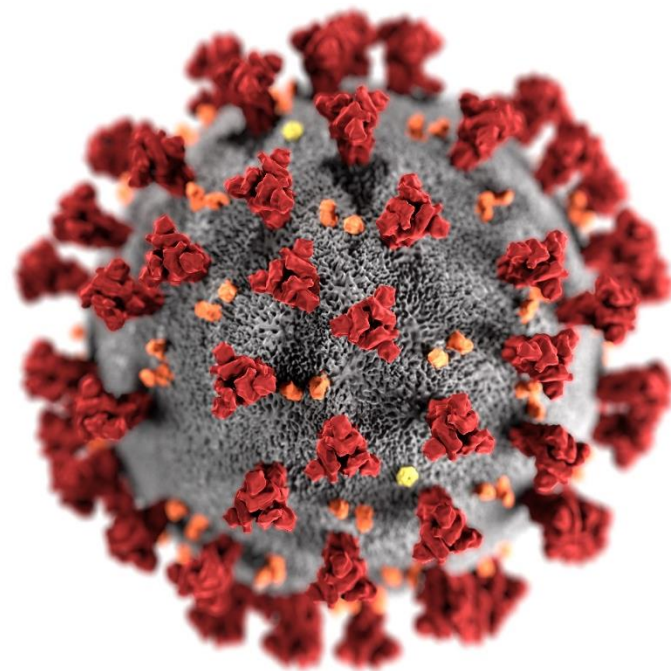


Update on Emerging SARS-CoV-2 Variants and Vaccine Considerations

CDR Heather Scobie PhD, MPH
ACIP Meeting
May 12, 2021



Background



SARS-CoV-2 Variants

- Multiple SARS-CoV-2 variants circulating globally
 - Viruses constantly change through mutation, so new variants are expected
 - After emerging, some disappear; others persist
- CDC and others are studying these variants to understand whether they:
 - Spread more easily from person to person
 - Cause milder or more severe disease in people
 - Detected by available diagnostic tests
 - Respond to therapeutics currently used to treat people for COVID-19
 - Change effectiveness of COVID-19 vaccines



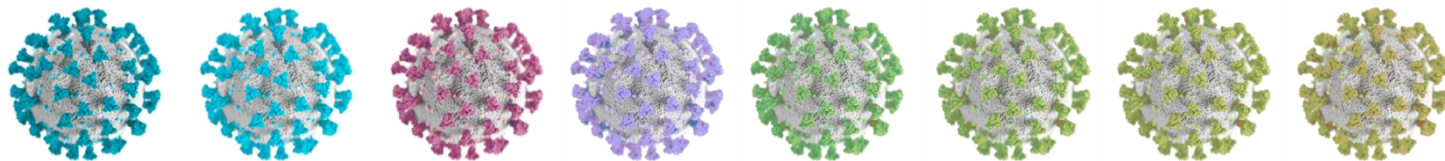
<https://www.cdc.gov/coronavirus/2019-ncov/transmission/variant.html>

Variant Classifications

- Established in collaboration with the SARS-CoV-2 Interagency Group (SIG)
- **Variant of Interest (VOI):** Genetic markers associated with changes to receptor binding, reduced antibody neutralization, reduced efficacy of treatments, potential diagnostic impact, or predicted increase in transmissibility or disease severity
- **Variant of Concern (VOC):** Evidence of increased transmissibility, more severe disease, significant reduction in neutralization by antibodies, reduced effectiveness of treatments or vaccines, or diagnostic detection failures
- **Variant of High Consequence (VOHC):** Clear evidence that prevention measures or medical countermeasures have significantly reduced effectiveness [**None yet**]

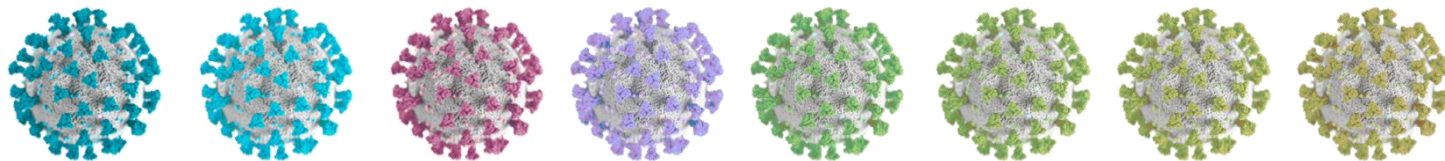


Variants of Interest



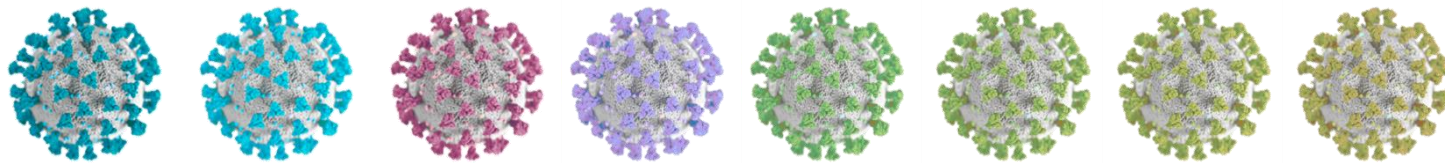
	B.1.526	B.1.526.1	B.1.525	P.2	B.1.617	B.1.617.1	B.1.617.2	B.1.617.3
First detected	New York	New York	UK/Nigeria	Brazil	India	India	India	India
No. of spike mutations	3-7	6-8	8	3-4	3	7-8	9-10	7
Receptor binding domain mutations	(S477N*) (E484K*)	L452R	E484K	E484K	L452R E484Q	L452R E484Q	L452R T478K	L452R E484Q
Attributes	<ul style="list-style-type: none"> • Reduced antibody efficacy • Reduced neutralization convalescent or vaccine sera 	<ul style="list-style-type: none"> • Potential reduced antibody efficacy • Potential reduced neutralization by vaccine sera 		<ul style="list-style-type: none"> • Potential reduced antibody efficacy • Reduced neutralization by vaccine sera 	<ul style="list-style-type: none"> • Potential reduced antibody efficacy • Reduced neutralization by vaccine sera 	<ul style="list-style-type: none"> • Potential reduced antibody efficacy • Potential reduced neutralization by vaccine sera 		

Variants of Interest



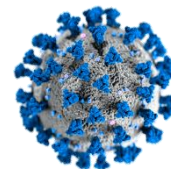
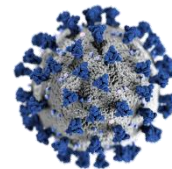
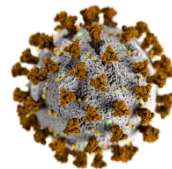
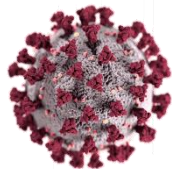
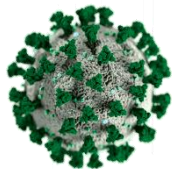
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Variants of Interest



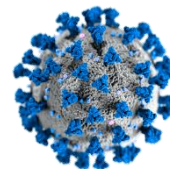
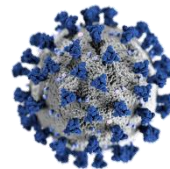
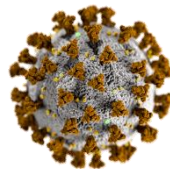
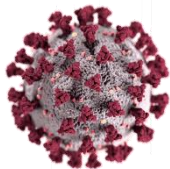
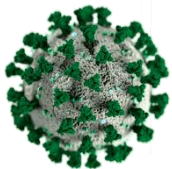
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Variants of Concern



	B.1.1.7	B.1.351	P.1	B.1.427	B.1.429
First detected	United Kingdom	South Africa	Japan / Brazil	California	California
No. of spike mutations	10-13	10	11	4	4
Receptor binding domain mutations	N501Y	K417N E484K N501Y	K417T E484K N501Y	L452R	L452R
Attributes	<ul style="list-style-type: none"> • 50% increased transmission • Minimal impact on neutralization by antibody therapies, convalescent or vaccine sera 	<ul style="list-style-type: none"> • 50% increased transmission • Reduced efficacy of some antibodies • Reduced neutralization by convalescent or vaccine sera 	<ul style="list-style-type: none"> • Reduced efficacy of some antibodies • Reduced neutralization by convalescent or vaccine sera 	<ul style="list-style-type: none"> • 20% increased transmission • Modest decrease in efficacy of some antibodies • Reduced neutralization by convalescent or vaccine sera 	<ul style="list-style-type: none"> • 20% increased transmission • Modest decrease in efficacy of some antibodies • Reduced neutralization by convalescent or vaccine sera

Variants of Concern



B.1.1.7

B.1.351

P.1

B.1.427

B.1.429

First detected

United Kingdom

South Africa

Japan / Brazil

California

California

No. of spike mutations

10-13

10

11

4

4

Receptor binding domain mutations

N501Y

K417N
E484K
N501Y

K417T
E484K
N501Y

L452R

L452R

Attributes

- **50%** increased transmission
- **Minimal** impact on neutralization by antibody therapies, convalescent or vaccine sera

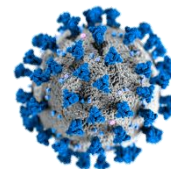
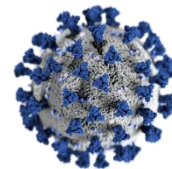
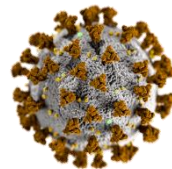
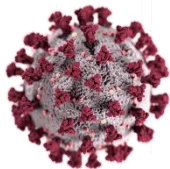
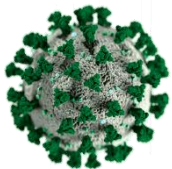
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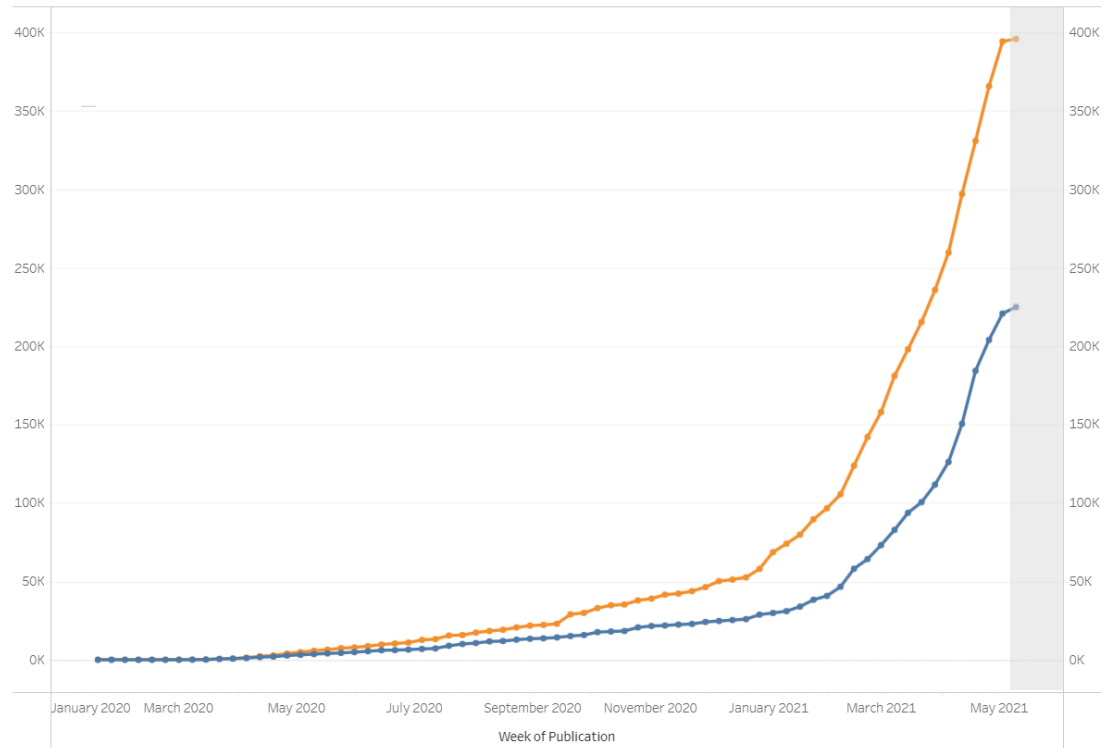
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Genomic Surveillance & Epidemiology of SARS-CoV-2 Variants



U.S. Sequences Available in Public Repositories

6%-9% of SARS-CoV-2 positive cases sequenced weekly



Data collection ongoing

■ US Sequences in NCBI ■ US Sequences submitted to GISAID

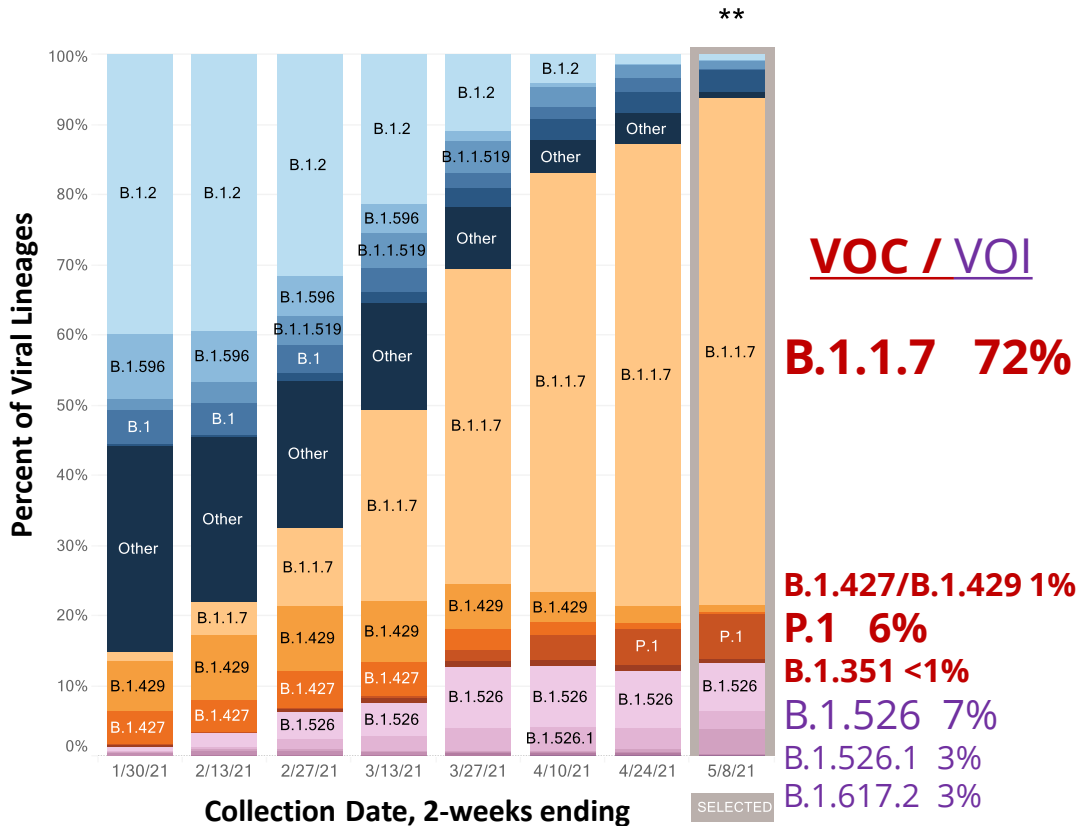
[CDC COVID Data Tracker](#)

As of 5/11/21

NCBI=National Center for Biotechnology Information; GISAID, a global initiative maintaining a repository of viral sequencing data

National SARS-CoV-2 Variant Proportions, United States

January 17 – May 8, 2021 with NOWCAST



Estimates for April 25-May 8, 2021

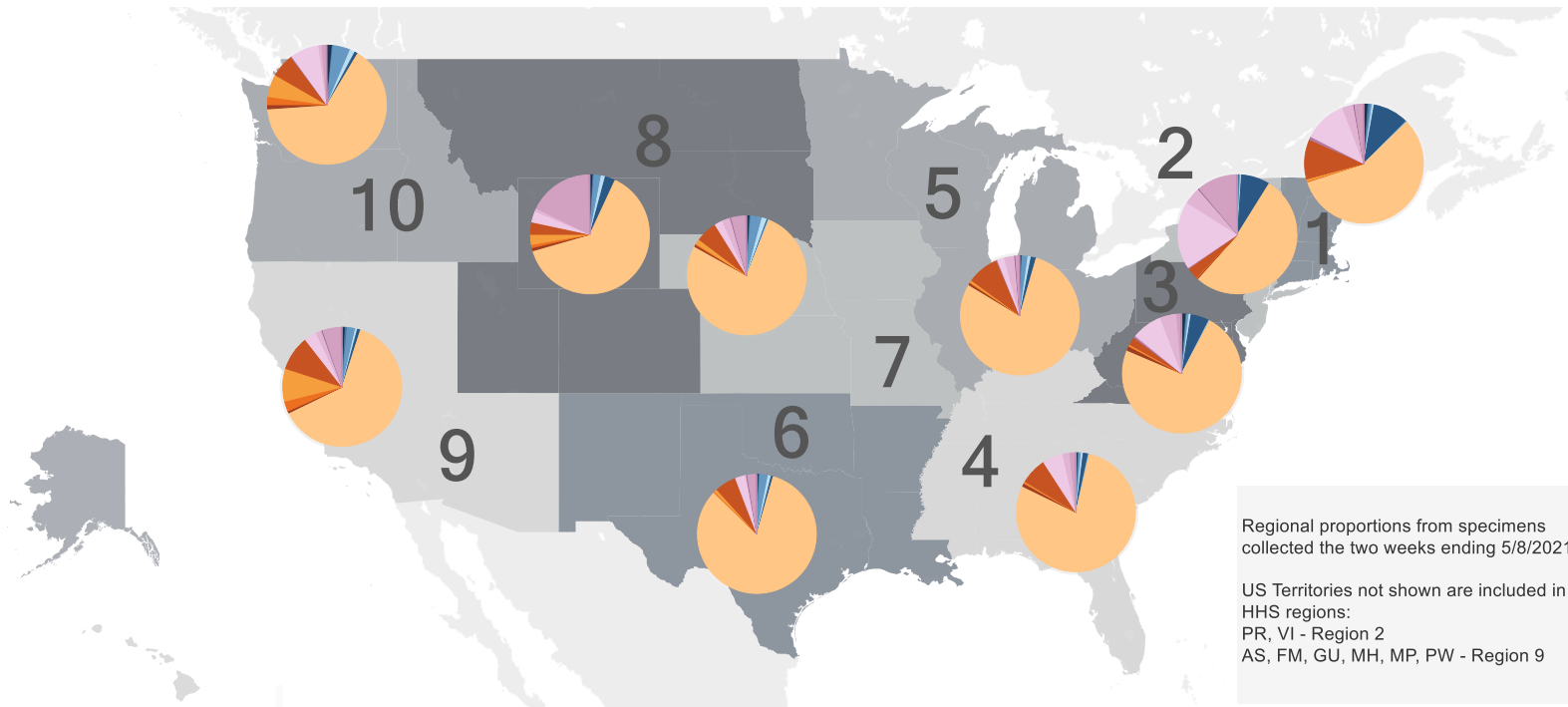
	Lineage	Type	%Total	95%PI	
Most common lineages	B.1.1.7	VOC	72.4%	67.4-77.1%	■
	B.1.526	VOI	6.8%	4.2-9.6%	■
	P.1	VOC	6.2%	3.7-9.1%	■
	B.1.617.2	VOI	3.3%	1.4-5.7%	■
	B.1.526.2	VOI	3.1%	1.4-5.1%	■
	B.1.526.1	VOI	2.8%	1.1-4.5%	■
	B.1.1.519		1.2%	0.3-2.3%	■
	B.1.2		0.7%	0.0-1.7%	■
	B.1		0.3%	0.0-1.1%	■
	B.1.596		0.1%	0.0-0.6%	■
Additional VOI/VOC lineages	B.1.429	VOC	0.9%	0.0-2.0%	■
	B.1.351	VOC	0.6%	0.0-1.4%	■
	B.1.427	VOC	0.4%	0.0-1.1%	■
	B.1.525	VOI	0.2%	0.0-0.8%	■
	B.1.617.1	VOI	0.2%	0.0-0.6%	■
	P.2	VOI	0.0%	0.0-0.3%	■
	B.1.617.3	VOI	0.0%	0.0-0.3%	■
Other*	Other	0.8%	0.0-4.0%	■	

* Other represents >200 additional lineages, which are each circulating at <1% of viruses

** These data include Nowcast estimates, which are modeled projections that may differ from weighted estimates generated at later dates

Regional SARS-CoV-2 Variant Proportions

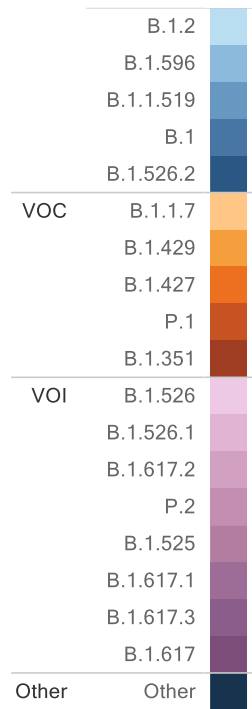
April 25 – May 8, 2021 with NOWCAST



Regional proportions from specimens collected the two weeks ending 5/8/2021.

US Territories not shown are included in HHS regions:
 PR, VI - Region 2
 AS, FM, GU, MH, MP, PW - Region 9

Lineage

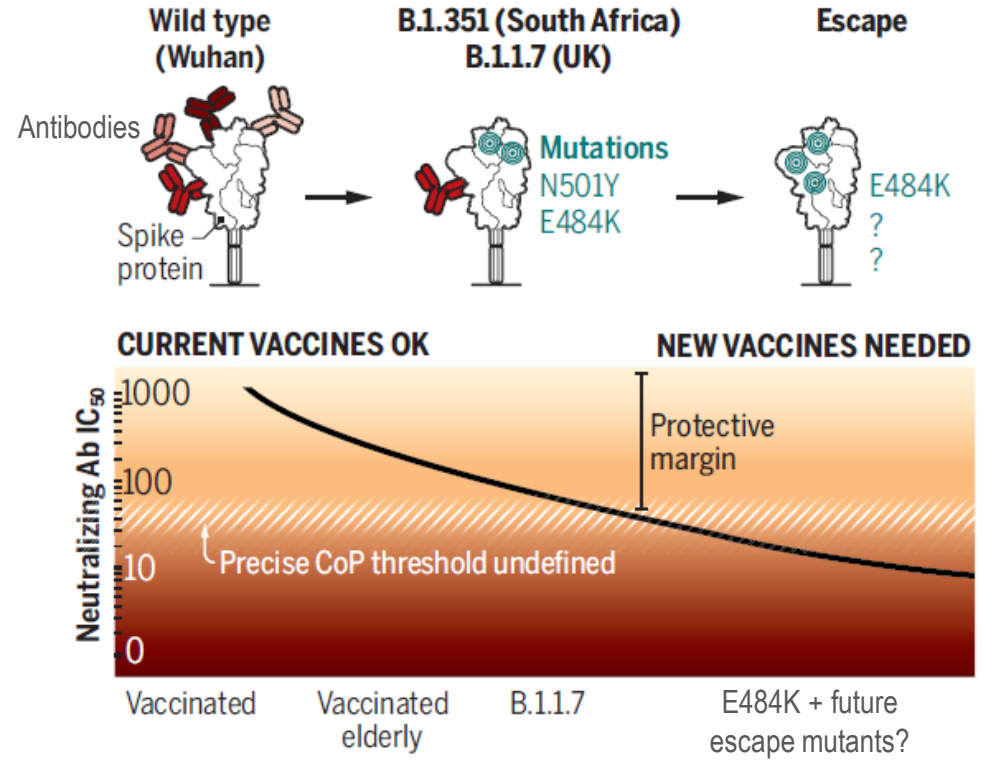


Vaccine Effectiveness Against SARS-CoV-2 Variants



Vaccine-Induced Antibody Protection and Variants

- Robust correlation between vaccine efficacy (VE) versus:
 - Neutralizing titer ($\rho = 0.79$)
 - Binding antibody titer ($\rho = 0.93$)
- **Correlate of protection, or threshold that protects against SARS-CoV-2, not yet determined**
- Variants result in reduced protective antibody levels
 - Lower VE and increased breakthrough infection?
 - Shorter duration of immunity?



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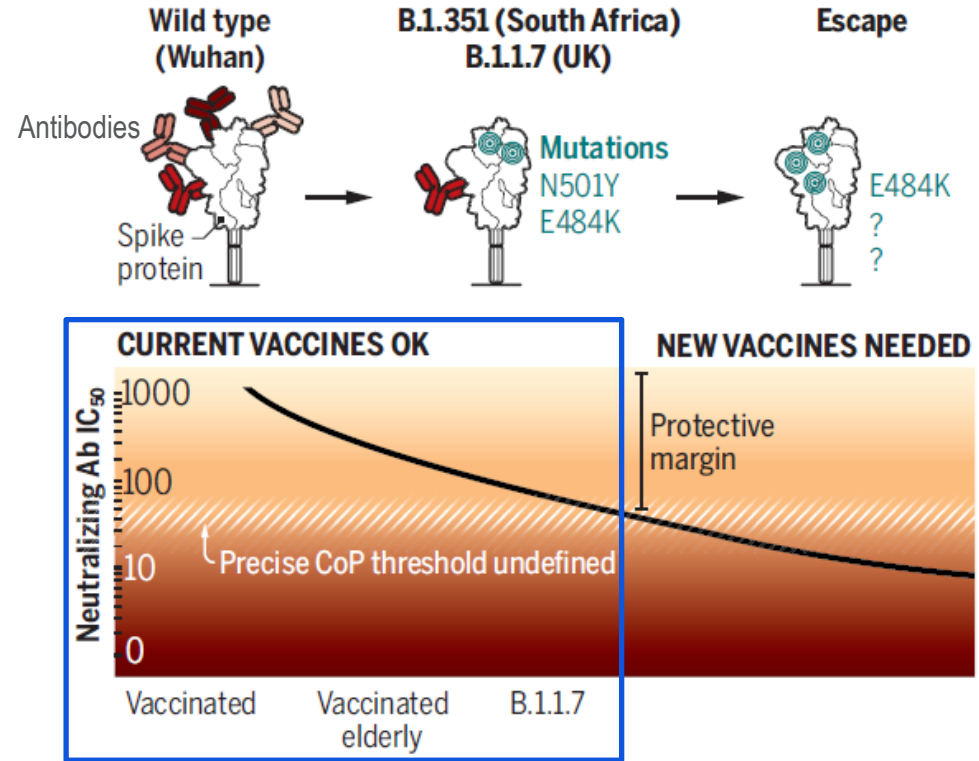
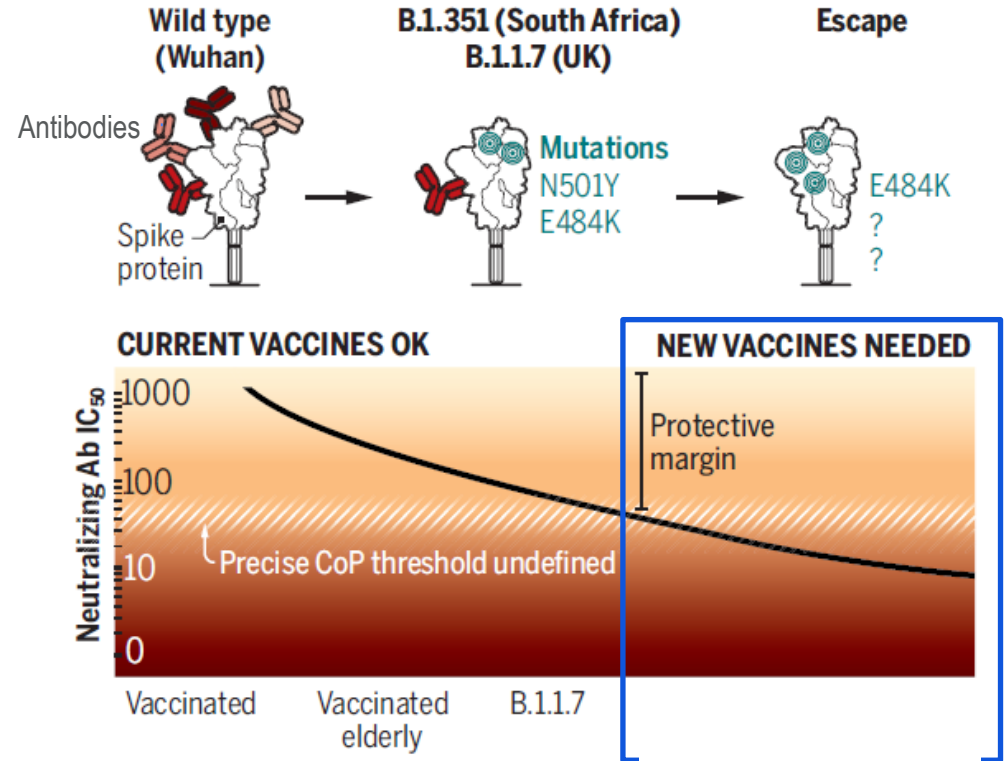


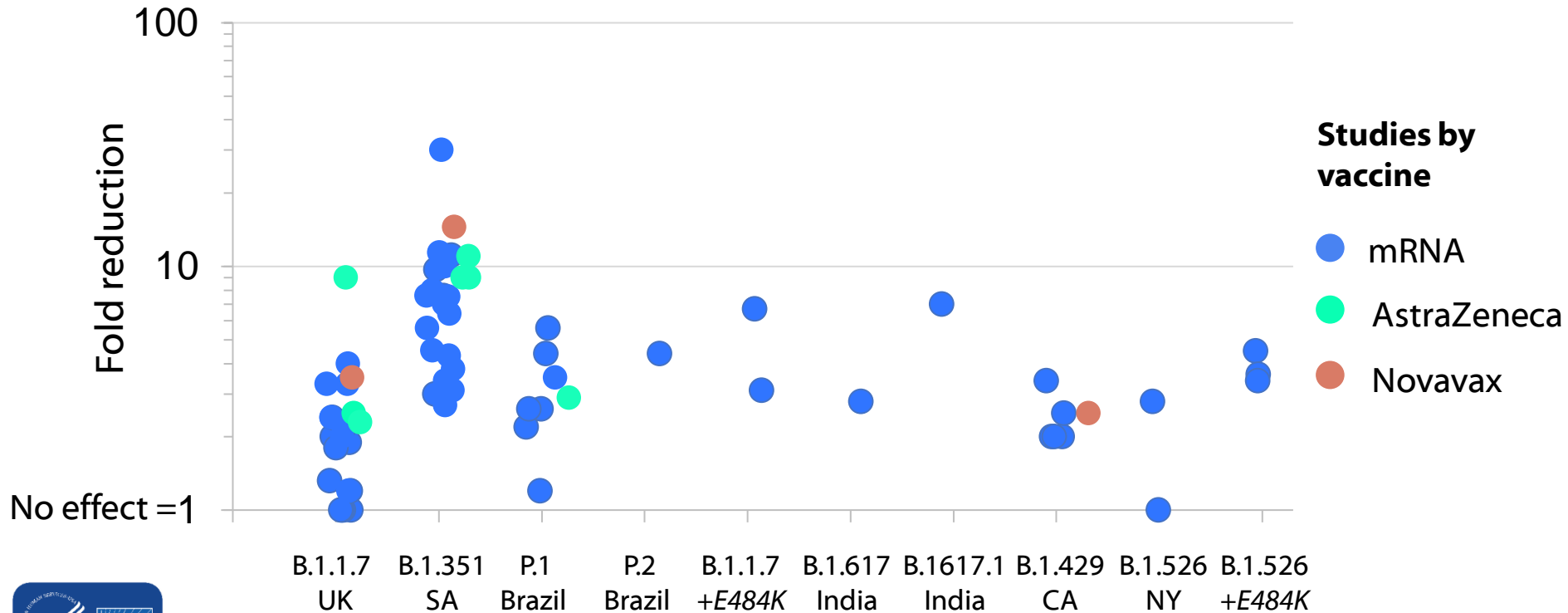
Figure Source: Altman et al (2021): <https://science.sciencemag.org/content/371/6534/1103>
Earle et al. medRxiv preprint (March 20, 2021): <https://doi.org/10.1101/2021.03.17.20200246>

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Reduced Neutralization Activity of Vaccine Sera Relative to Wildtype/Dominant Strain, by Study (n=31)



Discussion of Lab Studies

- Largest impacts: **B.1.351** (SA) > **P.1** (Brazil) > **B.1.1.7** (UK), **B.1.427/B.429** (CA)
- Difficult to estimate how results might translate to clinical protection
 - Neutralizing antibodies in sera from mRNA vaccine recipients higher than COVID-19 convalescent sera
- Variation in results may be explained by different experimental conditions
 - Neutralization assays — replicating & nonreplicating pseudovirus vs. SARS-CoV-2
 - Sera — time post-vaccination, or population (e.g., age, COVID-19 history)
 - Use of limited or full sets of spike mutations vs. clinical isolates of variants
- Limitation for all studies — small sample sizes and lack generalizability
 - Almost half of studies are preprints, not yet peer-reviewed



Vaccine Efficacy or Effectiveness (VE) Against Variants

Vaccine	Study type	VE
Pfizer	Post-EUA	<ul style="list-style-type: none"> • 90% against B.1.1.7 in Qatar* • 75% against B.1.351 in Qatar
Janssen	Pre-EUA	<ul style="list-style-type: none"> • 74% in U.S. • 66% in Brazil (69% of cases from P.2) • 52% in S. Africa (95% of cases from B.1.351)
Novavax	Pre-EUA	<ul style="list-style-type: none"> • 96% against non-B.1.1.7 in UK • 86% against B.1.1.7 in UK
	Pre-EUA	<ul style="list-style-type: none"> • 51% against B.1.351 in S. Africa
AstraZeneca	Pre-EUA	<ul style="list-style-type: none"> • 84% against non-B.1.1.7 in UK • 75% against B.1.1.7 in UK
	Pre-EUA	<ul style="list-style-type: none"> • 10% against B.1.351 in South Africa**

* >85% in UK & Israel (predominate B.1.1.7): <https://www.cdc.gov/coronavirus/2019-ncov/science/science-briefs/fully-vaccinated-people.html>

Abu-Raddad and Butt. Effectiveness of the BNT162b2 Covid-19 Vaccine against the B.1.1.7 and B.1.351 Variants | NEJM

<https://www.fda.gov/media/146217/download>

Novavax.: <https://ir.novavax.com/news-releases/news-release-details/novavax-covid-19-vaccine-demonstrates-893-efficacy-uk-phase-3>

Shinde et al. Efficacy of NVX-CoV2373 Covid-19 Vaccine against the B.1.351 Variant | NEJM

Madhi et al. Efficacy of the ChAdOx1 nCoV-19 Covid-19 Vaccine against the B.1.351 Variant | NEJM

Fmary et al. Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 variant of concern 202012/01 (B.1.1.7)- The Lancet **mild/moderate illness



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Vaccine	Study type	VE
Pfizer	Post-EUA	<ul style="list-style-type: none"> • 90% against B.1.1.7 in Qatar* • 75% against B.1.351 in Qatar
		100% for severe/critical disease
Janssen	Pre-EUA	<ul style="list-style-type: none"> • 74% in U.S. • 66% in Brazil • 52% in S. Africa
		73-82% for severe/critical disease in each country
Novavax	Pre-EUA	<ul style="list-style-type: none"> • 96% against non-B.1.1.7 in UK • 86% against B.1.1.7 in UK
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Investigating COVID-19 Vaccine Breakthrough Cases

- Despite high vaccine efficacy, vaccine breakthrough cases* expected
 - Some will be caused by variants, even if vaccine has similar effectiveness against variants
- Among 95 million fully vaccinated in U.S., 9,245 breakthrough infections** reported by state & territorial health departments to passive surveillance
 - Case investigation and whole genome sequencing to identify variants
- Starting soon – CDC project with Emerging Infections Program sites on frequency of SARS-CoV-2 variants among vaccinated and unvaccinated people

* **Vaccine breakthrough case:** Person with SARS-CoV-2 RNA or antigen detected in respiratory specimen collected ≥ 14 days after completing primary series of an FDA-authorized COVID-19 vaccine

** [COVID-19 Breakthrough Case Investigations and Reporting | CDC as of 4/26/21](#)

Tehran et al. <https://www.cdc.gov/mmwr/volumes/70/wr/mm7017e1.htm>



Do SARS-CoV-2 Variants Cause More Breakthrough Cases?

- One preprint study from Israel assessed variants of concern (VOC) in infections of Pfizer-vaccinated cases vs. unvaccinated matched controls
- Context: B.1.1.7 dominant strain; B.1.351 <1% of all specimens
- At least a week after 2nd dose — matched **OR = 8.0** for **B.1.351**
 - Among 149 pairs, 8 vaccinated and 1 unvaccinated persons had B.1.351
- 2 weeks after 1st dose to 1 week after 2nd dose — matched **OR = 2.6** for **B.1.1.7**
 - Among 245 pairs, 221 vaccinated and 205 unvaccinated persons had B.1.1.7
- Conclusion: breakthrough infection more frequent with VOCs
- Limitations: not yet peer-reviewed, small sample sizes (especially B.1.351)



Summary of Preliminary Data: Implications of SARS-CoV-2 Variants of Concern on Vaccine Effectiveness

- **B.1.1.7**
 - Exponential increase in prevalence in United States
 - Minimal impact on VE; attention needed for additional substitutions in receptor binding domain (RBD), such as E484K
- **B.1.351**
 - Currently low prevalence in United States
 - Moderate impact on VE for some vaccines, though may still provide protection against severe disease
- **P.1**
 - Increasing prevalence in United States; same 3 RBD mutations as B.1.351
 - Additional data needed on potential impact on VE



Boosters and Second-Generation Vaccines Against SARS-CoV-2 Variants

- Manufacturers launching booster studies of current vaccines and/or developing second-generation vaccines against B.1.351
- Moderna — preliminary phase 2 results of single 50 µg booster of authorized (mRNA-1273) and variant-specific vaccine (mRNA-1273.351)
 - 6-8 months after primary series (pre-booster), low/undetectable neutralizing antibody titers for B.1.351 and P.1, but titers against wild-type still likely protective
 - Both vaccines — acceptable safety; boosted immunity to all types (wild-type, B.1.351, P.1)
 - mRNA-1273.351 booster more effective than mRNA-1273 at neutralizing B.1.351
 - In progress — bivalent vaccine with 1:1 mix of original & variant vaccine (mRNA-1273.211)



Updates to Vaccines to Address SARS-CoV-2 Variants

- Periodic update of SARS-CoV-2 vaccines likely needed
- FDA defined data needed to support EUA amendment for a vaccine addressing emerging SARS-CoV-2 variants — immunogenicity studies
- U.S. SIG* developing an evaluation and risk assessment framework
 - Evidence needed to recommend whether modified vaccine needed
- WHO has role in global coordination, developing risk assessment framework



*SARS-CoV-2 Interagency Group (SIG)

<https://www.fda.gov/regulatory-information/search-fda-guidance-documents/emergency-use-authorization-vaccines-prevent-covid-19>

Variants: Implications for Vaccine Policy

- Current prevention measures and authorized vaccines offer protection against SARS-CoV-2 variants
 - Efforts needed to increase uptake
- Continue to monitor evidence:
 - Emergence and spread of SARS-CoV-2 variants
 - Vaccine effectiveness
 - Breakthrough infections in vaccinated or previously infected persons
 - Ability of postvaccination serum to neutralize emerging variant viruses
- ACIP will review evidence submitted for any next generation vaccines



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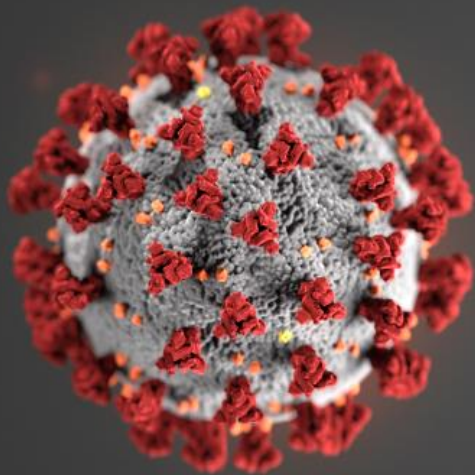
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