



Virtual Training on Antigen Surveillance: from Evolution to Immune Escape

SARS-CoV-2 variants: increased fitness and immune evasion

Delphine PLANAS, PhD
March 23rd, 2026

Objectives




- SARS-CoV-2 pathogenesis
- Overview of mRNA-based vaccines and SARS-COV-2 variant emergence
- Distinct evolution of Omicron XBB and BA.2.86/JN.1 lineages
- Future challenges and novel vaccine strategies



Objectives



- **SARS-CoV-2 pathogenesis**
 - Overview of mRNA-based vaccines and SARS-COV-2 variant emergence
 - Distinct evolution of Omicron XBB and BA.2.86/JN.1 lineages
 - Future challenges and novel vaccine strategies
- 

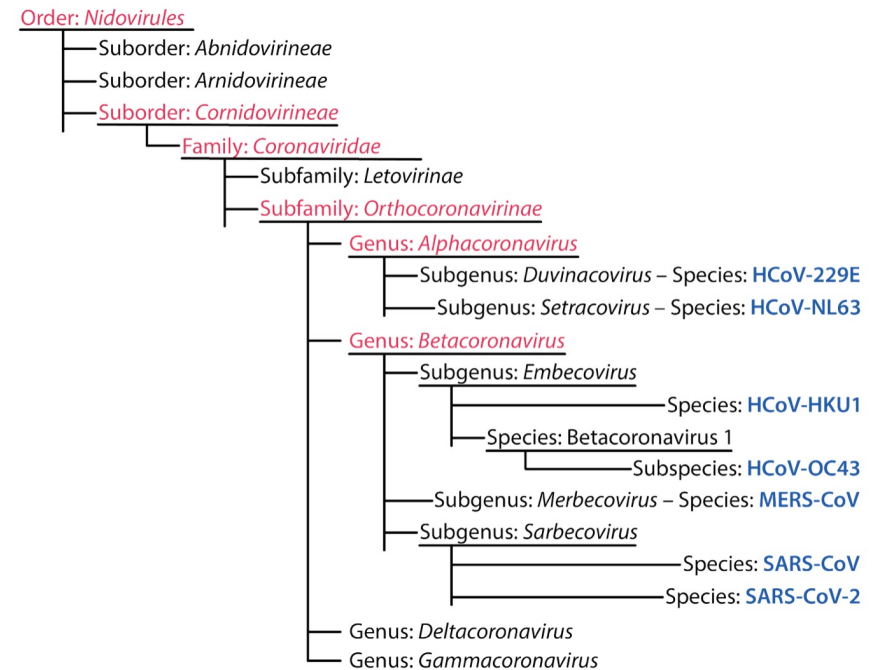
Emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)



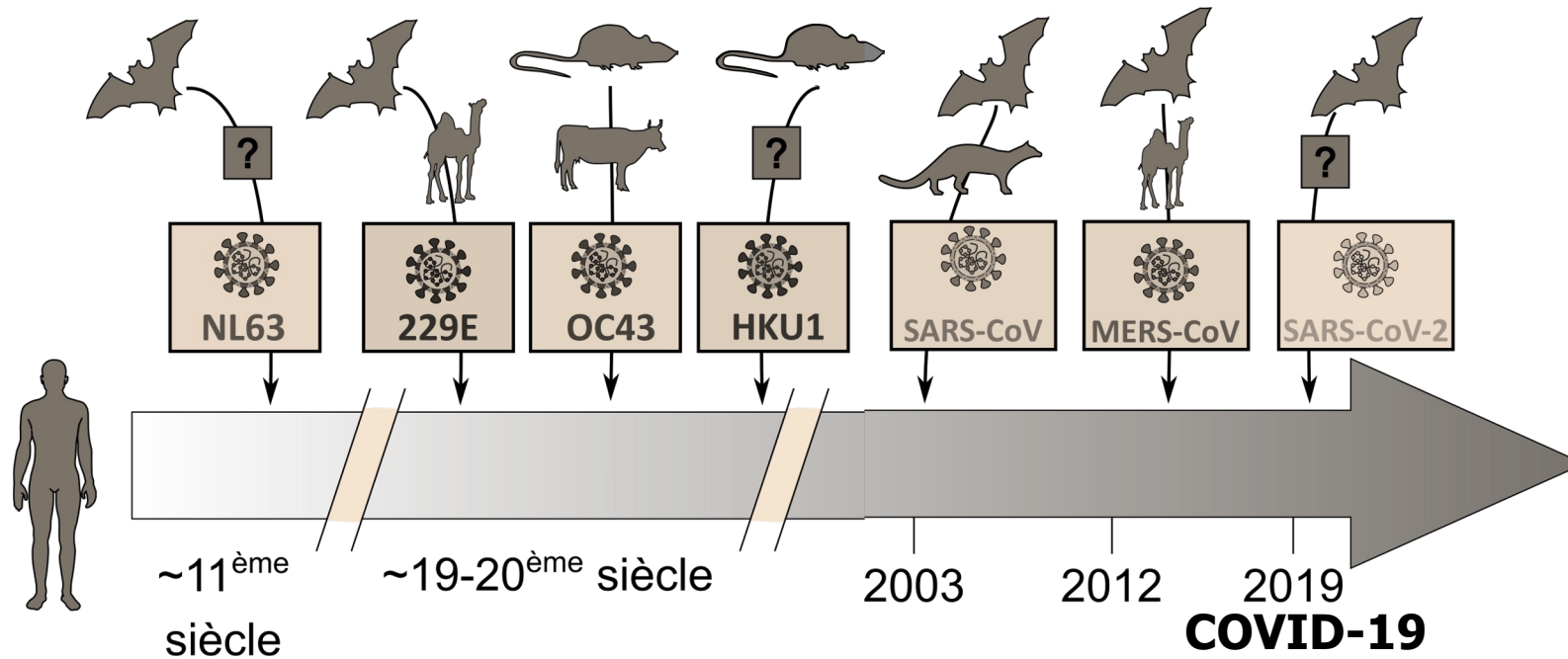
Pneumonia of unknown cause – China

Disease outbreak news
5 January 2020

On 31 December 2019, the WHO China Country Office was informed of cases of pneumonia of unknown etiology (unknown cause) detected in Wuhan City, Hubei Province of China. As of 3 January 2020, a total of 44 patients with pneumonia of unknown etiology have been reported to WHO by the national authorities in China. Of the 44 cases reported, 11 are severely ill, while the remaining 33 patients are in stable condition. According to media reports, the concerned market in Wuhan was closed on 1 January 2020 for environmental sanitation and disinfection.



Epidemic coronaviruses



Asymptomatic or mild cold
Rare complications

Asymptomatic, mild or severe cold
Frequent complications > 65

Case fatality ratio:

SARS-CoV: 5-10%

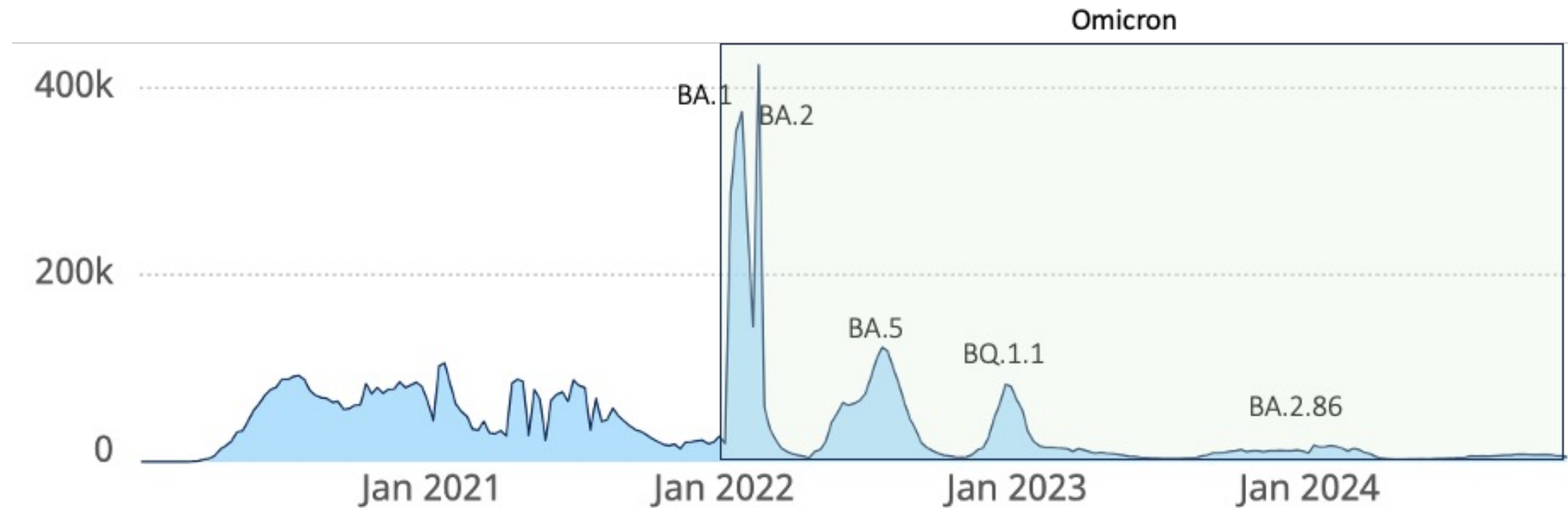
MERS-CoV: 35%

SARS-CoV-2: 0.5-3% before vaccination

Evolution of the COVID-19 pandemic



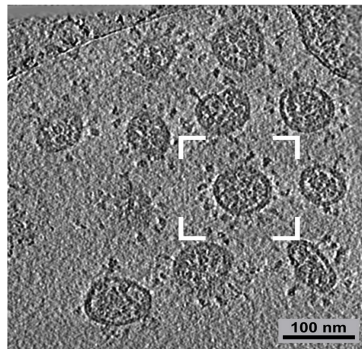
- Over 780 million people have been diagnosed with SARS-CoV-2 infection.
- 7 million deaths have been recorded.



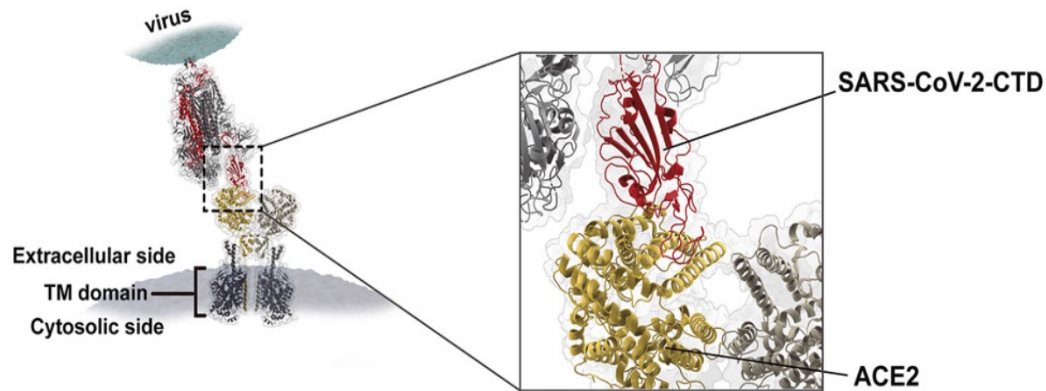
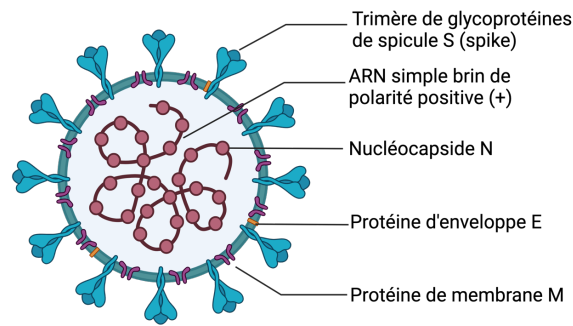
Data source: WHO COVID-19

Source: Official data collated by Our World in Data, Johns Hopkins University CSSE COVID-19 Data

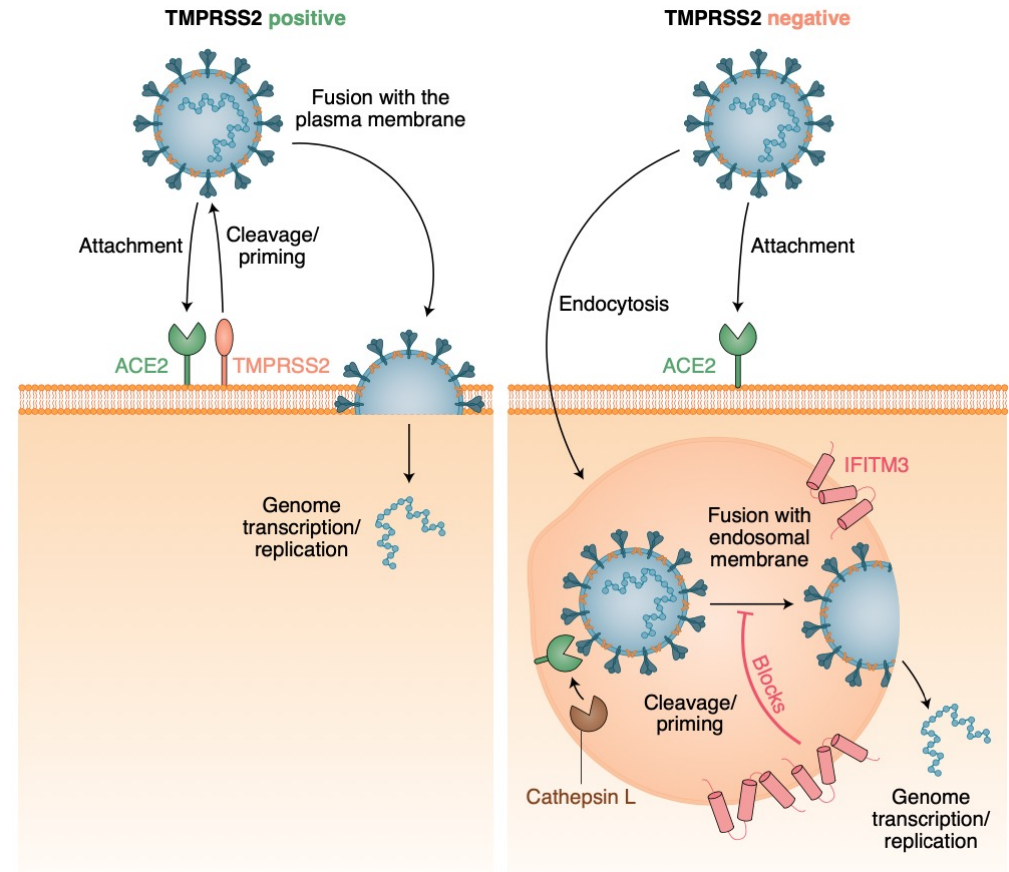
SARS-CoV-2 Spike protein binds to ACE2



H. Yao *et al.*, 2020

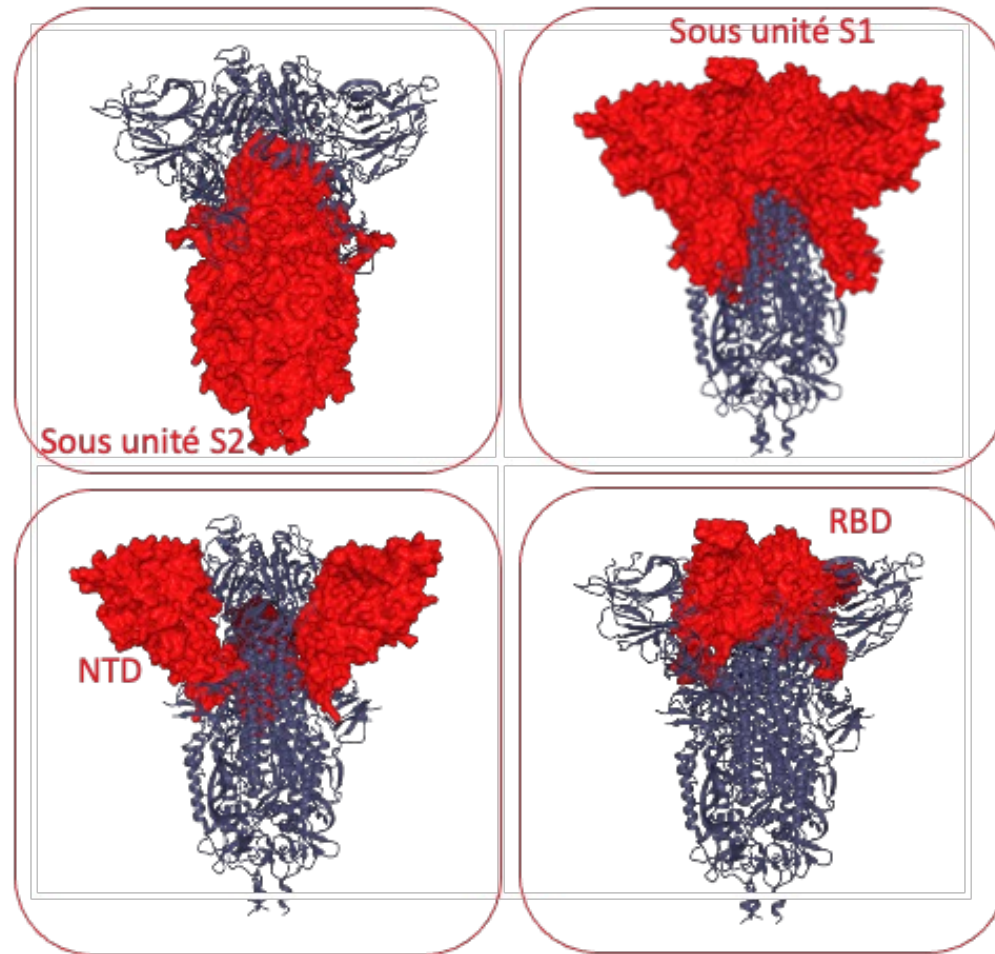
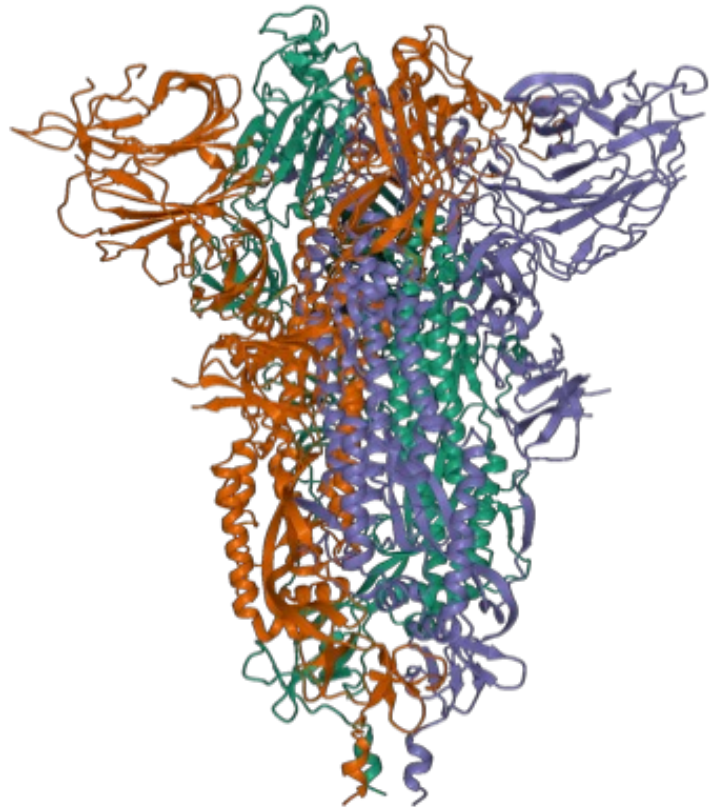
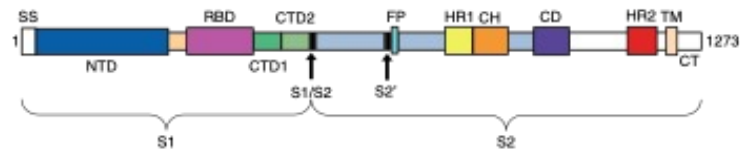


Wang *et al.*, Cell, 2020

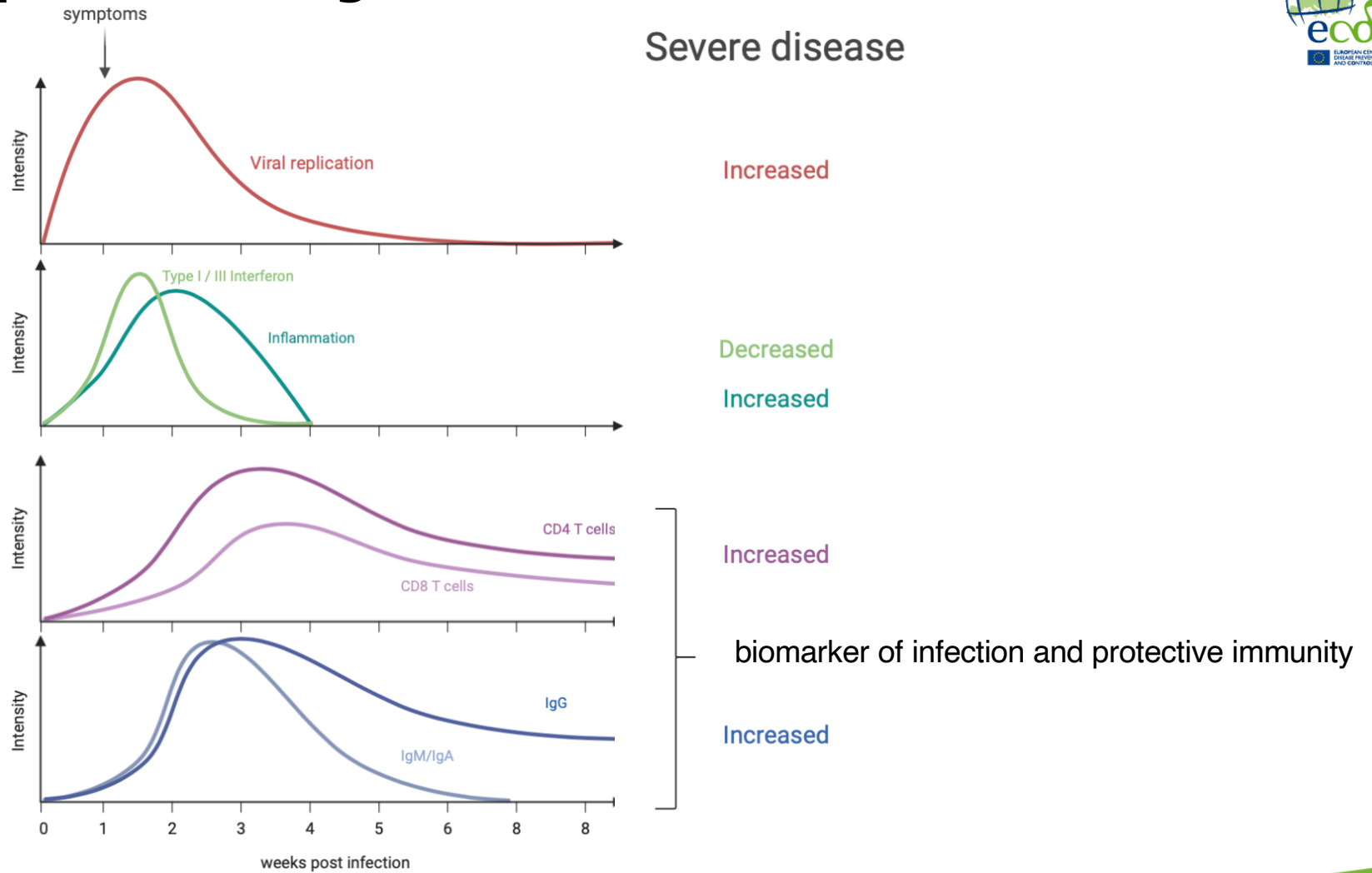


Markus Hoffmann and Stefan Pöhlmann., Nature Microbiology, 2021

SARS-CoV-2 Spike protein



Immune responses during COVID-19

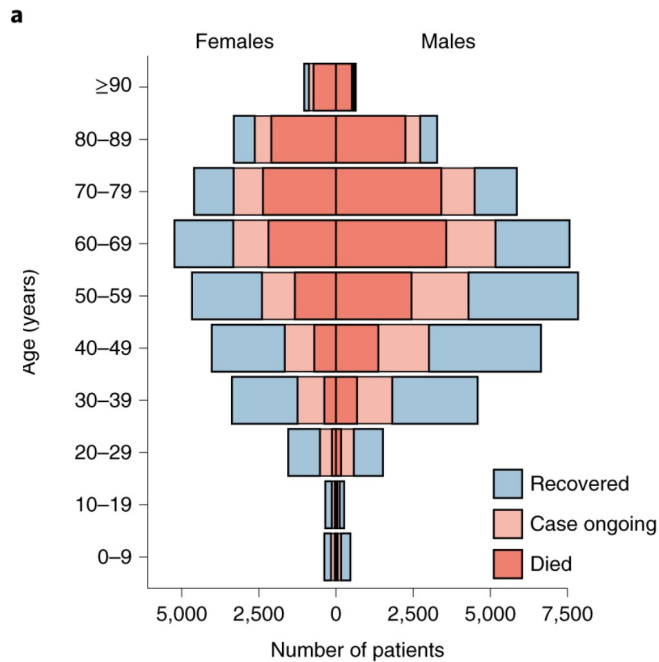
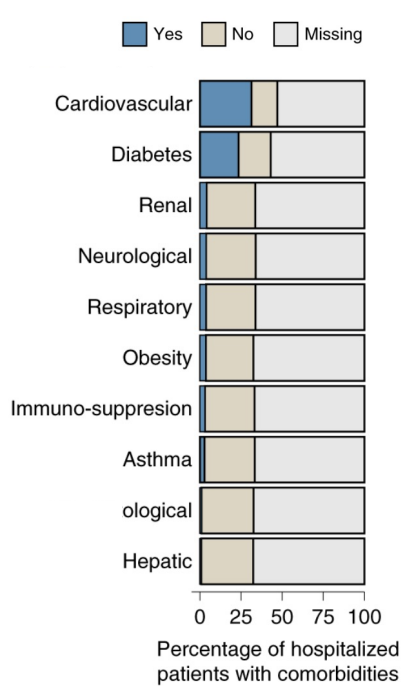


Adapted from Stephens and McElrath, JAMA, 2020 ; Zhang et al., Science 2020 ; Bastard et al., Science 2020 ; Hadjajd et al., Science 2020 ; Zheng et al., BMJ 2020; Sette and Crotty, Cell, 2021

Clinical features of COVID-19



Factors associated to severe disease



Marciel de Souza, Nat Hum Behav 2020

Asymptomatic infection

In Vo' (Italy), 40% of SARS-CoV-2-infected patients were asymptomatic.

	First survey		Second survey	
	Total positives	Percentage	Total positives	Percentage
Symptomatic at the time of sampling ^a	34	46.6	15	51.7
Presymptomatic at the time of sampling	10	13.7	1	3.4
Asymptomatic	29	39.7	13	44.8
Total	73		29	

Lavezzo et al., Nature, 2020

On the cruise ship *Diamond Princess*, 58% of infected individuals were asymptomatic.

Sakurai et al., NEJM, 2020

Correlates of protection (CoP) against SARS-CoV-2



Definition: A CoP is **an immune marker** that can be used to reliably **predict a vaccine's level of efficacy** in preventing a clinically relevant outcome.

Article

Correlates of protection against SARS-CoV-2 in rhesus macaques

Nature, 2021

<https://doi.org/10.1038/s41586-020-03041-6>
Received: 5 September 2020
Accepted: 25 November 2020
Published online: 4 December 2020
Check for updates

Katherine McMahan¹, Jingyou Yu¹, Noe B. Mercado¹, Carolin Loos^{3,7}, Lisa H. Tostanoski^{1,7}, Abishek Chandrasekar¹, Jinyan Liu¹, Lauren Peter¹, Caroline Atyeo^{2,4}, Alex Zhu¹, Esther A. Bondzie¹, Gabriel Dagotto¹, Makda S. Gebre^{1,4}, Catherine Jacob-Dolan^{1,4}, Zhenfeng Li¹, Felix Nampanya¹, Shivani Patel¹, Laurent Pessaint¹, Alex Van Ry¹, Kelvin Blade¹, Jake Valley-Ogunro¹, Mehtap Cabus¹, Renita Brown¹, Anthony Cook¹, Elyse Teow¹, Hanne Andersen¹, Mark G. Lewis¹, Douglas A. Lauffenburger¹, Galit Alter^{2,6} & Dan H. Barouch^{1,2,4,6,8}

RESEARCH

Science, 2020

CORONAVIRUS

Isolation of potent SARS-CoV-2 neutralizing antibodies and protection from disease in a small animal model

Thomas F. Rogers^{1,2*}, Fangzhu Zhao^{1,3,4*}, Deli Huang^{1*}, Nathan Beutler^{1*}, Alison Burns^{1,3,4}, Wan-ting He^{1,3,4}, Oliver Limbo^{3,5}, Chloe Smith^{1,3}, Ge Song^{1,3,4}, Jordan Woehl^{3,5}, Linlin Yang¹, Robert K. Abbott^{4,6}, Sean Callaghan^{1,3,4}, Elijah Garcia¹, Jonathan Hurtado^{1,4,7}, Mara Parren¹, Linghang Peng¹, Sydney Ramirez⁵, James Ricketts¹, Michael J. Ricciardi⁸, Stephen A. Rawlings², Nicholas C. Wu⁹, Meng Yuan⁹, Davey M. Smith², David Nemazee¹, John R. Tejarro¹, James E. Voss¹, Ian A. Wilson^{3,4,9}, Raees Andrabai^{1,3,4}, Bryan Briney^{1,4,7}, Elise Landais^{1,3,4,5}, Devin Sok^{1,3,4,5,†}, Joseph G. Jardine^{3,5,†}, Dennis R. Burton^{1,3,4,10,†}

“Passive transfer of neutralizing antibodies can prevent severe SARS-CoV-2 infection in multiple animal models.”

2021

nature
medicine

ARTICLES

<https://doi.org/10.1038/s41591-021-01377-8>

Check for updates

Neutralizing antibody levels are highly predictive of immune protection from symptomatic SARS-CoV-2 infection

David S. Khoury¹, Deborah Cromer¹, Arnold Reynaldi¹, Timothy E. Schlub^{1,2}, Adam K. Wheatley¹, Jennifer A. Juno¹, Kanta Subbarao^{3,4}, Stephen J. Kent^{3,5,6}, James A. Triccas^{7,8,9,10} and Miles P. Davenport^{1,10}

ARTICLES

<https://doi.org/10.1038/s41591-021-01540-1>

nature
medicine

Check for updates

OPEN

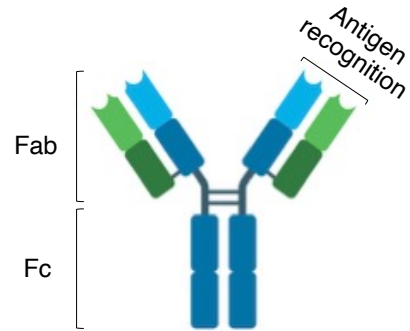
Correlates of protection against symptomatic and asymptomatic SARS-CoV-2 infection

Shuo Feng¹, Daniel J. Phillips¹, Thomas White², Homesh Sayal¹, Parvinder K. Aley¹, Sagida Bibi¹, Christina Dold¹, Michelle Fuskova¹, Sarah C. Gilbert¹, Ian Hirsch², Holly E. Humphries¹, Brett Jepson^{5,6}, Elizabeth J. Kelly¹, Emma Plested¹, Kathryn Shoemaker⁵, Kelly M. Thomas¹, Johan Vekemans⁷, Tonya L. Villafana⁵, Teresa Lambe^{5,9,35}, Andrew J. Pollard^{1,10,35}, Merryn Voysey^{1,10,35} and the Oxford COVID Vaccine Trial Group*

The global supply of COVID-19 vaccines remains limited. An understanding of the immune response that is predictive of protection could facilitate rapid licensure of new vaccines. Data from a randomized efficacy trial of the ChAdOx1 nCoV-19 (AZD1222) vaccine in the United Kingdom was analyzed to determine the antibody levels associated with protection against SARS-CoV-2. Binding and neutralizing antibodies at 28 days after the second dose were measured in infected and noninfected vaccine recipients. Higher levels of all immune markers were correlated with a reduced risk of symptomatic infection. A vaccine efficacy of 80% against symptomatic infection with majority Alpha (B.1.1.7) variant of SARS-CoV-2 was achieved with 264 (95% CI: 105, 806) binding antibody units (BAU)/ml; and 506 (95% CI: 135, not computed (beyond data range) (NC)) BAU/ml for anti-spike and anti-RBD antibodies, and 26 (95% CI: NC, NC) international unit (IU)/ml and 247 (95% CI: 101, NC) normalized neutralization titers (NF₅₀) for pseudovirus and live-virus neutralization, respectively. Immune markers were not correlated with asymptomatic infections at the 5% significance level. These data can be used to bridge to new populations using validated assays, and allow extrapolation of efficacy estimates to new COVID-19 vaccines.

“Neutralizing antibodies levels are highly predictive of immune protection from symptomatic infection.”

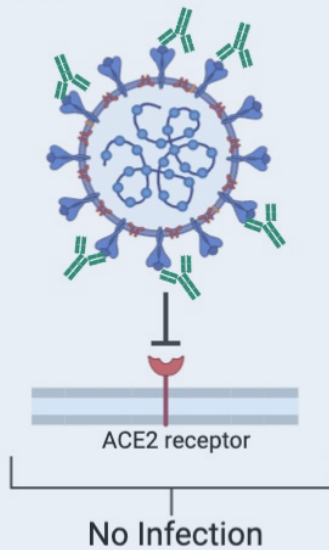
Immune properties of antibodies



- They often correlate with sterilizing immunity
- Their transfer may provide immune protection
- They are specific and target multiple epitopes

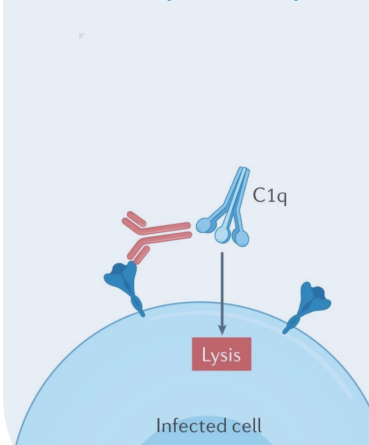
Neutralization

Neutralizing antibodies

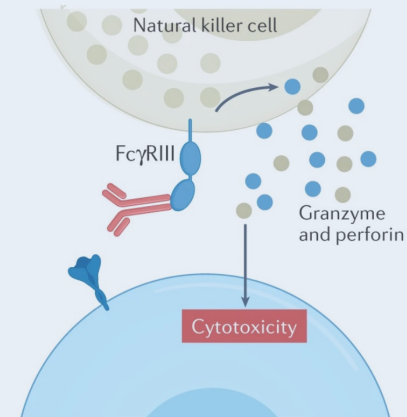


Fc-effector functions

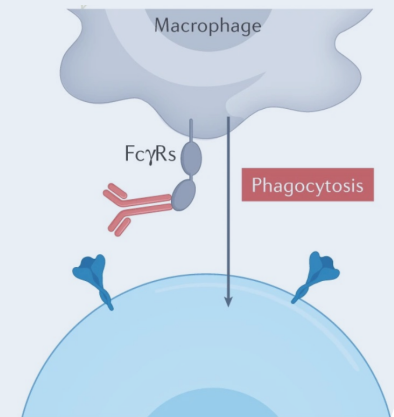
Complement-dependent cytotoxicity



Antibody-dependent cellular cytotoxicity

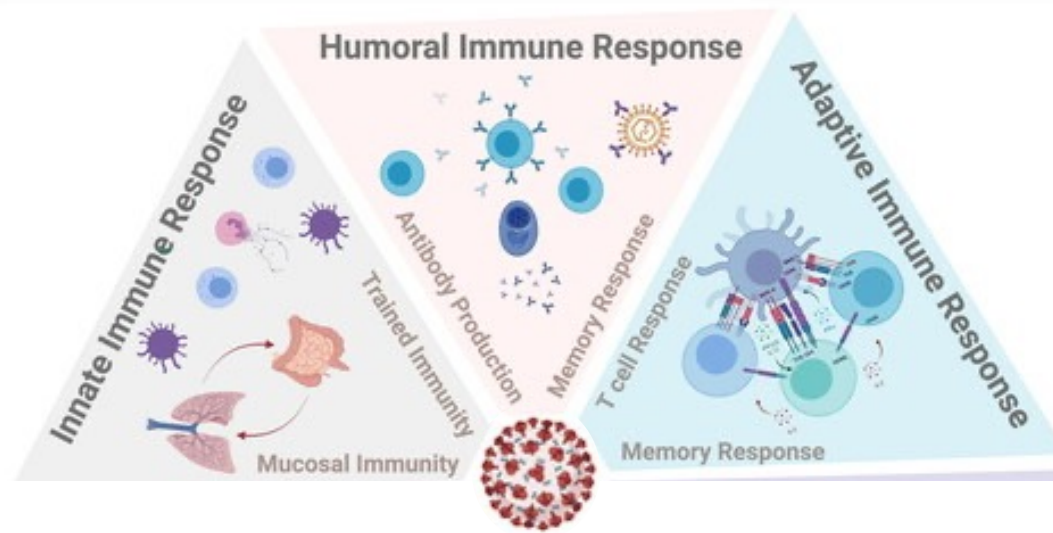


Antibody-dependent phagocytosis

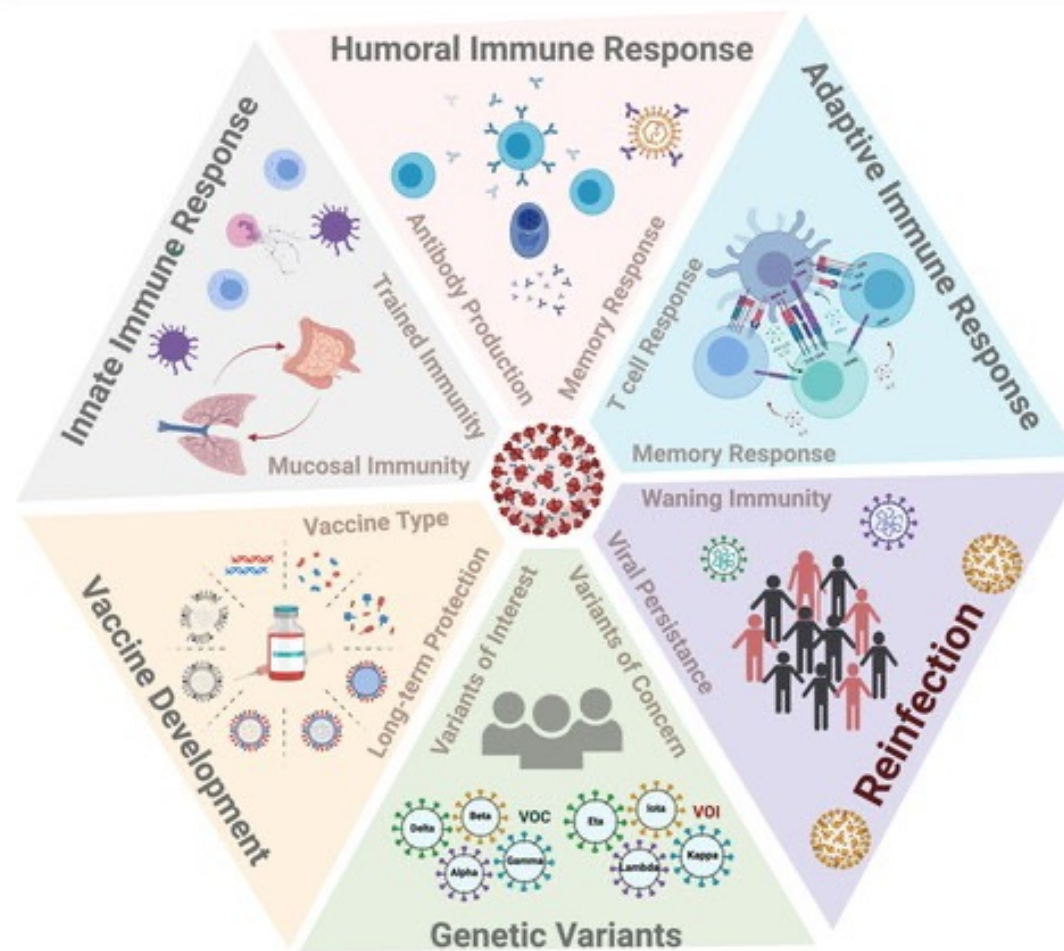


Pantaleo G et al., Nature, 2022

Protection against severe disease



Protection against severe disease



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Beginning of 2021: Implementation of COVID-19 Vaccination



The NEW ENGLAND JOURNAL of MEDICINE

New SARS-CoV-2 Variants — Clinical, Public Health, and Vaccine Implications

	Vaccine (Company)	Sample Size	Preexisting Variants	
			Efficacy in Preventing Clinical Covid-19	Efficacy in Preventing Severe Covid-19
			<i>no.</i>	<i>% (no. of events with vaccine vs. placebo)</i>
Viral vector	Ad26.COV2.S (Johnson & Johnson)	43,783	66 (NA)	85 (NA)
mRNA	BNT162b2 (Pfizer)	34,922	95 (8 vs. 162)	90 (1 vs. 9)
	mRNA-1273 (Moderna)	28,207	94 (11 vs. 185)	100 (0 vs. 30)
Viral vector	Sputnik V (Gamaleya)	19,866	92 (16 vs. 62)	100 (0 vs. 20)
Viral vector	AZD1222 (AstraZeneca)	17,177	67 (84 vs. 248)	100 (0 vs. 3)
Protein-based Inactivated virus	NVX-CoV2373 (Novavax)	15,000	89 (6 vs. 56)	100 (0 vs. 1)
	CoronaVac (Sinovac) ¶			
	Brazil	12,396	51 (NA)	100 (NA)
	Turkey	7,371	91 (3 vs. 26)	NA
Inactivated virus	BBIBP-CorV (Sinopharm)	NA	79 (NA)	NA

Efficacy of vaccines

Nov 2023

Research



Journal of the Royal Society of Medicine; 0(0) 1–10
DOI: 10.1177/01410768231216332

Temporal changes to adult case fatality risk of COVID-19 after vaccination in England between May 2020 and February 2022: a national surveillance study

Florence Halford , Kathryn Yates , Tom Clare , Jamie Lopez-Bernal, Meaghan Kall and Hester Allen

COVID-19 Vaccines and Epidemiology Division, UK Health Security Agency, London NW9 5EQ, UK

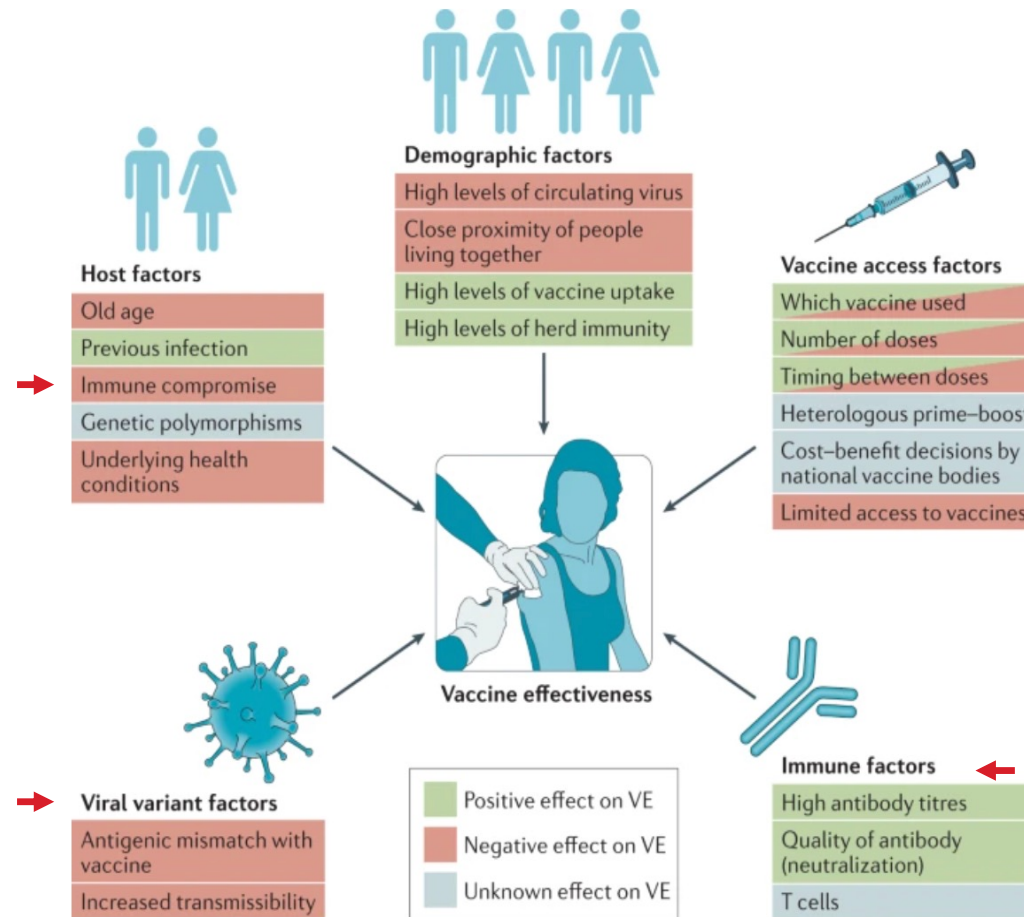
Corresponding author: Hester Allen. Email: hester.allen@ukhsa.gov.uk



Table 1. CFR of COVID-19 cases between 28 May 2020 and 28 February 2022, aged 18 years and over, by vaccination status or age band.

	Deaths (n)	Cases (n)	CFR (%)
Vaccination status			
Unknown	197	44,421	0.44
Unvaccinated	73,599	4,461,645	1.65
Age band			
Up to 6 months since last dose	11,400	5,032,493	0.23
Over 6 months since last dose	5346	1,077,589	0.50

Factors influencing vaccine effectiveness



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Emergence of SARS-CoV-2 variants in 2021



Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from linking epidemiological and genetic data

Erik Volz^{1*}, Swapnil Mishra^{1*}, Meera Chand⁴, Jeffrey C. Barrett⁵, Robert Johnson^{1*}, Lily Geidelberg¹, Wes R Hinsley¹, Daniel J Laydon¹, Gavin Dabrera⁴, Áine O'Toole³, Roberto Amato⁵, Manon Ragonnet-Cronin¹, Ian Harrison⁴, Ben Jackson³, Cristina V. Ariani⁶, Olivia Boyd¹, Nicholas J Loman^{4,6}, John T McCrone⁵, Sónia Gonçalves⁵, David Jorgensen¹, Richard Myers⁴, Verity Hill³, David K. Jackson⁵, Katy Gaythorpe¹, Natalie Groves⁴, John Sillitoe⁶, Dominic P. Kwiatkowski², The COVID-19 Genomics UK (COG-UK) consortium⁷, Seth Flaxman², Oliver Ratmann², Samir Bhatt¹, Susan Hopkins⁴, Axel Gandy², Andrew Rambaut⁸, Neil M Ferguson^{1*}

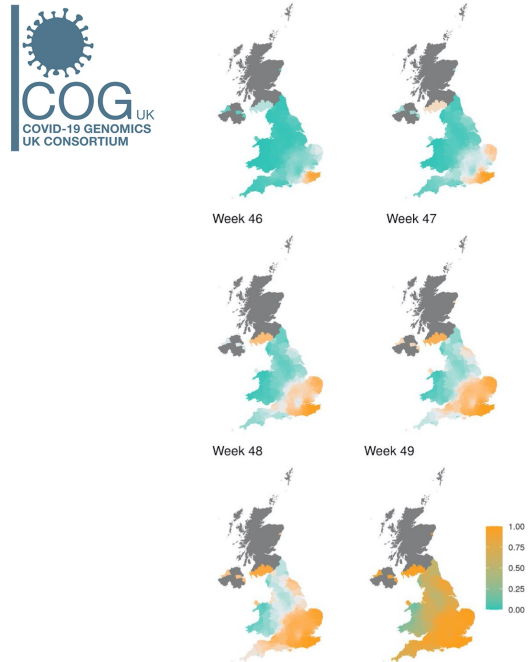
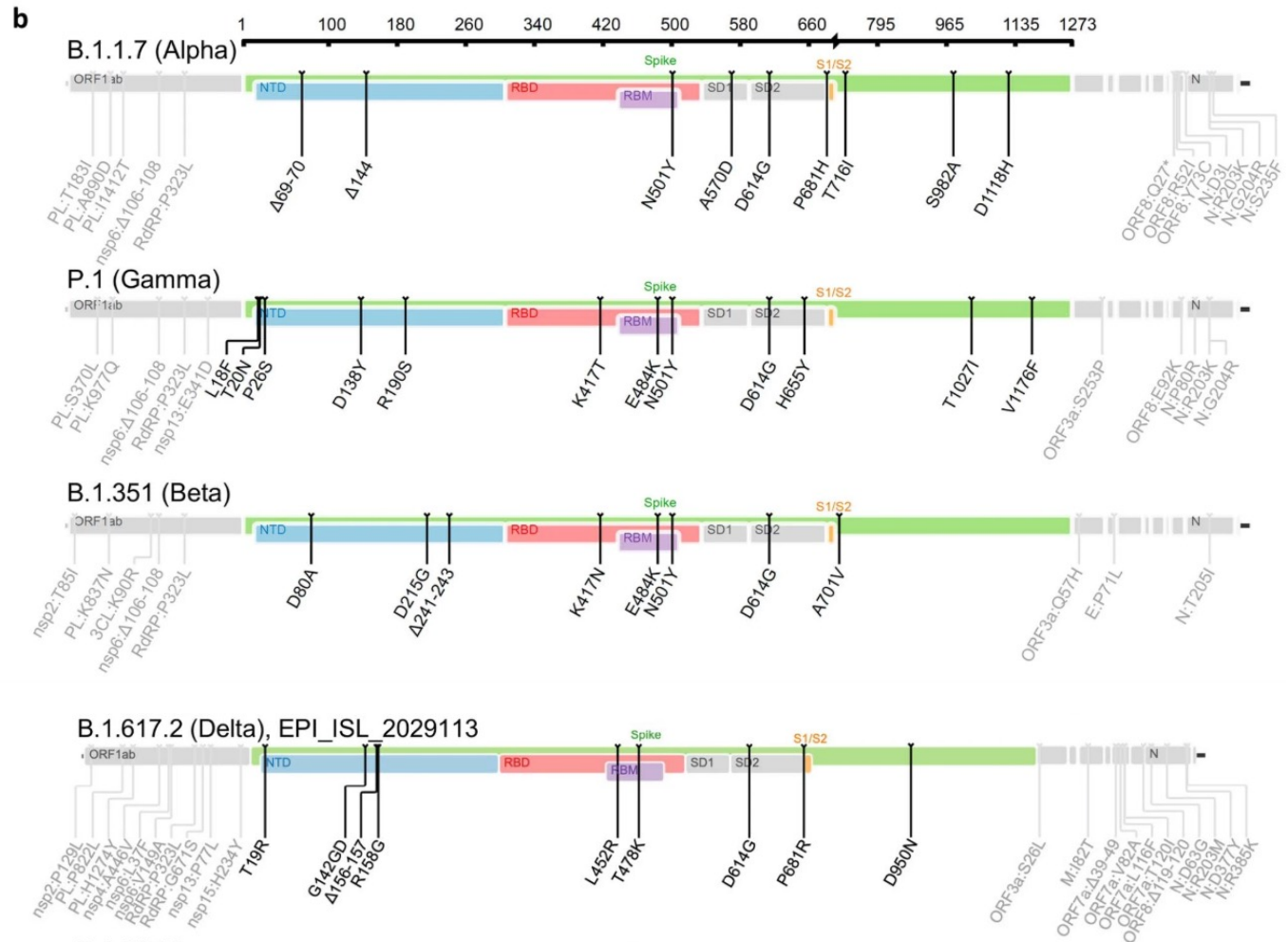


Figure S1 | Estimate of true positive rates for classification of B.1.1.7 infection given SGTF result (S-) as a function of time and UK region. The colour gradient shows the probability of sampling a B.1.1.7 sequence conditional on sampling any sequence with $\Delta 69-70$.



Emergence of Omicron variants

Nature Review

COMMENT

 Check for updates

Towards SARS-CoV-2 serotypes?

Etienne Simon-Loriere¹ and Olivier Schwartz^{2,3}

The magnitude of immune evasion of Omicron raises the question whether it should be considered as a distinct SARS-CoV-2 serotype. Here, we discuss lines of evidence in support or against the concept of SARS-CoV-2 serotypes, and the implications of this classification.

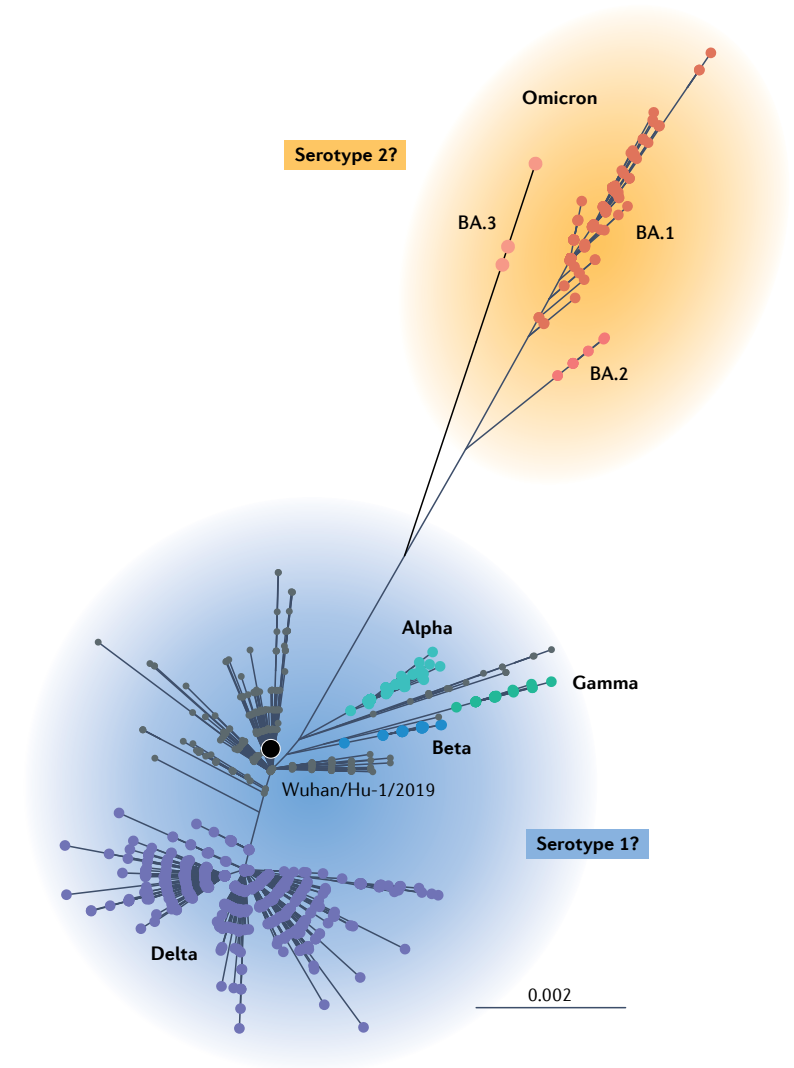
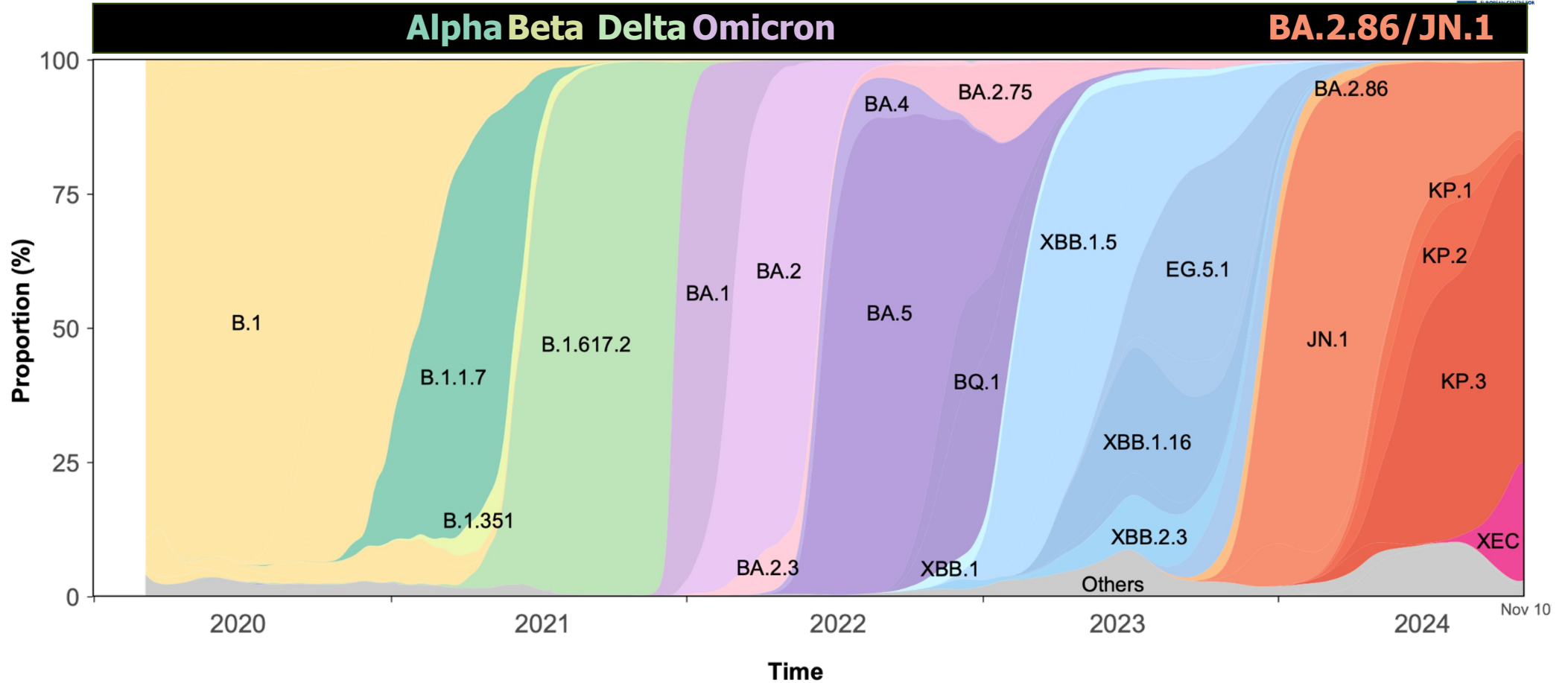
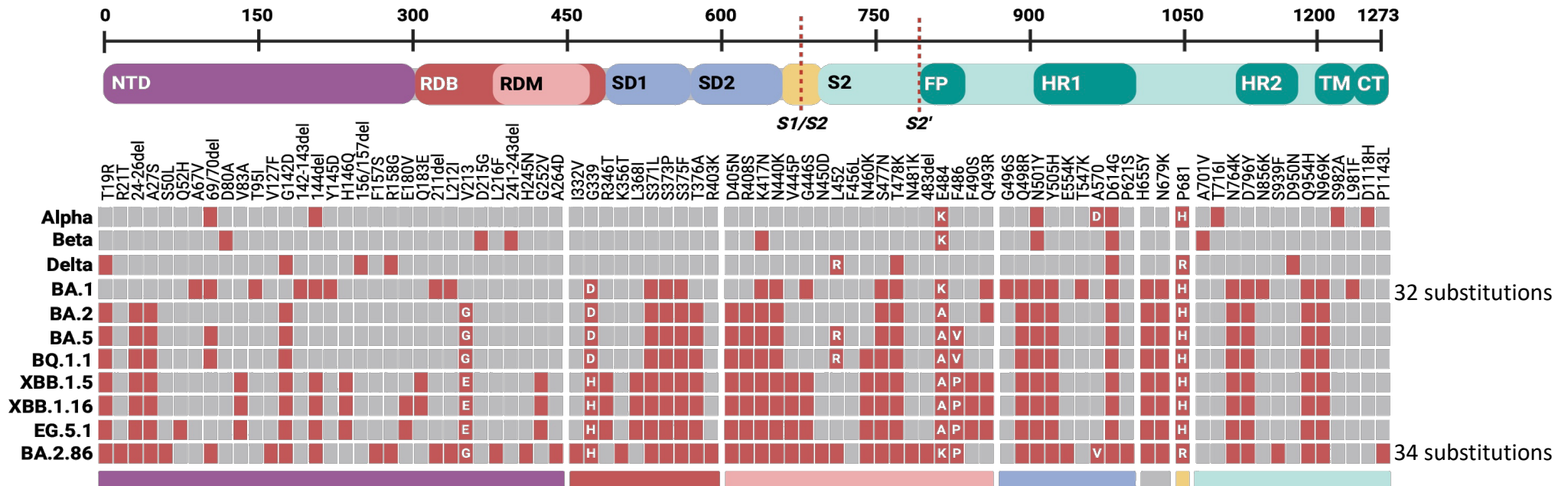


Fig. 1 | SARS-CoV-2 global evolution and Omicron divergence. Maximum likelihood phylogenies inferred from spike nucleotide sequences, scale corresponding to number of substitutions per site.

Global transitions in major variants



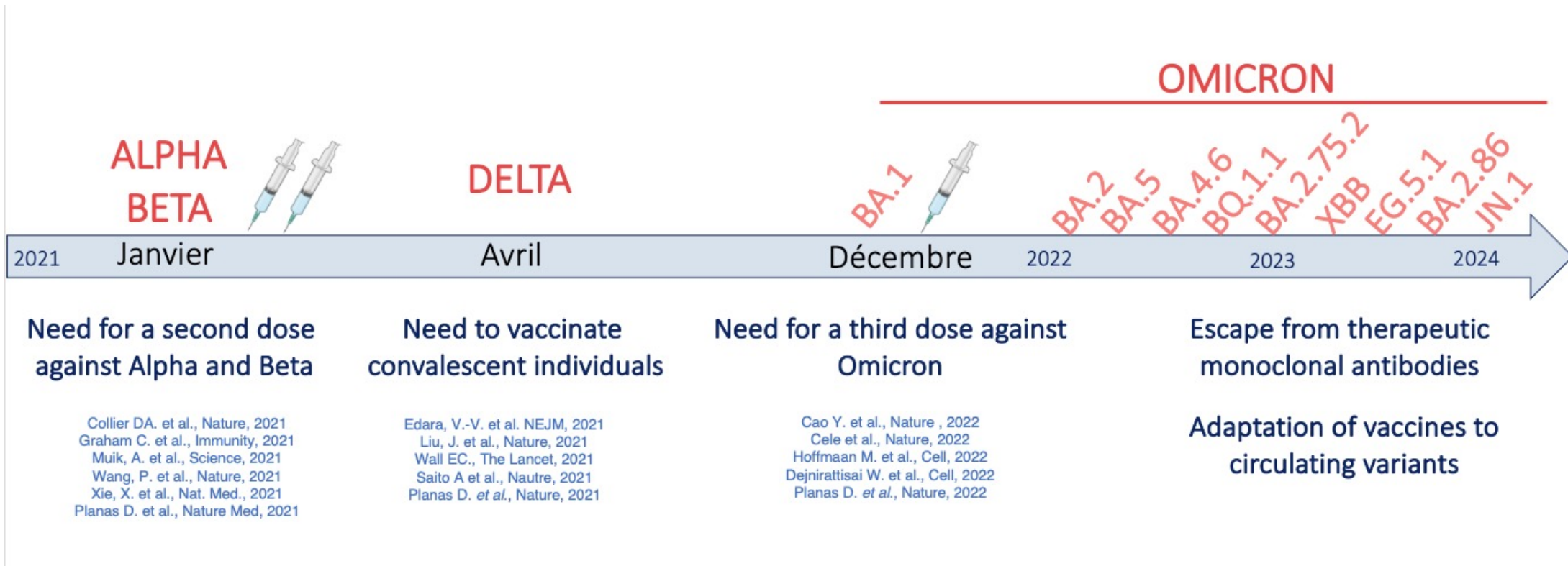
Evolutionary jump



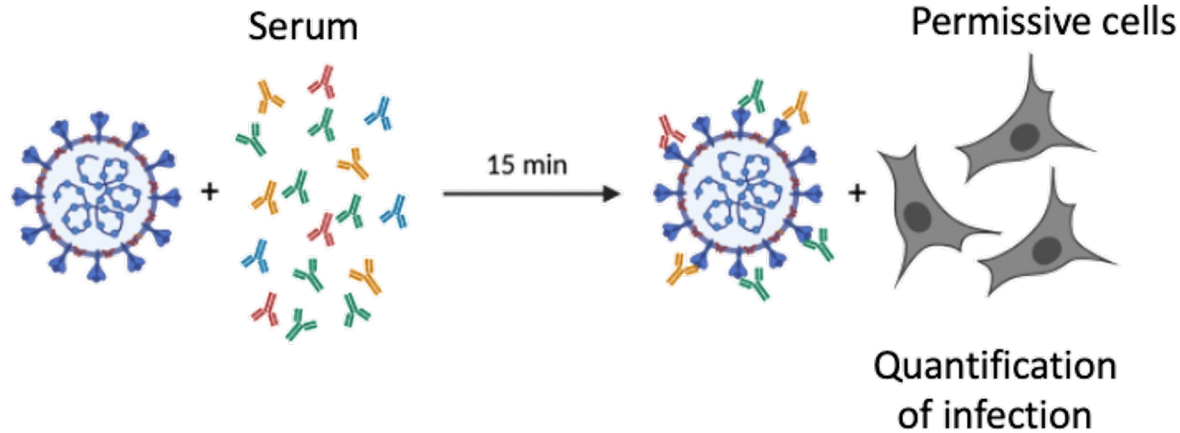
Mutations can effect different properties of the Spike:

- Binding affinity to the receptor ACE2.
- Spike fusogenicity – S1/S2 cleavage, conformational changes, receptor affinity.
- Evasion from the immune system e.g. neutralizing antibodies from previous infections or vaccina

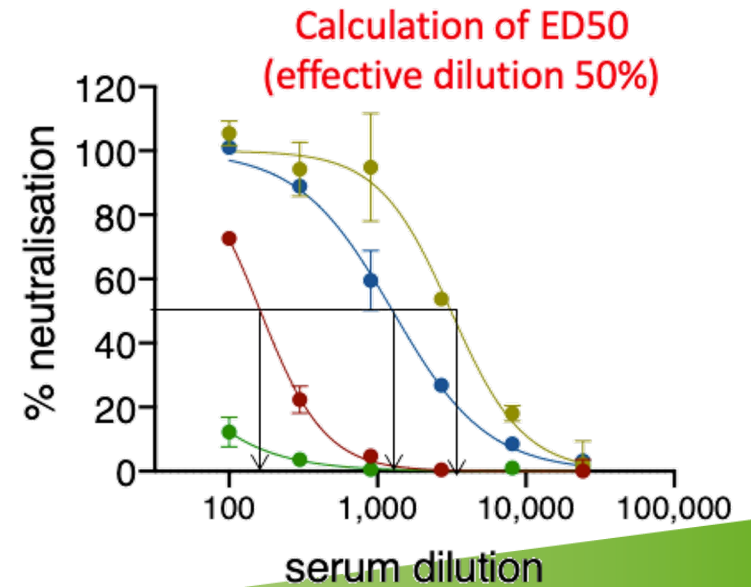
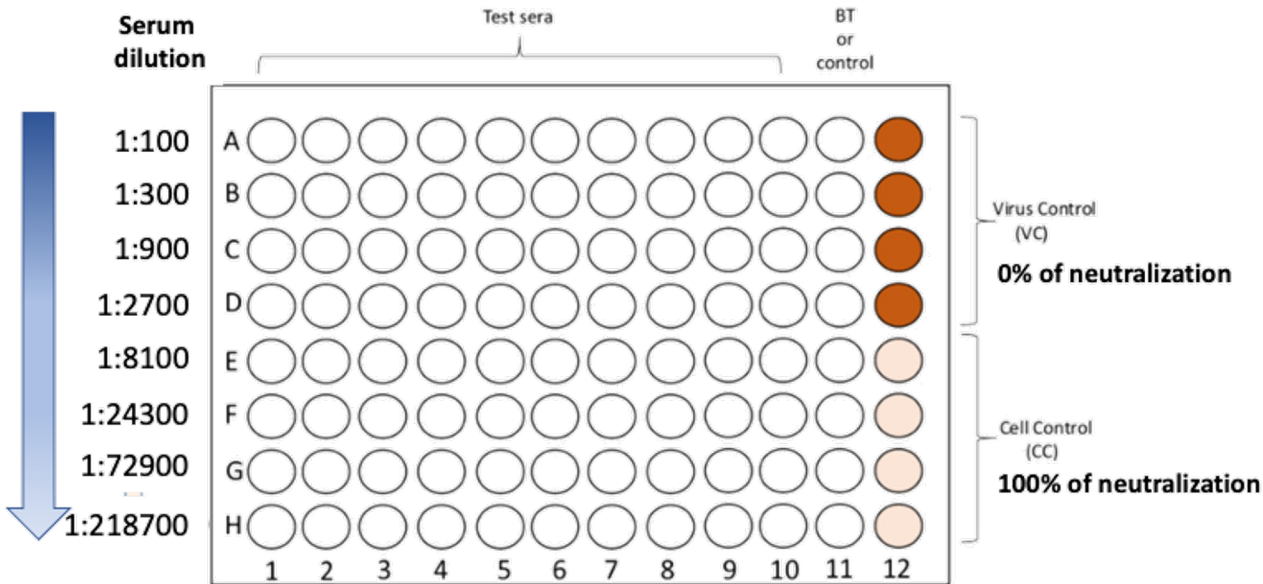
"Real-time" evaluation of SARS-CoV-2 antibody evasion



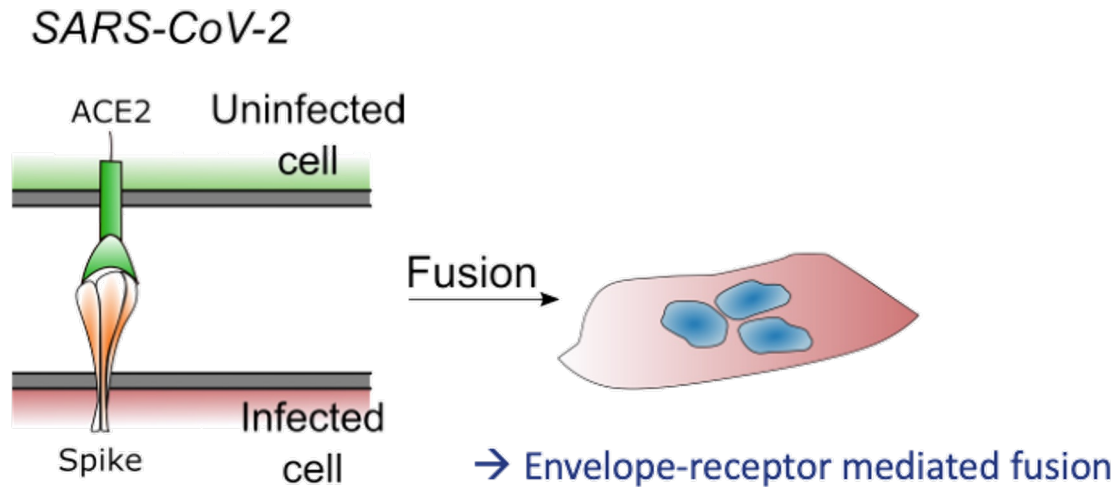
Principle of neutralization assay



- Cytopathic effect
- Detection of viral protein
- Detection of viral RNA
- Reporter system (pseudotype)



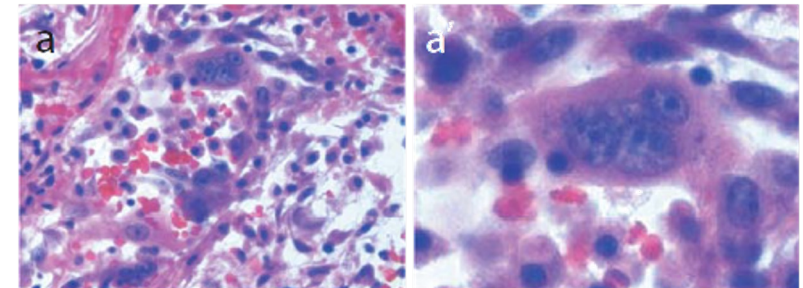
Syncytia formation in COVID-19 patients



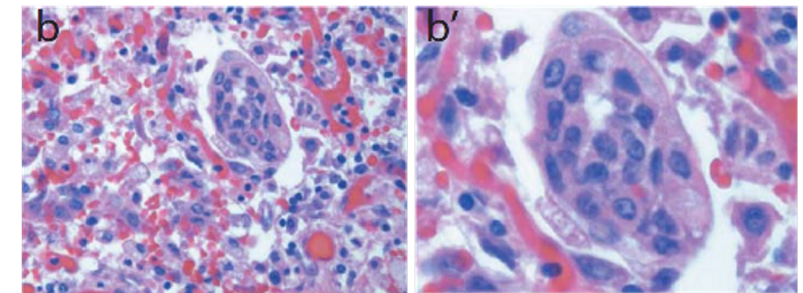
Persistence of viral RNA, widespread thrombosis and abnormal cellular syncytia are hallmarks of COVID-19 lung pathology

Rossana Bussani, Edoardo Schneider, Lorena Zentilin, Chiara Collesi, Hashim Ali, Luca Braga, Ilaria Secco, Maria Concetta Volpe, Andrea Colliva, Fabrizio Zanconati, Giorgio Berlot, Furio Silvestri, Serena Zacchigna and Mauro Giacca

- **Infected pneumocyte syncytia**
 - *Large number:* 20/41 (49%) patients
 - *Occasional:* 16/41 (39%) patients



Patient: 207.20
Staining: H&E

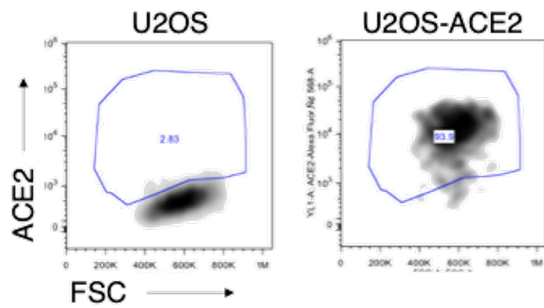


Patient: 210.20
Staining: H&E

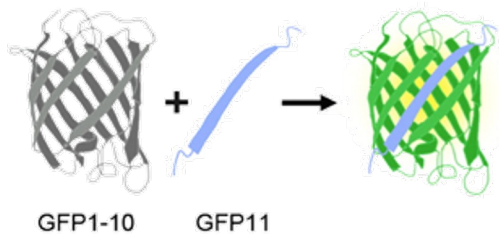
Figure 3

Bussani et al. *EBioMedicine*, 2020
Braga et al. *Nature*, 2021

Cell reporter system of SARS-CoV-2 infection



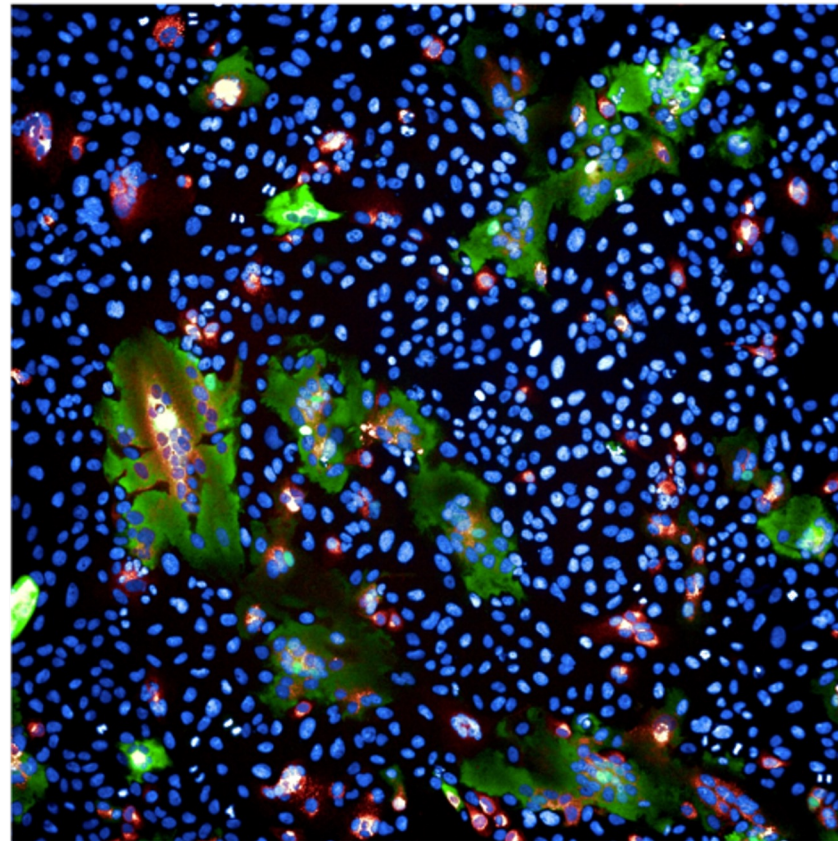
GFP split system



S-Fuse cells:

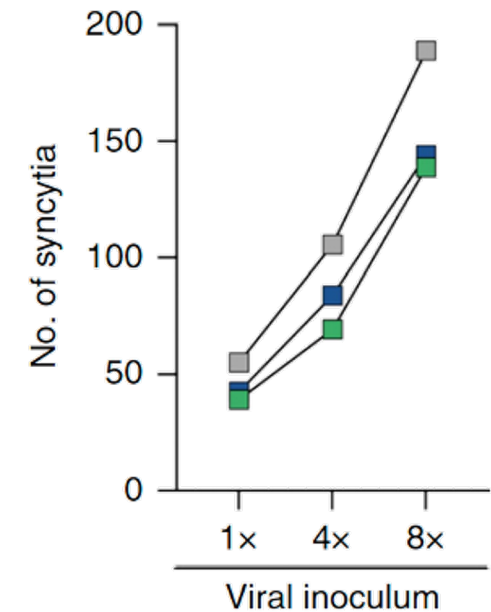
U2OS – ACE2 – GFP1-10
+
U2OS – ACE2 – GFP11

MOI 0.2 24h post-infection



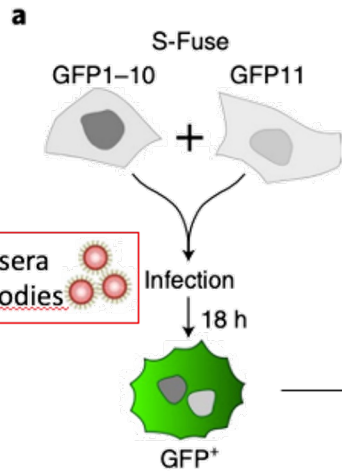
GFPsplit SARS-CoV-S DAPI

Buchrieser J et al., EMBO, 2021

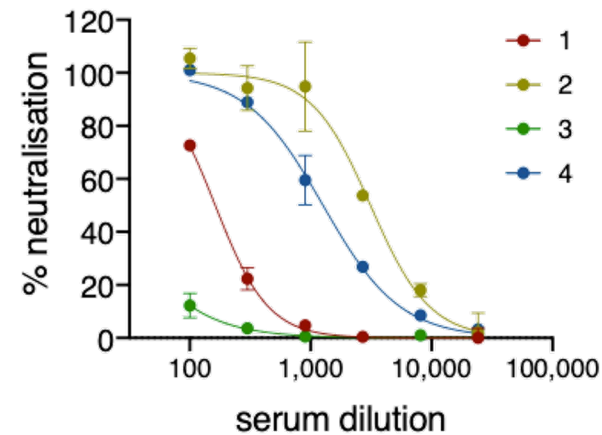
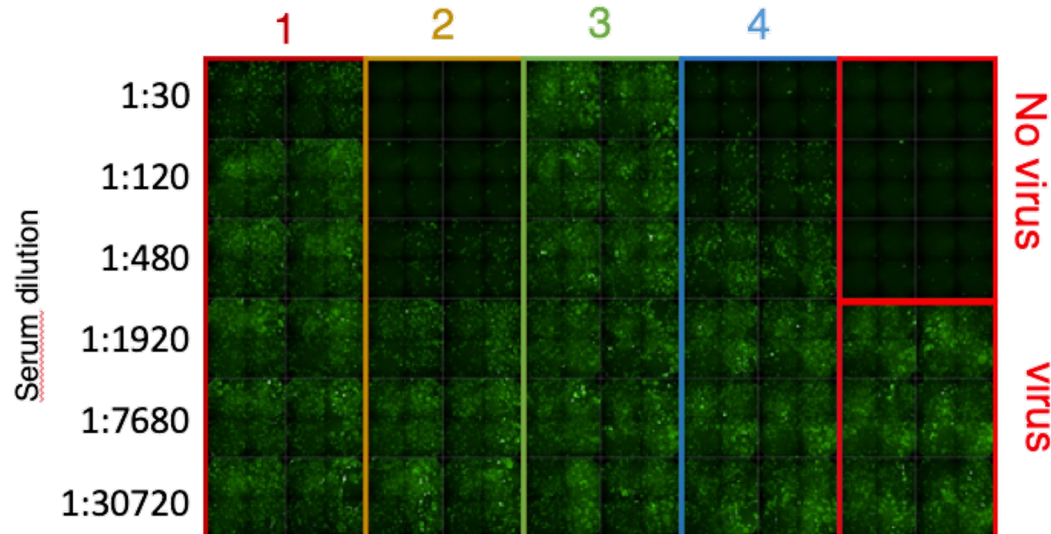
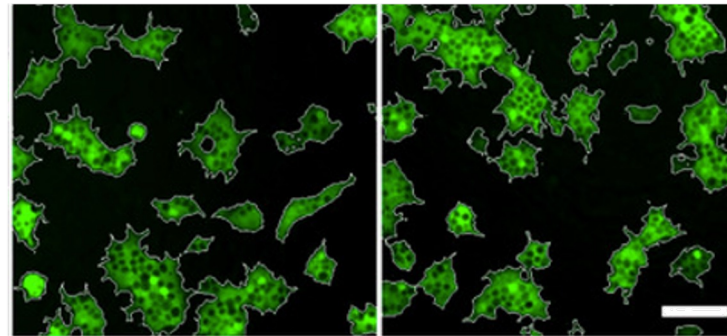


Planas D et al., Nature Med, 2021

S-Fuse neutralizing assay



Scoring of syncytia



Advantages:
 Live-virus
 GFP is read 18hours post-infection
 No staining is necessary

Disadvantages:
 BSL3 laboratory

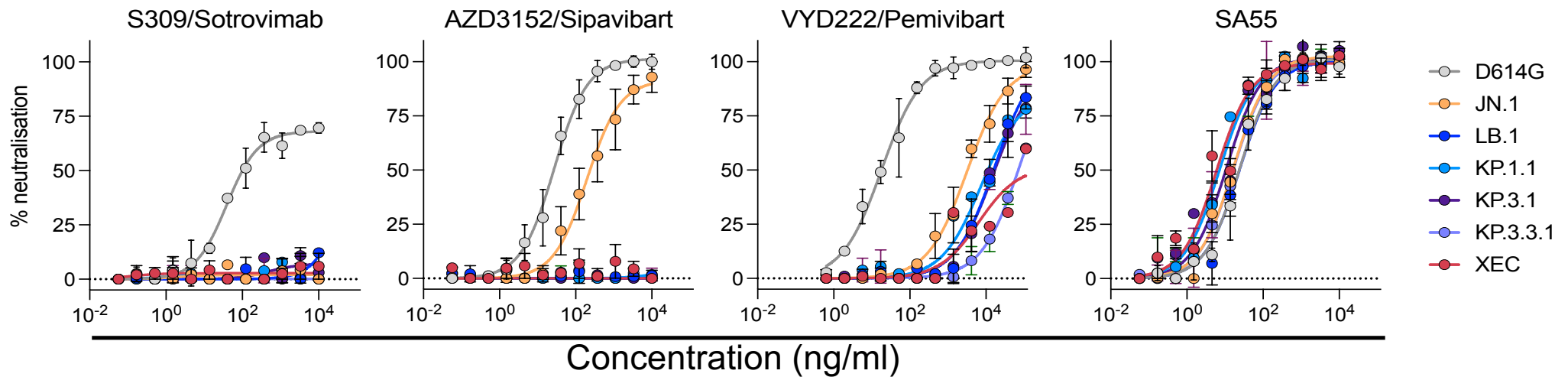
Escape of JN.1 subvariants including XEC to recently approved mAb



*Approved in July 2024 (EMA)
Not used in clinic*

*Approved in March 2024 (FDA)
Not used in clinic*

*Approved in China
Sinovac*



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Article | [Open access](#) | Published: 13 March 2024

Distinct evolution of SARS-CoV-2 Omicron XBB and BA.2.86/JN.1 lineages combining increased fitness and antibody evasion

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Nature Communications **15**, Article number: 2254 (2024) | [Cite this article](#)

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Aim:

Characterization of current SARS-CoV-2 variants:
a model for the diversification of an emerging virus.

Epidemiology and genetic evolution

Viral replication and fitness

Model of cell line to characterized SARS-CoV-2 variants:

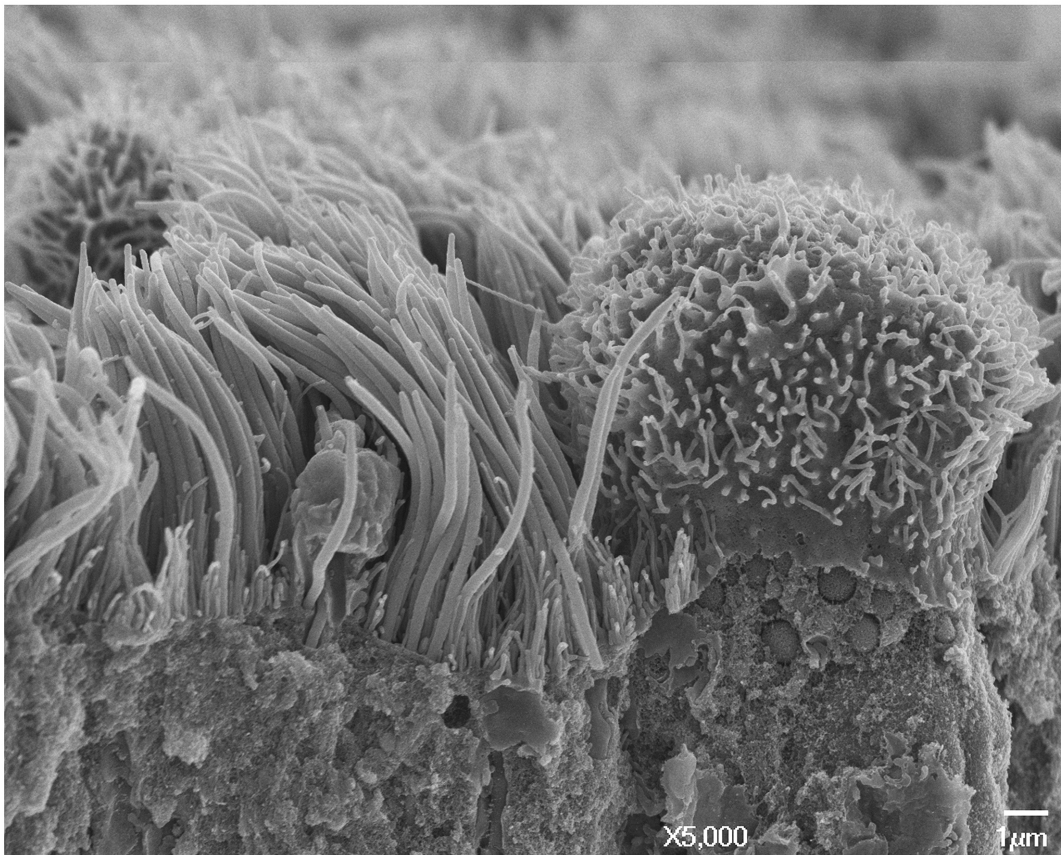
ACE2 affinity

Spike fusogenicity

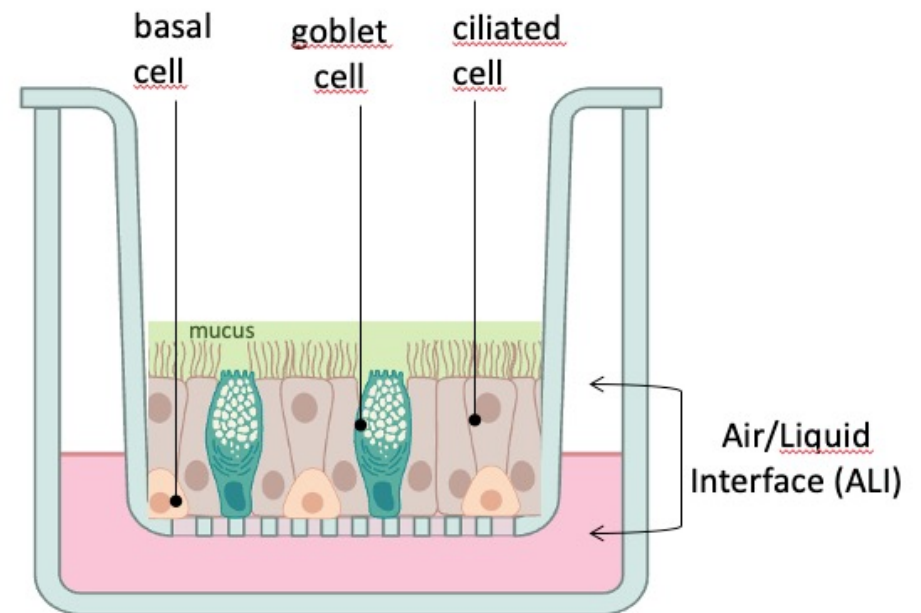
Sensitivity to antiviral drugs

Neutralizing Antibody escape

Multiplication of SARS-CoV-2 in airway epithelium model

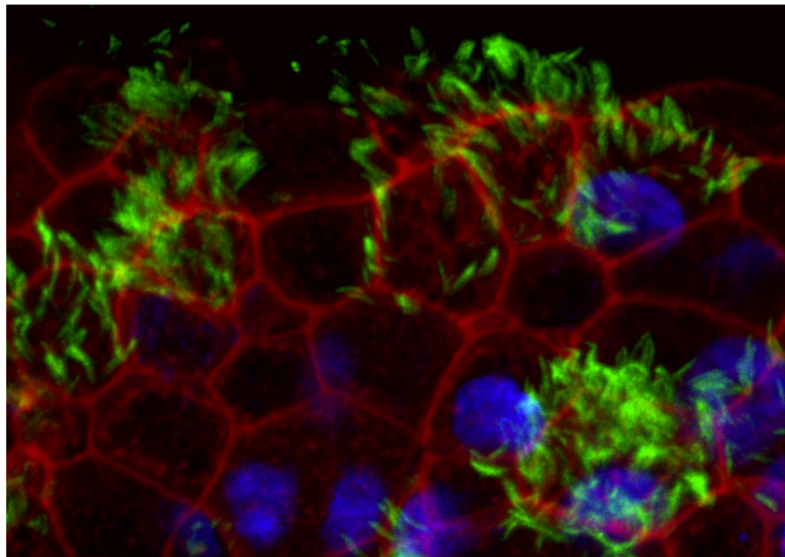


Vincent Michel @Institut Pasteur



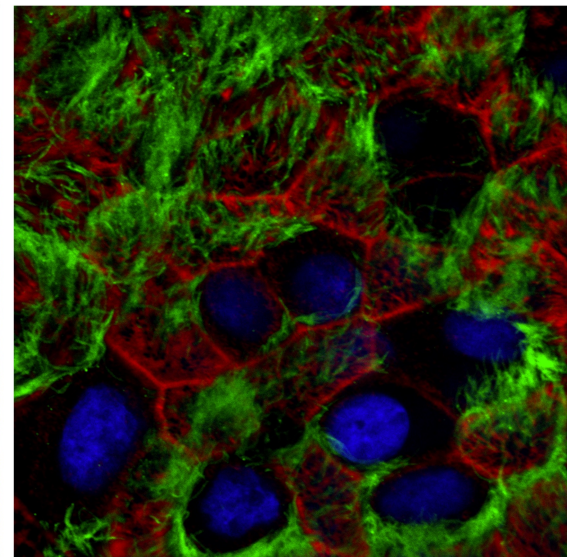
ACE2 and TMPRSS2 expression in human nasal epithelial cells (hNECs)

ACE2



ACE2
Actine
DAPI

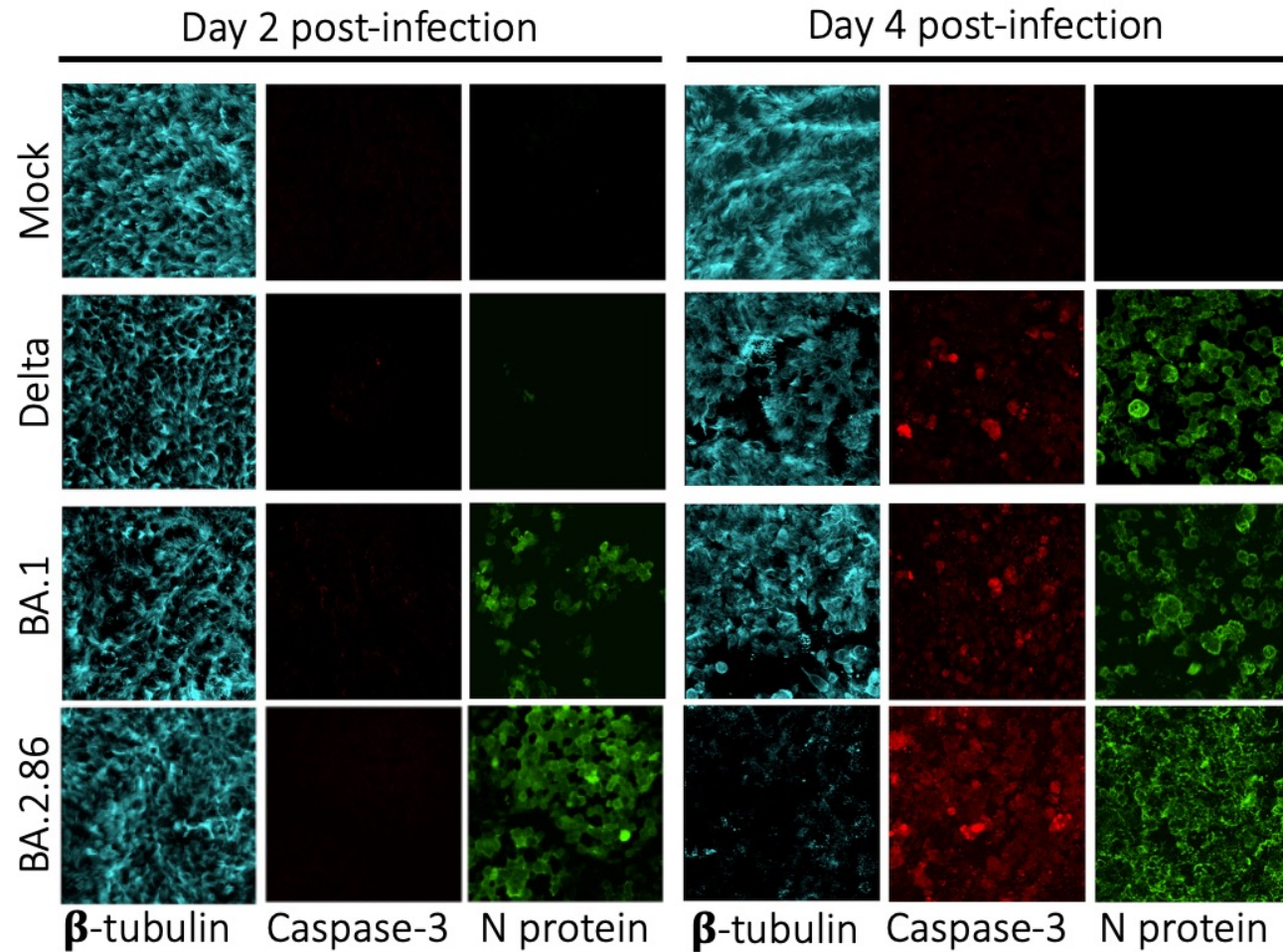
TMPRSS2



TMPRSS2
Actine
DAPI

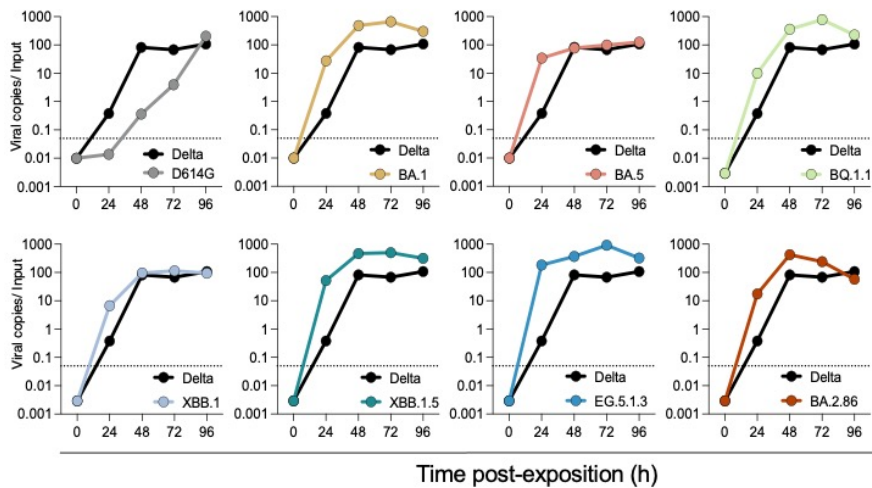
BA.2.86.1 seems to replicate faster than BA.1 and Delta variants

Viral input:
 $2 \cdot 10^3$ infectious particles/mL



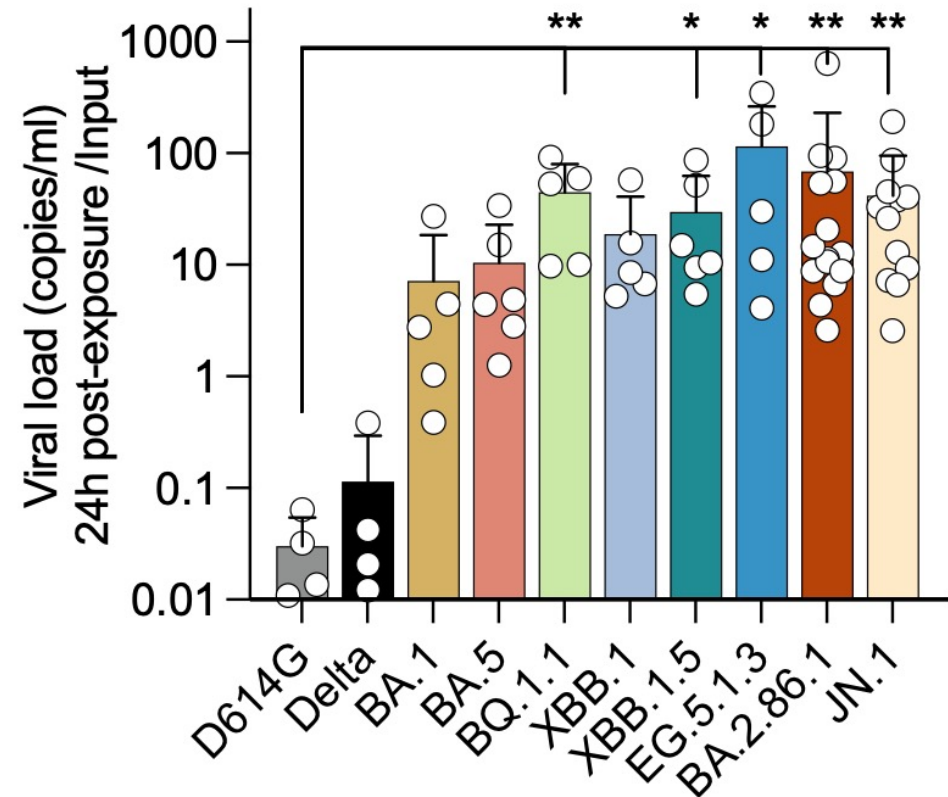
Post-Omicron variants replicate faster and higher compared to D614G and Delta.

Viral input: $2 \cdot 10^3$ infectious particules/mL



One representative experiment out of 3-5 experiments

Viral RNA release



Objectives



- SARS-CoV-2 pathogenesis
- Overview of mRNA-based vaccines and SARS-COV-2 variant emergence
- Distinct evolution of Omicron XBB and BA.2.86/JN.1 lineages
- **Future challenges and novel vaccine strategies**

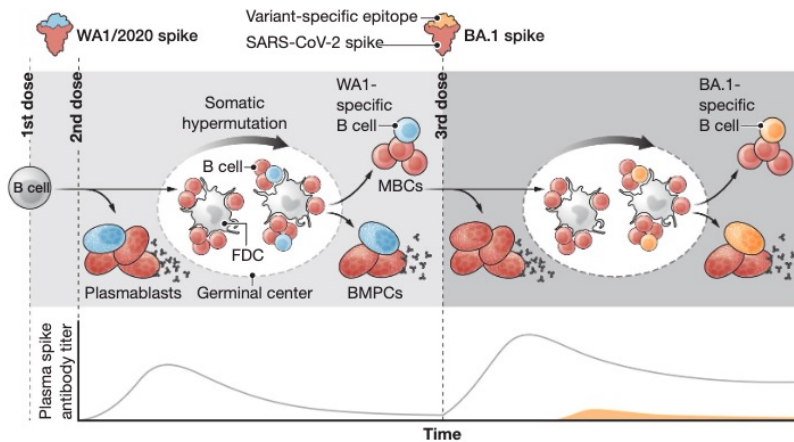
Variant-adapted vaccines

Science

Variant-adapted COVID-19 booster vaccines

Current vaccines should be tailored to combat future SARS-CoV-2 variants

By Florian Krammer^{1,2,3} and Ali H. Ellebedy^{4,5}

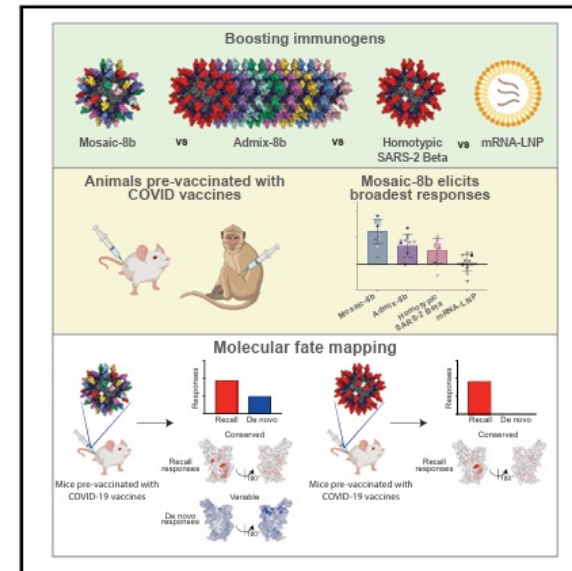


GRAPHIC: K. HOLOSKI/SCIENCE

Cell

Mosaic sarbecovirus nanoparticles elicit cross-reactive responses in pre-vaccinated animals

Graphical abstract



Authors

Alexander A. Cohen, Jennifer R. Keeffe, Ariën Schiepers, ..., Deborah H. Fuller, Gabriel D. Victora, Pamela J. Bjorkman

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In brief

Original antigenic sin, which describes the immunity generated against antigens as being shaped by the first exposure to a related antigen, is at play when investigating the potent cross-reactive antibody response as well as the protection of mosaic nanoparticles against previously vaccinated monkeys and mice. The mosaic particles present 8 SARS-like sarbecovirus receptor-binding domains and show promise in protecting COVID-19-vaccinated or -infected humans against future variants as well as animal coronaviruses with spillover potential.

Highlights

- Pan-sarbecovirus vaccine evaluated in pre-vaccinated monkeys and mice

Mucosal vaccines



The NEW ENGLAND JOURNAL of MEDICINE

CORRESPONDENCE

Mucosal IgA against SARS-CoV-2 Omicron Infection

TO THE EDITOR: Havervall et al. (Oct. 6 issue)¹ suggest that wild-type SARS-CoV-2 spike-specific mucosal IgA may provide protection against omicron (B.1.1.529) breakthrough infection. We detected salivary anti-receptor-binding domain (RBD) IgA antibodies against G614 RBD in 48 of 67 vaccinated healthy persons (72%) at 5 to 59 days after receiving a dose of messenger RNA (mRNA) vaccine — in 12 of 18 (67%) after dose 1, in 22 of 34 (65%) after dose 2, and in 14 of 15 (93%) after dose 3. We also observed these antibodies in 12 of 12 persons (100%) 8 to 43 days after they had had a breakthrough infection. Pre-vaccinated, noninfected persons served as con-

anti-RBD IgA and $P=0.003$ for salivary anti-RBD sIg) (Fig. 1C).

Thus, mRNA vaccines induced a low-level but durable (>6 months) sIgA response in a majority of persons in whom a higher level of sIgA was associated with protection. In agreement with the work by Havervall et al. and other studies,¹⁻⁴ our results suggest that the development of a mucosal booster vaccine dose should be further exploited to induce a stronger sIgA response.

Fanglei Zuo, Ph.D.

Harold Marcotte, Ph.D.

Lennart Hammarström, M.D., Ph.D.

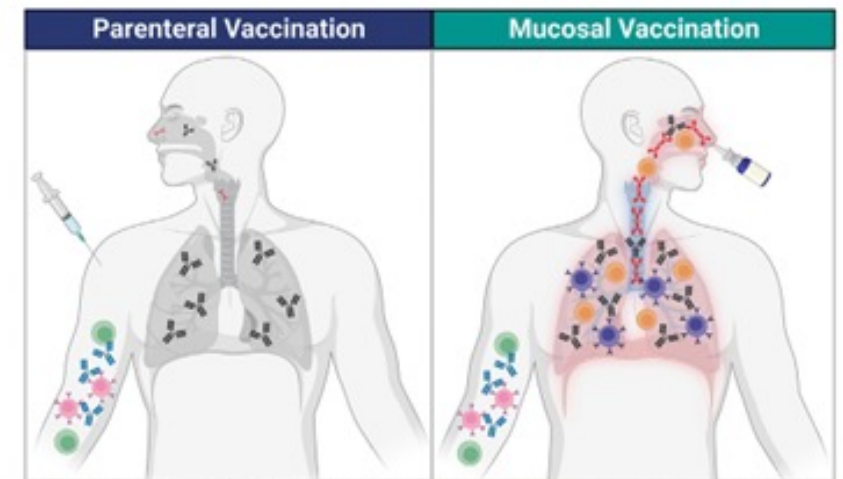
Qiang Pan-Hammarström, M.D., Ph.D.

eBioMedicine

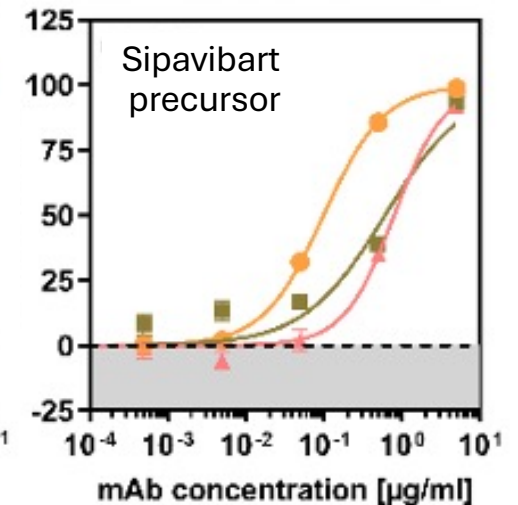
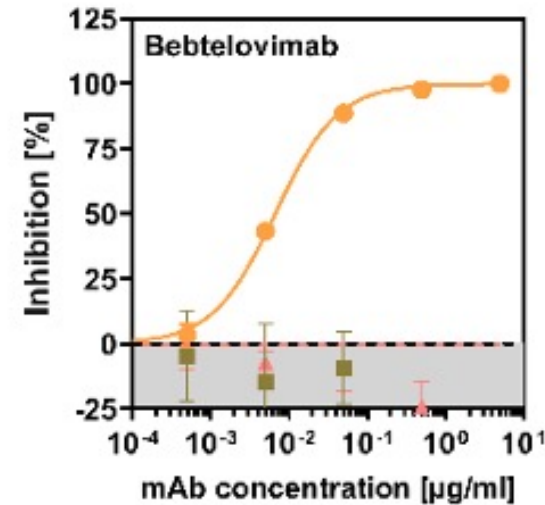
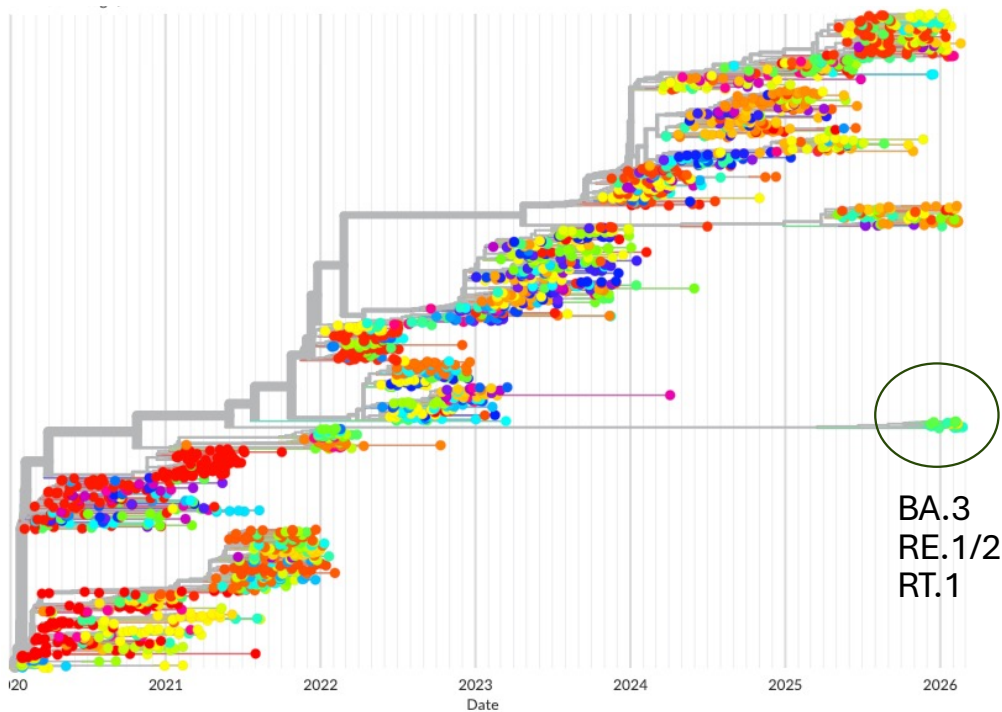
Part of THE LANCET Discovery Science

Mucosal vaccines for SARS-CoV-2: triumph of hope over experience

Devaki Pilapitiya, Adam K. Wheatley, and Hyon-Xhi Tan*



Emerging SARS-CoV-2 variant BA.3.2



Lu Zhang *et al.*, *Lancet Microbes*, 2026

LETTER ▶ [New Microbes New Infect.](https://doi.org/10.1016/j.nmni.2026.101727) 2026 Feb 18;70:101727. doi: [10.1016/j.nmni.2026.101727](https://doi.org/10.1016/j.nmni.2026.101727)

SARS-CoV-2 BA.3.2: epidemiological trends and implications for prophylactic antibodies

[Slim Fourati](#)^a, [Paul Loubet](#)^{b,*}

In summary



Emerging variants are often:

- more fit than previous variants
- less sensitive to sera from vaccinated individuals
- escape binding and neutralization by most therapeutic mAbs
- remain sensitive to Nirmatrelvir, Molnupiravir & Remdesivir

Remaining challenges

Fitness and tropism

Longer surveillance periods, impact and frequency of booster dose

Correlation between antibody levels, neutralizing titers and vaccine effectiveness

Local and systemic humoral responses in vaccine efficacy

Cellular immunity

Acknowledgements



Virus and Immunity Unit

Olivier Schwartz

Isabelle Staropoli

Jeanne Postal

Françoise Porrot

Florence Guivel-Benhassine

Julian Buchrieser

Nicoletta Casartelli

Mariam Znaidia

Eva Thuillier

Amélie Wileveau

Timothée Buel

Martin Groznica

Andrea Cottignies-Calamarte

Lisa Chakrabarti

Samuel Lebourgeois

Hyppolite Debarnot

Marne Azarias da Silva

Marie-Anne Rameix Welti
(Centre national de référence VIR)

Etienne Simon-Lorière

Matthieu Prot

Vincent Michel

Hugo Mouquet

Cyril Planchais

Felix Rey

Nathalie Aulner

UtechS PBI

University of Amsterdam

Marion Cornelissen

Martin Deijs

Lia Van Der Hoek

CHU Orléans

Laurent Hocqueloux

Thierry Prazuck

Hospices Civils de Lyon

Sophie Trouille-Assant



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ANR



mRNA vaccines for infectious diseases

