Ohnmar Soe, Kay Thi Aye, Wah Wah Aung, Yi Yi Kyaw, Aung Kyaw Kyaw, Theingi Win Myat, Aung Zaw Latt, Min Min Win, Aye Aye Win, Yin Min Htun, Khaing Mar Zaw, Phyu Win Ei, Kyaw Thu Hein, Lai Lai San, Nan Aye Thida Oo, Htin Lin, Nan Cho Nwe Mon, Khin Than Yee Khin Lapyae Htun, Lynn Pa Pa Aye, Yamin Ko Ko, Thitsar Htet Htet Htoo, Kham Mo Aung, Hnin Azili, Soe Soe Han, Ni Ni Zaw, Su Mon Win, Wai Myat Thwe, Thin Thin Aye, Myat Su Hlaing, Wai Yan Minn, Pyae Phyo Thu, Hlaing Myat Thu, Zaw Than Htun

DOI: 10.21203/rs.3.rs-91473/v1 Download PDF

DECLARATIONS: View author declarations.



https://doi.org/10.21203/rs.3.rs-91473/v1

Recent Finding

2nd week of the January-2021

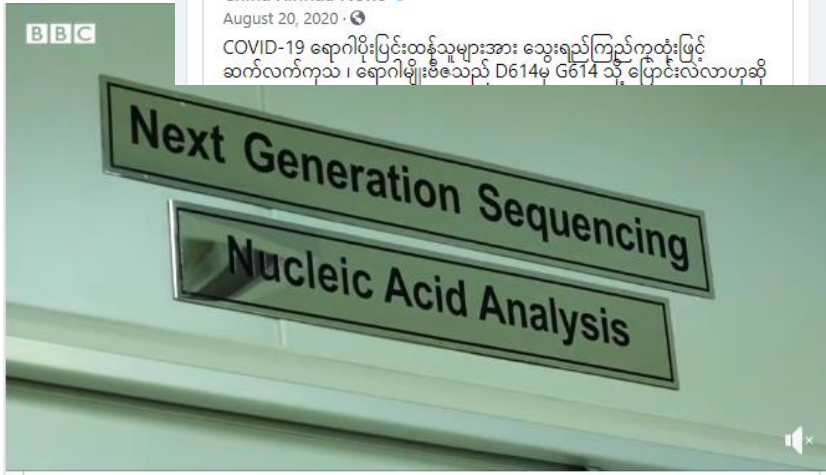
Total 11 samples (Jordan returnees -6, Bago-2, SOWCH -3)

Samples	Lineage	GISAID clade	Nextstain clade
All Jordan samples (n=6)	B.1.1.312	GR	20B
Bago samples (n=2)	B.1.36	GH	20A
Yangon samples (n=3)	B.1.36	GH	20A

Until now, no evidence on introduction of UK variant (B.1.1.7), 501Y.V2, Nigeria variant nor Cluster5 in Myanmar.

Dissemination of the findings and Public Awareness

China Xinhua News
August 20, 2020 ·
COVID-19 ရောဂါပိုးပြင်းထန်သူများအား သွေးရည်ကြည်ကုထုံးဖြင့် ဆက်လက်ကုသ ၊ ရောဂါမျိုးဗီဇသည် D614မှ G614 သို့ ပြောင်းလဲလာဟုဆို



BBC Burmese
August 21, 2020 ·
မြန်မာမှာတွေ့ရတဲ့ ကူးစက်မြန် ကိုဗစ်ပိုင်းရပ်စ်သစ် ဘယ်လိုအခြေအနေရှိလဲ
မြန်မာနိုင်ငံတွင်းမှာ ကူးစက်မြန်ပြီး မျိုးဗီဇပြောင်းလဲနေတဲ့ ကိုဗစ်-၁၉ ပိုင်းရပ်စ်ပိုးသစ်တွေ့ရှိနေတယ်လို့ ဆေးသုတေသနဦးစီးဌာနက တွေ့ရှိတဲ့သုတေသနပြုချက်တွေနဲ့ ထုတ်ပြောလာပါတယ်။ ဒီပိုင်းရပ်စ်ဗီဇသစ်က ဘယ်လို အန္တရာယ်ကြီးတာလဲ။ သူ့ရဲ့ဗီဇပြောင်းလဲမှုနဲ့ သဘောသဘာဝက ဘယ်လိုရှိပါသလဲ။ ဘယ်လောက်ထိ ကူးစက်မှုနှုန်းမြင့်မားပါသလဲ။ ဒီ

The Standard Time Daily
Favorites · August 20, 2020 ·
#Latest_NEWS
■ ပြင်းထန်သည့် COVID-19 မျိုးဗီဇပြောင်းလဲမှုရှိနေပြီဖြစ်သည့်အတွက် ဒုတိယလှိုင်းဖြစ်နိုင်ခြေရှိဟုဆို
COVID-19 ရောဂါကိုဖြစ်စေသည့် SARS-CoV-2 ပိုးရဲ့ပြင်းထန်တဲ့မျိုးဗီဇပြောင်းလဲမှုကို တွေ့ရှိနေပြီဖြစ်တဲ့အတွက် အဲဒီကူးစက်မှုမြန်တဲ့ ပိုးအမျိုးအစားများမှ ပြည်တွင်းကူးစက်မှု ဖြစ်လာပါက ဒုတိယလှိုင်း ဖြစ်နိုင်ခြေရှိတယ်လို့ ဆေးသုတေသနဦးစီးဌာနက သိရပါတယ်။

တနလ်း၊ ဩဂုတ် ၂၄၊ ၂၀၂၀ | မြန်မာ့အလင်း | ပြည်တွင်းသတင်း | ၇

ပြည်ထောင်စုဝန်ကြီး ဒေါက်တာမြင့်ထွေးထံ ဆေးသုတေသနဦးစီးဌာနက မြန်မာနိုင်ငံတွင် တွေ့ရှိရသည့် SARS-CoV-2 ပိုင်းရပ်စ်ပိုး၏ မျိုးဗီဇတစ်ခုလုံးကို လေ့လာသော သုတေသနဆောင်ရွက်ခဲ့မှုနှင့် ကာကွယ်ဆေးသုတေသနလုပ်ငန်းများနှင့် စပ်လျဉ်း၍ ရှင်းလင်းတင်ပြ

နေပြည်တော် ဩဂုတ် ၂၃

ကျန်းမာရေးနှင့်အားကစားဝန်ကြီးဌာန ပြည်ထောင်စုဝန်ကြီး ဒေါက်တာမြင့်ထွေးထံ ဆေးသုတေသနဦးစီးဌာနက "မြန်မာနိုင်ငံတွင် တွေ့ရှိရသည့် SARS-CoV-2 ပိုင်းရပ်စ်ပိုး၏ မျိုးဗီဇတစ်ခုလုံးကို လေ့လာသောသုတေသန" ဆောင်ရွက်ခဲ့မှုနှင့် ကာကွယ်ဆေးသုတေသနလုပ်ငန်းများနှင့် စပ်လျဉ်း၍ ရှင်းလင်းတင်ပြမှု အစည်းအဝေးကို ယမန်နေ့ ညနေပိုင်းတွင် ဆေးသုတေသနဦးစီးဌာန(ရန်ကုန်)၌ ကျင်းပသည်။ (ယာပုံ)

ရှေးဦးစွာ ဆေးသုတေသနဦးစီး ရှင်းလင်းတင်ပြ

ဌာန၊ ကာကွ
ညွှန်ကြား
ထွန်းက
တွင် ၁၉၉၀
မှ ထုတ်လုပ်
အသားဝါ(ဘ
ထုတ်လုပ်နိုင်
ခဲ့ပြီး ၁၉၉၇
ထုတ်လုပ်နိုင်
တွင် ကိုရီးယ
ကမ္ဘာ့၊
ပူးပေါင်း၍ R
B Vaccine c

မှု၊ ဓာတ်ခွဲ ဆောင်ရွက်ကာ "မြန်မာနိုင်ငံတွင် ပုံသဏ္ဌာန်၊ အခြားနိုင်ငံများတွင် ရှိနေသော်လည်း အဆိုပါ အထောက်
၁၀ ခုအနက် ဖြစ်ပွားနေသည့် SARS-CoV-2 ဖြစ်ပွားသည့်ရောဂါပိုးနှင့် တူညီမှု အပုံများမရှိတော့ပါက ကုန်ကျစရိတ်
ပြောင်းလဲမှု ပိုင်းရပ်စ်ပိုးကို မော်လီကျူးနည်းပညာ ရှိ၊ မရှိနှင့် ရောဂါပြင်းထန်စေနိုင်မှု များစွာ သုံးစွဲရမည်ဖြစ်သဖြင့်
ငြင်းလဲမကြောင့် ဖြင့် ဆောင်ကြွသွေလျာခြင်း"ကို ပမာဏတိုကို သိရှိနိုင်ကာ ရောဂါ ကာကွယ်ဆေးအမျိုးမျိုးကို မိမိတို့

Future Direction

- Genomic Surveillance is essential compartment of the pandemic
- Genomic and molecular surveillance have to be conducted.
- Surveillance network
- Sample data bank (pathogen/host)

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Thank
You