The future of COVID-19: evolutionary and immunological lessons from other viruses

[redacted]

Department of Infectious Disease Epidemiology
London School of Hygiene & Tropical Medicine

NITAG meeting
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Motivation

- Childhood immunisation programmes have led to elimination of viruses with little antigenic variation – such as measles and rubella – in many countries.

- But viruses such as influenza undergo frequent antigenic turnover, necessitating regular vaccine updates and re-vaccination.

- What might the future of COVID-19 look like?

Effectiveness of available vaccines

Pathogen	Vaccine effectiveness (%, mean, 95% CI)	Basic reproduction number, R_0
Measles	96 (72–99)	12.0 (6.0–18.0)
Mumps	86 (65–92)	4.2 (3.6–4.5)
Rubella	89 (58–97)	4.7 (3.4–7.8)
Varicella	95 (92–97)	6.5 (3.3–16.9)
SARS-CoV-2 (pre-B.1.1.7)	86 (76–97)*	2.7 (1.5–3.8)
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Influenza A/H1N1 (post-2009)	61 (57–65)	1.4 (1.2–2.0)
Influenza A/H3N2	33 (22–43)	2.1 (1.6–2.5)
Influenza B	54 (46–61)	2.1 (1.6–2.5)

*two dose BNT162b2 effectiveness against infection, with single dose at 72% (58-86%) [Hall et al, SSRN]

Hodgson et al. CMMID working paper, 2021

Are vaccines sufficiently effective to reach herd immunity in theory?

$HIT = 1 - 1/R_0$

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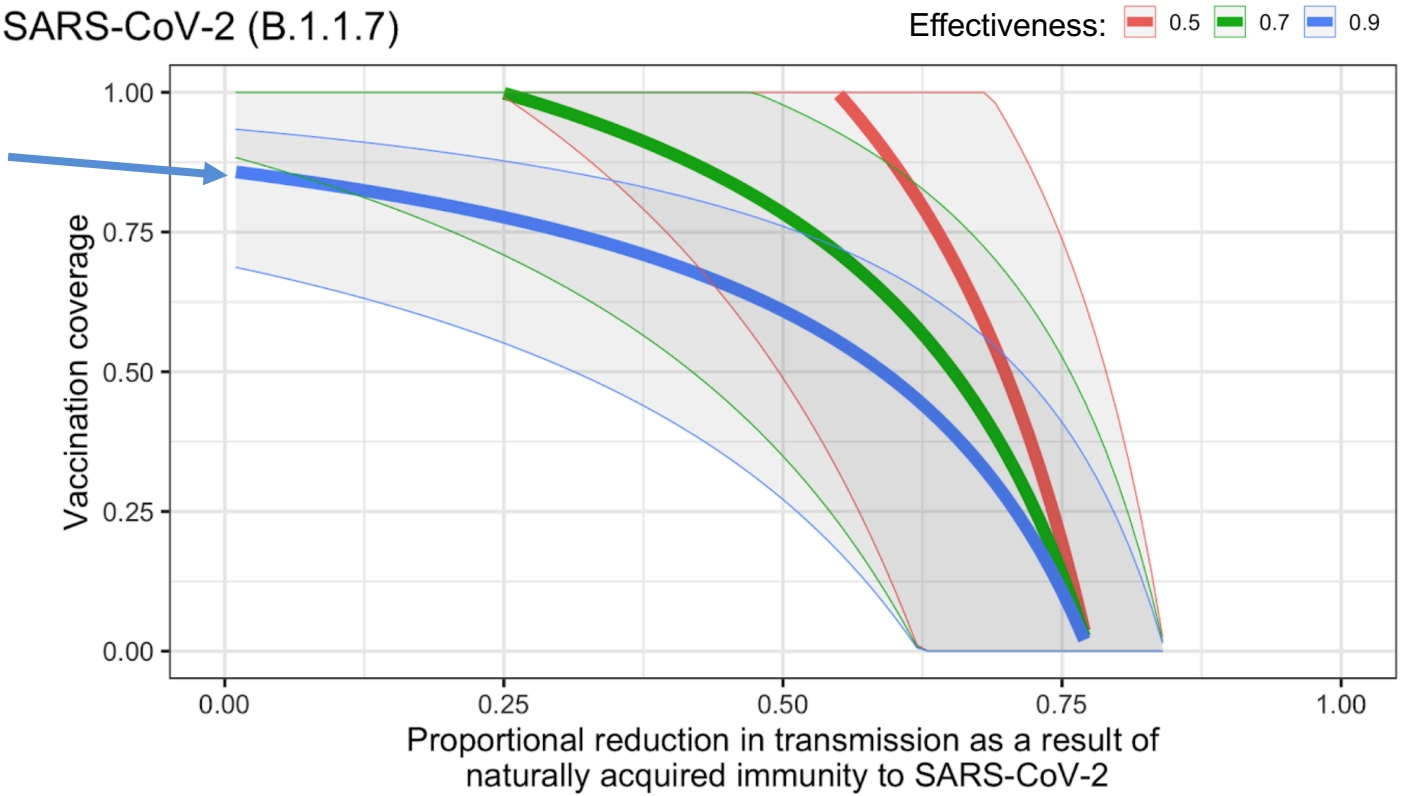
What about additional immunity from natural infections?

Plausible based on early two dose BNT162b2 data



Hodgson et al. CMMID working paper, 2021

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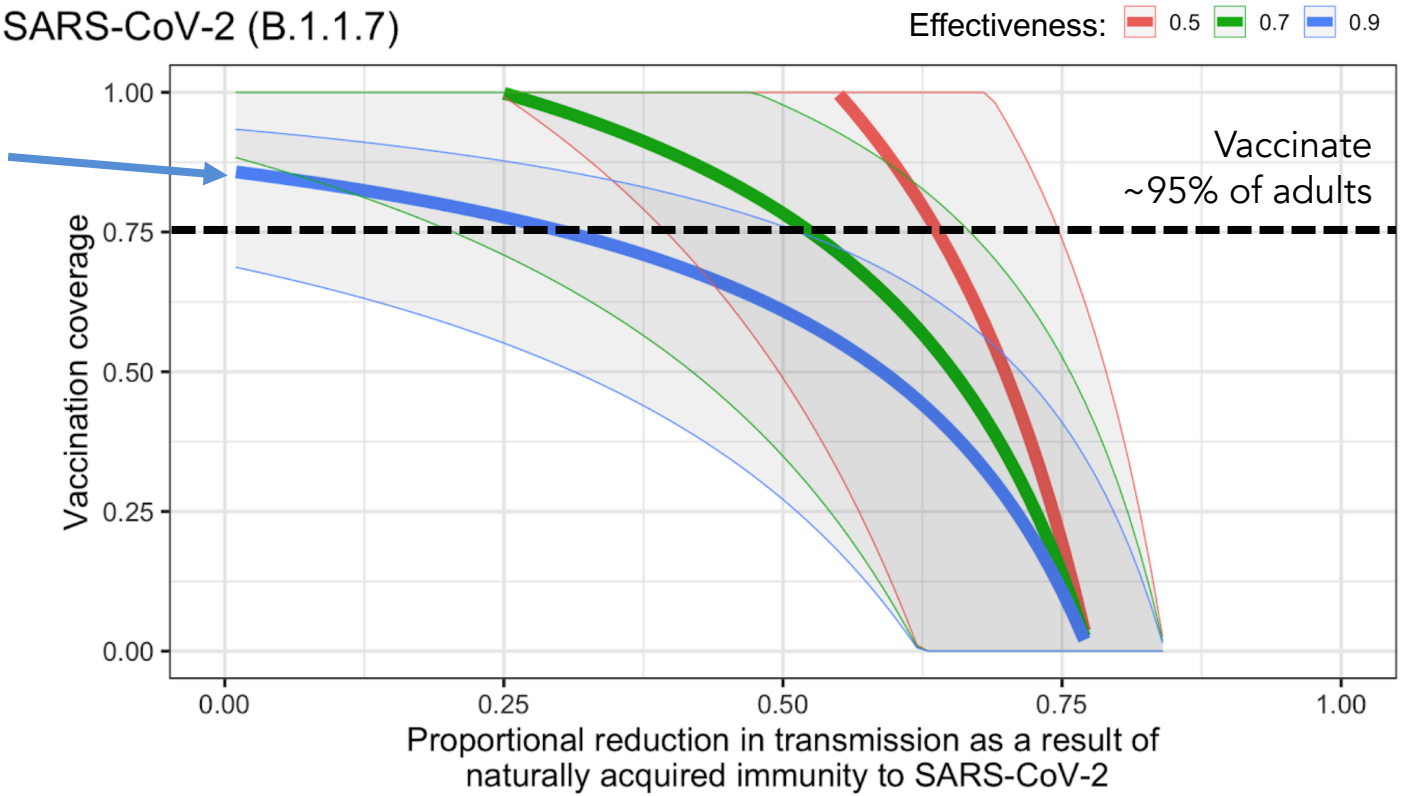

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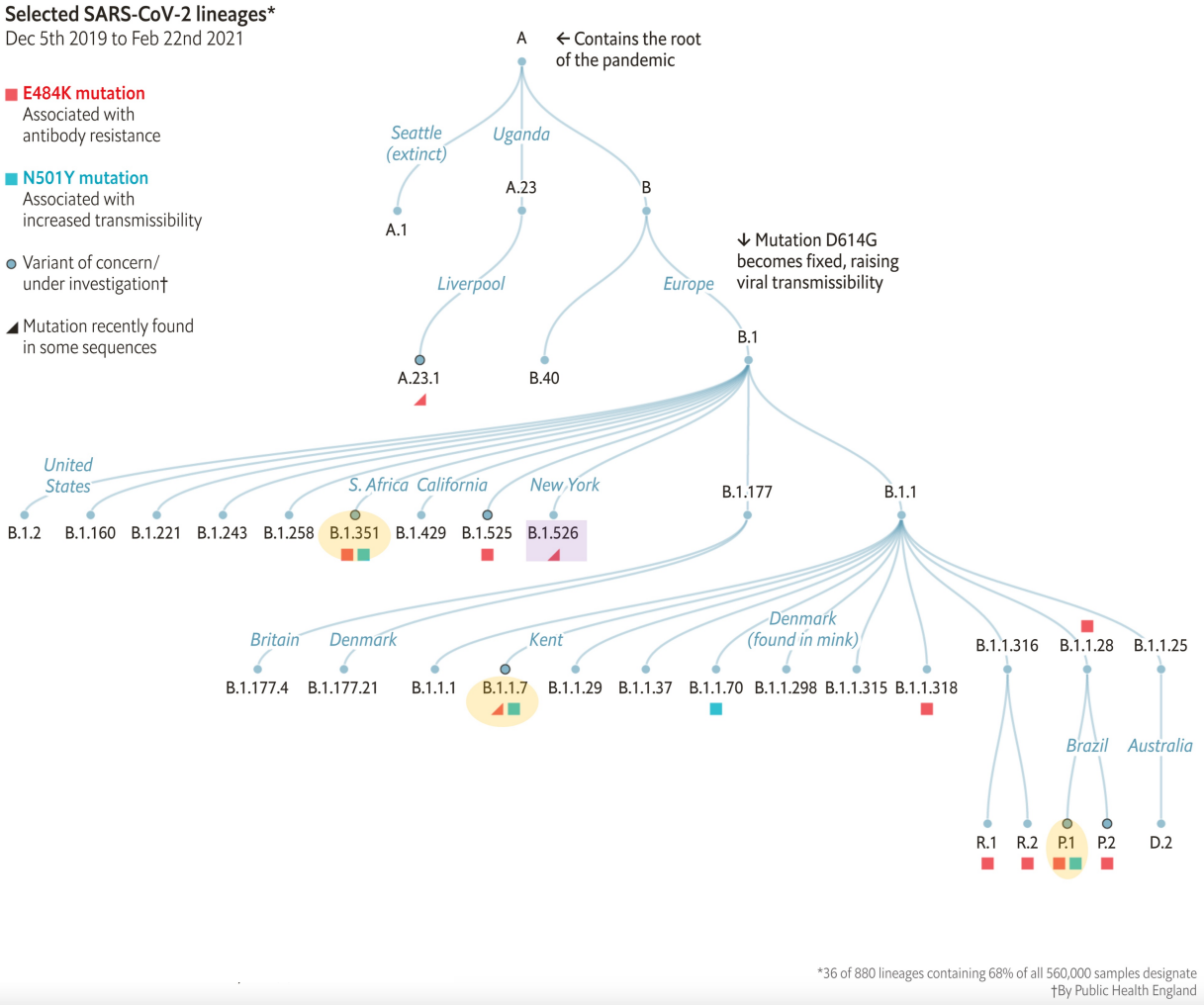
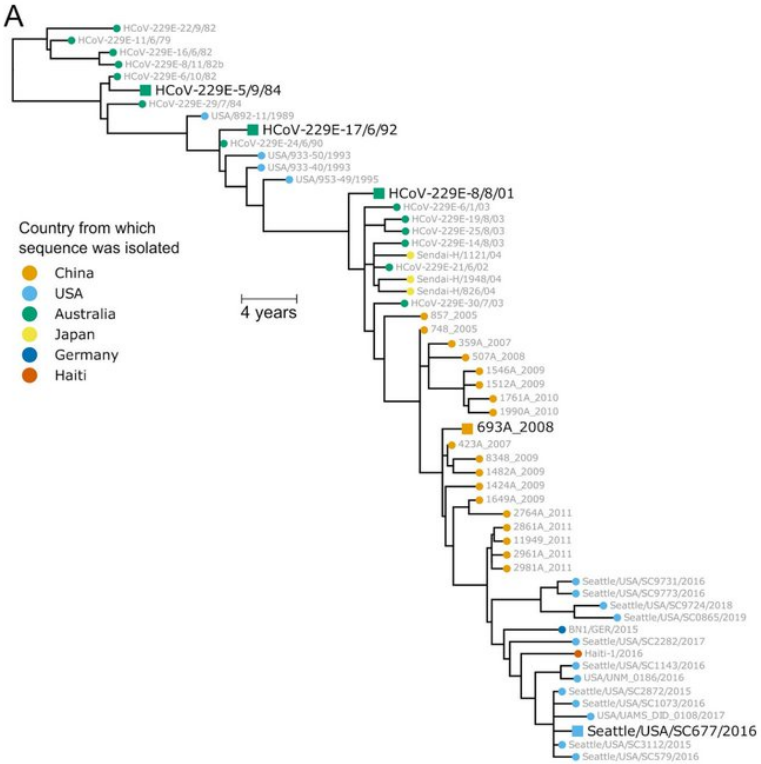


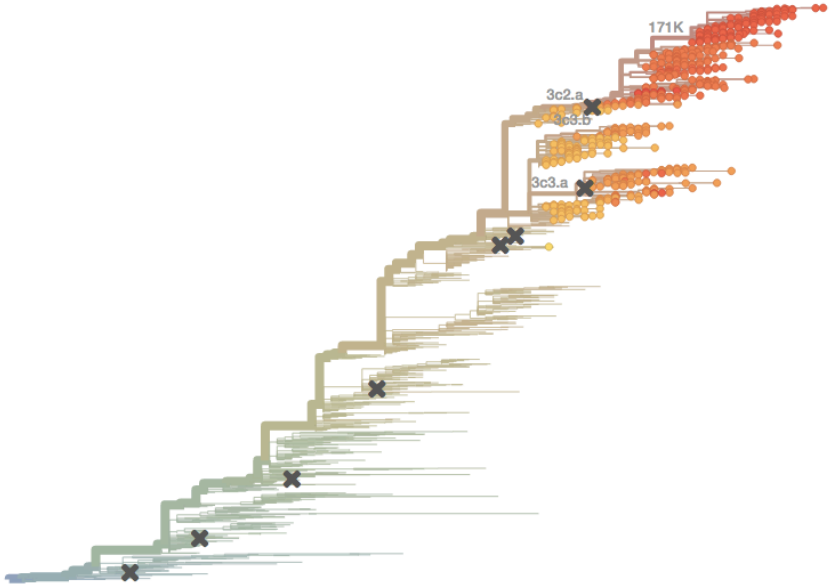
The Economist

Seasonal coronaviruses undergo antigenic evolution like influenza

Human coronavirus 229E:



Influenza A/H3N2 (2005–17):



Eguia et al. MedRxiv, 2021
nextflu.org

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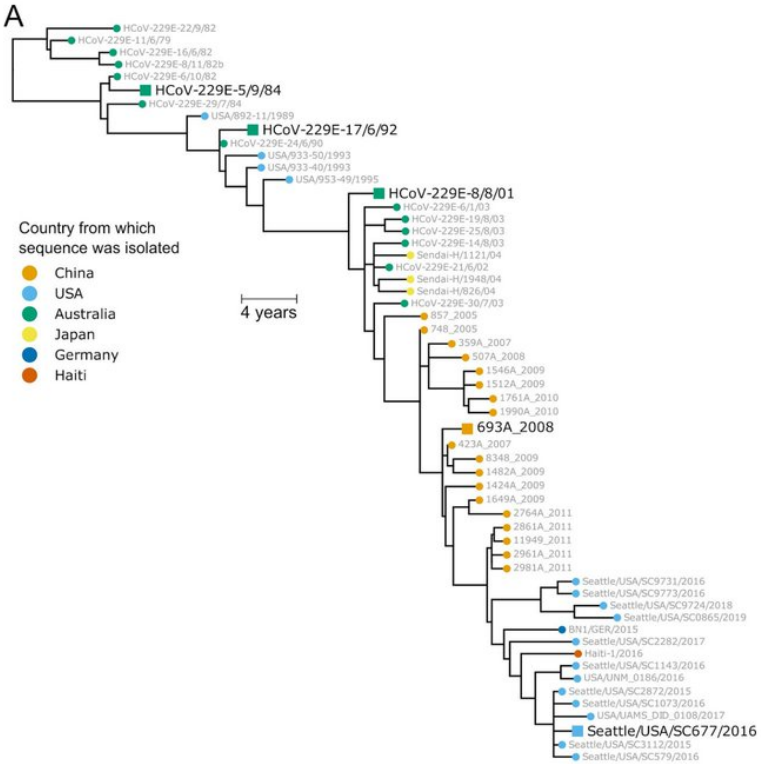

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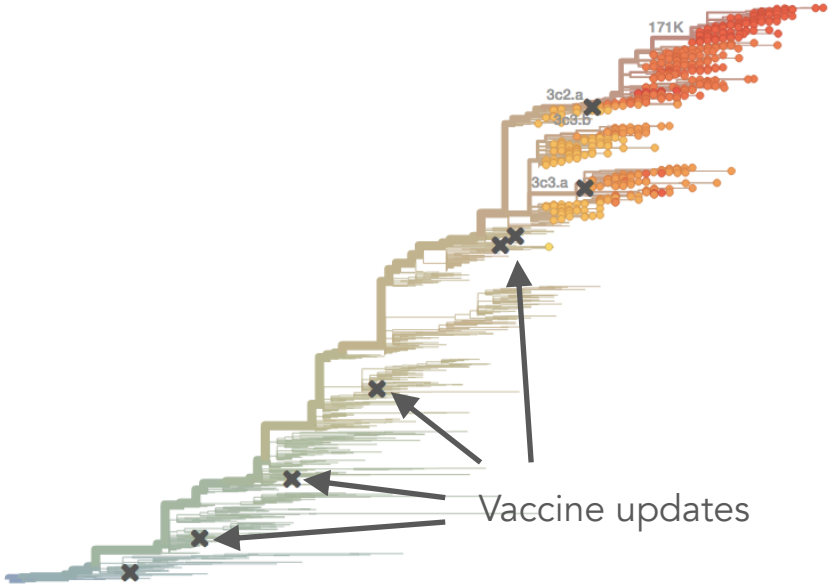

Eguia et al. MedRxiv, 2021
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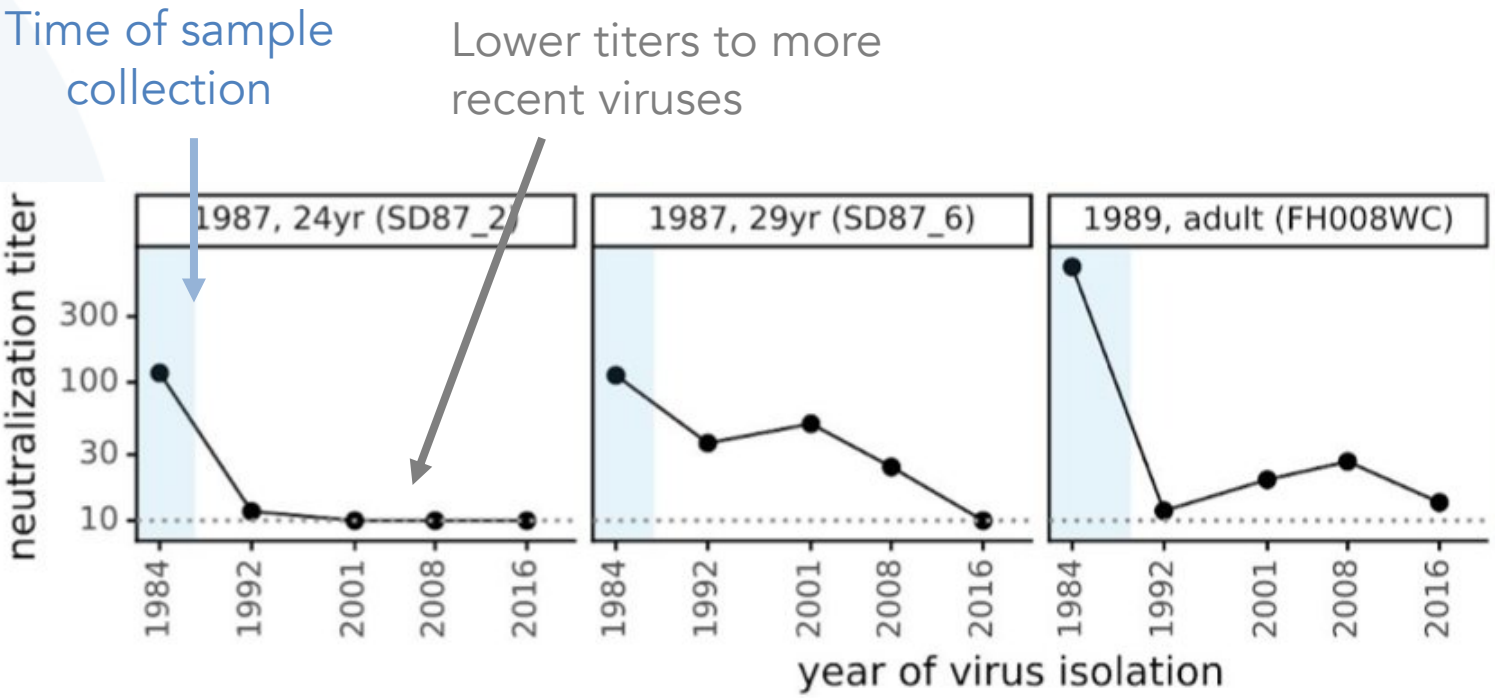
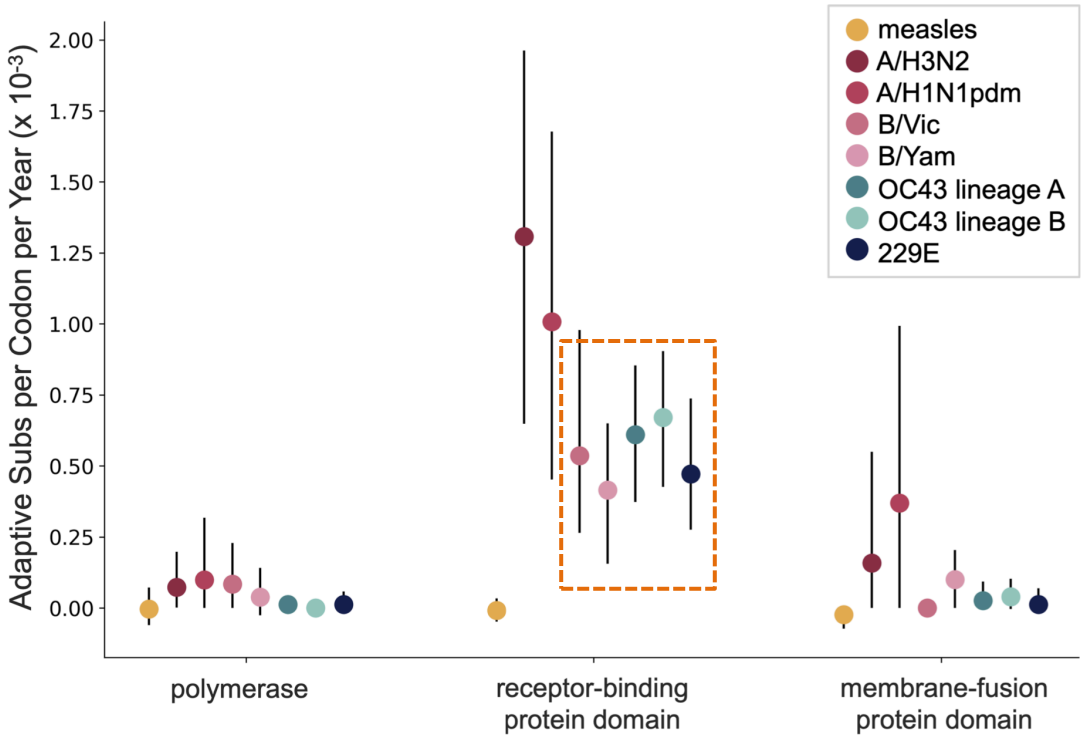
HCoV-229E antibody responses reduced to subsequent viruses



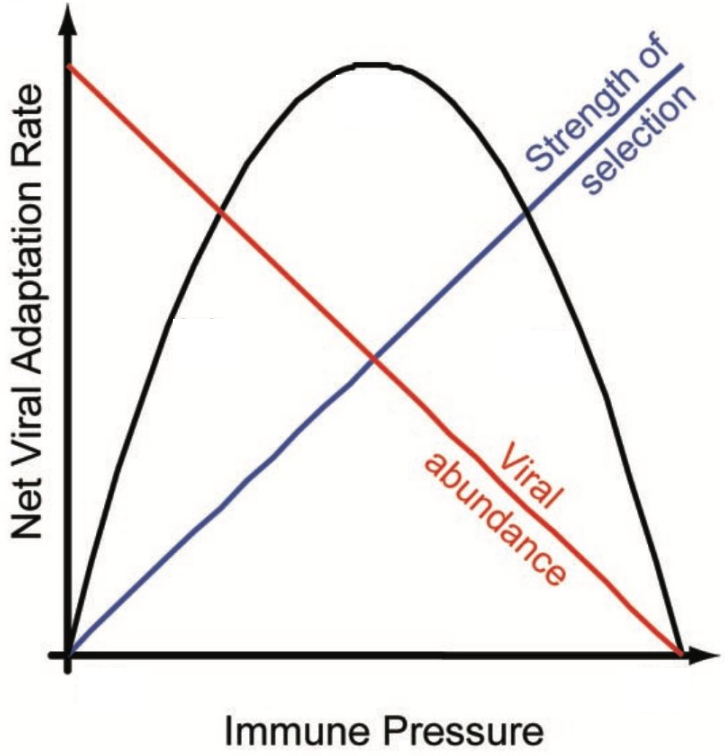
Eguia et al. MedRxiv, 2021

Adaptation rate in receptor-binding domain similar to influenza B



Kistler et al, eLife, 2021

Immune escape depends both on prevalence and selection pressure



Grenfell et al, Science, 2004
Saad-Roy et al, Science, 2021

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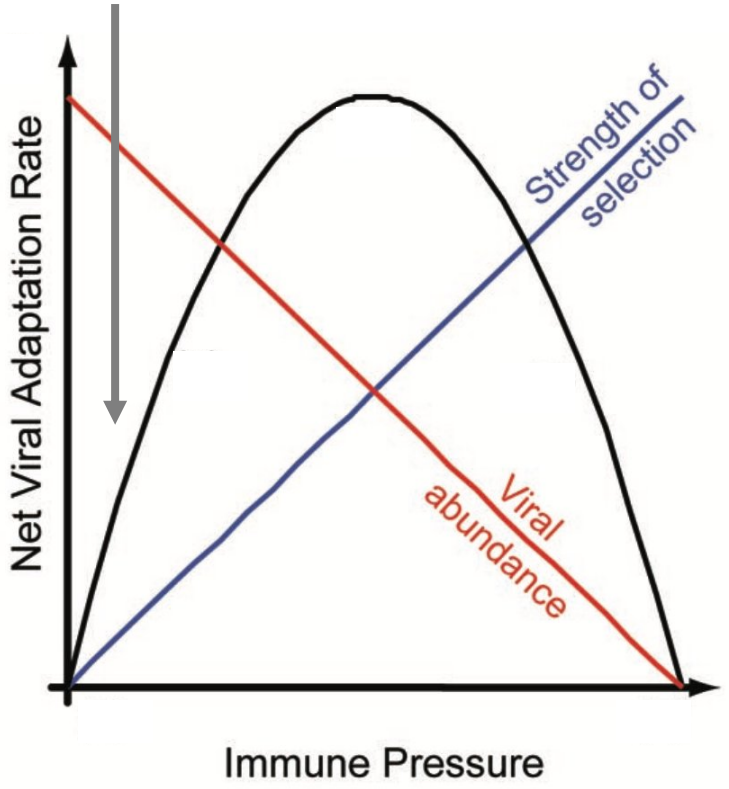
Early COVID-19
epidemics in 2020



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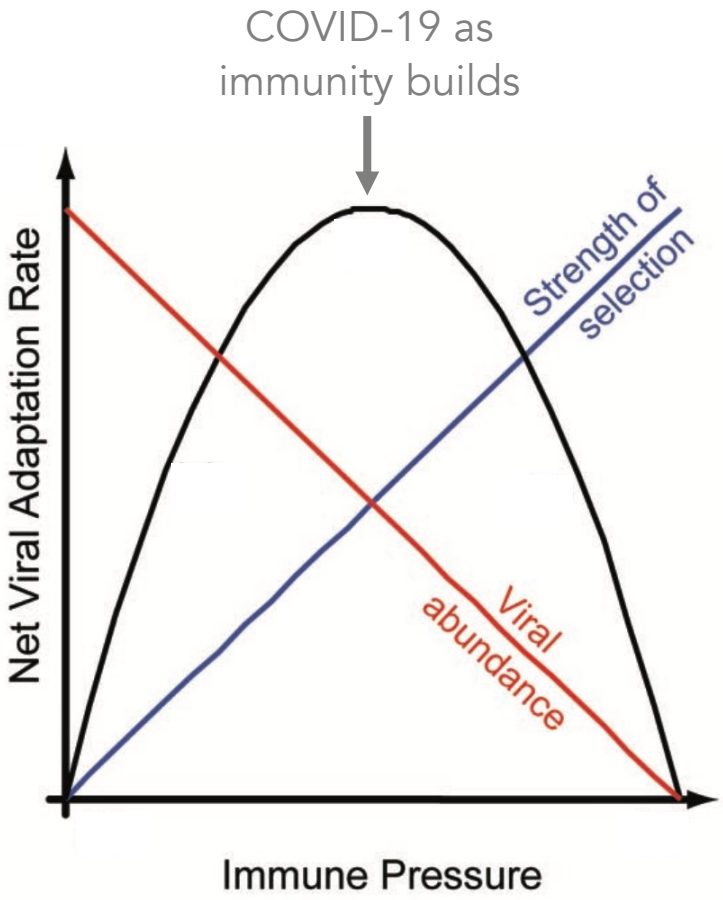

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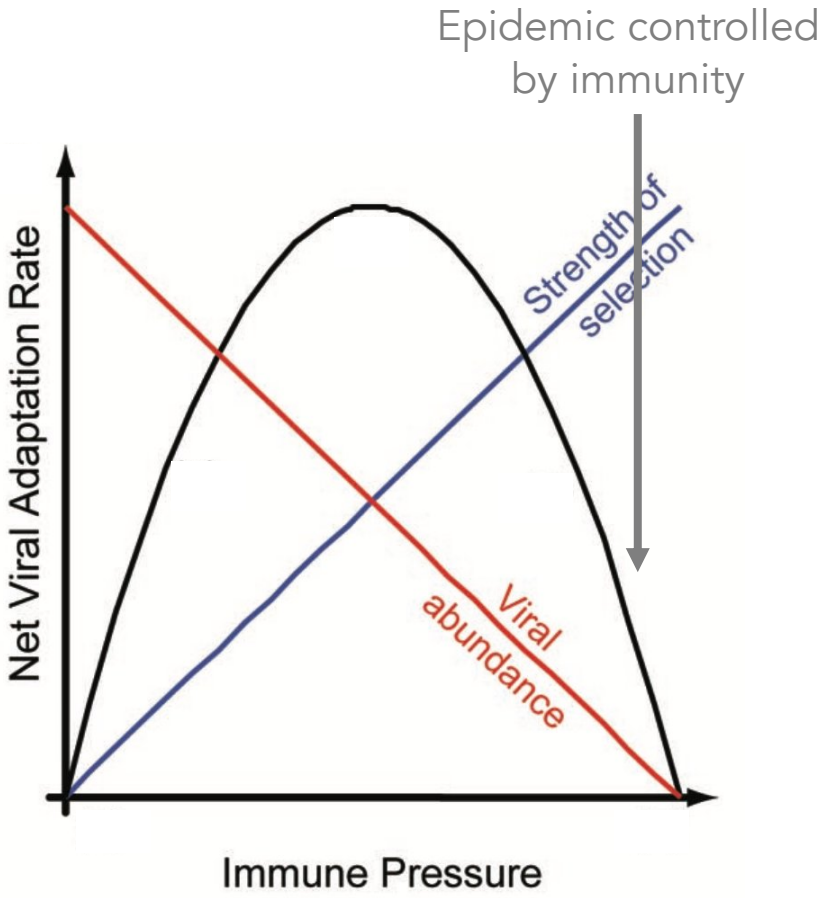
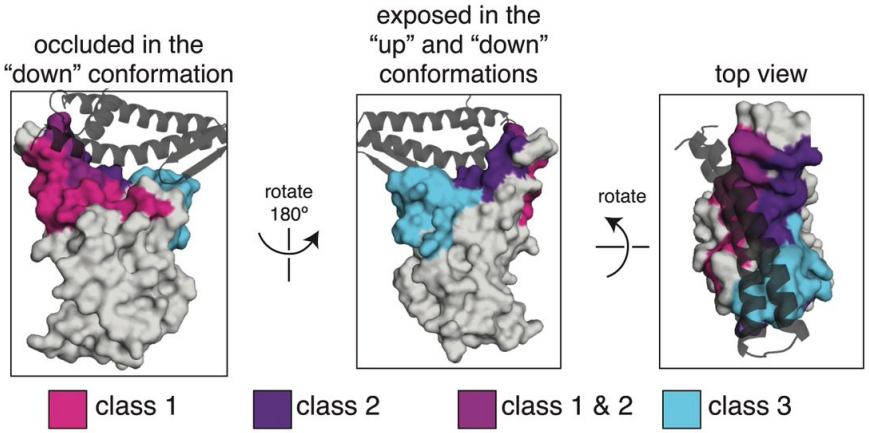


Grenfell et al, Science, 2004
Saad-Roy et al, Science, 2021

Also need to consider combinations of mutations

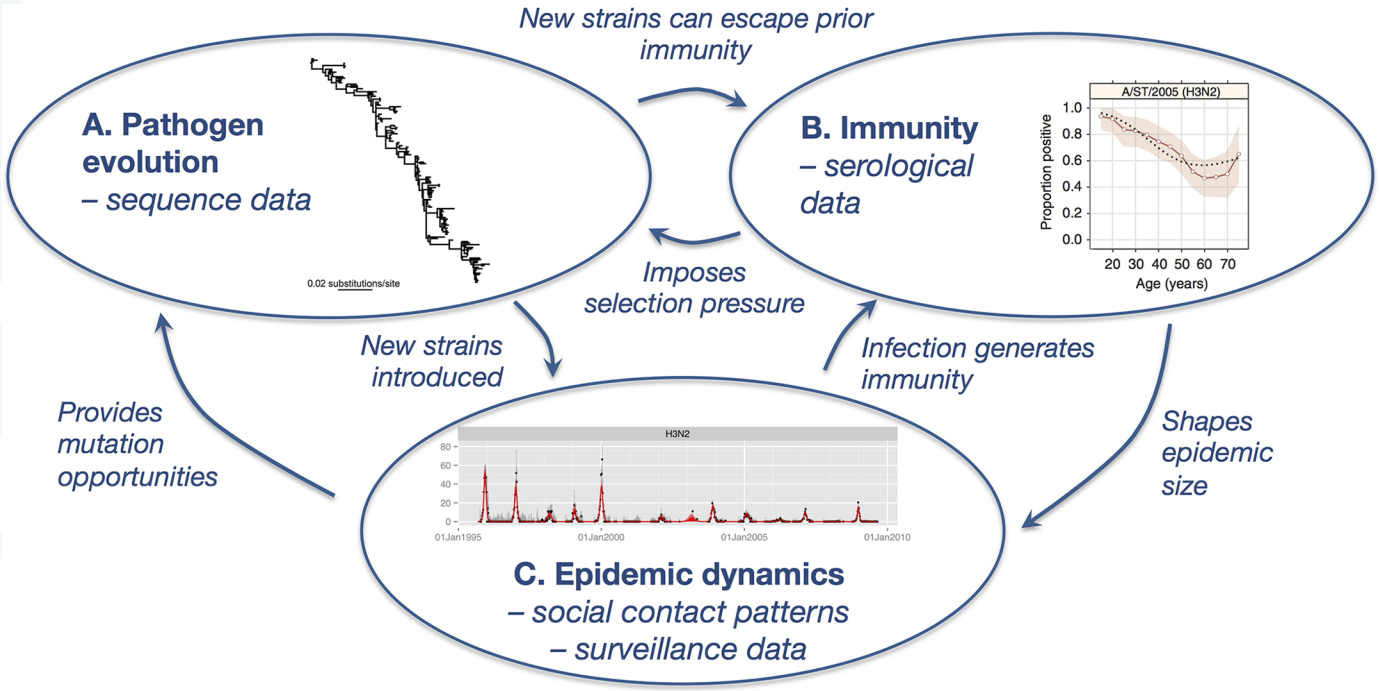
Locations of mutations that escape common monoclonal antibodies:



	escape mutations		
viral lineage	class 1	class 2	class 3
B.1.1.7	–	–	–
B.1.351	K417N	E484K	–
P.1	K417T	E484K	–
P.2	–	E484K	–
B.1.429	–	–	L452R
B.1.526	–	E484K	–

Greaney et al, MedRxiv, 2021

Standardised genomic, immunological and epidemiological data could provide insights into future multi-variant dynamics



Kucharski et al, PLOS Path, 2017

Summary

- Influenza B and seasonal coronaviruses could be useful conceptual model for future SARS-CoV-2 evolutionary dynamics

- Vaccination-induced herd immunity against B.1.1.7 unlikely with current vaccines unless: i) children also vaccinated or ii) substantial natural immunity also accumulated.

- Potential for SARS-CoV-2 immune escape largest in areas of high prevalence and accumulating immunity

- Standardisation and sharing of multiple data sources will be important for tracking evolutionary dynamics