

SARS-CoV-2

Variants of concern:

What to know?

Swiss Society of Tropical and Travel Medicine FMH - Formation continue

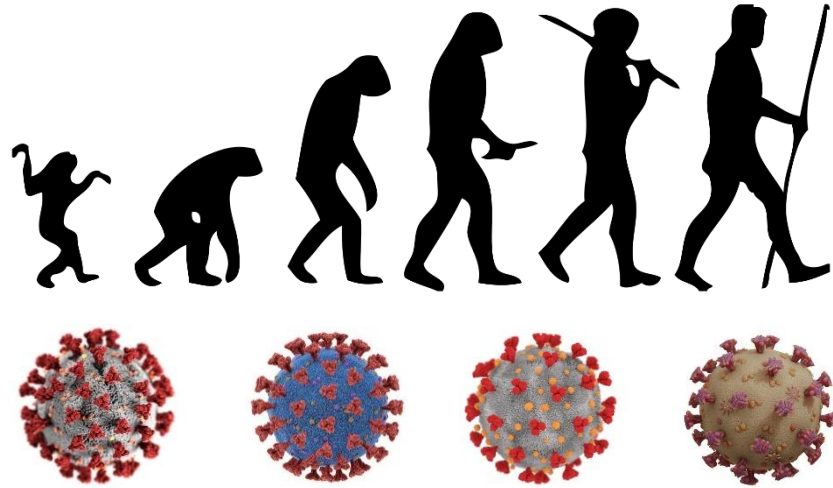
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Acknowledgements: E Boehm



Variant:

Natural evolution of a virus over time (mutations)

Favoured by selection pressure

Acquisition and selection of properties which confer an advantage

Mutations and impact on viruses

- Types of mutations

- Insertion
- Deletion
- Substitution



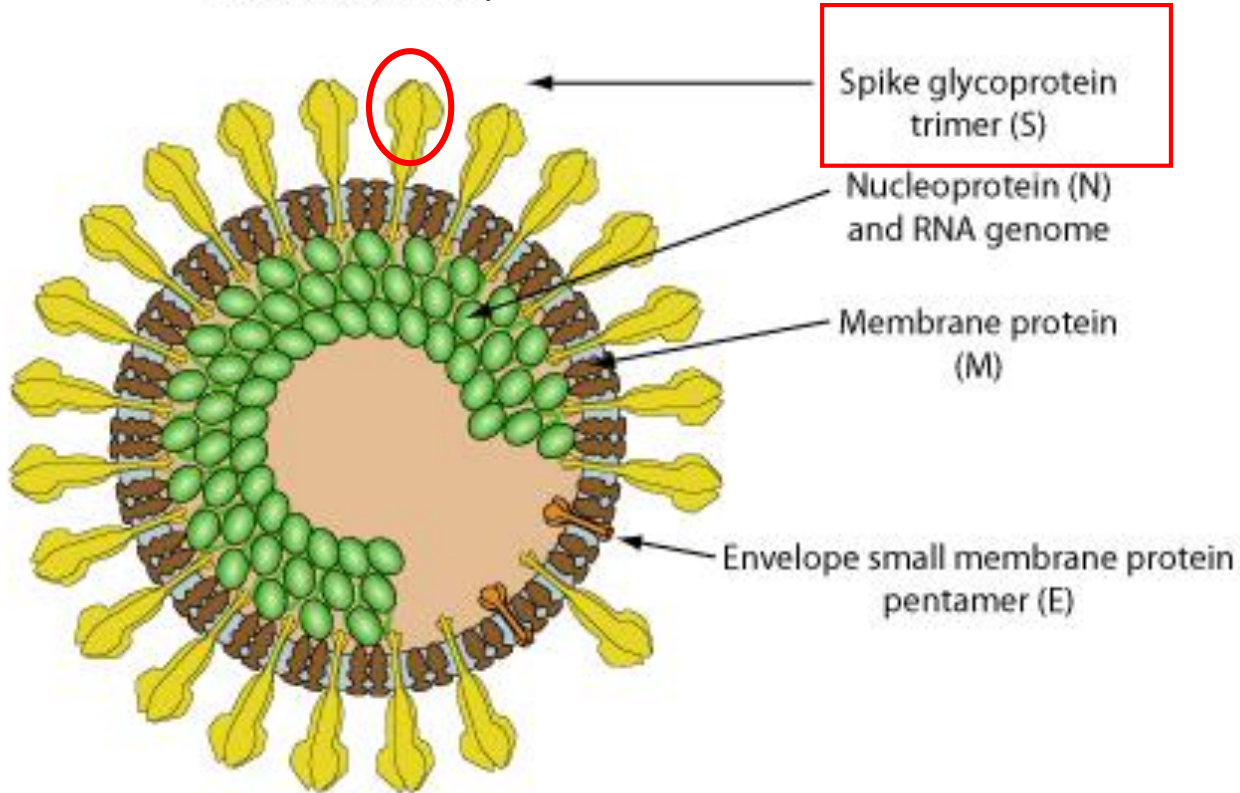
- Impact:

- Neutral
- Negative
- Positive



- Synonymous
- Non-synonymous

SARS coronavirus / SARS-CoV-2



Spike glycoprotein trimer (S)

Nucleoprotein (N) and RNA genome

Membrane protein (M)

Envelope small membrane protein pentamer (E)

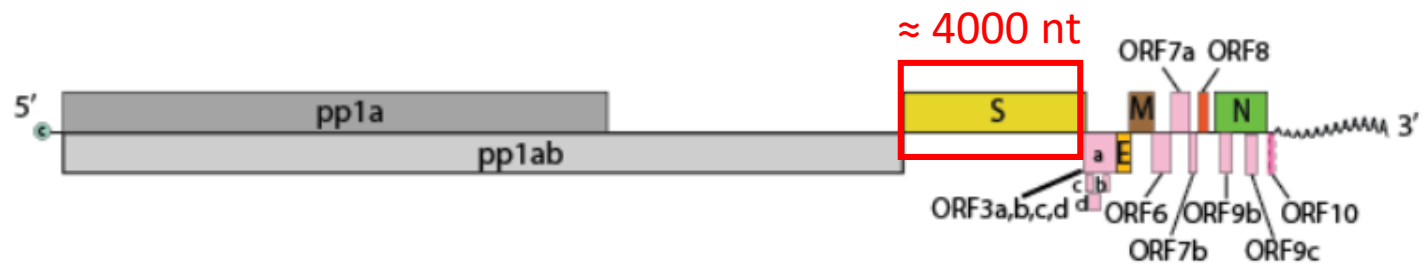
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SIB Swiss Institute of Bioinformatics

Single-stranded + RNA
Genome size 30 kb

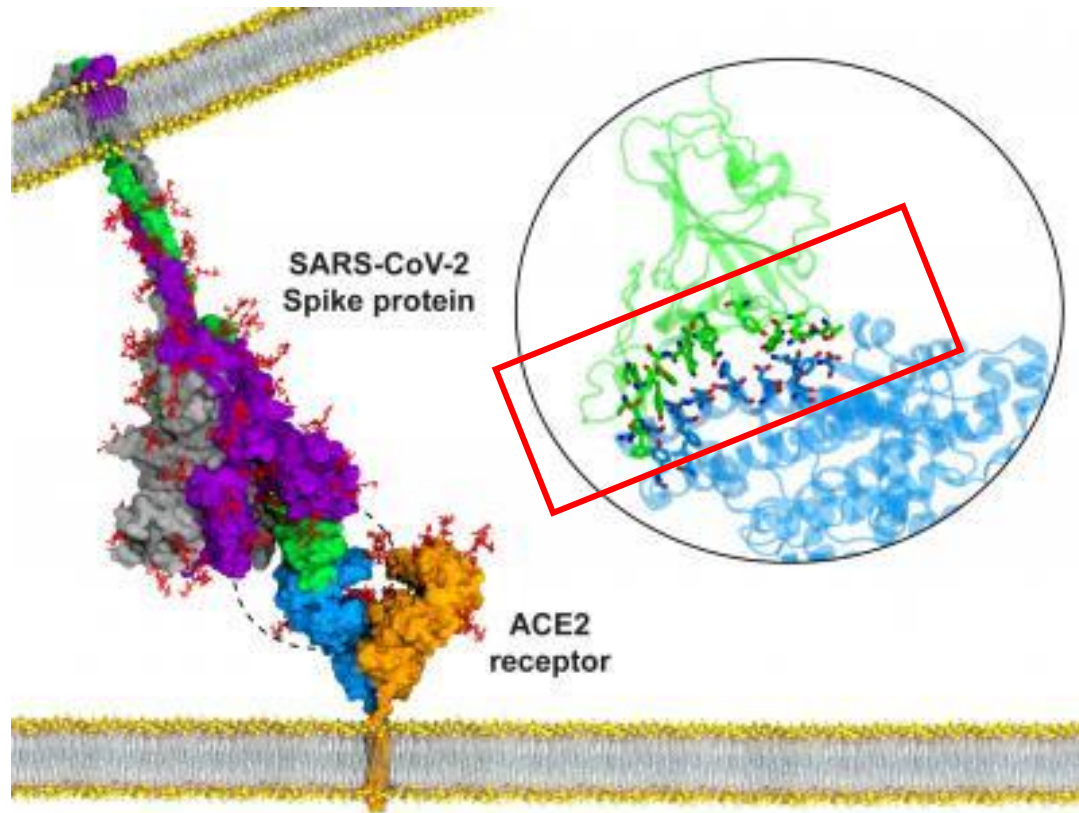
RNA-dependent RNA polymerase
(proofreading reactivity)

Rate of substitutions: 9.9×10^{-4} to 1.12×10^{-3} substitutions per site per year

SARS-CoV-2: 1-2 nt per month/lineage



Interaction between the Spike protein and its receptor



Mutation of the S protein:

- Modification of the entry efficiency of the cell
- Modification of neutralising antibodies (natural infection and vaccines)

Neutralizing antibodies : prevent infection by targeting the Spike

-> no binding to the receptor ACE2 anymore
(principle of vaccination)

Adapted from : https://www.krisp.org.za/ngs-sa/ngs-sa_updates_covid-19_analysis_narratives_reports/token/18

«Variants of concern»

Accumulation of high number of mutations (> 10-20)

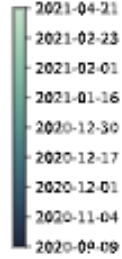
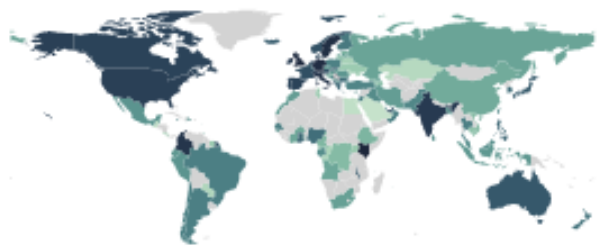
Most of them on the **S gene**

WHO denomination	Lineage	Country of first identification	Main important mutations
Alpha	B.1.1.7	UK	N501Y, Del 69-70
Beta	B.1.351	South-Africa	N501Y, E484K, K417N
Gamma	P.1	Brazil	N501Y, E484K, K417T
Delta	B.1.617	India	L452R, P681R, +/-E484Q

- Increase in transmissibility
- Severity/virulence
- Possible immune escape
 - Reinfection risk
- Reduced vaccine efficacy
- Diagnostic failure
- Treatment failure

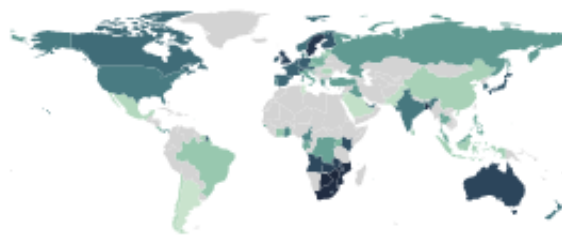
B.1.617 – First identified in India

- 3 sub-lineages: B.1.617.1, B.1.617.2, B.1.617.3
- B.1.617.2 (delta) considered a VOC by WHO since May 2021
(increased transmissibility: dominant in the UK)
- «Double mutant»?
 - 7 mutations on the S gene, > 15 mutations along the whole genome
 - L452R (RBD): increased affinity of the virus to its ACEII receptor (Chen, JMB, 2020)
 - P681R: increased transmissibility (near furin cleavage site)
 - E484Q: (only in B.1.617.1/3) : immune escape



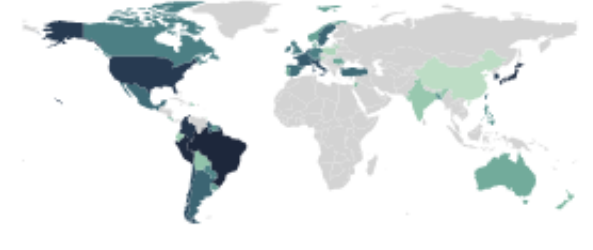
B.1.1.7 report

Alpha
 First identification in UK
 September 2020



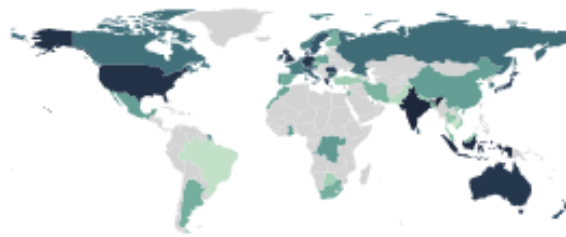
B.1.351 report

Beta
 First identification South-Africa
 May 2020



P.1 report

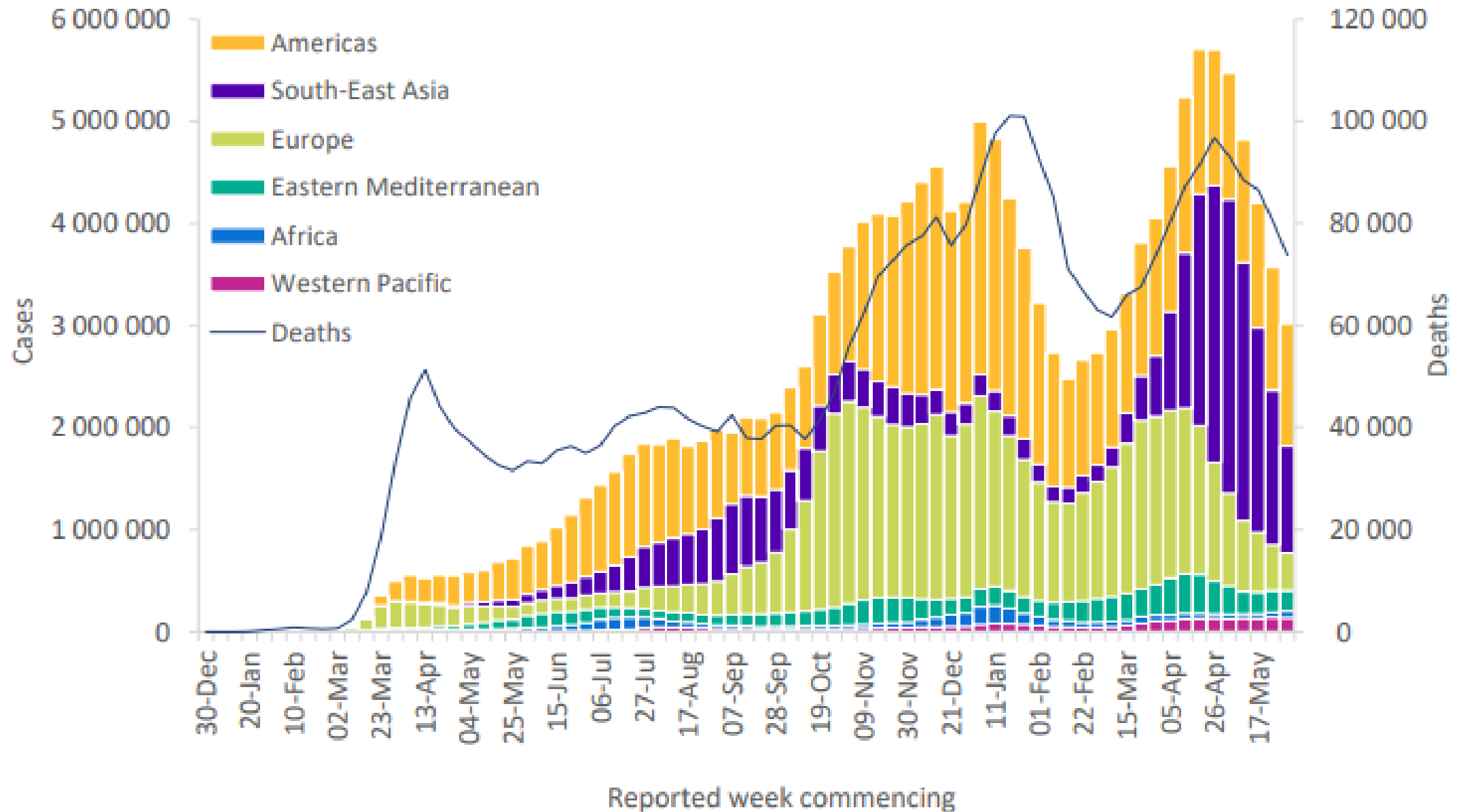
Gamma
 First identification in returning
 travellers from Brazil
 November 2020



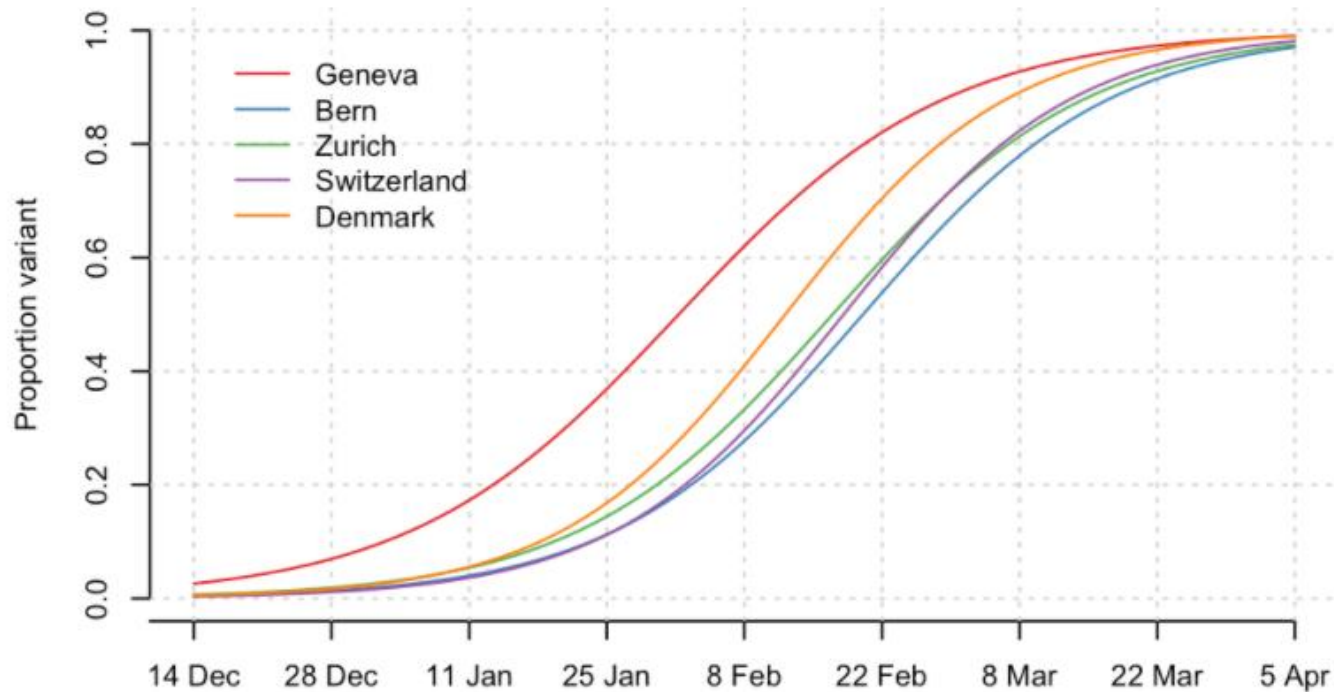
B.1.617.2 report

Delta
 First identification en India, October 2020

Figure 1. COVID-19 cases reported weekly by WHO Region, and global deaths, as of 6 June 2021**



501Y or B.1.1.7 in all regions



C. Althaus' group: <https://ispmbern.github.io/covid-19/variants/>

<https://cevo-public.github.io/Quantification-of-the-spread-of-a-SARS-CoV-2-variant/>

B.1.1.7 Alpha variant:

- Increased transmissibility 20-50%
- Replaced previously circulating variants

Increased transmissibility

B.1.1.7 Alpha	B.1.351 Beta	P.1 Gamma	B.1.617.2 Delta
30-50% more transmissible than previous variants (↑ Rt) ↑ secondary attack rate	Increased transmissibility (1.5 time?)	Increased transmissibility (2.5 time?)	≈40% more transmissible than alpha (outcompetes alpha) ↑ (Rt) ↑ secondary attack rate
In all age groups Secondary attack rate still lower in children			Spreading in non vaccinated population (children(?))

Increased in VL? Increased shedding duration? Increased growth rate (shorter generation time)?

Public health and social measures effective against all variants

Severity

B.1.1.7 Alpha	B.1.351 Beta	P.1 Gamma	B.1.617.2 Delta
Possible increased risk of hospitalisation, severity and mortality (epidemiological data)	Possible increased risk of in-hospital mortality Not confirmed (low evidence data)	Possible increased risk of hospitalization Not confirmed (low evidence data)	Increased risk of hospitalization Under study (?) Increased severity in Syrian Golden Hamster
Not confirmed based on data relying on sequencing			

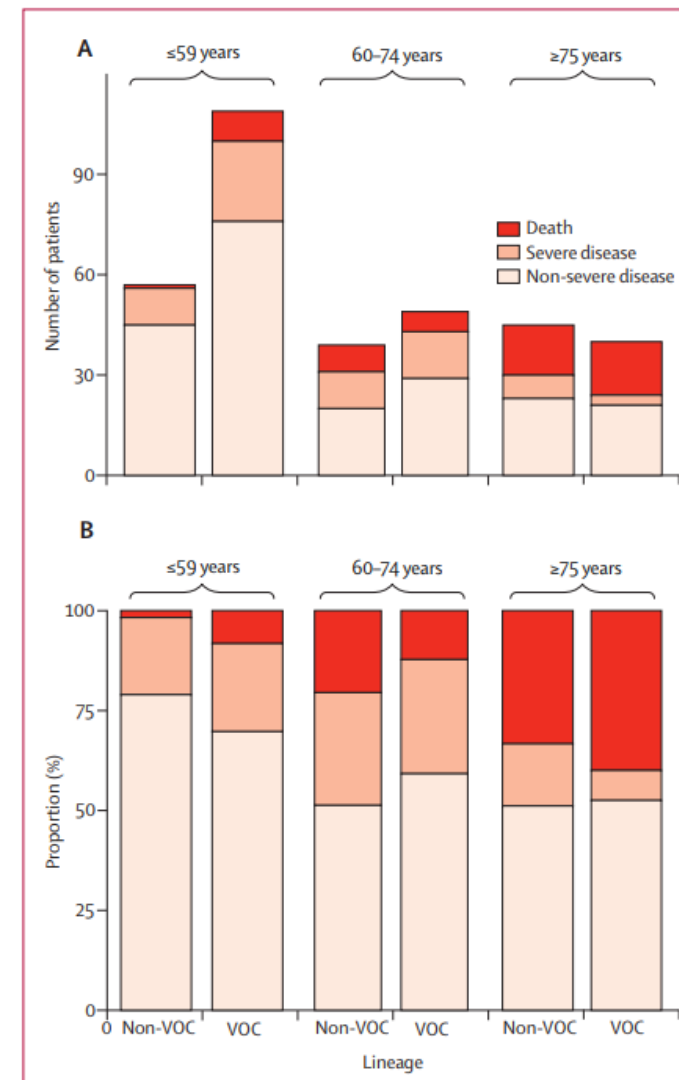


Figure 1: Severity of illness across patient age groups and by presence of VOC or non-VOC SARS-CoV-2 infection

Figure shows absolute counts (A) and proportion of patients (B). Non-severe disease was defined as reaching a WHO ordinal scale of less than 6 by day 14 after symptom onset. Severe disease was defined as reaching an ordinal scale point of 6 or higher. Death was defined as those who had died by day 28 after the first positive swab. VOC=variant of concern.

Possible immune escape

- Mechanism:
 - Mutations in antigenic supersites (RBD and N-terminal domain of S) with decreased neutralizing capacities of monoclonal antibodies and polyclonal sera
 - E484K, K417N/T, Del69-70, L452R, ...

In vitro neutralization data studies give no indication on the effectiveness of **cell-mediated immunity**, which is conserved against variants

Immune escape to monoclonal antibodies

	B.1.1.7	B.1.351	P.1	B.1.617
Monoclonal antibodies Eli Lilly	Partial resistance to etesevimab Conserved efficacy of bamlanivimab	Partial resistance to etesevimab (501Y, E484K, 417N/T) Resistance to bamlanivimab (452R, E484K, 417N/T)		
Regeneron	Conserved efficacy of carisivimab and imdevimab	Partially resistant to casirivimab (E484K, 452R) Neutralization effective with imdevimab		
	Preserved <i>in vitro</i> efficacy of the cocktail casirivimab/imdevimab against all variants			
VIR-7831 (GSK)	maintained activity (press release) binds to a highly conserved epitope of the spike protein			(?)

Variants and vaccines:

In vitro neutralization data (pseudoviruses or full virus)

	B.1.1.7 Alpha	B.1.351 Beta	P.1 Gamma	B.1.617.2 Delta
Pfizer mRNA BTN162b2	From no to minimal decreased neutralization Impact of age Impact of number of doses	Minimal to substantial decreased neutralization (esp. only 1 dose) Effect linked to E484K	Minimal to moderate decreased neutralization Effect linked to E484K	Modest to moderate decreased neutralization (esp. only 1 dose) Impact of age Impact of number of doses
Moderna mRNA 1273				
Astra-Zeneca	Minimal to moderate decreased neutralization	Moderate to substantial decreased neutralization (esp. only 1 dose)	Minimal decreased neutralization	Moderate to Substantial loss (esp. only 1 dose)
Novavax	From no to minimal decreased neutralization	Not available	Not available	Not available

Variants and vaccine efficacy/effectiveness

	B.1.1.7 Alpha	B.1.351 Beta	P.1 Gamma	B.1.617.2 Delta	Previous circulating variants
mRNA (Pfizer/Moderna)	51% effective 1d > 90% effective 2d	76% effective 2 doses (infection) 100% (?) against severe disease	No data	(symptomatic disease) 33% effective 1d 88% effective 2d	> 90% efficacy after 2 doses
Astra-Zeneca	51% 1d - 73% 2d (symptomatic disease) 26% (infection)	10% (symptomatic disease)	No data	(symptomatic disease) 33% effective 1d 60% effective 2d	75% - 84% efficacy (2d)
Janssen (J&J) 1 dose (Ad26.COV2.S)		57% efficacy 100% against severe cases	No data	No data	72% efficacy (USA)
Novavax NVX- CoV2373 (protein-based)	85.6% efficacy N= 62 events, 32 B.1.1.7 Only one severe case	51% efficacy (95% CI: 19.9 – 80.1) N= 44 events No severe case	No data	No data	89% efficacy (UK)

Vaccines against SARS-CoV-2 variants

- Decreased effectiveness of some vaccines against some SARS-CoV-2 variants against infection or symptomatic disease

**Retained protection against B.1.1.7 (alpha),
but decreased against B.1.351 (beta) & B.1.617.2 (delta)**

- **Protection depends on:**
 - vaccine type
 - number of vaccine doses
 - time elapsed since the last dose
 - characteristics of the patients: age, immunosuppression, ...
- **Preserved protection against severe disease (?)**

Other variants to monitor...

- **All variants that include E484K**
 - P.2 (Zeta)
 - P.3 (Theta): 501Y+484K!
 - B.1.525 (Eta)
 - B.1.526 (Iota): part of the lineage carries E484K, the other S477N
 - B.1.1.7 + E484K (Alpha with the 484K: cluster detected in Switzerland)
 - A.VOI.V2
 - A.23.1 + E484K ... and likely more to come
- **All variants that include E484Q:** Likely similar to the E484K mutation
 - B.1.617.1 (Kappa) and B.1.617.3 : L452R+E484Q
- **All variants that include L452R:** slightly more transmissible relative to N501, resistance to bamlanivimab
 - B.1.427/429: (Epsilon): L452R
 - B.1.617.1 (Kappa): L452R+E484Q
 - Paris/Mondor variant HMN.19B : N501Y+L452R
 - C.36.3
- And more to come (?)

Conclusion

- New emerging variants have become dominant
- Public health measures still effective despite higher transmissibility
- **Phenotypic difference** with increased severity (?)
- Some mutations have an **impact on immune therapeutics** (consider local epidemiology when initiating treatment)
- Decreased **vaccine** efficacy *in vitro* but **may still protect against severe disease**
 - Need for real-life clinical data & vaccine adaptation
- No impact yet on RT-PCR detection (multiplex)
- **Monitoring** is crucial

Thank you for you attention!

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