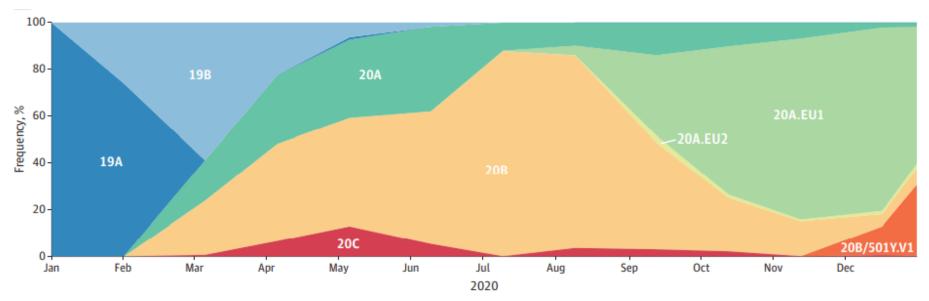


It is Time to Make Pan-Sarbecovirus Vaccines

By Stanley A. Plotkin

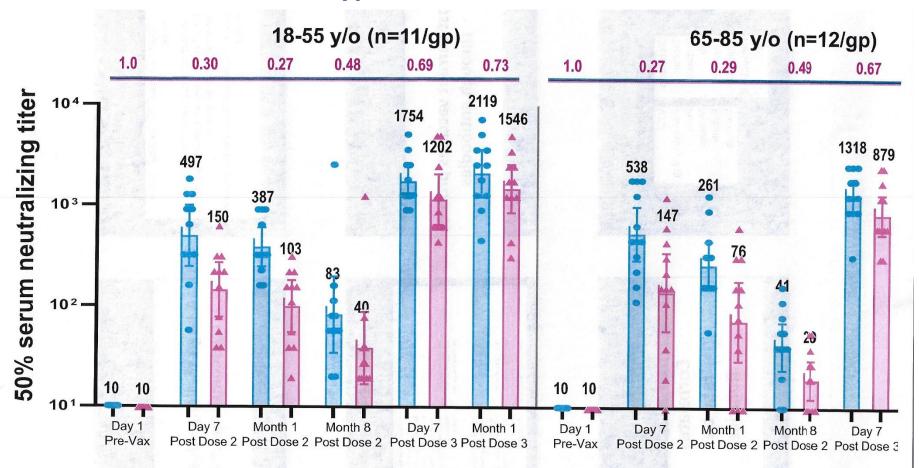
WHO Dec 2021 V2 Dec. 3, 2021

Frequencies of circulating lineages of SARS-CoV-2 over time



Lauring, A., Hodcroft, E., JAMA 2021;325;6

Covid-19 Vaccine: Neutralization Titers Much Higher Post 3rd Than Post 2nd for Wild Type and Beta Variants^{1,2}





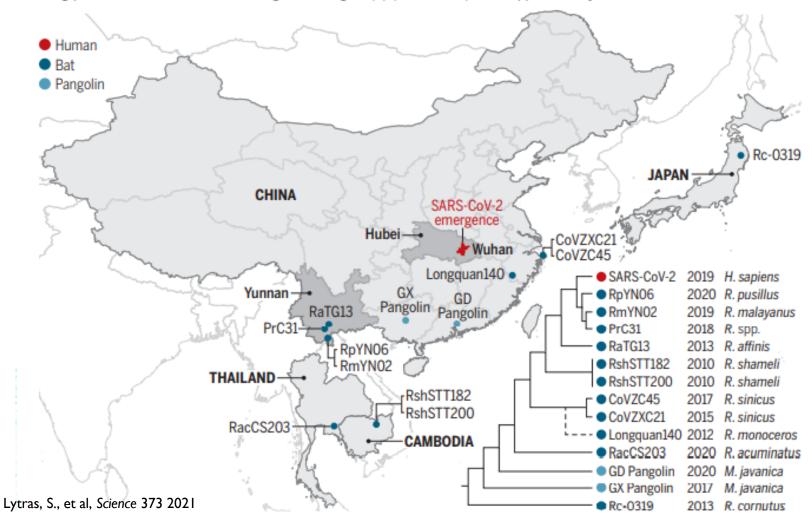
1. Initial data, Phase 1 sentinel subjects received dose 1 & 2 of 30mcg BNT162b2 21 days apart, subjects then came back and received BNT162b2 30 mcg as a 3rd 2. Samples were tested against each variant separately; PRNT: Plaque Reduction Neutralizing Test; GMR: Geometric Mean Ratio; WT: Wild Type; LOD: Limit of

Second Quarter 2021 Earnings

Data submitted for publication

Sarbecoviruses closely related to SARS-CoV-2

Coronaviruses that are evolutionarily closest to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have been sampled in China, Cambodia, Japan, and Thailand (5). The phylogenetic tree, inferred from a genomic region minimized for recombination (5), shows sarbecoviruses closely related to SARS-CoV-2. Host species for each virus, horseshoe bat (*Rhinolophus*), human (*Homo sapiens*), and pangolin (*Manis javanica*) and the year of sample collection are shown in the key. Longquan140 is inferred from another genomic region (5) (dashed line). See supplementary table S1 for more details.



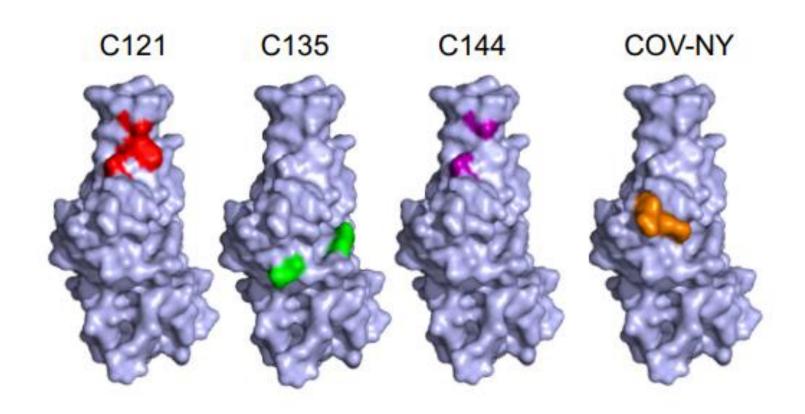
Impact of SARS-CoV-2 Variants on Vaccine Efficacy and Effectiveness

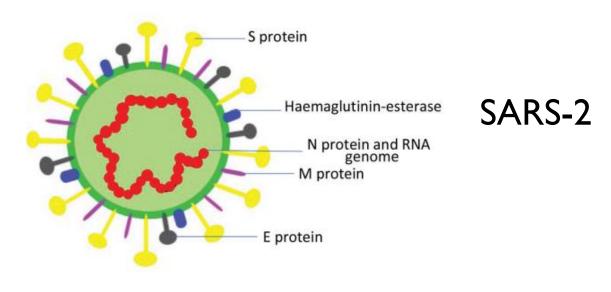
	Vaccine-mediat	ediated Protection	
SARS-CoV-2 Variant (also known as)	AZD I 222 (AstraZeneca University of Oxford)	BnT I 62b2 (Pfizer – BionTech)	
Wuhan reference strain	55–81%	95%	
Alpha, B. I. I. 7 (British/ Kent; VOC 202012/01; 20B/501Y.VI	75%	90%	
Beta, B.1.351 (South African; 20H/501Y.V2)	10%	75%	
Gamma, P.1 (B.1.1.28.1)	Unknown	No evidence of reduced protection	
Delta, B.1.617.2	92% effective against hospitalization; one-dose effectiveness estimated at 60–71%	Lower mean plaque reduction neutralization titres but sera can neutralize titres of at least 40; one dose of vaccine is 88% effective	

The degree to which SARS-CoV-2 will adapt to evade neutralizing antibodies is unclear. Using a recombinant chimeric VSV/SARS-CoV-2 reporter virus, we show that functional SARS-CoV-2 S protein variants with mutations in the receptor-binding domain (RBD) and N-terminal domain that confer resistance to monoclonal antibodies or convalescent plasma can be readily selected.

Weisblum, Schmidt, et al, eLife 2020;9

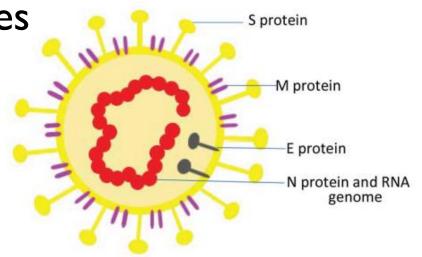
Neutralization of rVSV/SARS-CoV-2/GFP RBD mutants by monoclonal antibodies





Structures of

Coronaviruses

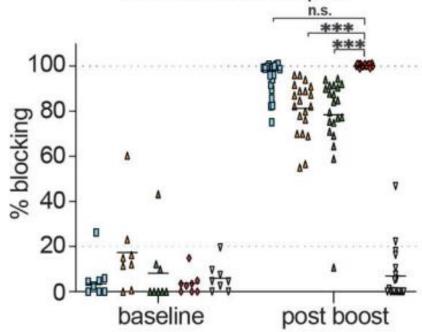


SARS-I

Genetic design of chimeric Sarbecovirus spike vaccines

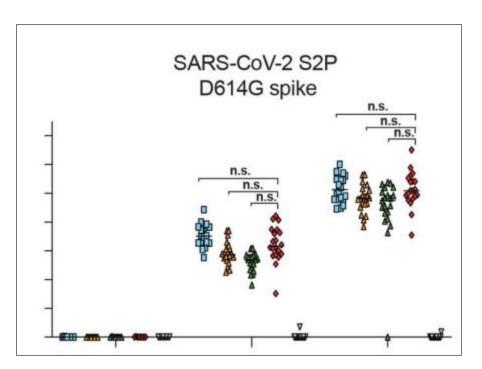
Chimera	RBD	NTD	S2
1	SARS-CoV	HKU3-1	SARS-CoV-2
2	SARS-CoV-2	SARS-CoV	SARS-CoV
3	SARS-CoV	SARS-CoV-2	SARS-CoV-2
4	RsSHC014	SARS-CoV-2	SARS-CoV-2

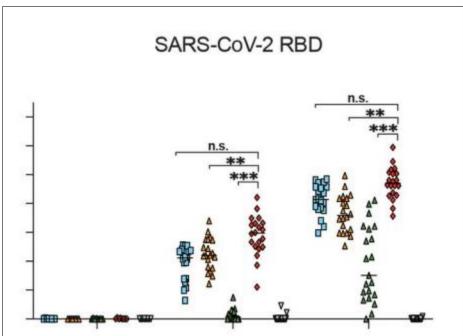
hACE2 blocking of SARS-CoV-2 spike

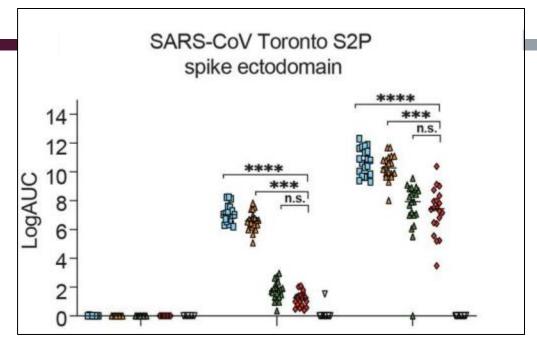


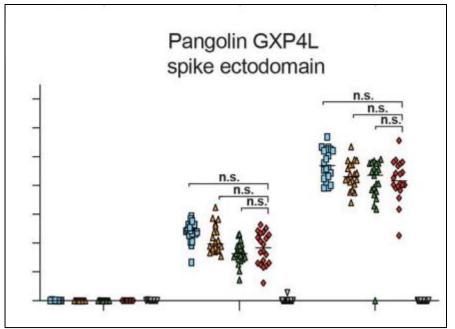
mRNA vaccine group

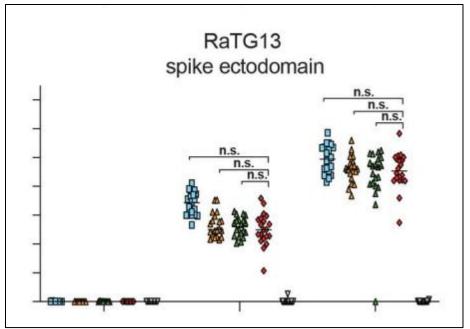
- Group 1: chimeras 1-4 prime/boost
- → Group 2: chimeras 1-2 prime and 3-4 boost
- Group 3: chimera 4 prime/boost
- Group 4: SARS-CoV-2 spike furin KO prime/boost
- Group 5: Norovirus capsid prime/boost

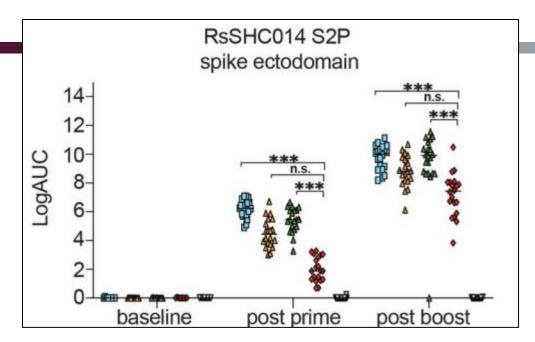


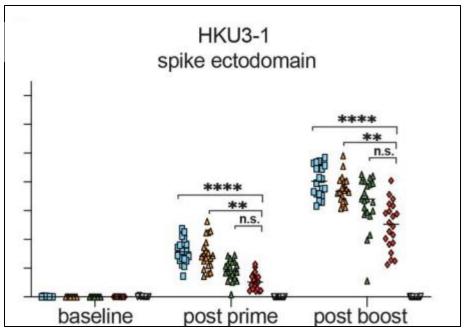


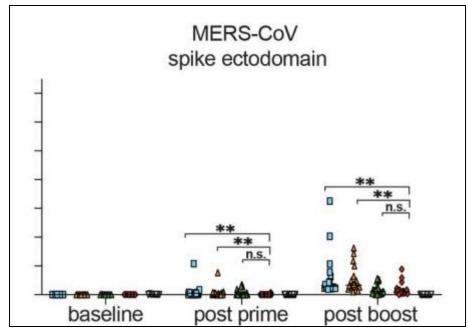




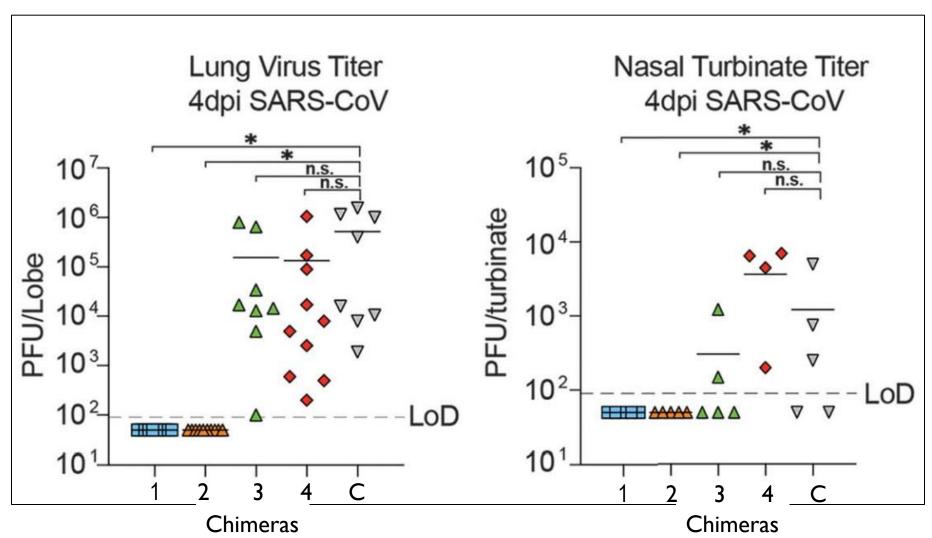




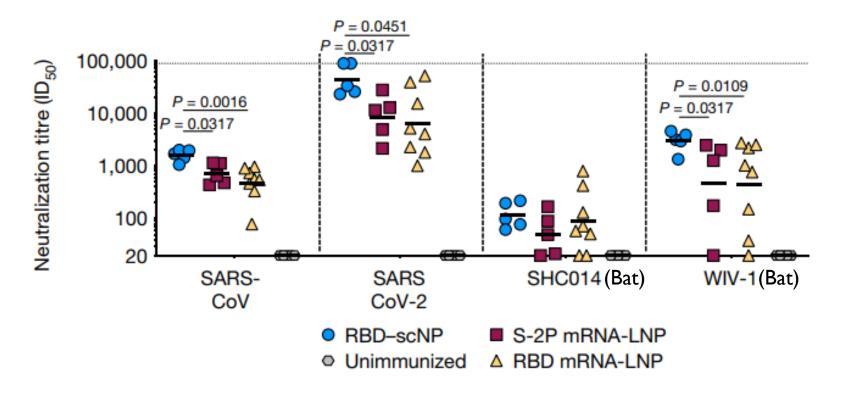




In vivo protection against Sarbecovirus challenge after mRNA-LNP vaccination



Serum cross-neutralization of infections with SARS-related betacoronaviruses induced by RBD-sortase-A nanoparticle in monkeys



Spike-specific CD4+ and CD8+T cell vaccine responses quantitatively and qualitatively differ in SARS-CoV-2 naive versus previously infected individuals

