

SARS-CoV-2 Update (2019-nCoV)

Baric Laboratory University of North Carolina





Outline

- Introduction
- Emerging Coronaviruses
 - SARS-CoV
 - Pre-pandemic SARS-like Bat-CoV
 - Drivers of Epidemic Disease Outbreaks

The Outbreak

- Origins
- SARS-CoV 2
 - Genome Organization and relatedness
- COVID-19 Disease

Countermeasures

- Vaccines
- Broad based CoV nucleoside inhibitors

Summary





Timeline: Emerging Nidoviruses

Virus	Species	Emergence
HCoV-NL63	Human	500-800 years
HCoV-229E	Human	200-300 years
HCoV-OC43	Human	~120 years
PEDV	Porcine	~25 years < 2012 in US
PRRSV	Porcine	~25 years
rBCoV	Bovine	~25 years
SARS-CoV	Human	~16 years ~7 years Cross Species Movement 21st Century 3 months
MERS-CoV	Human	~7 years Accelerating Cross Species
SADS-CoV (HKU2)	Porcine	~2 years Movement 21st Century
SARS-CoV 2	Human	3 months

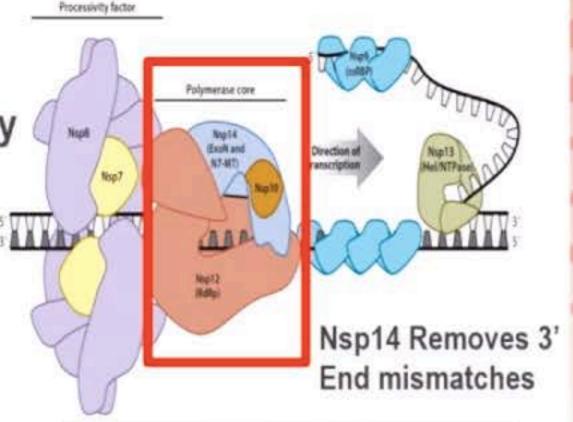
Fu et al., 2018 Infect Genetic Evolution; Peiris JS et al., Lancet 2003, Huynh J et al., J.Virol 2012; Zaki AM et al., N Engl J Med. 2013, Mole B. Nature. 2013; Zhou P et al., Nature 2018

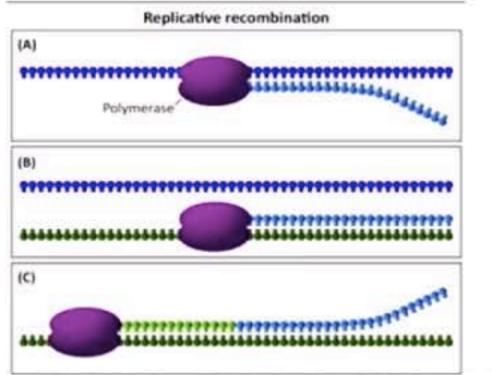


Drivers of CoV Evolution

- □ CoV Genome Size: 32Kb
- CoV Mutation Rate
 - 10⁻⁶ Regulated Fidelity (nsp14: ExoN)
 - Environmental Change
 - Fidelity rates change
- High Rates RNA Recombination
 - 25% during mixed infections
 - Modular evolution

CoV Replicase Complex



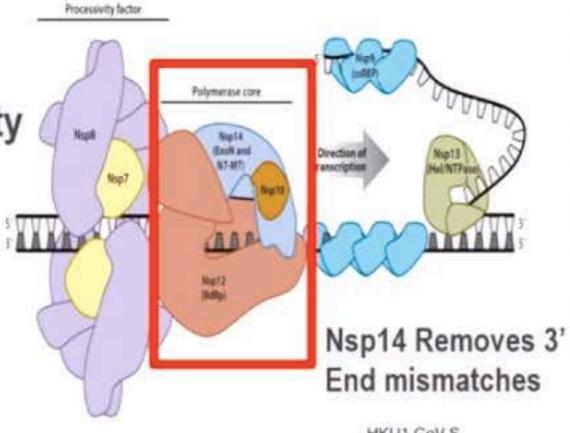


Position Piece: CoV: An RNA Proofreading Machine Regulates Replication and Fidelity (RNA Biol, 2011), Dudas G. Virus Evolution 2016; Eckerle et al., Plos Pathogens 2010; Graham et al., Nature Medicine 2012; Smith et al., Plos Path 2014

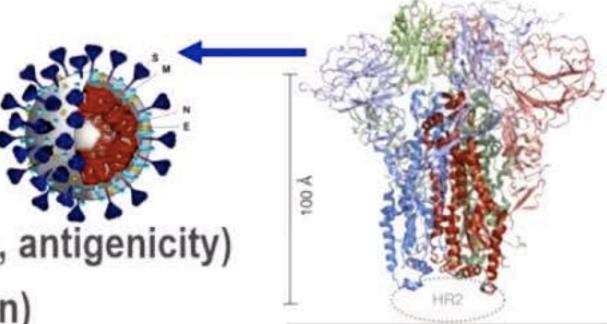


Drivers of CoV Evolution

- □ CoV Genome Size: 32Kb
- CoV Mutation Rate
 - 10⁻⁶ Regulated Fidelity (nsp14: ExoN)
 - Environmental Change
 - Fidelity rates change
- High Rates RNA Recombination
 - 25% during mixed infections
 - Modular evolution
- Plastic Surface Glycoprotein
 - Tolerates high rates of mutation
 - Deletions and Insertions (tropism, antigenicity)
 - Recombination (modular evolution)
 - Host range, tissue tropism, transmissibility



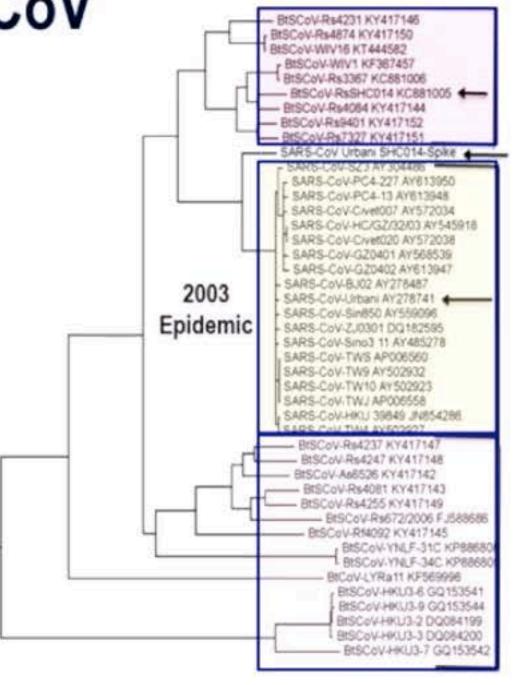
CoV Replicase Complex





Origins of the Group 2B SARS and SARS-like CoV

- □ SARS-CoV Origins (Yellow)
 - bats
 - Open Markets and Civet Intermediate Hosts
- SARS-like bat CoV (Pink)
 - Pre-epidemic potential (high/low)
 - Bats, low level seroprevalence in people residing near bat hibernacula
- □ SARS-CoV 2
 - Bats
 - Open Market Origins?



State of Knowledge Before Dec 2019



SARS-CoV Emergence in 2002 in China

8,096 cases, 774 deaths, in 32 countries, Nov 1 2002 - July 31 2003

Most Likely Model

WIV-16 (97-98% Identical)



Civet Strains (99.5%)







Bat to Human to Civet

Intermediate host

Bat to Civet to Human

Is SARS-CoV Extinct?

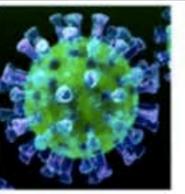


BtCoV Bats Animals

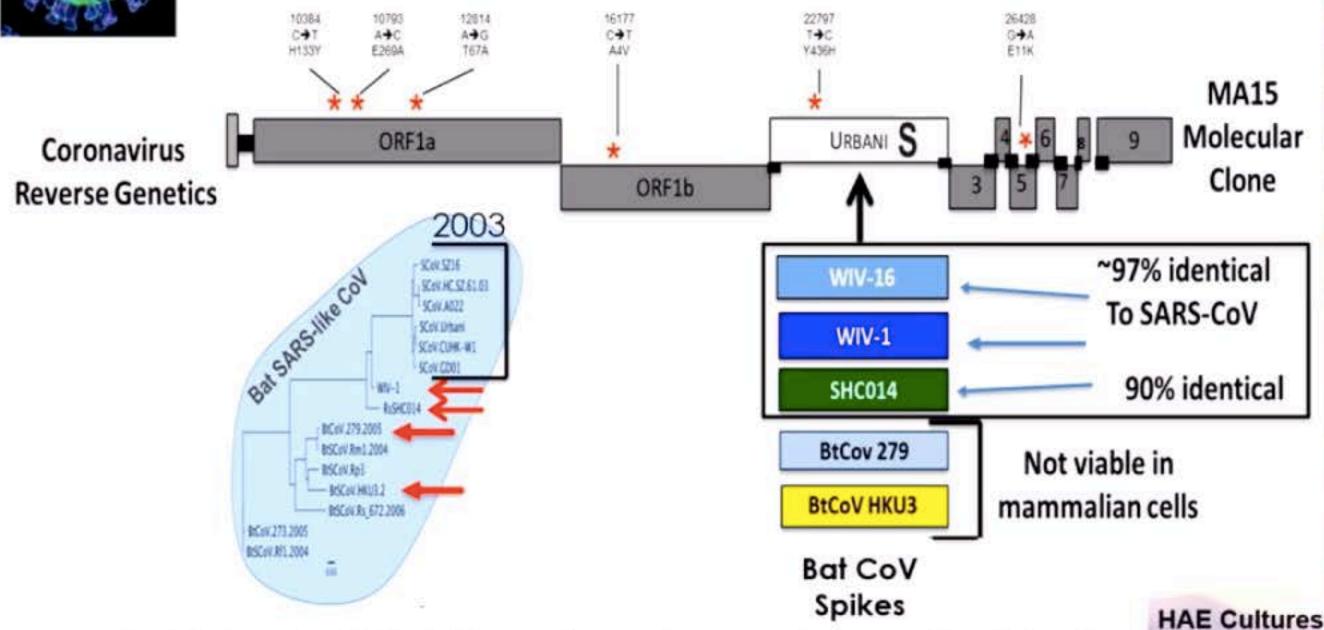


Threat Level?





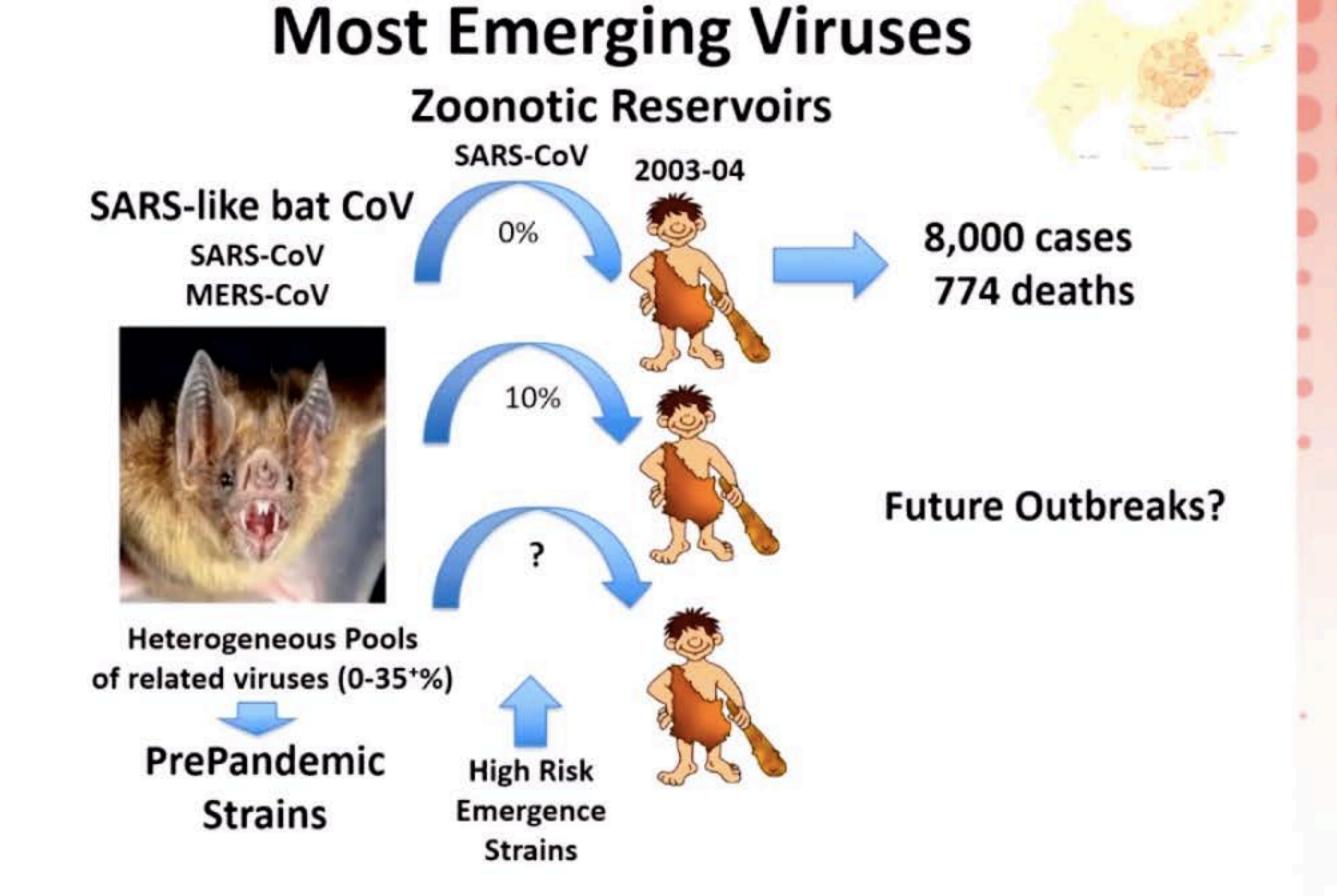
SARS MA15 Molecular Clone

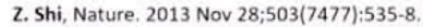


Replicate like SARS-CoV on primary human airway epithelial cells Use human receptor as well as SARS-CoV (if yes) Synthesize full length genomes, recover full length virus

Rockx et al., JV 2007; Becker et al., PNAS 2008; Menachery et al., Nature Medicine, 2015; Menachery et al., PNAS 2017

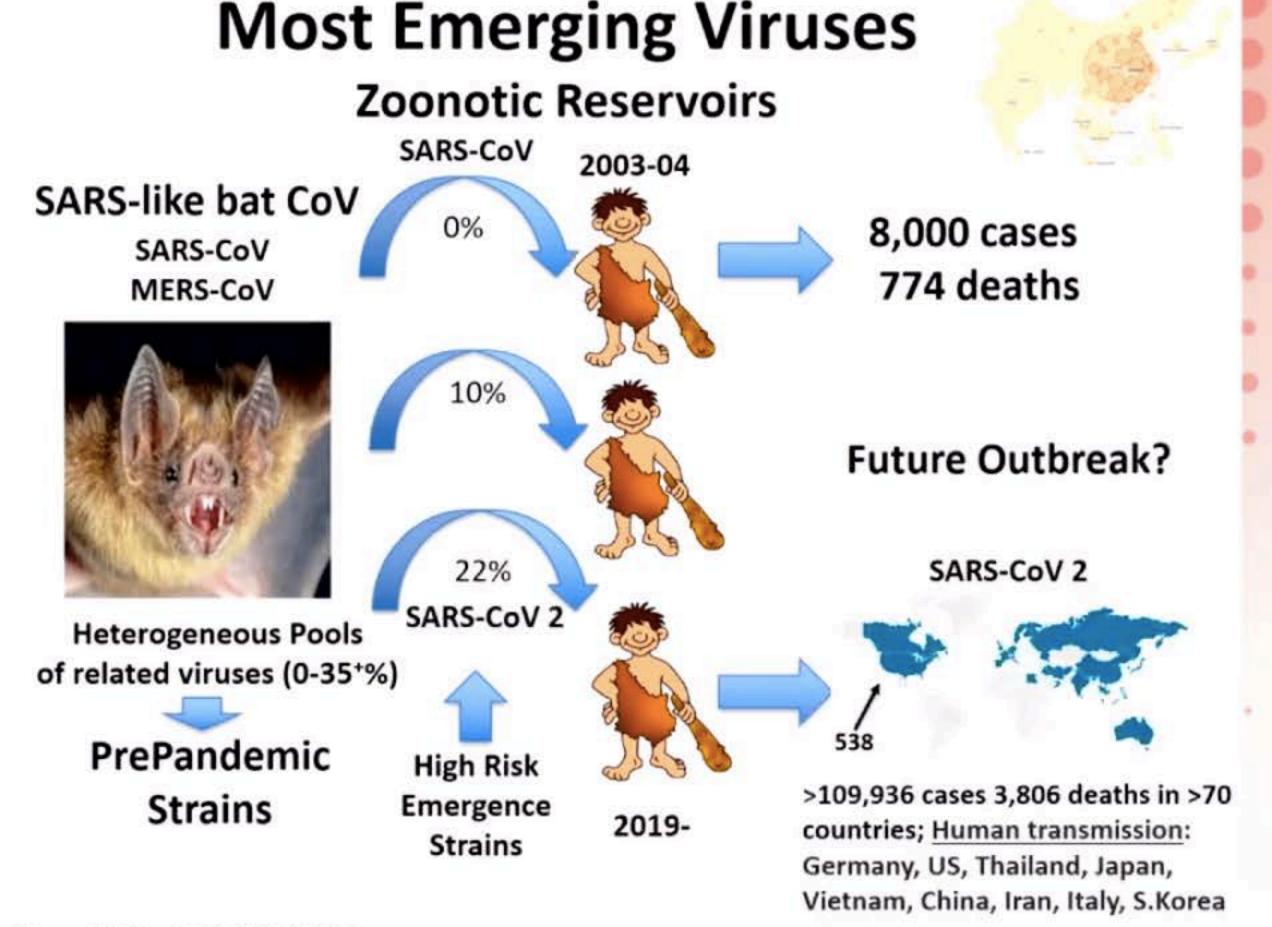






Sheahan et al., JV 2008; Becker PNAS 2008; Menachery V et al., Nature Medicine 2015, Menachery PNAS 2016; Simon et al., mBIO 2017

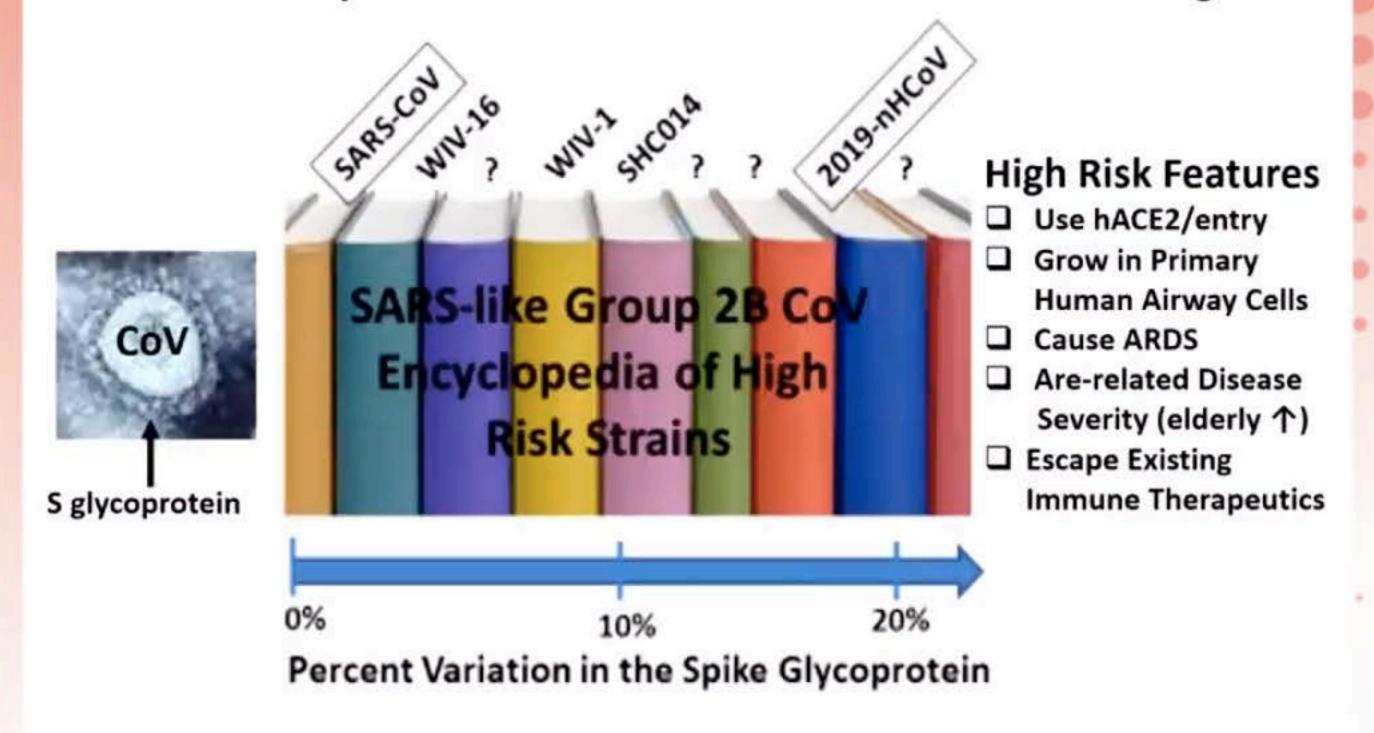








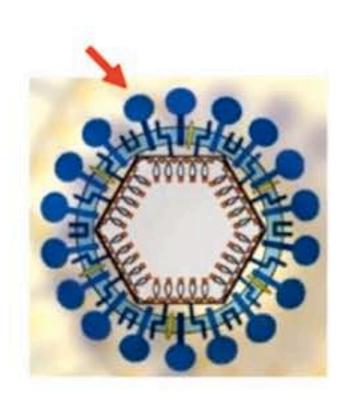
Known Group 2B SARS-like CoV Poised for Human Emergence

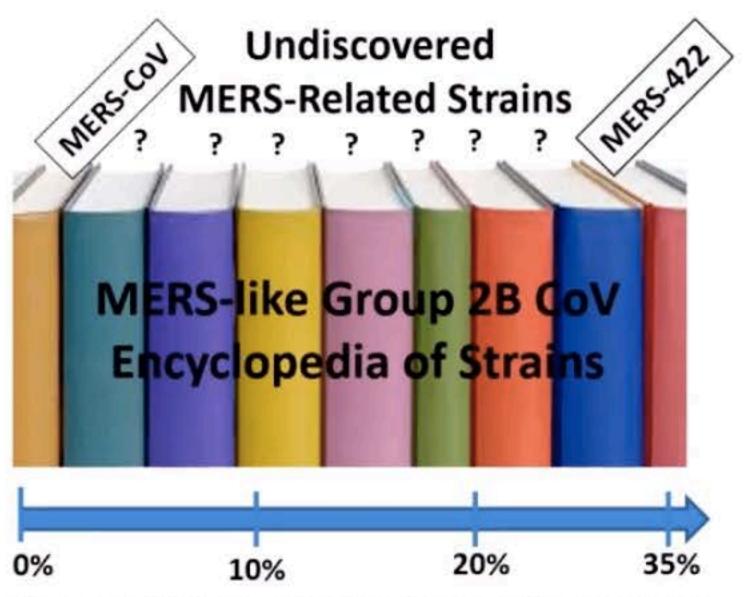


Platform to develop/test broad based vaccines, hmAB and antiviral drugs



Known Group 2C MERS-like CoV Poised for Human Emergence

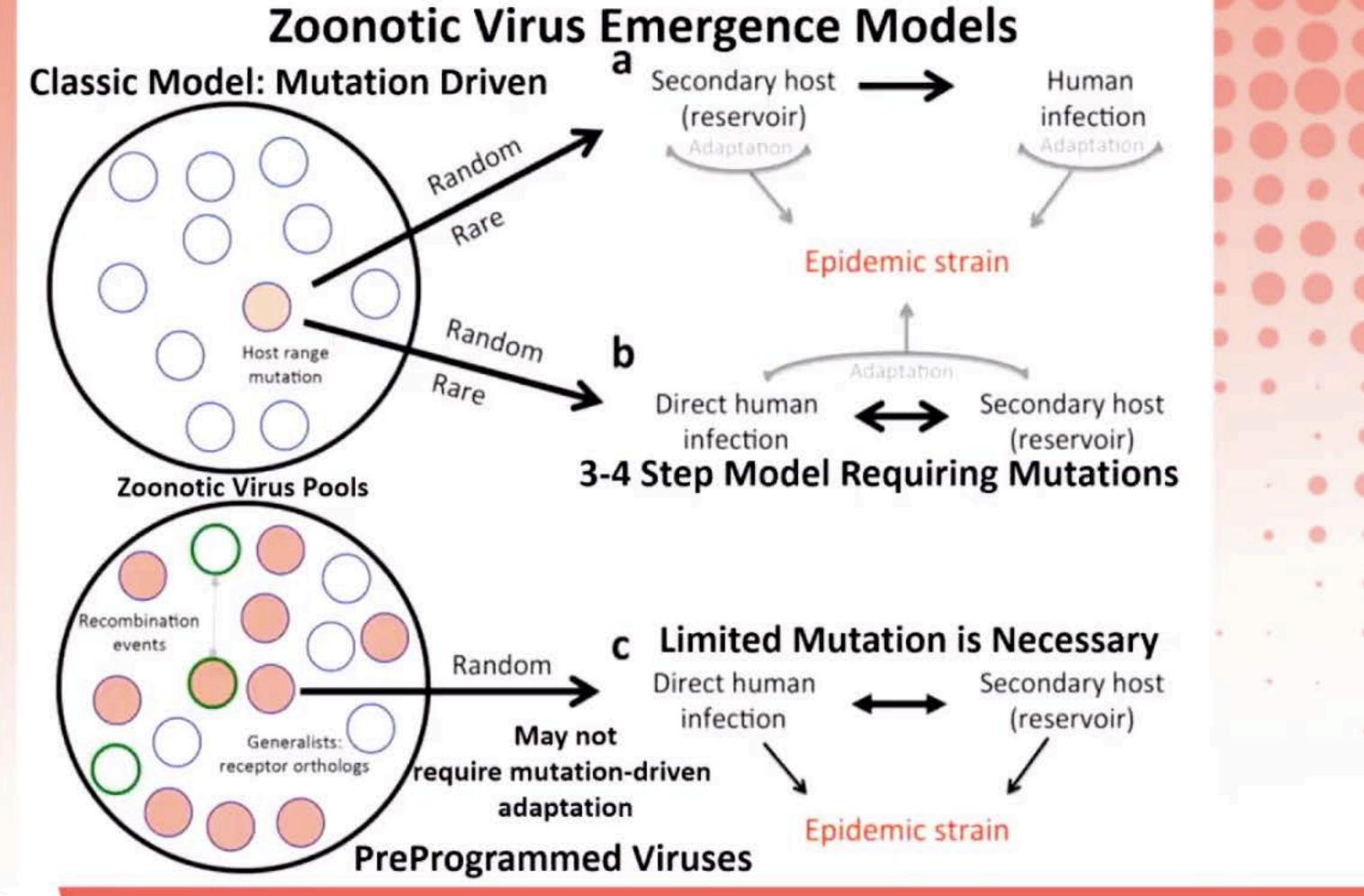




Percent Variation in the Spike Glycoprotein

- -MERS-like bat CoV (China) 65% Identity with MERS-CoV Spike
- -Uses hDPP4 as a receptor for docking and entry
- -Replicate efficiently in primary human airway epithelial cells







SARS-CoV 2

- Emerged Early Dec in Wuhan China (Dec 1)
- Began as Cluster of Cases Associated with Open Markets (Dec 31)
 - No Evidence of Human to Human Transmission
 - Not Very Pathogenic
 - Not SARS-CoV, Likely a Novel Virus



<u>Never</u> under-estimate epidemic potential of an emerging virus

- Wuhan Open Fish Market Closed (Jan 1, 2020)
- Identified as a SARS-like Coronavirus on Jan 7th, 2020
 - distant relative to the SARS-CoV (kissing cousin)
- Genome Length Sequence Reported (5 isolates) (~9-11th)
- 15 HCW infected, China Confirms Person to Person Spread (~20th)



UPDATE ON NEWLY DISCOVERED CORONAVIRUS

	SARS CoV	MERS CoV	SARS-CoV 2
Virion Structure	Enveloped RNA virus	Enveloped RNA virus	Enveloped RNA virus
Outbreak period	2003-2004	2012-present	Dec 2019-present
Initial site of isolation	Guangdong province, China	Saudi Arabia	Wuhan, China
No. of countries/cases	29	27	>70
No. of cases (mortality)	8,096 (9.6%)	2,494 (~34%)	~109,936 (N=3,806)(3.4%)* >6,129 critical (~14%)
No. of cases U.S.	8	2 (2014)	538 (WA, IL, CA, AZ, Mass, Wis
Reservoir (intermediate host)	Bats (palm civet)	Bats (dromedary camels)	Bats (likely a zoonosis)
Incubation period	2-7 days (range, 2-21)	2-7 (range, 2-14 days)	2-14 days (mean 5-6)
Infectivity, rho	1.8-2.5	0.3-1.3	~3 (2.4-3.8)*
Super spreaders	Yes	Yes (common)	Yes (many examples)
Asymptomatic/mild Spread	No	Rare	Yes/Yes
Attack Rate	10.3% to 60%	4 to 20%	20-30%, 80% (early study)?
Transmission (including to HCP)	Droplet/Direct, Airborne/Indirect?	Droplet/Direct, Airborne/Indirect?	Droplet/Direct, Airborne/Indirect/Fecal
Treatment (PEP)	Supportive (none)	Supportive (none)	Supportive (drugs CU)
Infection Prevention	Airborne, contact, face shield	Airborne, contact, face shield	Airborne, contact, face shield

^{*}About 83% of cases are mild or asymptomatic, Mortality Rates are age Stratified:

80+=14.8%, 70-79=8%; 60-69=3.6%, 50-59=1.3%, 40-49=0.4%, <40=0.2%, less than 15=0%.



Cause of Death: ARDS

Emerging CoV and IAV

SARS-CoV H7N9 2019-nCoV

H1N1-2009 1918 H1N1

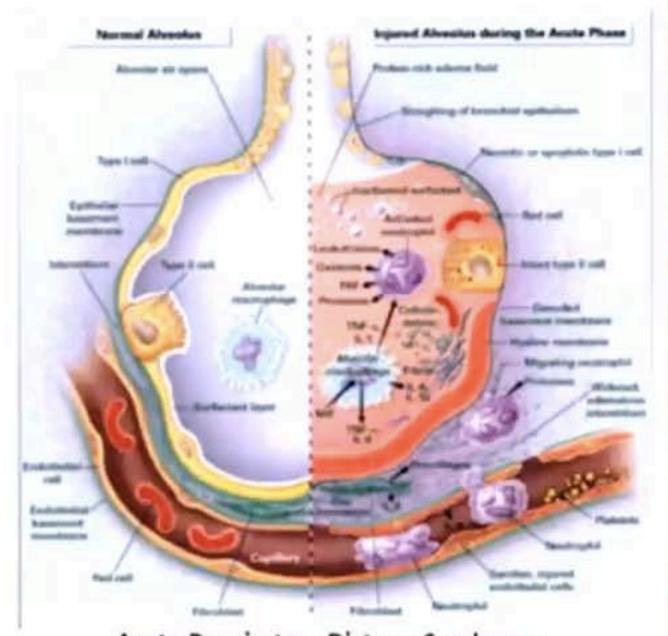
MERS-CoV H5N1

Acute Respiratory Distress Syndrome (ARDS) (SARS, MERS, 2019-nCoV)

- End stage lung disease
- ~30% mortality, ~17% require respiratory assistance (13% invasive ventilators)
- Little evidence 2nd bacterial infections

ARDS:

- ~75,000 deaths in US
- 1 million deaths worldwide
- Progress: Pulmonary Fibrosis
- 5 million deaths/worldwide



Acute Respiratory Distress Syndrome (hypoxia, oxygen insufficiency, organ failure, death)

Infections in children generally mild, males generally develop more serious disease

Wang et al., 2020, JAMA Clinical Characteristics of 138 Hospitalized Patients With2019 NovelCoronavirus-Infected Pneumoniain Wuhan, China

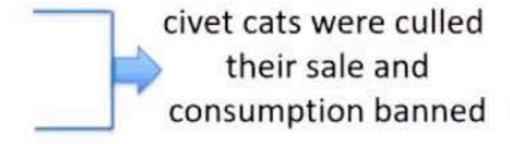


SARS-CoV Outbreak Drivers

Animal Markets-Civets







Hospitals: Epicenters for Disease Expansion



Health Care Workers
Super-spreader Events

Barrier Nursing

- Transmission occurs 24-36 hrs after Disease Onset
 - -Community spread limited
 - Few asymptomatic cases

Vulnerable to quarantine Contact Tracing

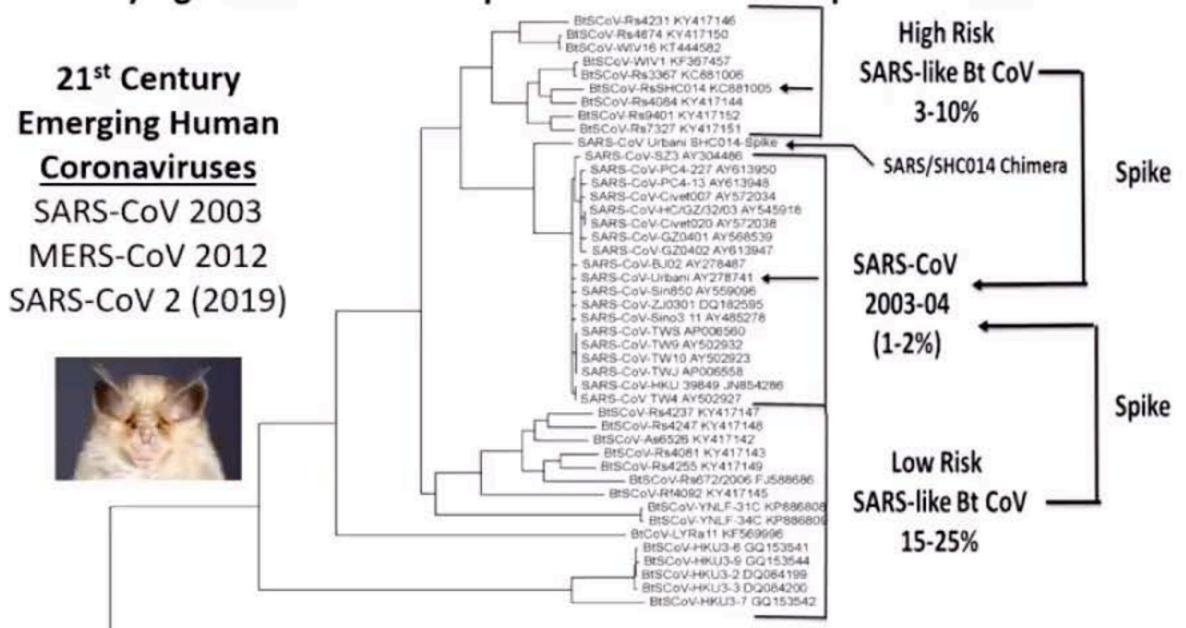
Ro=<1.0 (epidemic goes extinct)

Public Health Response

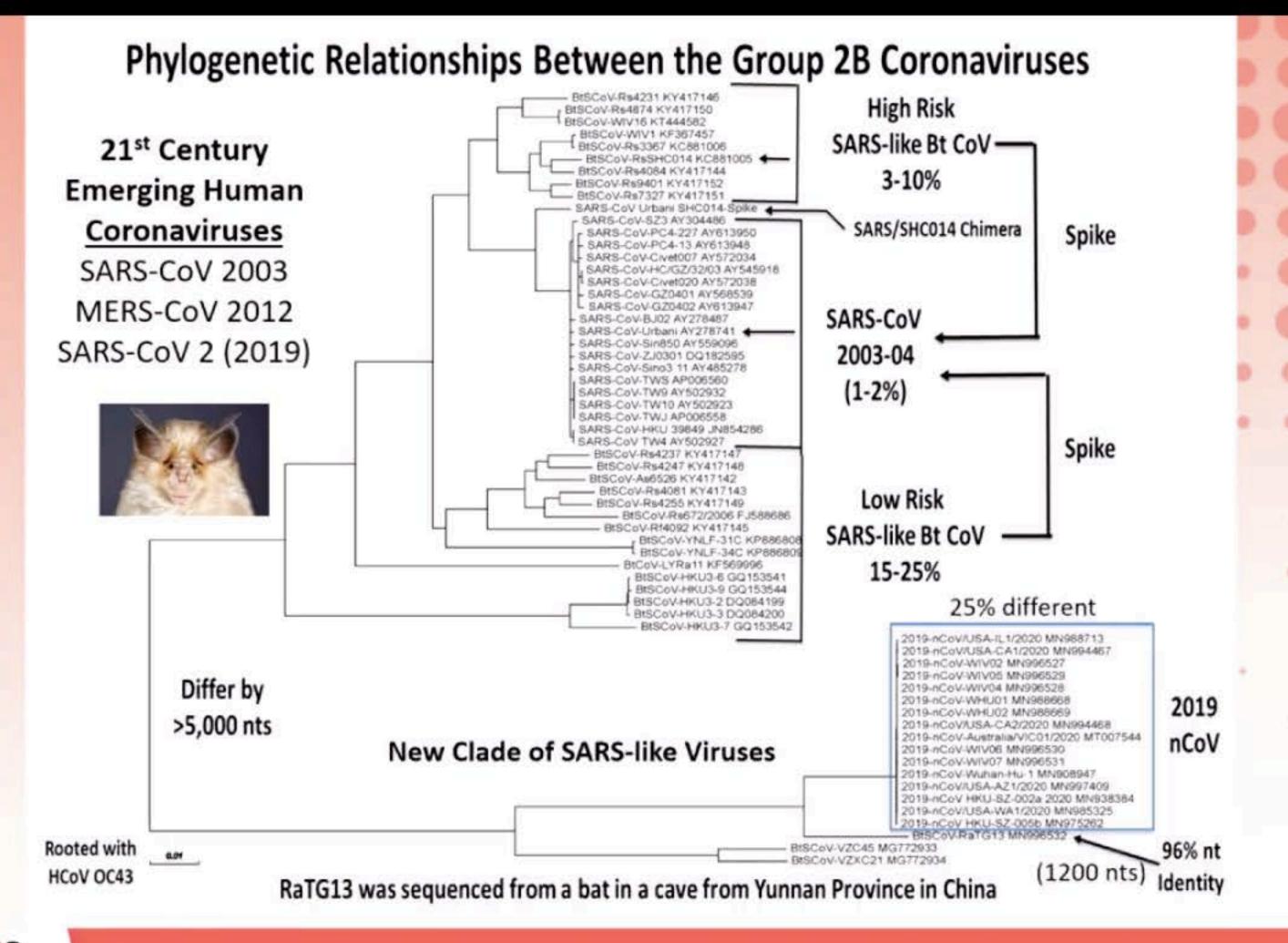
We not so fortunate with SARS-CoV 2 (difficult)



Phylogenetic Relationships Between the Group 2B Coronaviruses

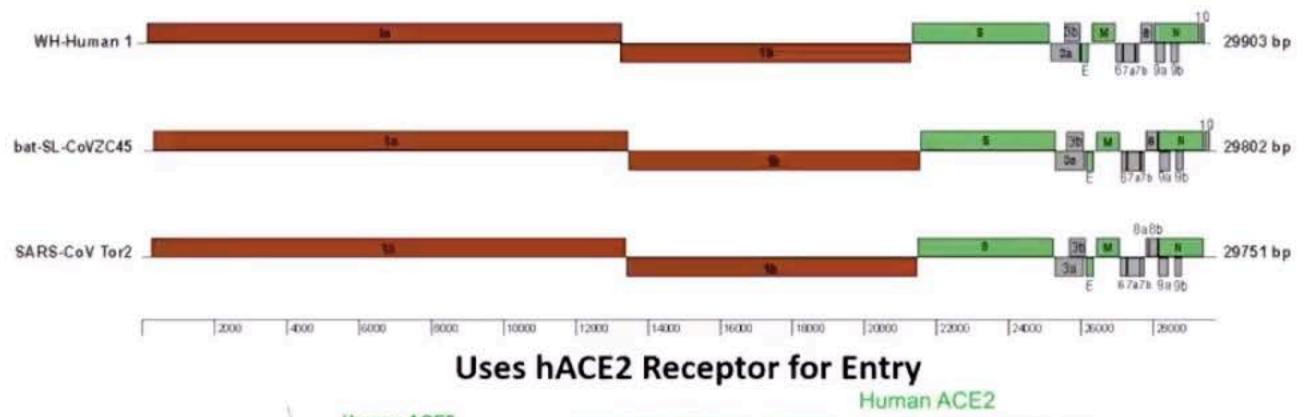


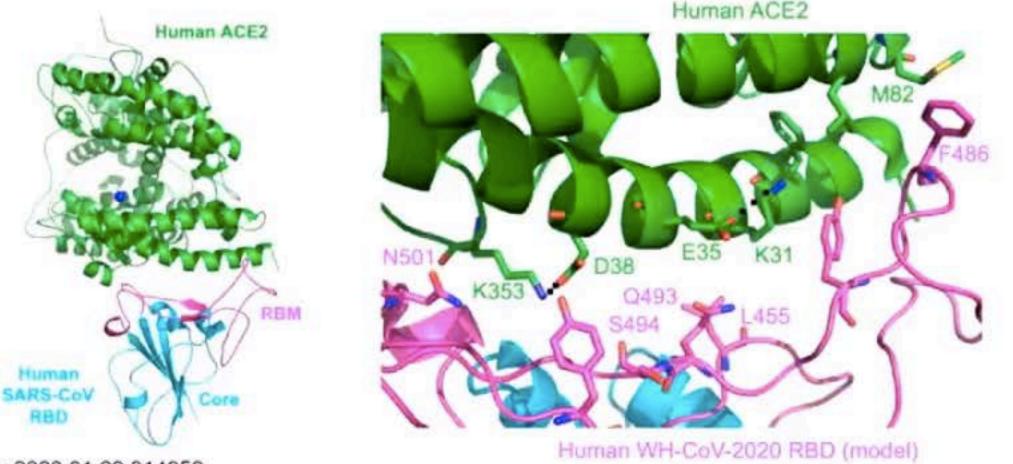


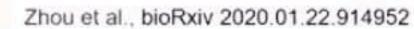




SARS-CoV 2 Genome Organization









SARS-like CoV Group 2B S-RBD ACE2 Interface Sites*

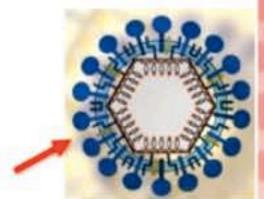
	Virus	402	426	436	440	442	472	473	475	479	484	486	487	488	491	
	SARS-CoV	T	R	Y	Y	Y	L	N	Y	N	Y	T	T	G	Y	
	CUHK-W1	T	R	Y	Y	Y	L	N	Y	N	Y	T	T	G	Y	Use
Little Biot	GD03	T	R	Y	Y	Y	9	N	Y	N	Y	Т	S	G	Y	hACE2
High Risk	HC/SZ/61/03	T	R	Y	Y	Y	9	N	Y	R	Y	T	S	G	Y	cACE2
Strains	WIV16	T	R	Y	Y	2.	F	N	Y	N	Y	T	N	G	Y	bACE2
	Rs3367	T	R	Y	Y	5	F	N	Y	N	Y	T	N	G	Y	mACE2
	WIV1	T	R	Y	Y	5.	F	N	Y	N	Y	T	N	G	Y	MACEZ
	SHC014	T	N	γ	Y	W	P	N	Y	R	F	T	Α	G	Н	7/14
Low Risk	PDF2386	T	N	-	Y	16	L	G	Y	K	1	T	٧	G	Υ	
Strains	ZXC45	T	A		Y	8				S	N.	N	٧	2	Y	
Strains	ZXC21	T	A		Y	8				S	N	N	٧	P	Y	L
	RaTG13 BtCoV	T	K	F	Y	4.0	L	N	Y	7	Υ	T	D	G	Н	?
2019 nCoV	WUH Original	T	N	Υ	Y	L	F	N	Υ	Q	Q	T	N	G	Y	8/14
2025 11004	WUH 402121	T	N	Υ	Υ	L	F	N	Υ	Q	Q	T	N	G	Υ	0/14
	Rp3	T	A		Υ	- 8	-			S	Y	S	٧	þ.	Y	
	HKU3	T	. A		Y	- 5				5	N.	N	V	P	Y	
Low Risk	Rm1	T	A		Y	5				S	Y	S	1	p	Y	
Strains	279	T	A		Y	5				S	Y	S	+		Y	
	Rf1	T	A		Y	5				S	N.	N	٧	p.	Y	
	273	T	A		Y	8				S	* * :	N	٧		Y	

14 Contact Interface Sites that Bind the ACE2 Receptor
Variation across Interface Site Can Alter Orthologue Species ACE2 Receptor Usage

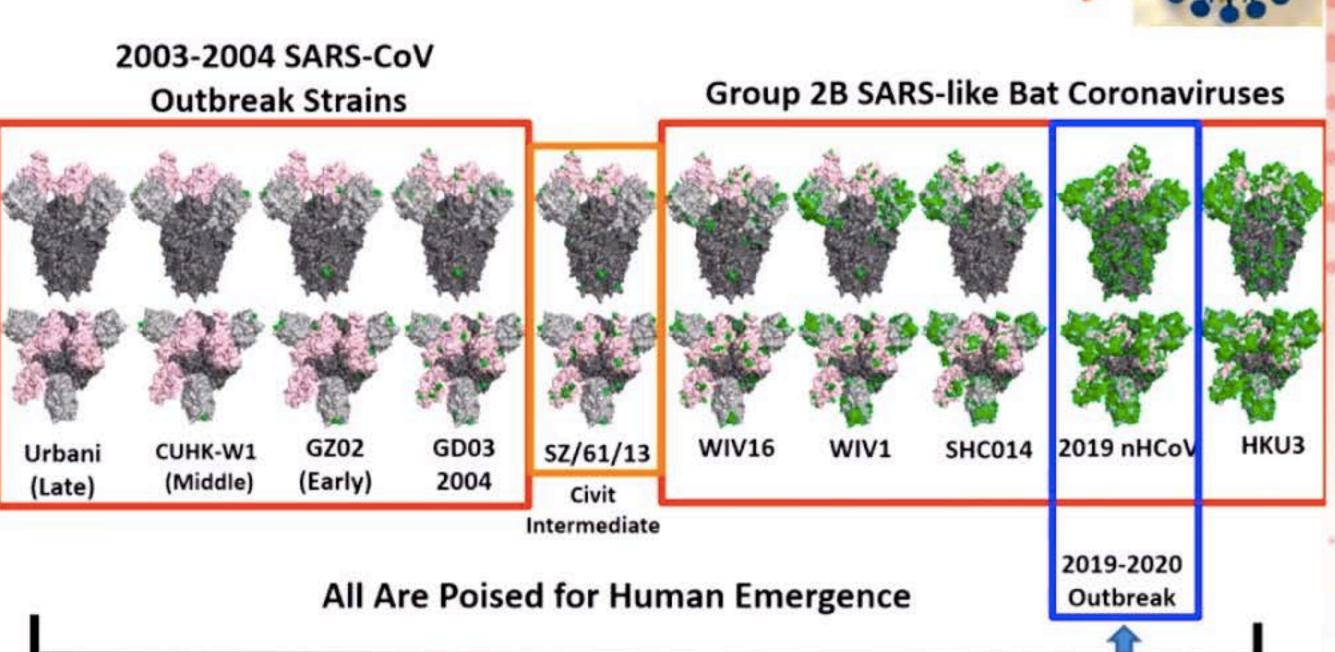
^{*}Conservations based on BLOSUM62 Matrix



Immune Therapeutic Countermeasures



variation



Antigenic Distance is Large, SARS-CoV Immune Therapeutics (hmAB) and Vaccines likely Fail

Broadly active drugs/vaccines are essential to control zoonotic CoV



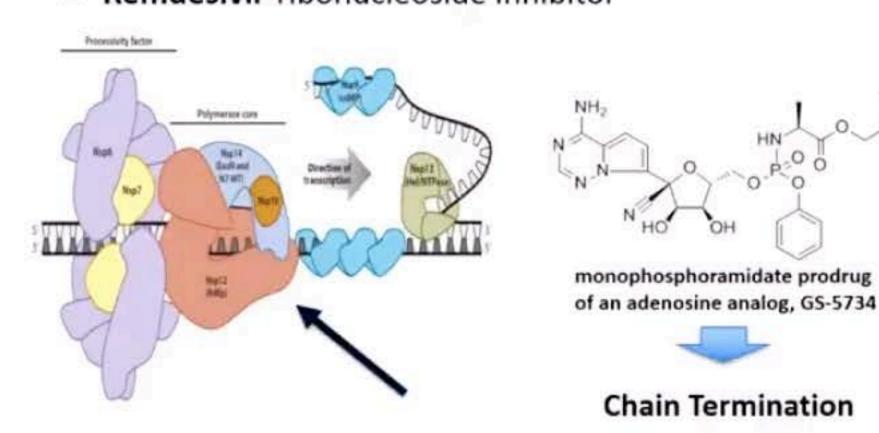
SARS Vaccine Complications

- Vaccine efficacy in aged populations can reduce performance
- Heterogeneous group 2b SARS-like CoV pool may vary by as much as 35% (compared with SARS)
- Th2 Immune Pathology after Vaccination
 - DIV SARS-CoV Vaccine + Alum Adjuvant
 - Adjuvanted S glycoprotein Vaccines
- Evidence for Enhancing Antibodies (controversial)
 - Primates
 - Cell Culture
- SARS-CoV 2 ??—we don't know (right adjuvant)



Therapeutic Interventions

- No approved drugs, immune therapeutics and vaccines against any group 2b coronavirus
- Experimental Drugs (nsp12-RdRp target)
 - Remdesivir-ribonucleoside inhibitor











- Combination lopinavir, ritonavir, and interferon beta tested in China?
- Therapeutic antibodies (MERS, likely soon for SARS-CoV 2)

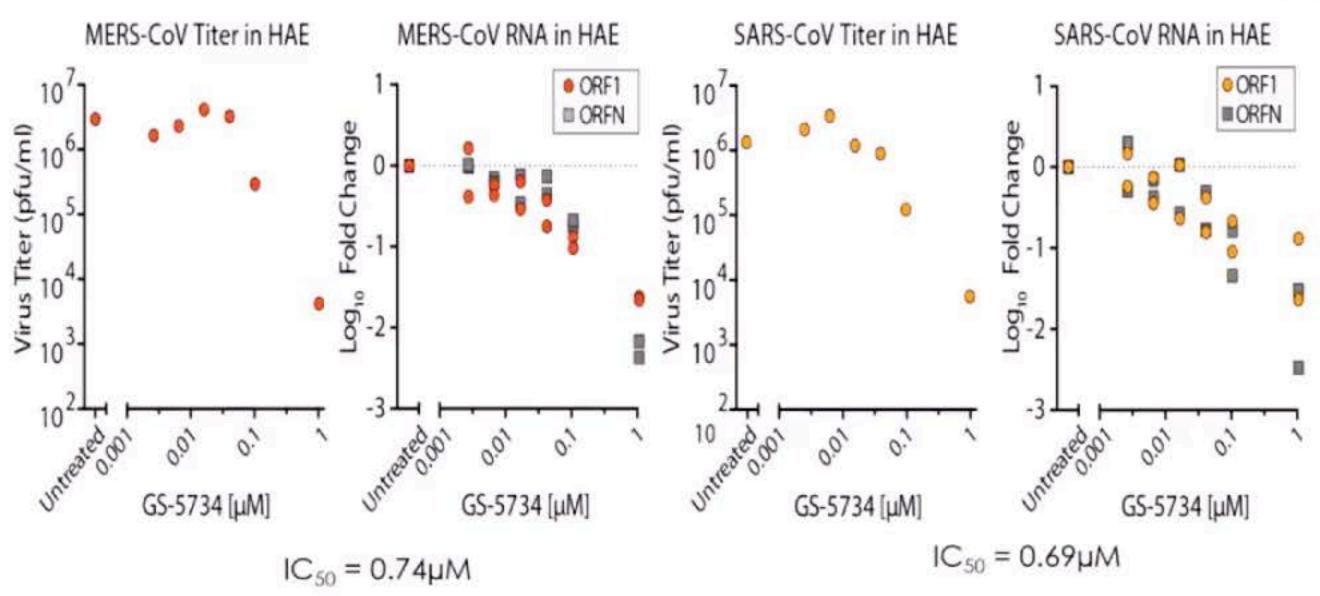
Sheahan et al., Nature Communications 11, 222 (2020)

Sheahan et al., Sci Transl Med. 2017 Jun 28;9(396).



Antiviral effect in primary human cells

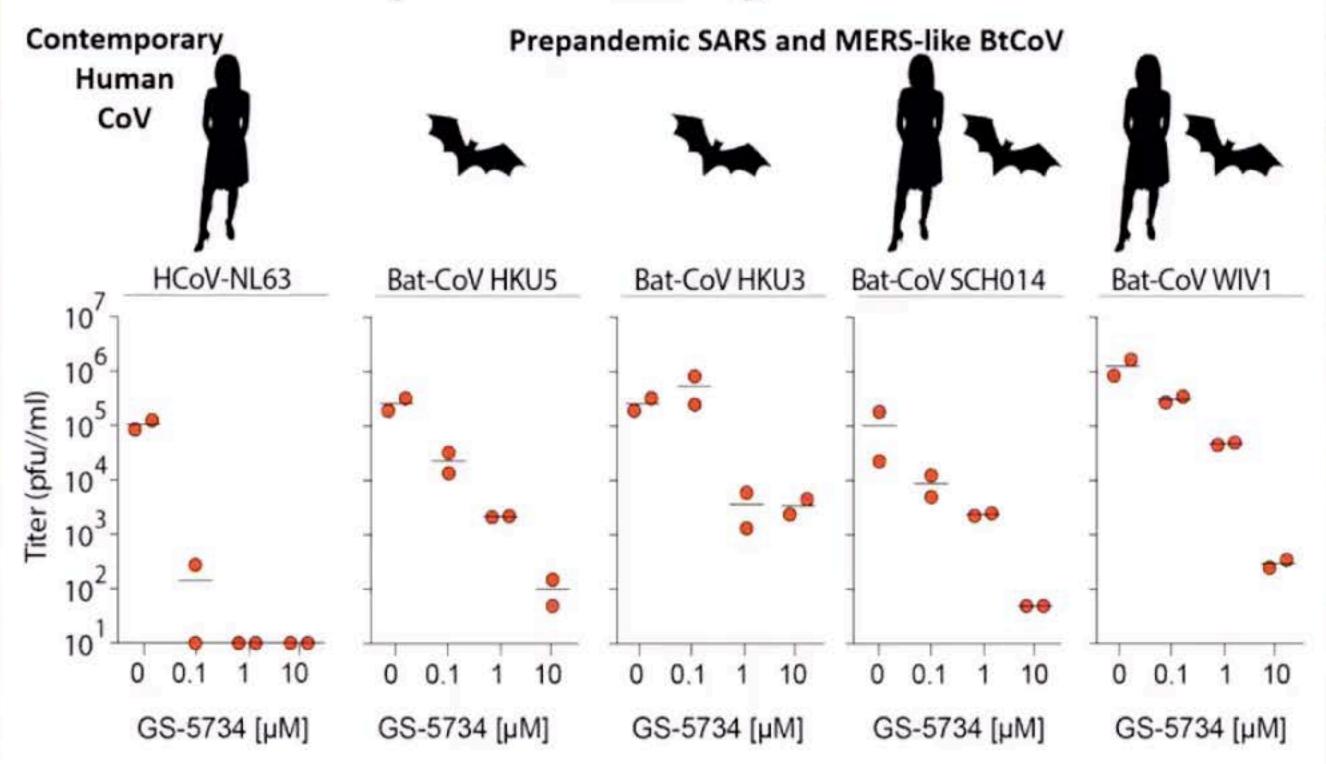




Sheahan et. al 2017 Science Translational Medicine 2017 Jun 28;9(396)



Efficacy of GS-5734 against diverse CoV

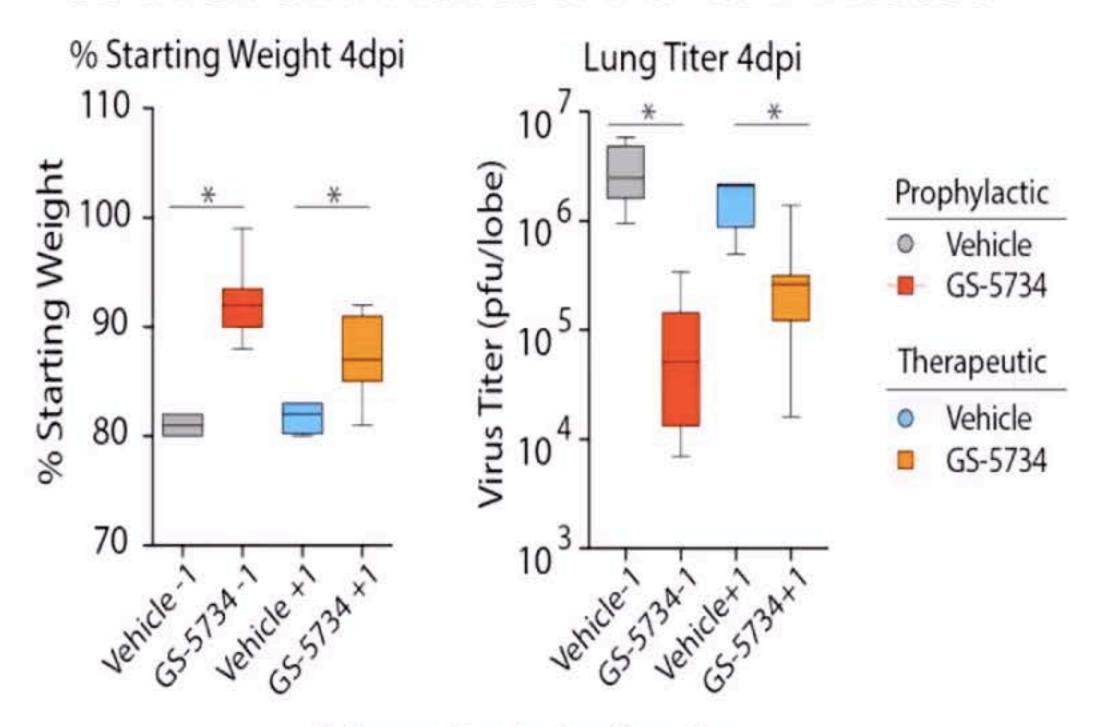


GS5734 Also Inhibits SARS-CoV 2 replication in cells in culture

Sheahan et. al 2017 Science Translational Medicine 2017



GS-5734 diminishes SARS-CoV Disease



Enhances Respiratory Function

Effective against SARS-like HKU3 in Aged animals

Predict efficacy against SARS-CoV 2

Sheahan et. al 2017 Science Translational Medicine 2017



Clinical Testing of Remdesivir for Treatment of COVID-19

Five randomized controlled trials in hospitalized patients with diagnosed COVID-19

COVID-19 Location Sponso		Sponsor	Study size (randomization)	First patient enrolled	Primary endpoint		
Severe Double-blind Placebo- controlled	ouble-blind China Medical University		N = 453 (2:1) 10d RDV:Placebo	Feb 6, 2020	Time to clinical improvement by Day 28		
Mild/Moderate Double-blind Placebo- controlled	Wuhan, China	Capital Medical University, China	N = 308 (1:1) 10d RDV:Placebo	Feb 13, 2020	Time to clinical recovery by Day 28		
All hospitalized* Double-blind Placebo- controlled	Global	NIAID	N = 394 (1:1) 10d RDV:Placebo	Feb 21, 2020	Clinical status at Day 15 based on 7-point ordinal scale		
Severe Open-label	Global	Gilead	N = 400 (1:1) 10d RDV:5d RDV	Enrollment not yet started	Normalization of fever and O ₂ saturation by Day 14		
Moderate Open-label	Global	Gilead	N = 600 (1:1:1) 10d:5d RDV: Placebo	Enrollment not yet started	Hospital discharge by Day 14		

^{*} Stratified by disease severity at enrollment



Future: 2019 nHCoV

- Another nucleoside inhibitor drug, EIDD 1931 is under FDA review
 - Manuscript is under review
- We have tested both drugs in vitro against 2019 nCoV, in vivo studies are in process







Baric Laboratory

Acknowledgements

Adam Cockrell

Emily Gallichotte



Lisa Gralinski

Lisa Lindesmith Michael Mallory

Ande West Kendra Gully

Ethan Fritch Ariana Brown

Alexandra Schaefer

Trevor Scobey

Tommy Baric

Amy Sims

Sarah Leist

Jesica Swanstrom

Paul Brewer-Jensen

Boyd Yount

Ellen Young

Caitlin Edwards

Jenny Munt

Kenny Dinnon



DEPARTMENT OF EPIDEMIOLOGY

Tim Sheahan Lab (UNC) Ron Swanstrom Lab (UNC)

Mark Denison Lab

Gilead Sciences Inc.





George Painter



Emory Institute for Drug Development



Rich Whitley, UAB





