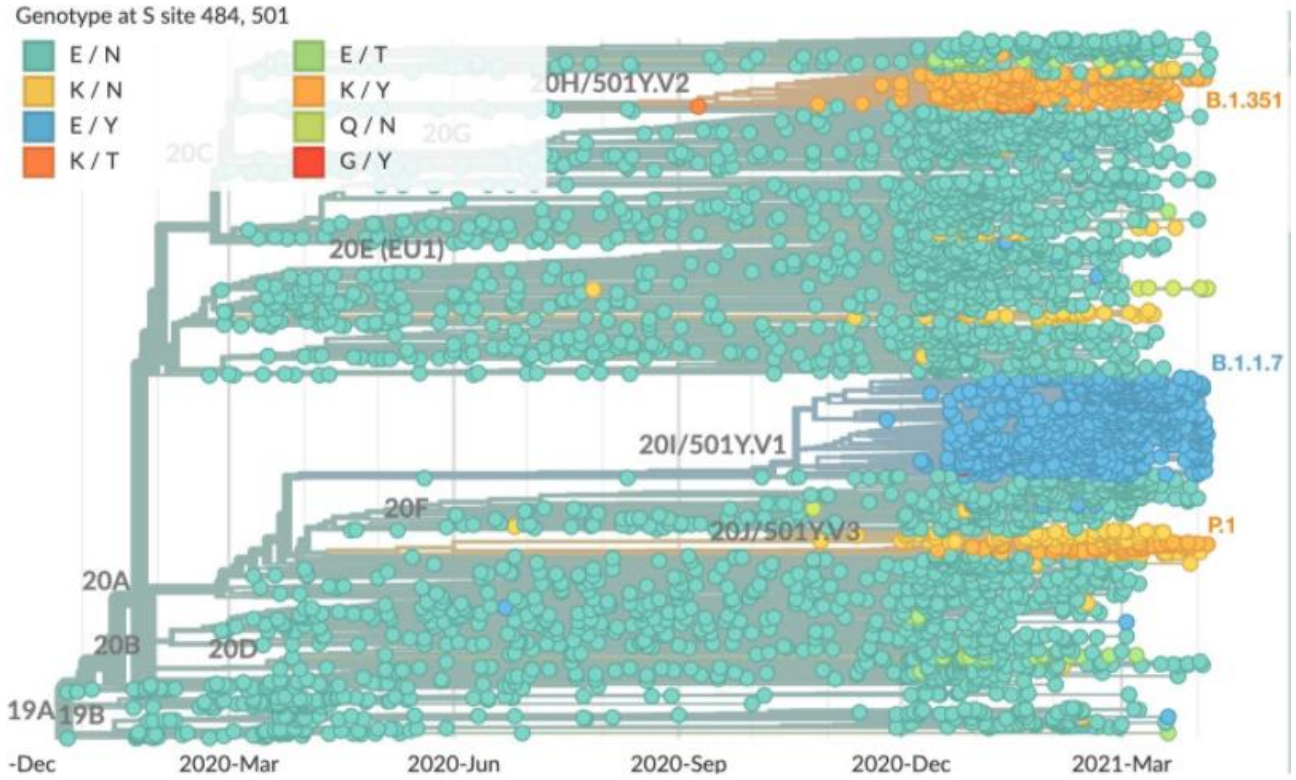
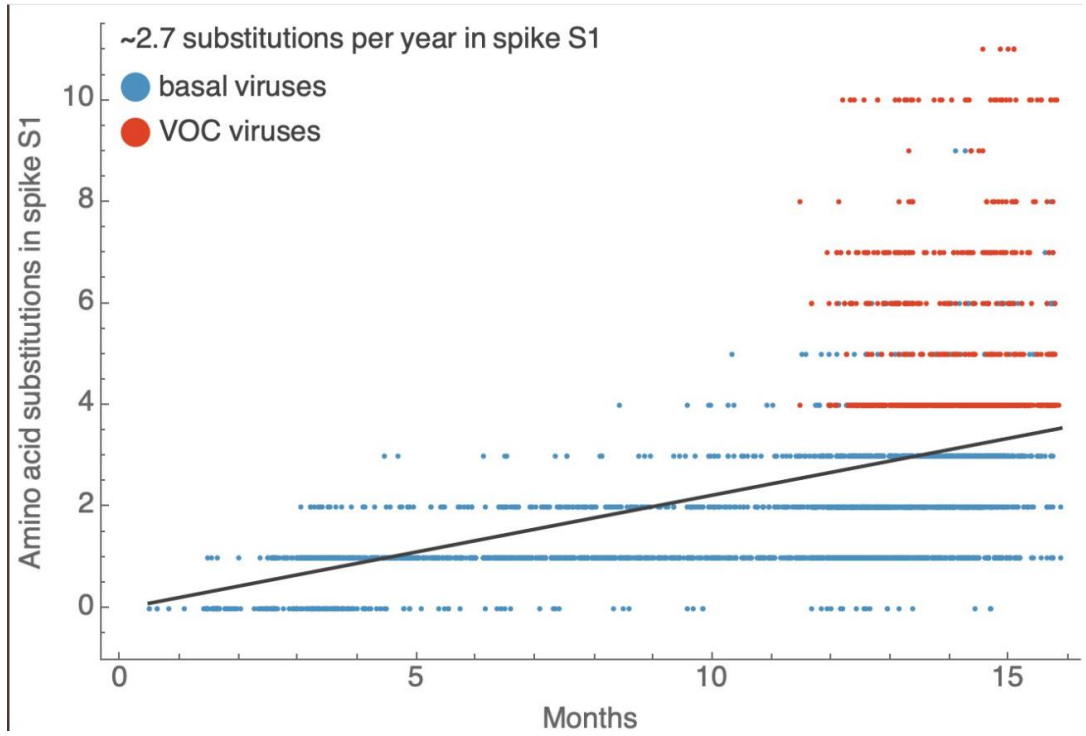
Sars-CoV-2 Varyantları ve Etkileri: Bildiklerimiz, Bilmediklerimiz

Kenan Midilli

İÜ-C Tıbbi Mikrobiyoloji Anabilim Dalı

Tıbbi Viroloji Bilim Dalı


Genotype at S site 484, 501
E / N
K / N
E / Y
K / T
E / T
K / Y
Q / N
G / Y
20C
20G
0H/501Y.V2
B.1.351
20E (EU1)
B.1.1.7
20I/501Y.V1
20F
20J/501Y.V3
P.1
20A
20B
20D
19A
19B
-Dec
2020-Mar
2020-Jun
2020-Sep
2020-Dec
2021-Mar


~2.7 substitutions per year in spike S1
basal viruses
VOC viruses
Amino acid substitutions in spike S1
0
2
4
6
8
10
0
5
10
15
Months

VOI = Variant of Interest

Referans izolata kıyasla fenotip değişikliği gösteren ya da fenotipik değiişikliğe yol açtığı bilinen ya da kuşkulanılan amino asit değşiklikleri olan SARS-CoV-2 izolatı

veya

Toplumda bulaştığı bilinen; vaka kümeleri oluşturan ya da başka ülkelerde de saptanan SARS-CoV-2 izolatı

veya

DSÖ’nün SARS-CoV-2 Değerlendirme Çalışma Grubu ile birlikte değerlendirmeye aldığı bir VOI

VOC = Variant of Concern

- Bulaşıcılığı artmış veya COVID-19 epidemiyolojisini olumsuz yönde etkileyebilecek
- Virulansı artmış ya da klinik tabloda değişikliğe yol açmış
- Halk sağlığı veya sosyal önlemlerin etkinliğine azaltan ya da mevcut tanı kitleri, aşı veya terapötiklerin etkinliğini azaltan

veya

DSÖ’nün SARS-CoV-2 Değerlendirme Çalışma Grubu ile birlikte değerlendirmeye aldığı bir VOC

https://www.gov.uk/government/publications/covid-19-variants-genomically-confirmed-case-numbers/variants-distribution-of-cases-data#differences-between-a-variant-of-concern-and-a-variant-under-investigation

The previous variant names frequently include similar numbers with similar or repeating patterns. This makes referring to them verbally challenging. To overcome this challenge, a revised nomenclature has been agreed involving dropping the first 2 numbers of the year and replacing the 2-month numbers with a 3-letter abbreviation. This shortens the name and reduces the degree of repeated sequences of numbers.

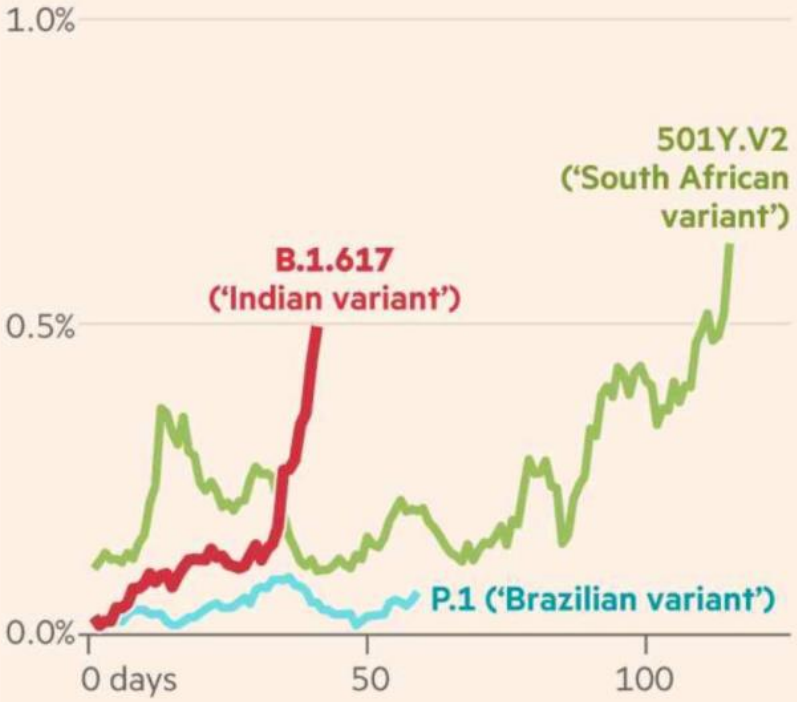
- 501.Y.B.1.7 → VOC-20DEC-01
- 501.B.351 → VOC-20DEC-02
- 501Y.B.28 (p1) → VOC-21JAN-02

- P.2 → VUI-21JAN-01
- A.23.1 wE484K → VUI-21FEB-01
- B.1.525 → VUI-21FEB-03
- ……

Variant	Other names by which this variant may be known*	Lineage	Country in which first detected	Total confirmed cases^	New cases since last update (data up to 7 April)
VUI-21JAN-01	VUI-202101/01	P.2	Brazil	59	0
VUI-21FEB-01	VUI-202102/01	A.23.1 with E484K	England, UK	79	0
VOC-21FEB-02	VOC-202102/02	B.1.1.7 with E484K	England, UK	43	0
VUI-21FEB-03	VUI-202102/03	B.1.525 (previously designated UK1188)	England, UK	361	+27
VUI-21FEB-04	VUI-202102/04	B1.1.318	TBC	113	+9
VUI-21MAR-01	VUI-202103/01	B1.324.1 with E484K	TBC	2	0
VUI-21MAR-02	N/A	P.3	TBC	5	0
VUI-21APR-01	N/A	B.1.617	India	77	Initial update

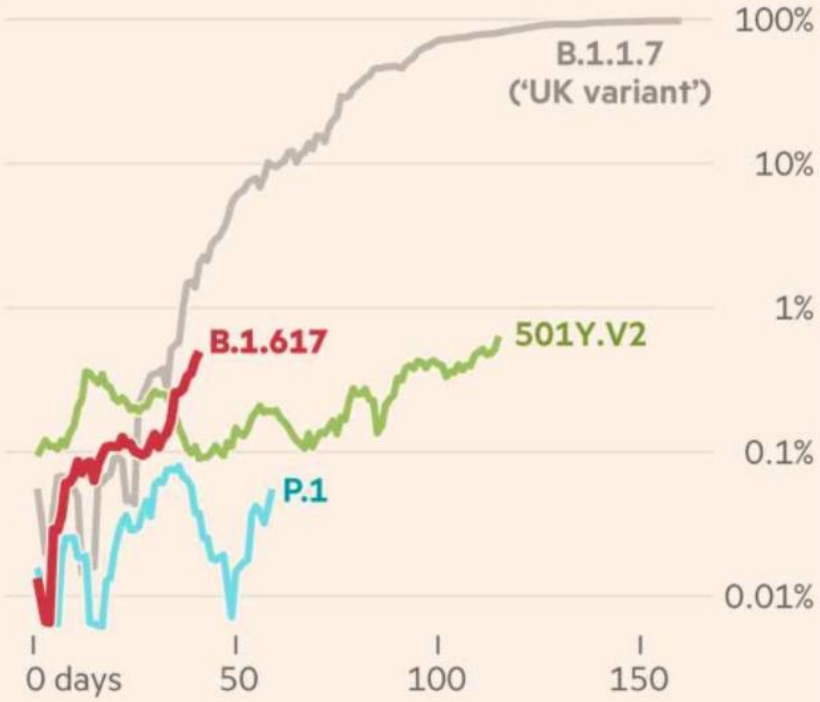
The new variant first discovered in India appears to be spreading rapidly...

Each variant as a share of all sequenced cases in the UK, by number of days since it was first identified in the UK



...and confirmed cases are growing at a similar rate to B.1.1.7 at the same stage of its emergence

Each variant as a share of all sequenced cases in the UK **(log scale)**, by number of days since it was first identified in the UK



Source: FT analysis of GISAID data

© FT

CDC

- A US government interagency group developed a Variant Classification scheme that defines three classes of SARS-CoV-2 variants:
  - Variant of Interest
  - Variant of Concern
  - Variant of High Consequence
- The B.1.1.7, B.1.351, P.1, B.1.427, and B.1.429 variants circulating in the United States are classified as variants

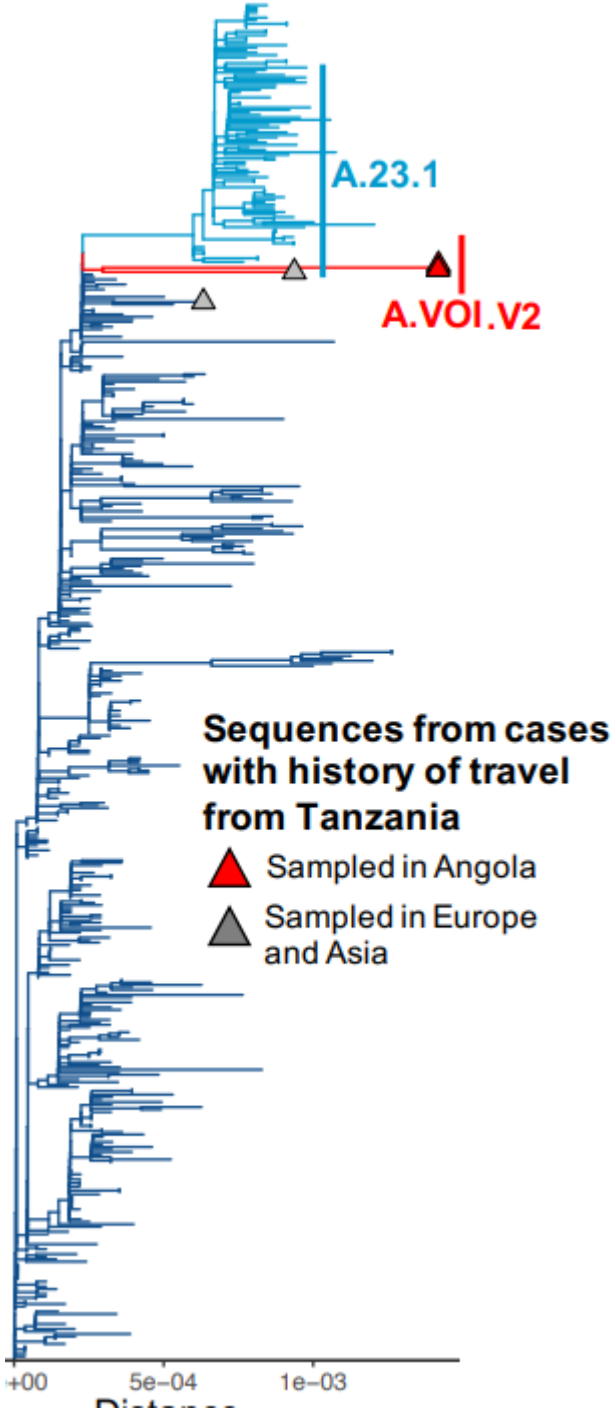
Current variants of interest in the United States that are being monitored and characterized are listed in the table below. The table will be updated when a new variant of interest is identified.

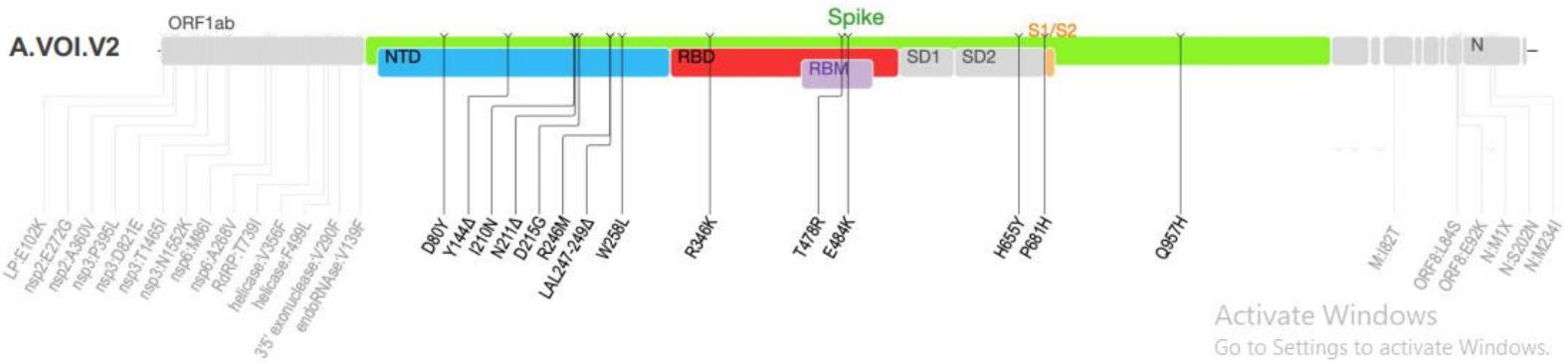
Name (Pango lineage)	Substitution	Name (Nextstrain[a])	First Detected	BEI Reference Isolate[b]	Predicted Attributes
B.1.526	**Spike:** (L5F*), T95I, D253G, (S477N*), (E484K*), D614G, (A701V*) **ORF1a:** L3201P, T265I, Δ3675/3677 **ORF1b:** P314L, Q1011H **ORF3a:** P42L, Q57H **ORF8:** T11I **5'UTR:** R81C	20C	New York/November 2020		• Potential reduction in neutralization by monoclonal antibody treatments • Potential reduction in neutralization by convalescent and post-vaccination sera
B.1.525	**Spike**: A67V, Δ69/70, Δ144, E484K, D614G, Q677H, F888L **ORF1b**: P314F **ORF1a**: T2007I **M**: I82T **N:** A12G, T205I **5'UTR**: R81C	20C	New York/December 2020		• Potential reduction in neutralization by monoclonal antibody treatments • Potential reduction in neutralization by convalescent and post-vaccination sera
P.2	**Spike**: E484K, D614G, V1176F **ORF1a**: L3468V, L3930F **ORF1b**: P314L **N:** A119S, R203K, G204R, M234I **5'UTR**: R81C	20J	Brazil/April 2020		• Potential reduction in neutralization by monoclonal antibody treatments • Potential reduction in neutralization by convalescent and post-vaccination
B.1.427	L452R D614G	20C/S:452R	US-California		• ~20% increased transmissibility [21] • Significant impact on neutralization by some, but not all, EUA therapeutics • Moderate reduction in neutralization using convalescent and post-vaccination sera [21]
B.1.429	S13I W152C L452R D614G	20C/S:452R	US-California		• ~20% increased transmissibility [21] • Significant impact on neutralization by some, but not all, EUA therapeutics • Moderate reduction in neutralization using convalescent and post-vaccination sera [21]

DSÖ

Table 3: Overview of variants of interest (VOIs), as of 13 April 2021*

Nextstrain clade	PANGO lineage	GISAID clade	Alternate names	First detected by	Earliest samples	Key spike mutations
20C	B.1.525	G/484K.V3	-	United Kingdom and Nigeria	Dec 2020	H69-V70 deletion; Y144 deletion; Q52R; E484K; Q677H; D614G; and F888L
20C/S.452R	B.1.427/B.1.429	GH/452R.V1	CAL.20C/L452R	United States of America	Jun 2020	L452R; W152C; S13I; and D614G
20B/S.484K	B.1.1.28.2, alias P.2	GR	-	Brazil	Apr 2020	L18F; T20N; P26S; F157L; E484K; D614G; S929I; and V1176F
Not yet assigned	B.1.1.28.3, alias P.3	Not yet assigned	PHL-B.1.1.28	Philippines and Japan	Feb 2021	141-143 deletion E484K; N501Y; and P681H
20C	B.1.526 with E484K or S477N	GH	-	United States of America	Nov 2020	L5F; T95I; D253G; D614G; A701V; and E484K or S477N
20C	B.1.616	GH	-	France	Jan 2021	G142 deletion; D66H; Y144V; D215G; V483A; D614G; H655Y; G669S; Q949R; and N1187D





Activate Windows
Go to Settings to activate Windows.

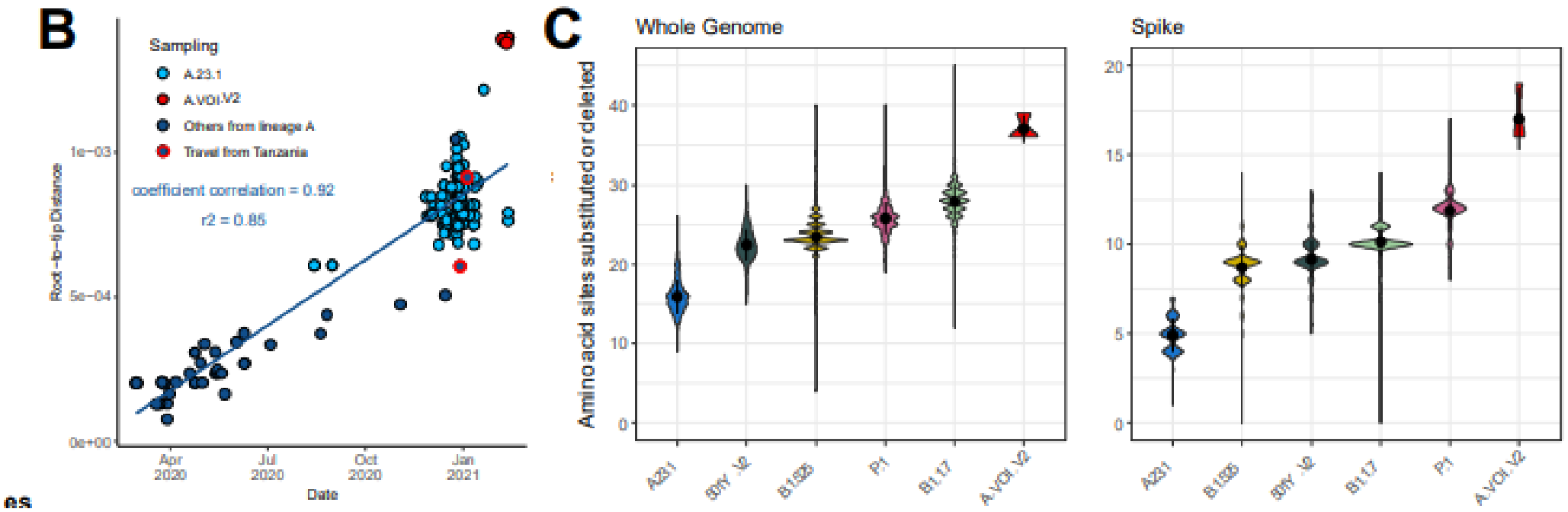
Comment on this paper

A novel variant of interest of SARS-CoV-2 with multiple spike mutations detected through travel surveillance in Africa

Tulio de Oliveira, Silvia Lutucuta, Join Nkengasong, Joana Morais, Joana Paula Paixão, Zoraima Neto, Pedro Afonso, Julio Miranda, Kumbelembe David, Luzia Inglês, Amilton Pereira Agostinho Paulo Raisa Rivas Carralero, Helga Reis Freitas, Franco Mufinda, Sofonias Kifle Tessema, Houriiyah Tegally, Emmanuel James San, Eduan Wilkinson, Jennifer Giandhari, Sureshnee Pillay, Marta Giovanetti, Yeshnee Naidoo, Aris Katzourakis, Mahan Ghafari, Lavanya Singh, Derek Tshiabuila, Darren Martin, Richard J Lessells

doi: https://doi.org/10.1101/2021.03.30.21254323

This article is a preprint and has not been peer-reviewed [what does this mean?]. It reports new medical research that has yet to be evaluated and so should *not* be used to guide clinical practice.



Tanzanya canavarı! 😱 👀

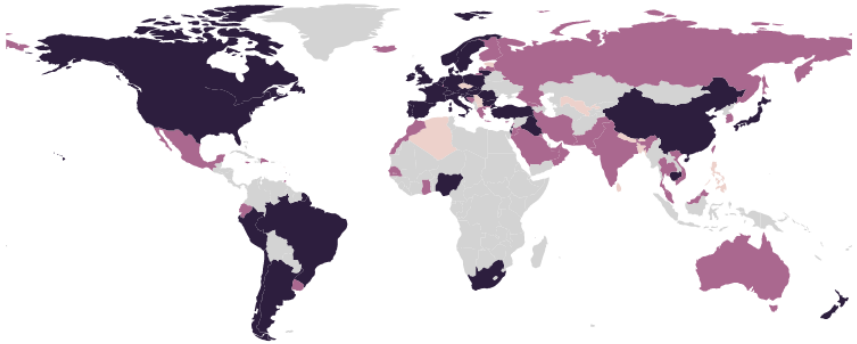
11'i S bölgesinde olmak üzere 31 amino asit değişikliği

S bölgesinde 3 delesyon
RBD: R346K, T478R ve E484K)
NTD: 5 amino asit değişikliği ve 3 delesyon (Y144Δ, R246M, SYL247-249Δ ve W258L)
S1/S2 civarı: H655Y ve P681H

AKILDAKİ SORULAR

- Varyantların bulaşıcılığı
- Varyantların klinik etkileri
- Varyantlarla mücadele üzerine etkileri
- Varyantların geçirilmiş infeksiyonla edinilmiş bağışıklıktan etkilenme durumları
- Varyantların aşılama ile elde edilmiş bağışıklıktan etkilenme durumları
- Varyantların izlenmesi
- Yeni varyantların ortaya çıkma riski
- Aşı seçimi ve varyantlar
- Aşıların güncellenmesi – Pan-SARS-CoV 2 aşısı *«dream vaccine»*

501Y.V.1 (B 1.1.7)

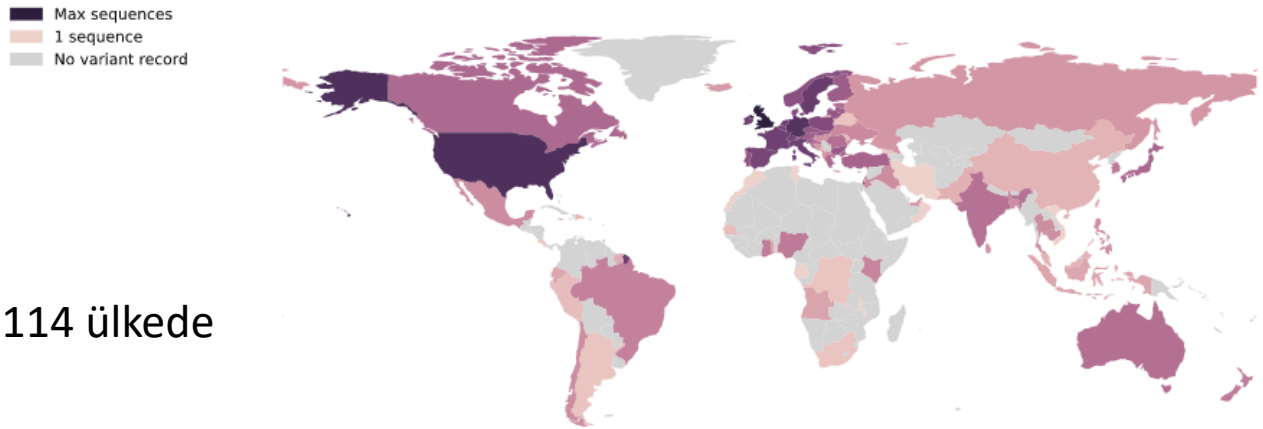


Mutasyonlar	23
Amino asit değişiklikleri	orf1ab:T1001I, orf1ab:A1708D, orf1ab:I2230T, del:11288:9, del:21765:6, del:21991:3, orf8:Q27*, Orf8:R52I, Orf8:Y73C, N:D3L, N:S235F **S:HV 69-70 deletion, S: Y144 deletion, S: N501Y, S: A570D, S: P681H, S: T716I, S: S982A, S: D1118**
Bulaşma hızı	%40-75 daha yüksek; ikincil atak hızı 3 puan daha yüksek (%10'a karşılık %13)
Hospitalizasyon gereksiniminde artış	>%50 (Danimarka)
Mortalite	X 1.3
Nötralizan antikorlardan etkilenme	Anlamlı bir değişiklik yok. Aşı ile bağışıklama sonrası yabanıl tipe göre yaklaşık 2 kat; K484E eklenlendiğinde 7-9 kat (Biontech)
Aşı denemeleri	Minimum; AZ ve Novavax: %10 daha düşük

Figure 3. Countries, territories and areas reporting SARS-CoV-2 VOC 202012/01 as of 13 April 2021

Figure 3 | Map of B.1.1.7 sequence counts

Map showing the logged number of sequences of the variant in each country. Countries with more sequences are show

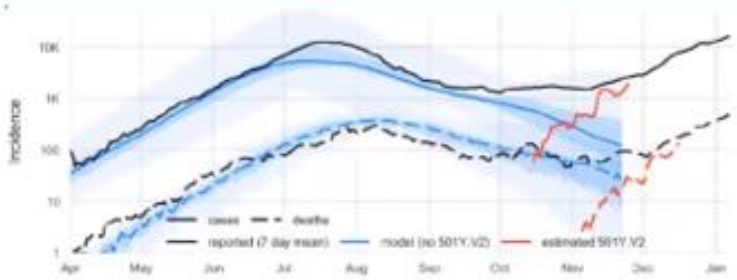


114 ülkede

501Y.V.2 (B.1.351)

Mutasyonlar	21
Amino asit değişiklikleri	E:P71L, N:T205I, orf1a:K1655N **S:D80A, S:D215G, S:K417N, S:A701V, S:N501Y, S:E484K**
Bulaşma hızı	Artış: 1.50
Hospitalizasyon gereksiniminde artış	X1.2 (?)
Mortalite	Artmış; özellikle yaşlılar ve komorbiditesi olanlarda daha belirgin
Nötralizan antikorlardan etkilenme	KP'ya karşı 9.4; aşılanmışlardan elde edilen serumlara karşı 10.3-12.4 kat dirençli.
Aşı denemeleri	Novavax ve JJ aşıları %60 civarında; AZ: hafif ve orta infeksiyonları önlemede etksiz
Reinfeksiyon	Olasılıkla yüksek

Increased transmissibility of 501Y.V2



CMMID, LSHTM & SACEMA (Carl Pearson *et al.*)

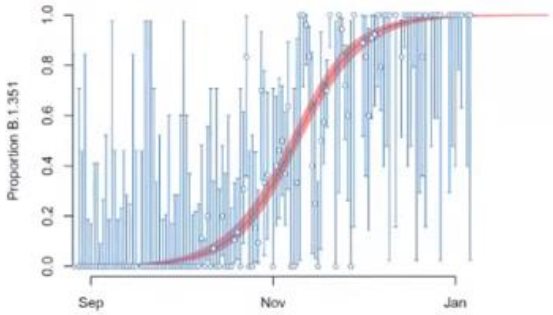
CovidM: age-structured mathematical model

501Y.V2 - **1.50 (95%CrI 1.20-2.13) times as transmissible** as previously circulating lineages

BUT, same effect could be explained by 501Y.V2 evading 21% (95% CrI 11-36%) of previously acquired immunity, without any increased transmissibility

https://cmmid.github.io/topics/covid19/sa-novel-variant.html

Increased transmissibility of 501Y.V2



Christian Althaus *et al.* (Bern) – unpublished data

501Y.V2 - **48%** (95%CI 43%-53%) or **67%** (95%CI 60%-74%) increase in transmissibility, assuming generation time of 5 or 7 days respectively

This analysis does not consider immune escape

501Y.V2 and risk of re-infection

Novavax phase 2b vaccine trial – placebo arm

- Antibody testing at enrolment (anti-spike IgG) – 31% positive

	N	Any symptomatic COVID-19		Moderate-severe COVID-19	
		n	% (95% CI)	n	% (95% CI)
Seronegative	1516	80	5.3 (4.3-6.6)	47	3.1 (2.3-4.1)
Seropositive	674	35	5.2 (3.6-7.2)	21	3.1 (1.9-4.7)

- Results suggested prior infection offers no protection from re-infection – caution given risk of bias (e.g. differential risks of exposure seropositive vs. seronegative participants)
- Results recently updated to 90 days follow-up – 7.9% seronegative vs. 4.4% seropositive

Shinde V, *et al*. medRxiv 2021
https://ir.novavax.com/node/15661/pdf

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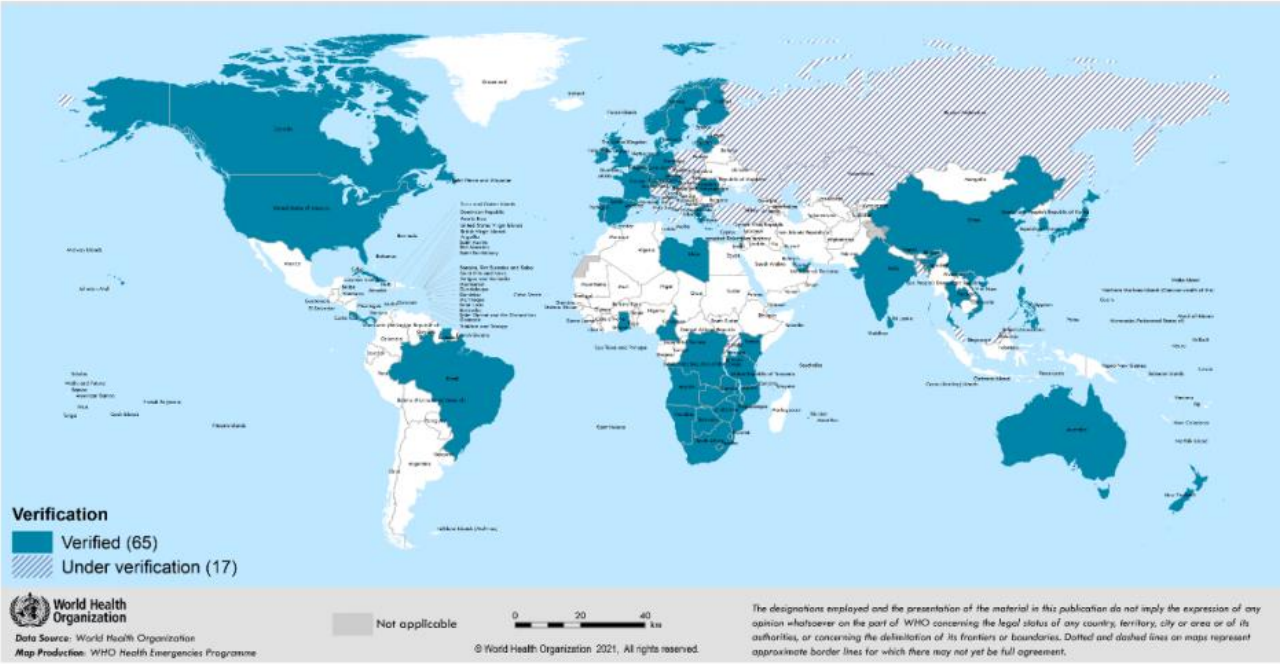
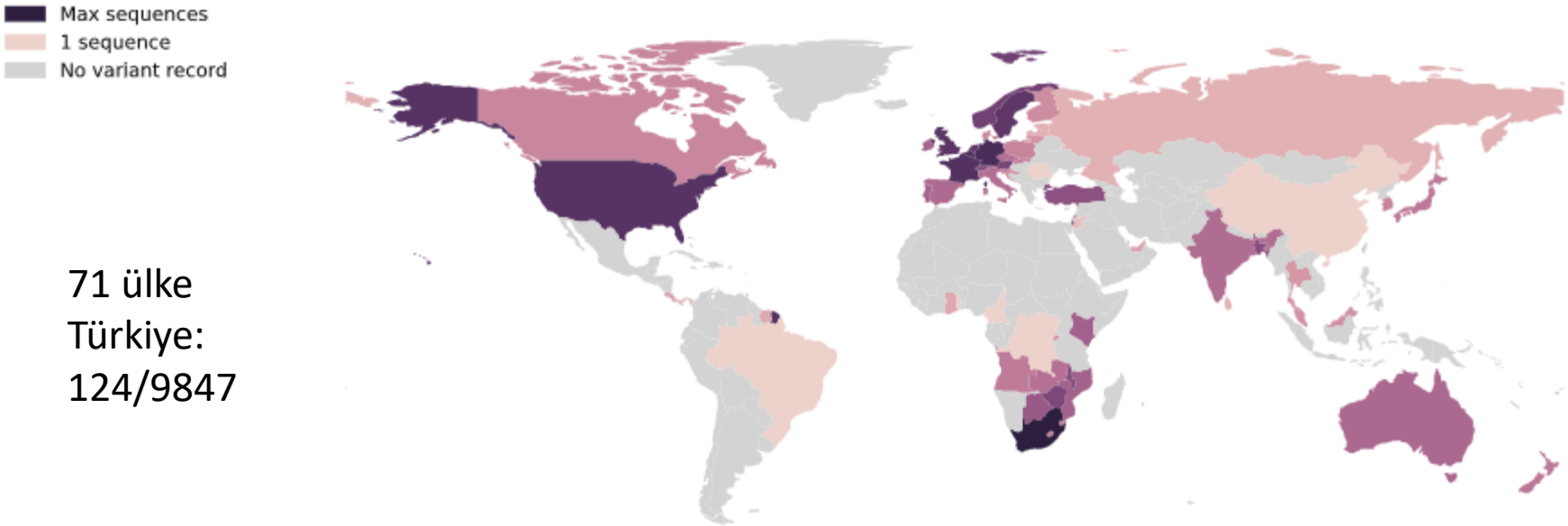
Figure 4. Countries, territories and areas reporting SARS-CoV-2 501Y.V2 as of 13 April 2021

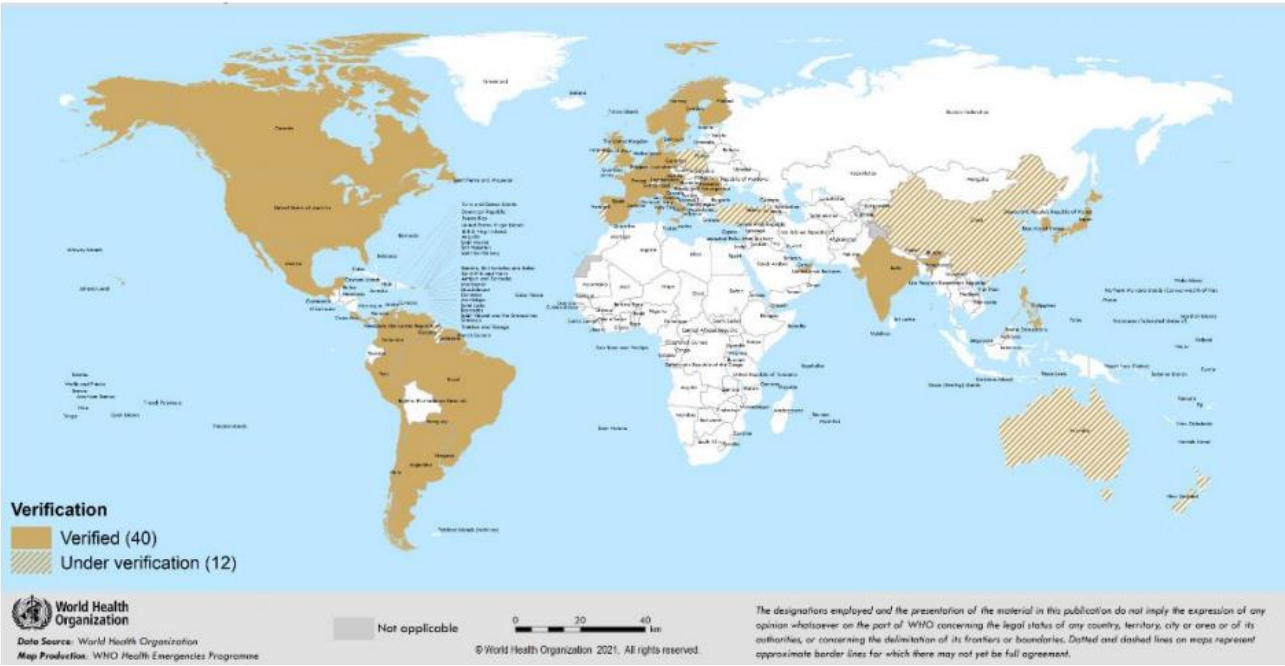


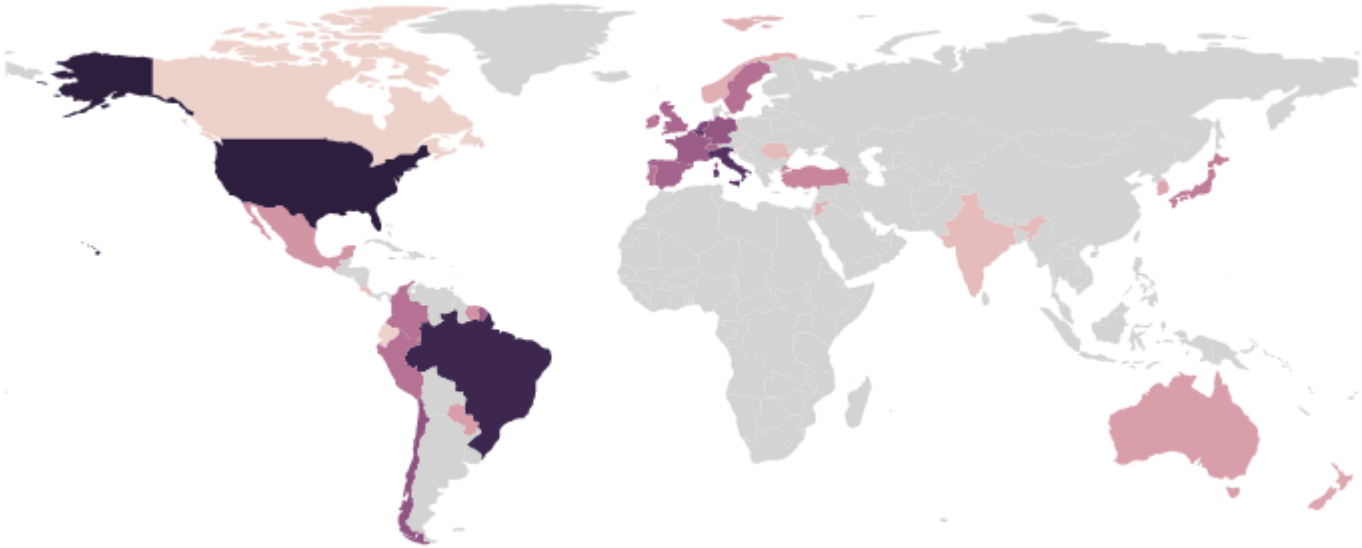


71 ülke
Türkiye:
124/9847

501Y.V.3 (B 1.1.28.1 ya da P.1)

Mutasyonlar	17
Amino asit değişiklikleri	orf1ab:S1188L, orf1ab:K1795Q, del:11288:9, orf3a:G174C, orf8:E92K, N:P80R **S:L18F, S:T20N, S:P26S, S:D138Y, S:R190S, S:K417T, S:E484K, S:N501Y, S:H655Y, S:T1027I**
Bulaşma hızı	Yüksek (X1.4-2.2)
Hospitalizasyon	??
Mortalite	X 1.1-1.8??
Nötralizan antikorlardan etkilenme	Konvelasan plazmaya karşı 6.5 kat düşüş; aşılanmışlarda (m-RNA) 2-3 kat Bir başka çalışmada aşı yanıtlarına (Biontech) 10.3-12.4 kat; konvelesan plazmaya karşı 9.4 kat daha dirençli
Reinfeksiyon	Daha önceden kazanılmış bağışıklık %25-61 oranında koruyucu → Reinfeksiyon





37 ülkede
Türkiye 12/3674

P1 bulaşıcılık: 1.7-2.4 kat daha yüksek

Geçirilmiş infeksiyonun P1'e karşı koruyuculuğu: %54-79

Brazil warns women to delay pregnancy amid Covid-19 surge

Advice comes as country's clinicians claim P1 Covid variant more aggressive during pregnancy

- Coronavirus - latest updates
- See all our coronavirus coverage

▲ A healthcare worker assists a pregnant woman, in a hospital in Santarem, Brazil. A health ministry official advised women to 'delay pregnancy until a better moment'. Photograph: Tarso Sarraf/AFP/Getty Images

Brazil has warned women to delay getting pregnant until the worst of the pandemic passes, saying the virus variant that is devastating the South American country appears to affect expectant mothers more than earlier versions of the coronavirus.

B.1.617: Hindistan varyantı

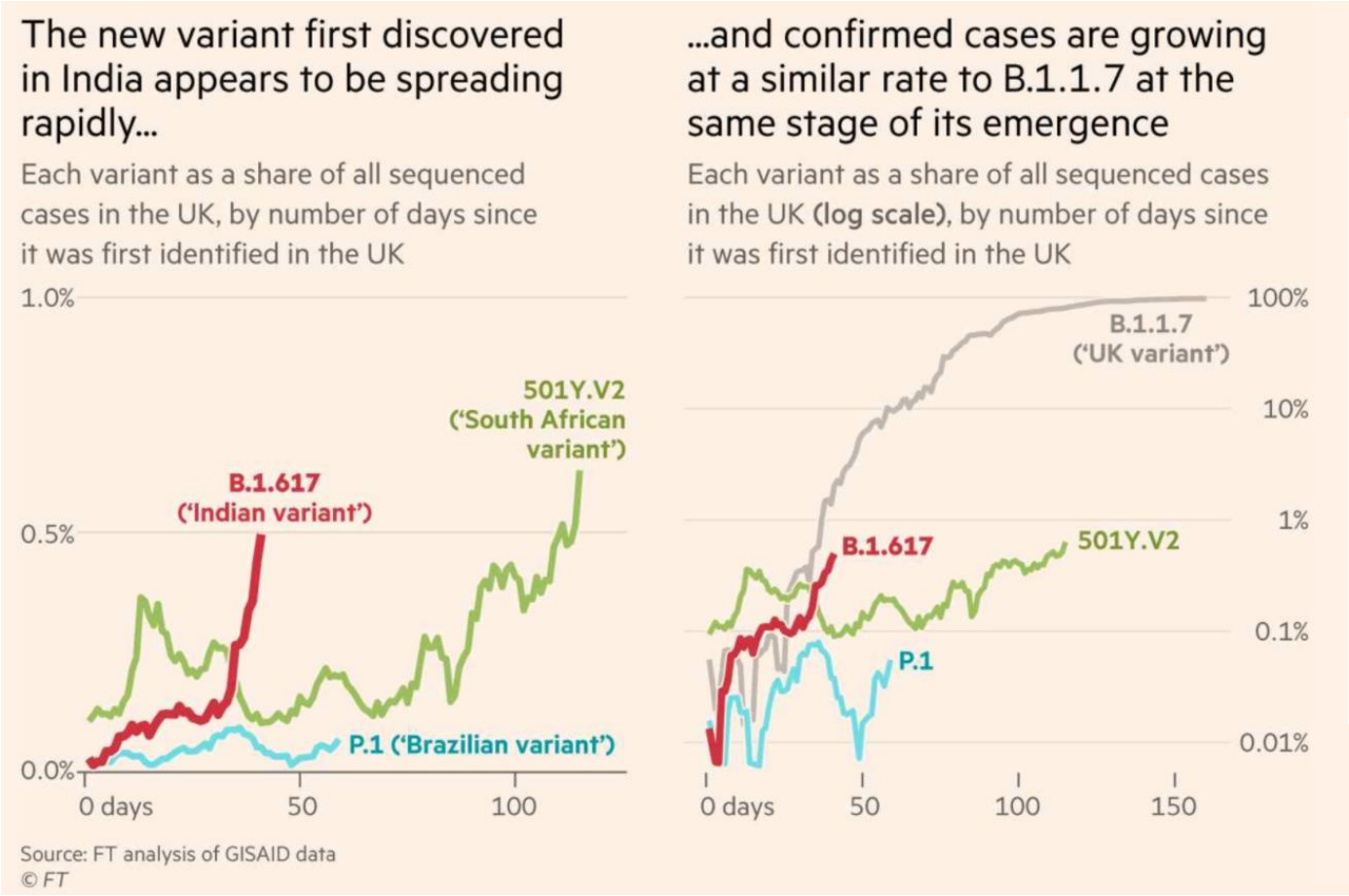
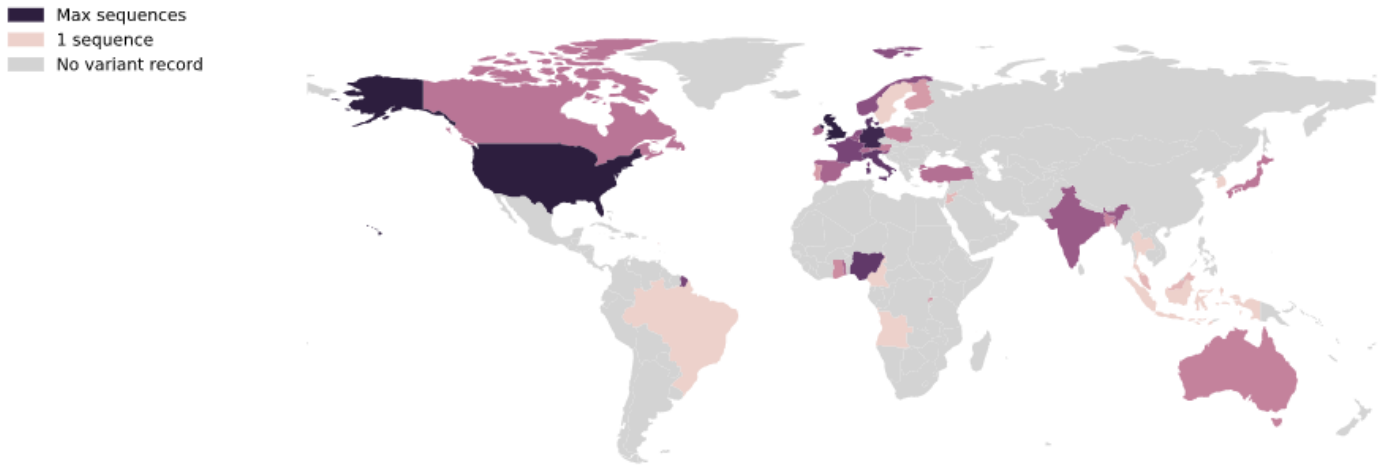


Figure 3 | Map of B.1.525 sequence counts

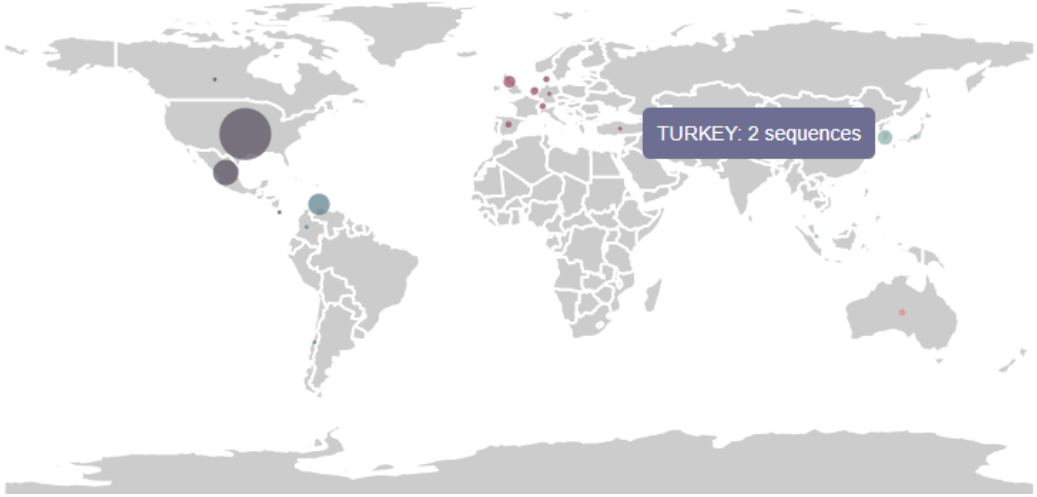
Map showing the logged number of sequences of the variant in each country. Countries with more sequences are shown in darker colours.

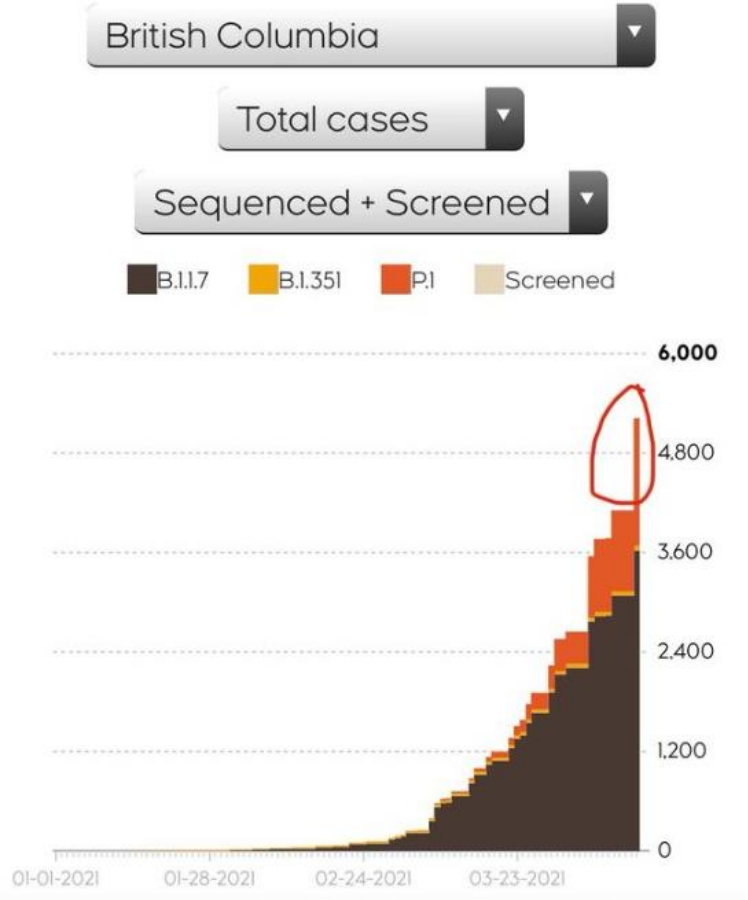


Türkiye 14 sekans

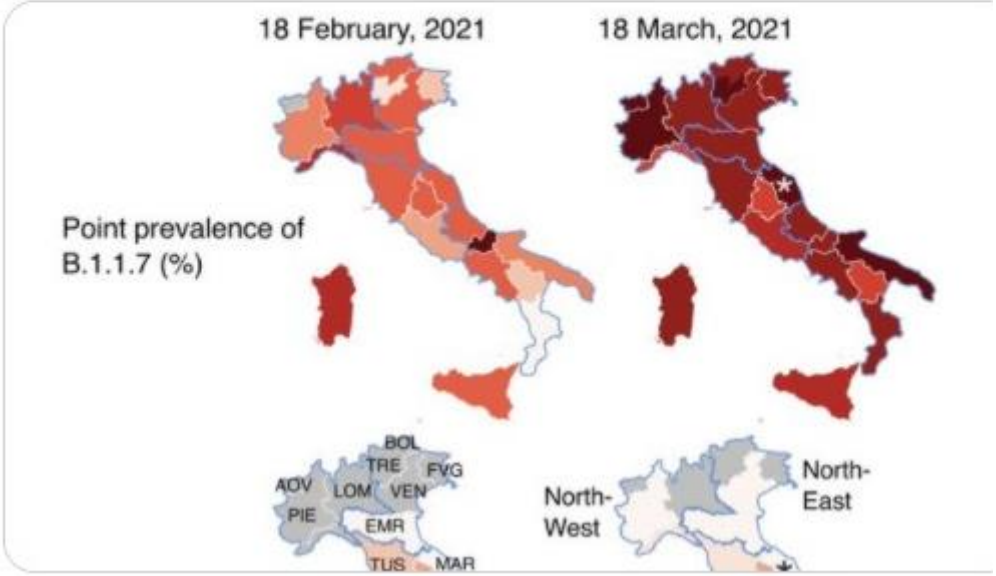
Lineage B.1.427

GO TO PARENT LINEAGE: B.1

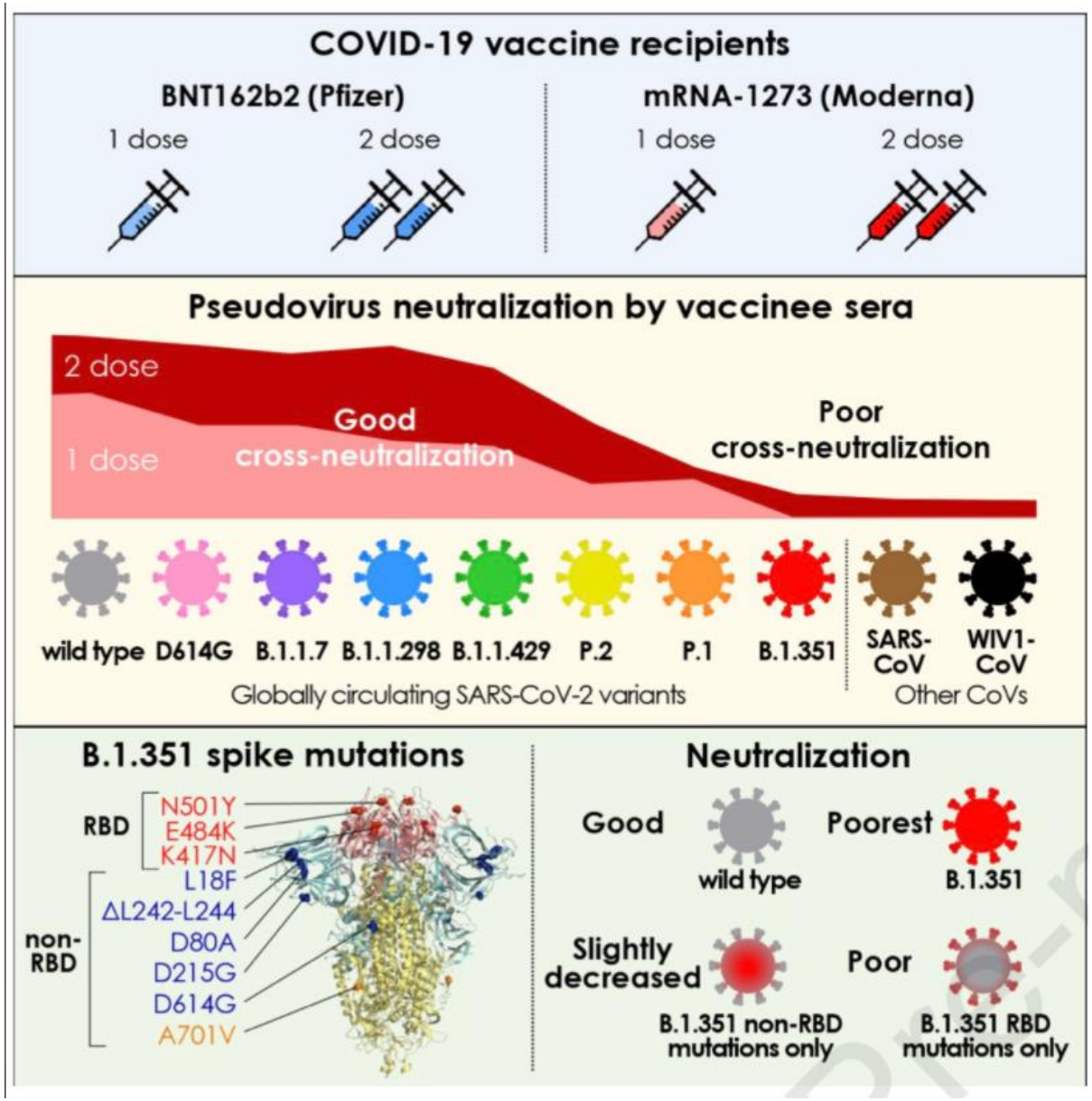




B.1.1.7 was dominant in Italy already on Feb 18 (54% of all cases), and increased by Mar 18 (86%). P.1 was quite common in Central Italy (5% of cases nationally, ~10-35% in Central Italy) on Feb 18 and did not increase b Mar 18. B.1.351 was rarely detected in both surveys. 2/9



As of April 13, there were 5,162 cases infected with variants of concern (VOC) (confirmed by sequencing) with onset up to week 13 in BC. Of those, 3,588 (70%) were infected with variant B.1.1.7; 1,510 (29%) were infected with variant P.1; and 64 (1%) were infected with variant B.1.351. Episode dates range from week 51 to week 13. Adults 20-49 years of age comprised 61% of all SARS-CoV-2 VOC cases in BC, and also comprised 2,041 (57%) of the B.1.1.7; 1,053 (70%) of the P.1 variants and 32 (50%) of the B.1.351 that were detected.

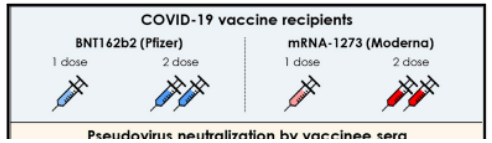

COVID-19 vaccine recipients
BNT162b2 (Pfizer)
1 dose
2 dose
mRNA-1273 (Moderna)
1 dose
2 dose
Pseudovirus neutralization by vaccinee sera
2 dose
1 dose
Good
cross-neutralization
Poor
cross-neutralization
wild type
D614G
B.1.1.7
B.1.1.298
B.1.1.429
P.2
P.1
B.1.351
SARS-CoV
WIV1-CoV
Globally circulating SARS-CoV-2 variants
Other CoVs
B.1.351 spike mutations
RBD
N501Y
E484K
K417N
non-RBD
L18F
ΔL242-L244
D80A
D215G
D614G
A701V
Neutralization
Good
wild type
Poorest
B.1.351
Slightly decreased
B.1.351 non-RBD mutations only
Poor
B.1.351 RBD mutations only

Cell

Article

Multiple SARS-CoV-2 variants escape neutralization by vaccine-induced humoral immunity

Graphical abstract



Authors

Wilfredo F. Garcia-Beltran, Evan C. Lam, Kerri St. Denis, ..., A. John Iafrate, Vivek Naranbhai, Alejandro B. Balazs

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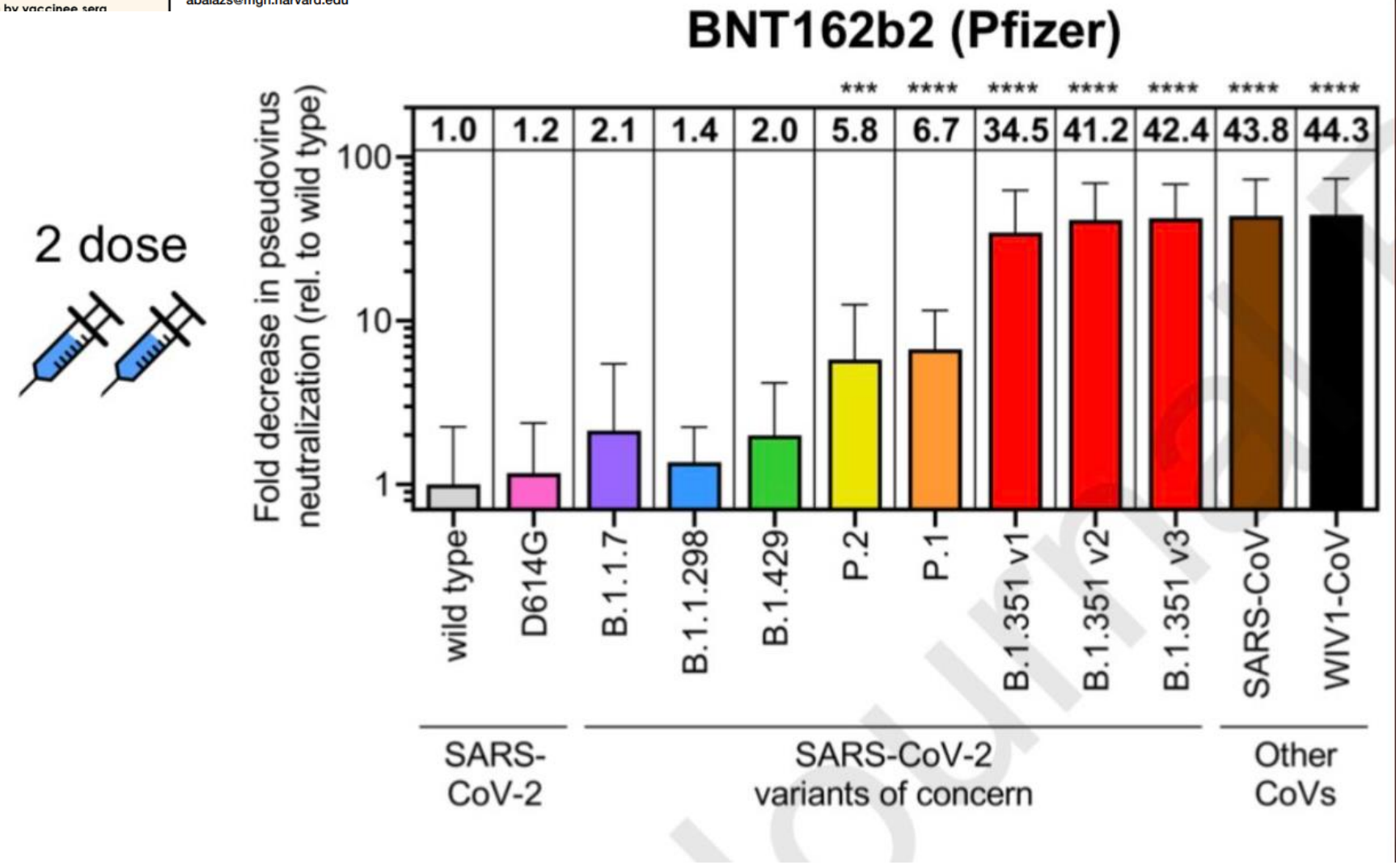
abalazs@mgh.harvard.edu

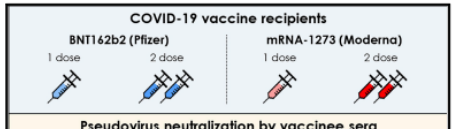


Cell

Article

Multiple SARS-CoV-2 variants escape neutralization by vaccine-induced humoral immunity

Graphical abstract



Authors

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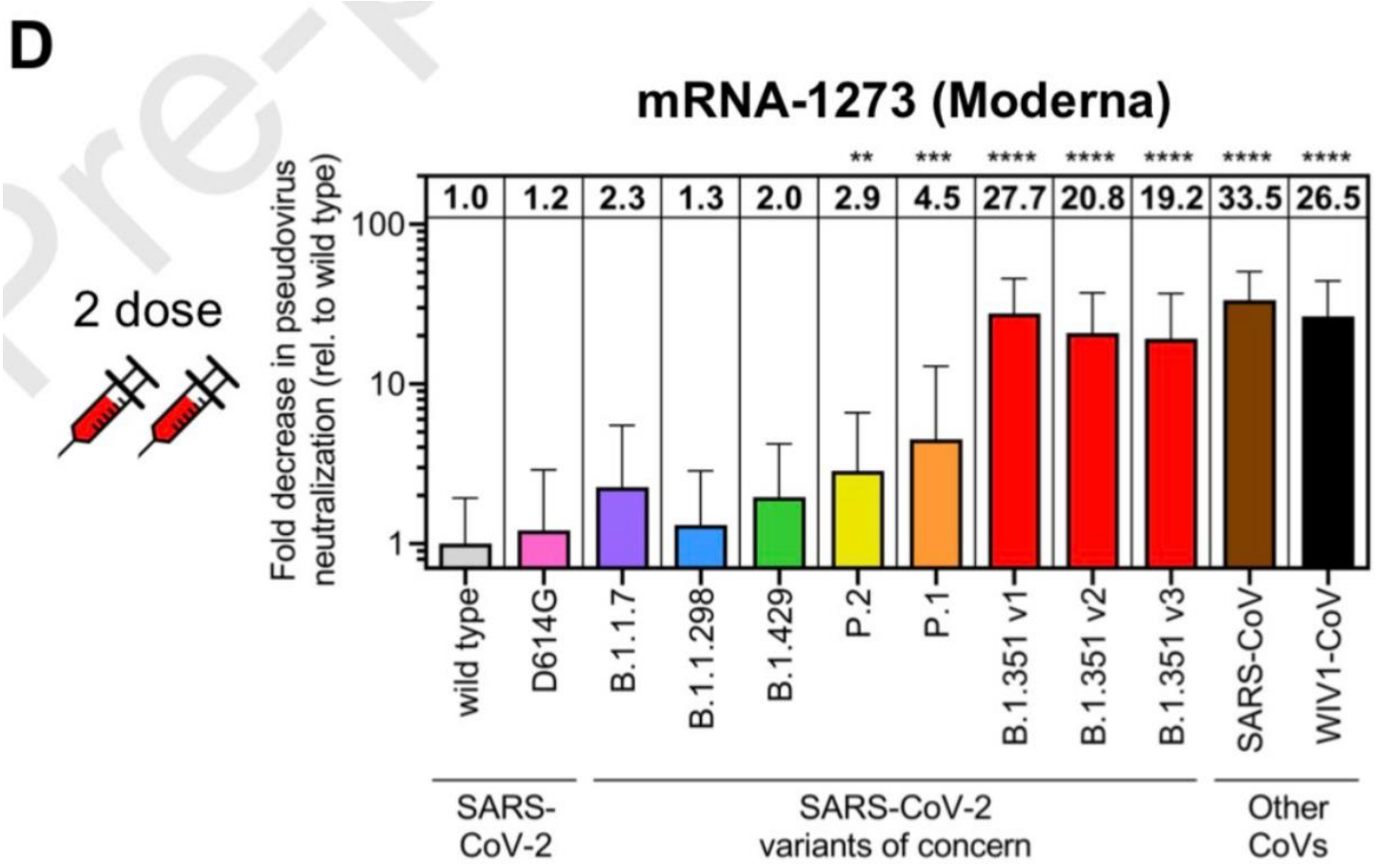
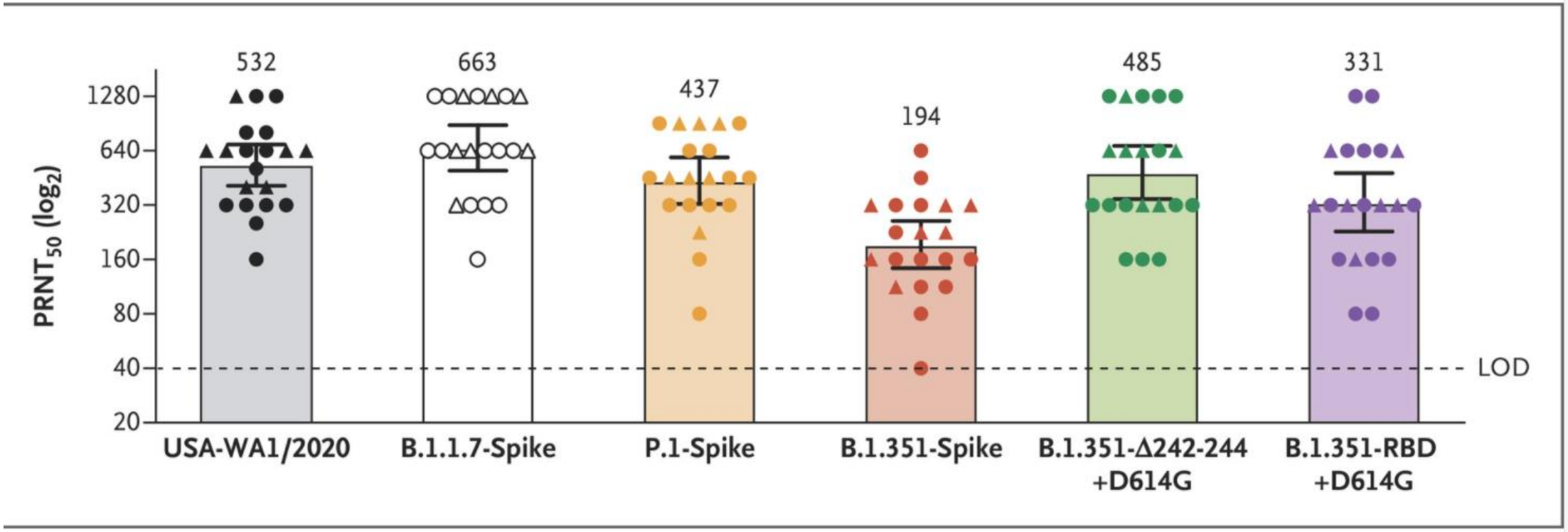


Pfizer’in iki doz sonrası kendi çalışması



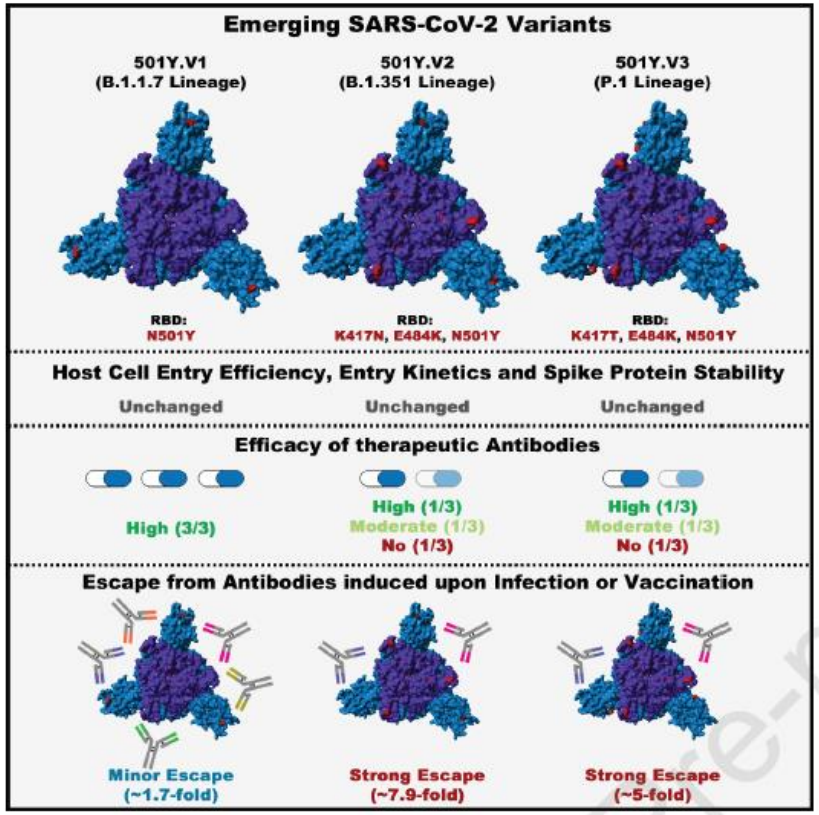
April 15, 2021
N Engl J Med 2021; 384:1466-1468
DOI: 10.1056/NEJMc2102017

Journal Pre-proof

SARS-CoV-2 variants B.1.351 and P.1 escape from neutralizing antibodies

Markus Hoffmann, Prerna Arora, Rüdiger Groß, Alina Seidel, Bojan F. Hörnich, Alexander S. Hahn, Nadine Krüger, Luise Graichen, Heike Hofmann-Winkler, Amy Kempf, Martin S. Winkler, Sebastian Schulz, Hans-Martin Jäck, Bernd Jahrsdörfer, Hubert Schrezenmeier, Martin Müller, Alexander Kleger, Jan Münch, Stefan Pöhlmann

PII: S0092-8674(21)00367-6



Aşı: Biontech

Humoral and cellular immune responses against SARS-CoV-2 variants and human coronaviruses after single BNT162b2 vaccination.

Metodi Stankov, Anne Cossmann, Agnes Bonifacius, Alexandra Jablonka, Gema Morillas Ramos, Nina Goedecke, Anna Zychlinsky Scharff, Christine Happle, Anna-Lena Boeck, Anh Thu Tran, Isabell Pink, Marius M Hoeper, Rainer Blasczyk, Martin Winkler, Inga Nehlmeier, Amy Kempf, Heike Hofmann-Winkler, Markus Hoffmann, Britta Eiz-Vesper, Stefan Poehlmann, Georg Behrens

doi: https://doi.org/10.1101/2021.04.16.21255412

İkinci dozdan sonra T hücre yanıtları gelişiyor

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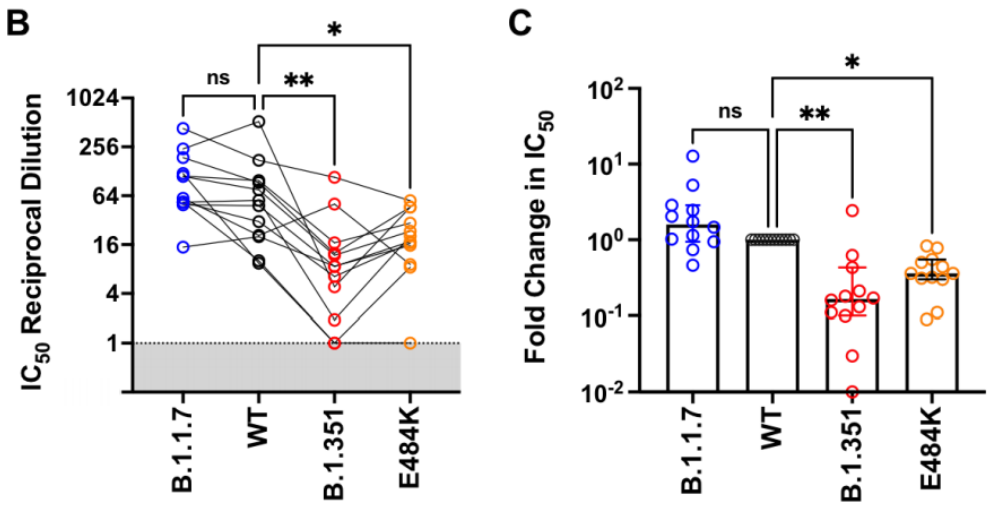
Qualitatively distinct modes of Sputnik V vaccine-neutralization escape by SARS-CoV-2 Spike variants

Satoshi Ikegame, Mohammed N.A. Siddiquey, Chuan-Tien Hung, Griffin Haas, Luca Brambilla, Kasopefoluwa Y. Oguntuyo, Shreyas Kowdle, Ariel Esteban Vilardo, Alexis Edelstein, Claudia Perandones, Jeremy P. Kamil, Benhur Lee

SPUTNIK V AŞISI



	B.1.1.7	WT	B.1.351	E484K
GMT	87.1	49.4	7.9	17.0
Lower 95% CI	49.5	23.4	3.2	8.6
Upper 95% CI	154	105	19.5	33.8

	B.1.351	E484K
Median Fold-Change	6.1	2.8
Lower 95% CI	2.3	1.8
Upper 95% CI	10.1	3.3

Figure 2. Neutralization activity of antibody responses elicited by the Sputnik V vaccine.

- M-RNA aşıları daha fazla koruyuculuk? Daha uzun süre koruyuculuk?

Novavax https://ir.novavax.com/news-releases/news-release-details/novavax-confirms-high-levels-efficacy-against-original-and

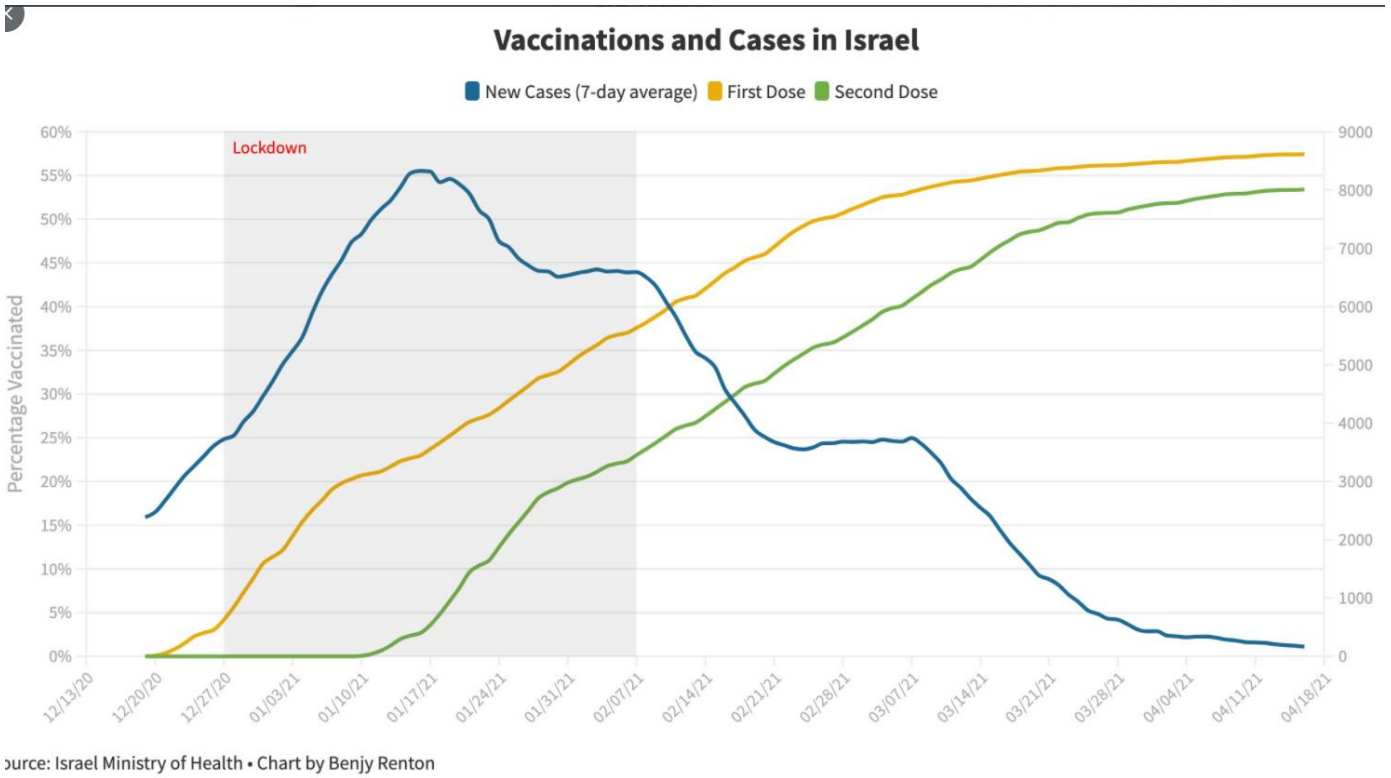
📌96% effective against symptomatic #COVID19

📌86% for #B117 variant from UK🇬🇧

📌55% for #B1351 variant from South Africa🇿🇦 (among HIV-negative)

📌100% protection against severe disease (all populations) 🧵
ir.novavax.com/news-releases/...

İYİ HABER.....



KÖTÜ HABER:

Aşı sonrası infeksiyonlarda V2 8 kat daha yüksek.

Evidence for increased breakthrough rates of SARS-CoV-2 variants of concern in BNT162b2 mRNA vaccinated individuals

Talia Kustin*[1,2], Noam Harel*[1,2], Uriah Finkel[3], Shay Perchik[3], Sheri Harari[1,2], Maayan Tahor[1], Itamar Caspi[1], Rachel Levy[1], Michael Leschinsky[3], Shifra Ken Dror[4], Galit Bergerzon[4], Hala Gadban[4], Faten Gadban[4], Eti Eliassian[5], Orit Shimron[5], Loulou Saleh[6], Haim Ben-Zvi[6], Doron Amichay[7,8], Anat Ben-Dor[7], Dana Sagas[9], Merav Strauss[9], Yonat Shemer Avni[10,11], Amit Huppert[12,13], Eldad Kepten[3], Ran D. Balicer[3], Doron Nezer[14*], Shay Ben-Shachar[3,13*†], Adi Stern[1,2†]

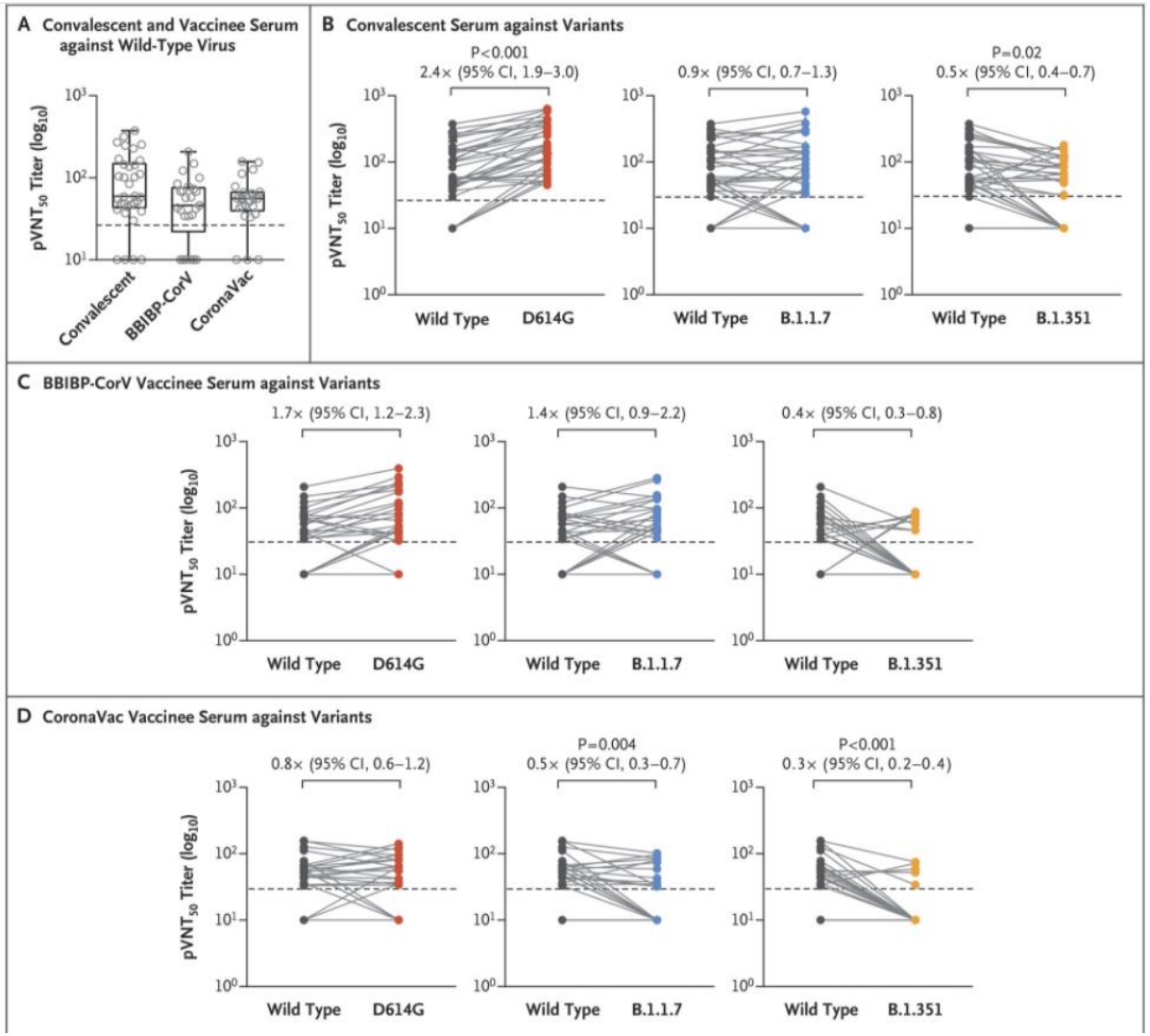
CORRESPONDENCE

Susceptibility of Circulating SARS-CoV-2 Variants to Neutralization

April 6, 2021
DOI: 10.1056/NEJMc2103022
Metrics

TO THE EDITOR:

The emergence of two variants of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) —



We next assessed the neutralizing activity of convalescent serum and vaccinee serum against D614G, B.1.1.7, and B.1.351 variants as compared with wild-type pseudovirus. The convalescent serum was significantly more effective (by a factor of 2.4; 95% confidence interval [CI], 1.9 to 3.0) in neutralizing the D614G pseudovirus, had a similar effect to that of the wild-type virus in neutralizing the B.1.1.7 variant, and was significantly less effective (by a factor of 0.5; 95% CI, 0.4 to 0.7) in neutralizing the B.1.351 pseudovirus (Figure 1B). Moreover, 9 of 30 convalescent serum samples showed complete loss of neutralizing activity against B.1.351. For the BBIBP-CorV vaccinee serum samples, although the GMTs of neutralization against the variants were not significantly different from the GMTs against the wild-type virus, 20 serum samples showed complete or partial loss of neutralization against B.1.351 (Figure 1C). For the CoronaVac vaccinee serum samples, we observed a marked decrease in the GMTs in the serum neutralization of B.1.1.7 (by a factor of 0.5; 95% CI, 0.3 to 0.7) and B.1.351 (by a factor of 0.3; 95% CI, 0.2 to 0.4). In addition, most of the serum samples showed complete or partial loss of neutralization against B.1.351 (Figure 1D).

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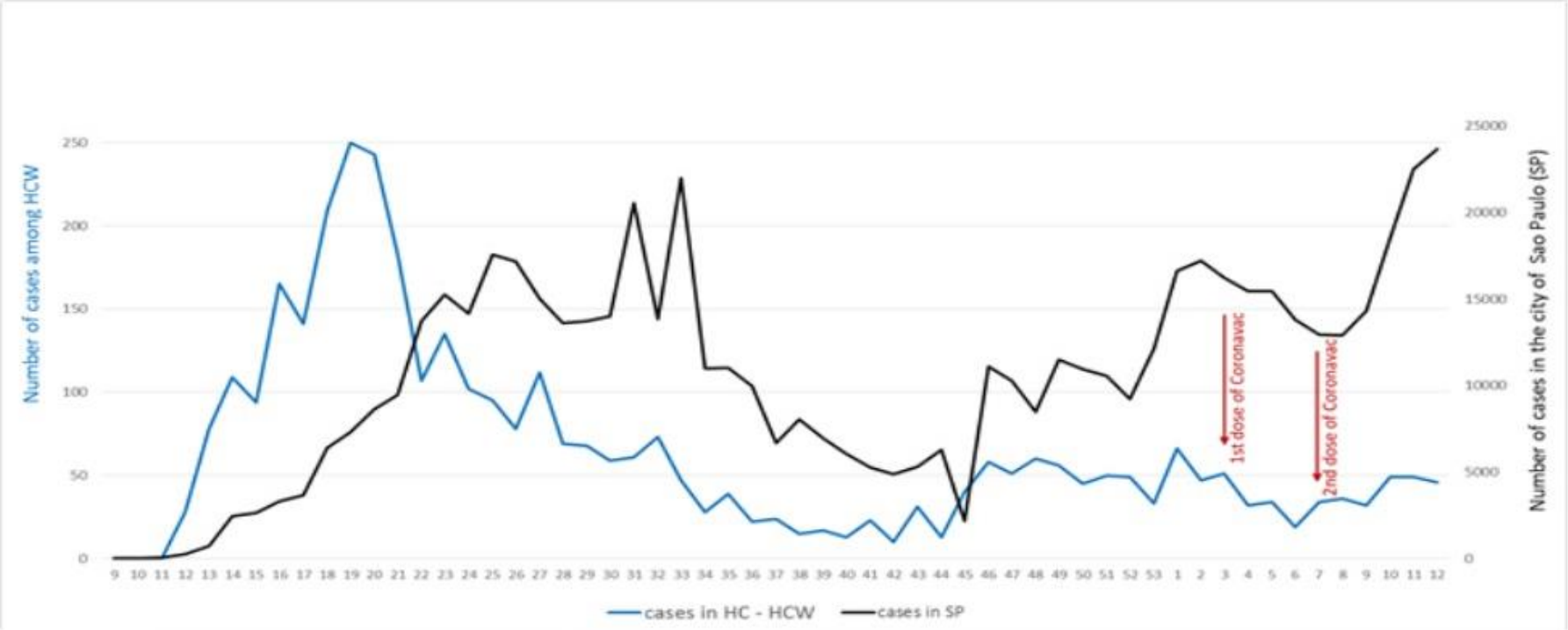
Performance of vaccination with CoronaVac in a cohort of healthcare workers (HCW) - preliminary report

Elizabeth de Faria [1], Ana Rubia Guedes [2], Maura S. Oliveira [2], Moacyr Vergara de Godoy

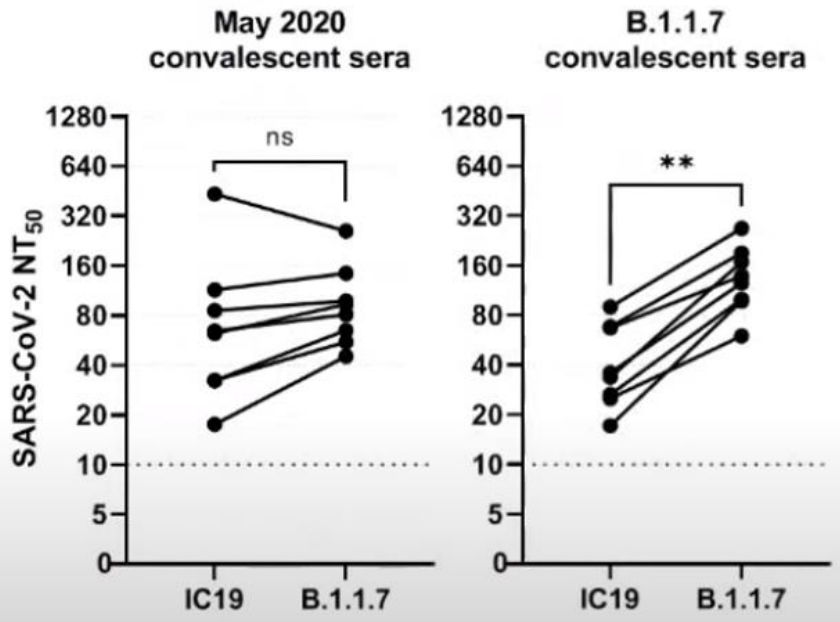
Figure 1: Graphical representation of the number of weekly COVID-19 cases in the city of São Paulo (SP) and among healthcare workers (HCW) of Hospital das Clinicas (HC) (University of São Paulo). Arrows mark the adminstration of the 2 doses of CoronaVac in HC's HCW.

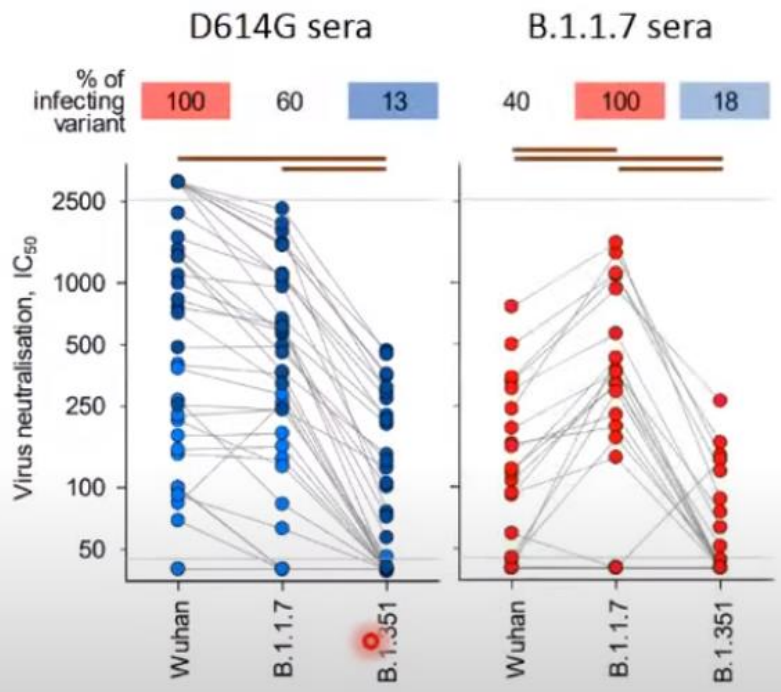


1. Dozdan sonra %50
2. Dozdan sonra %67

Baskın köken P1

Çapraz koruyuculuk





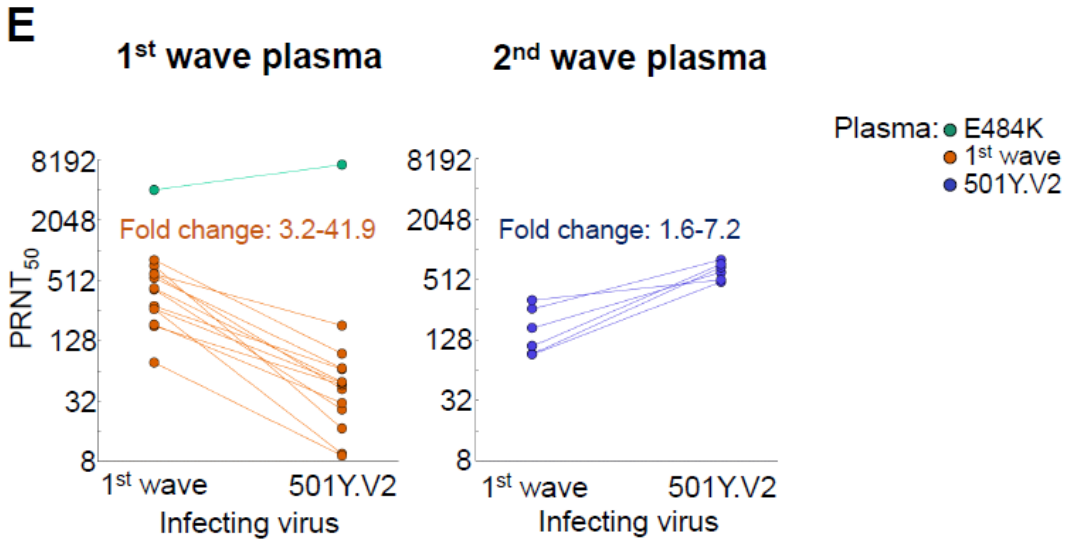
Brown et al.
https://www.biorxiv.org/content/10.1101/2021.02.24.432576v1

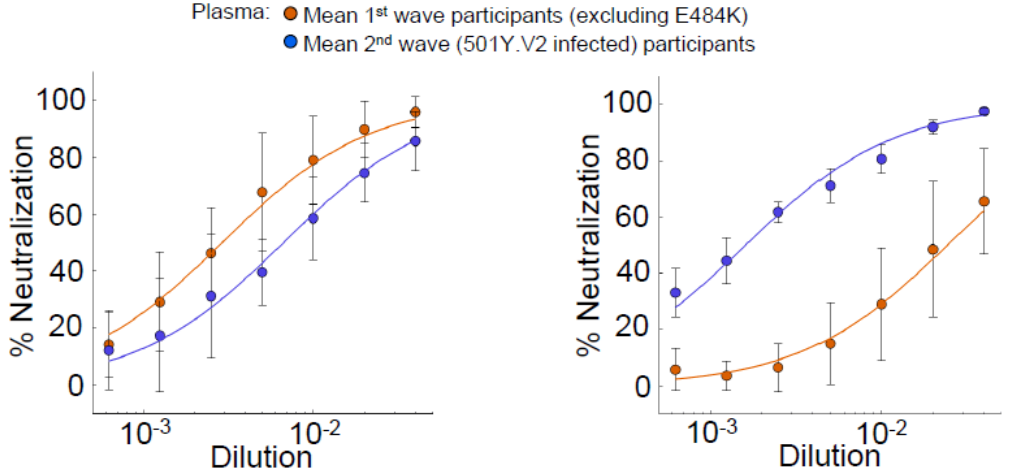
Reduced antibody cross-reactivity following infection with B.1.1.7 than with parental SARS-CoV-2 strains

Nikhil Faulkner1,21,*, Kevin W. Ng1,*, Mary Wu2,*, Ruth Harvey3,*, Saira Hussain3,4,... ....., Rupert Beale8, Steve J. Gamblin9, Crick COVID-19 Consortium, John McCauley3, Rodney Daniels3, Michael Howell, David L.V. Bauer4, Eleni Nastouli10,12, SAFER Investi

Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma

Sandile Cele[1,2], Inbal Gazy[2,3,4], Laurelle Jackson[1], Shi-Hsia Hwa[1,5], Houriiyah Tegally[3], Gila Lustig[6], Jennifer Giandhari[3], Sureshnee Pillay[3], Eduan Wilkinson[3], Yeshnee Naidoo[3], Farina Karim[1,2], Yashica Ganga[1], Khadija Khan[1], Mallory Bernstein[1], Alejandro B. Balazs[7], Bernadett I. Gosnell[8], Willem Hanekom[1,5], Mahomed-Yunus S. Moosa[8], NGS-SA[§], COMMIT-KZN Team[§§], Richard J. Lessells[2,3,6], Tulio de Oliveira[2,3,6,9*], Alex Sigal[1,2,10*]





Plasma $PRNT_{50}$

Virus variant	Plasma source: 1st wave	Plasma source: 501Y.V2	Fold change HM/HT
1st wave	344.0 (275.4-458.0)	149.7 (132.1-172.8)	2.3
501Y.V2	41.1 (32.7-55.50)	619.7 (517.8-771.5)	15.1
Fold change HM/HT	8.4	4.1	

Homologous (HM)
Heterologous (HT)

501 Y. V2 konvelasan plazma varyant 1'i de etkili bir biçimde nötralize ediyor. Aşı ???

Table 1. Summary Results on SARS-CoV-2 Vaccine Trial Efficacy and Viral Neutralization of the B.1.1.7, P.1, and 501Y.V2 Variants, as Compared with Preexisting Variants.*

Vaccine (Company)	Preexisting Variants			Neutralization by Pseudovirion or Live Viral Plaque Assay			Efficacy in Settings with 501Y.V2 Variant
	Sample Size	Efficacy in Preventing Clinical Covid-19	Efficacy in Preventing Severe Covid-19	B.1.1.7 Variant	P.1 Variant	501Y.V2 Variant	
	no.	*% (no. of events with vaccine vs. placebo)*					%
Ad26.COV2.S (Johnson & Johnson)	43,783	66 (NA)	85 (NA)	NA	NA	NA	57†, 85‡
BNT162b2 (Pfizer)	34,922	95 (8 vs. 162)	90 (1 vs. 9)	Decrease by 2×	Decrease by 6.7×	Decrease by ≤6.5×	NA
mRNA-1273 (Moderna)	28,207	94 (11 vs. 185)	100 (0 vs. 30)	Decrease by 1.8×	Decrease by 4.5×	Decrease by ≤8.6×	NA
Sputnik V (Gamaleya)	19,866	92 (16 vs. 62)	100 (0 vs. 20)	NA	NA	NA	NA
AZD1222 (AstraZeneca)	17,177	67 (84 vs. 248)	100 (0 vs. 3)	NA	NA	Decrease by ≤86× to complete immune escape	22§
NVX-CoV2373 (Novavax)	15,000	89 (6 vs. 56)	100 (0 vs. 1)	Decrease by 1.8×	NA	NA	49§
CoronaVac (Sinovac)¶							
Brazil	12,396	51 (NA)	100 (NA)	NA	NA	NA	NA
Turkey	7,371	91 (3 vs. 26)	NA	NA	NA	NA	NA
BBIBP-CorV (Sinopharm)	NA	79 (NA)	NA	NA	NA	Decrease by 1.6×	NA

Varyant taraması *vs (+)* Genomik sürveyans

Riskler:

- Artan infeksiyon sayısı
- Aşılama
- Uzun birinci doz – ikinci doz aralıkları
- Aşıların koruyuculukları? Süresi
- Salgın uzadıkça reinfeksiyonların da artması
- Aşı adaletsizlikleri

Öncelikli gruplar:

- Bağışıklığı baskılanmış kişilerdeki uzamış infeksiyonlar
- Klinik ya da epidemiyolojik açıdan dikkat çeken durumlar
- Aşı ya da doğal infeksiyon sonrası gelişen reinfeksiyonlar
- Coğrafi yoğunlaşma olan bölgeden gelenler

Table A1. Number of sequences required, >100,000 total number of cases per time unit and geographic unit (no population size correction)

Expected prevalence of variant among all circulating viruses	Number of sequences required per time unit and geographic unit of desired resolution			
	Only detect presence of variant viruses with 95% confidence (no precision)	Determination of proportion of variant		
		Low precision (95% relative CI ±50%)	Medium precision (95% relative CI ±25%)	High precision (95% relative CI ±10%)
25.00%	12	46	184	1 152
10.00%	30	138	553	3 457
5.00%	60	292	1 168	7 299
2.50%	120	599	2 397	14 982
1.00%	300	1 521	6 085	38 032
0.50%	599	3 058	12 232	76 448
0.25%	1 198	6 131	24 525	153 280
0.10%	2 995	15 351	61 404	383 776

Table A2. Number of sequences required, 100 000 total number of cases per time unit and geographic unit

Expected prevalence of variant among all circulating viruses	Number of sequences required per time unit and geographic unit of desired resolution			
	Only detect presence of variant viruses with 95% confidence (no precision)	Determination of proportion of variant		
		Low precision (95% relative CI ±50%)	Medium precision (95% relative CI ±25%)	High precision (95% relative CI ±10%)
25.00%	12	46	184	1 139
10.00%	30	138	550	3 342
5.00%	60	291	1 154	6 803
2.50%	120	596	2 341	13 030
1.00%	299	1 498	5 736	27 553
0.50%	595	2 967	10 899	43 326
0.25%	1 184	5 777	19 695	60 518
0.10%	2 908	13 308	38 044	79 329

RT-PCR ile Tarama:

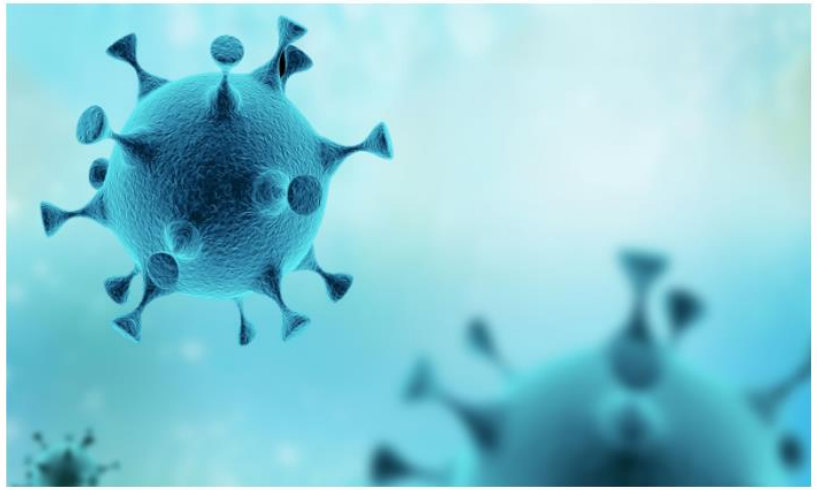
- del 60/70 → V1
- Del 144 → V1 ve Cal.
- Del 241-43 → V2 (%82.1)
- Del 3675-77 → V1 /(%97.5); V2 (%93.9); V3 (%93.3); B1 526 (%98.4)
  B1.526.2 (98.9)

GT Global Times

CHINA / SOCIETY

Chinese COVID-19 vaccines have neutralizing effect on mutant strains found in South Africa, UK

By Global Times
Published: Mar 28, 2021 09:25 PM



coronavirus Photo:VCG

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Preliminary study suggests CoronaVac neutralizes novel variants of SARS-CoV-2

March 24, 2021

PT ES

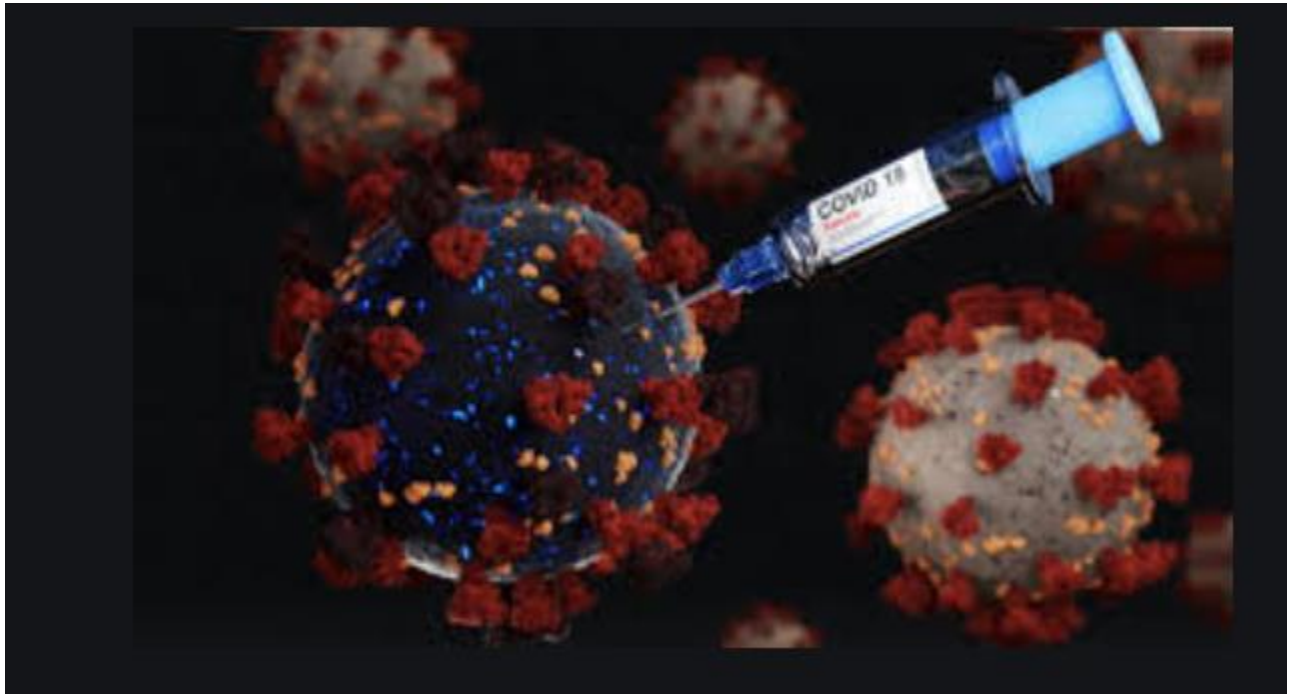
Laboratory trial by Butantan Institute in partnership with the University of São Paulo involved inoculation of variants P.1 and P.2 into cultured cells containing blood serum from vaccinated subjects. The results were satisfactory, according to the researchers (*photo: São Paulo State Government*)

By Maria Fernanda Ziegler | Agência FAPESP – A preliminary study conducted by Butantan Institute in the state of São Paulo, Brazil, suggests the CoronaVac vaccine, developed by Chinese pharmaceutical company Sinovac Biotech, can neutralize variants P.1 and P.2 of SARS-CoV-2. Epidemiologists believe P.1, the more transmissible variant first detected in Manaus, is one of the causes of the recent jump in COVID-19 cases and deaths, alongside the relaxing of mobility restrictions in and after the holiday season and the slow pace of vaccination.

- Bazı varyantların klinik, bulaşıcılık, mortalite üzerindekietkileri ile ilgili güvenilir veriler eksik
- Varyantların baskın hale gelme olasılıkları

- Aşı ile ilgili sorular.... Sorular...

- Kaynağı kısıtlı bölgelerde varyant takibi
- Daha fazla varyantın ortaya çıkması


COVID 19