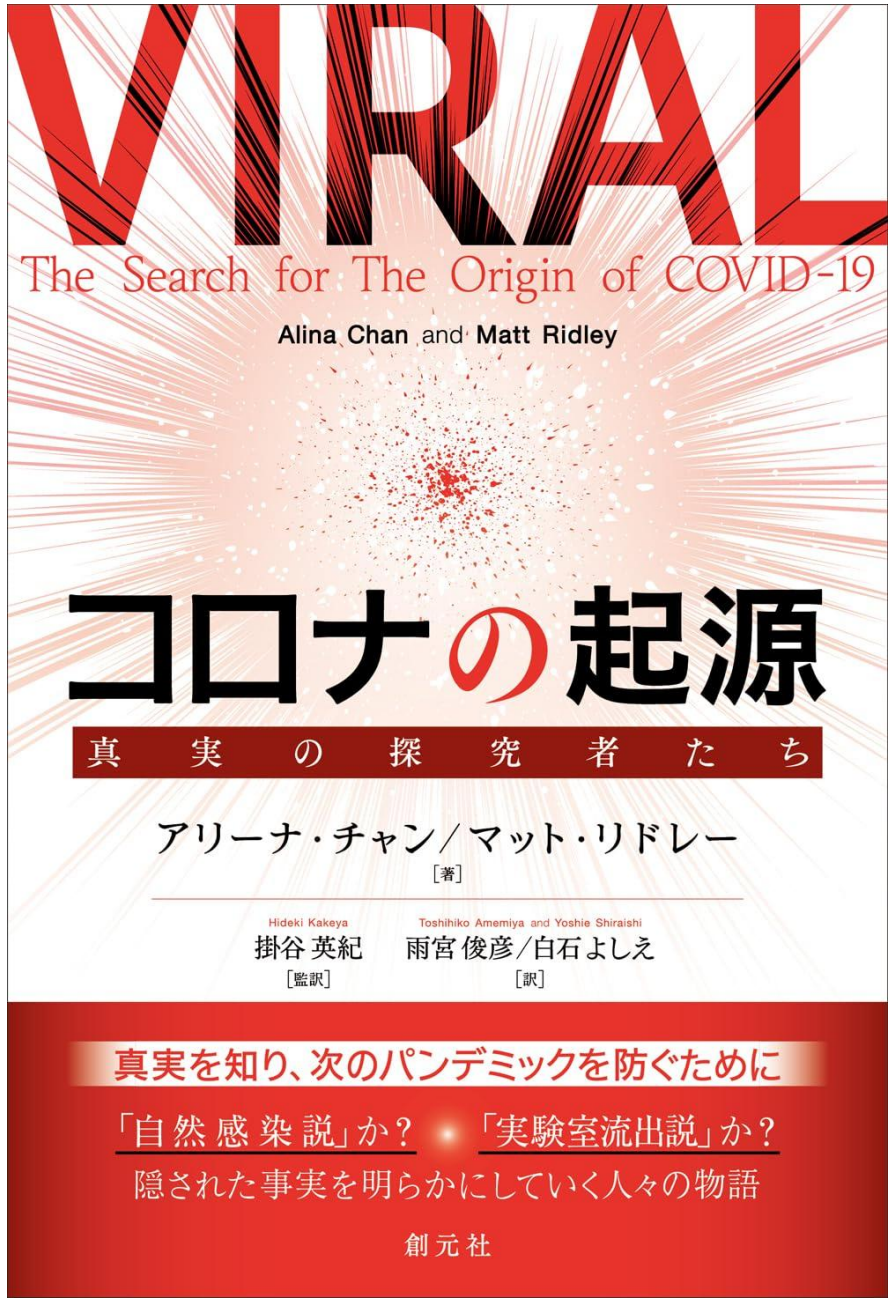
監訳者解説
「コロナの起源
真実の探究者たち」

掛谷英紀



https://www.amazon.co.jp/dp/4422360213/

https://www.youtube.com/watch?v=s1nm9PT1bYE

目次

- SARS-CoV-2研究所起源の生物学的証拠
- DEFUSE計画とウイルス学者の隠蔽工作
- 情報機関の分析
- 考察（気候変動問題との類似性）

SARS-CoV-2研究所起源の生物学的証拠

疫学的証拠

- 8万のサンプルを検査しても中間宿主が見つからず

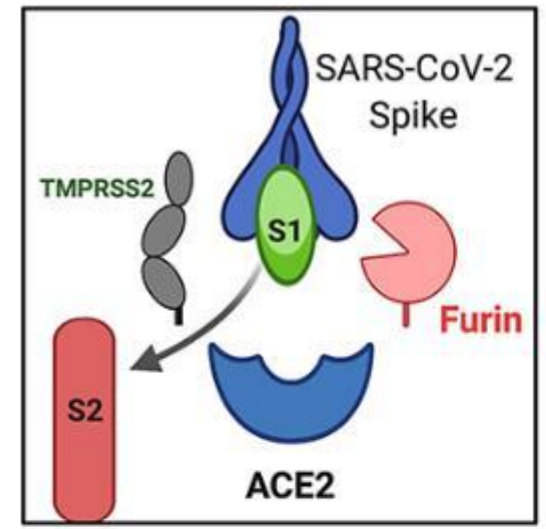
分子的証拠

- 流行初期からのヒトACE2受容体結合力の最適化
- フーリン切断部位の挿入
- 制限酵素切断部位の人工合成に好都合な配置

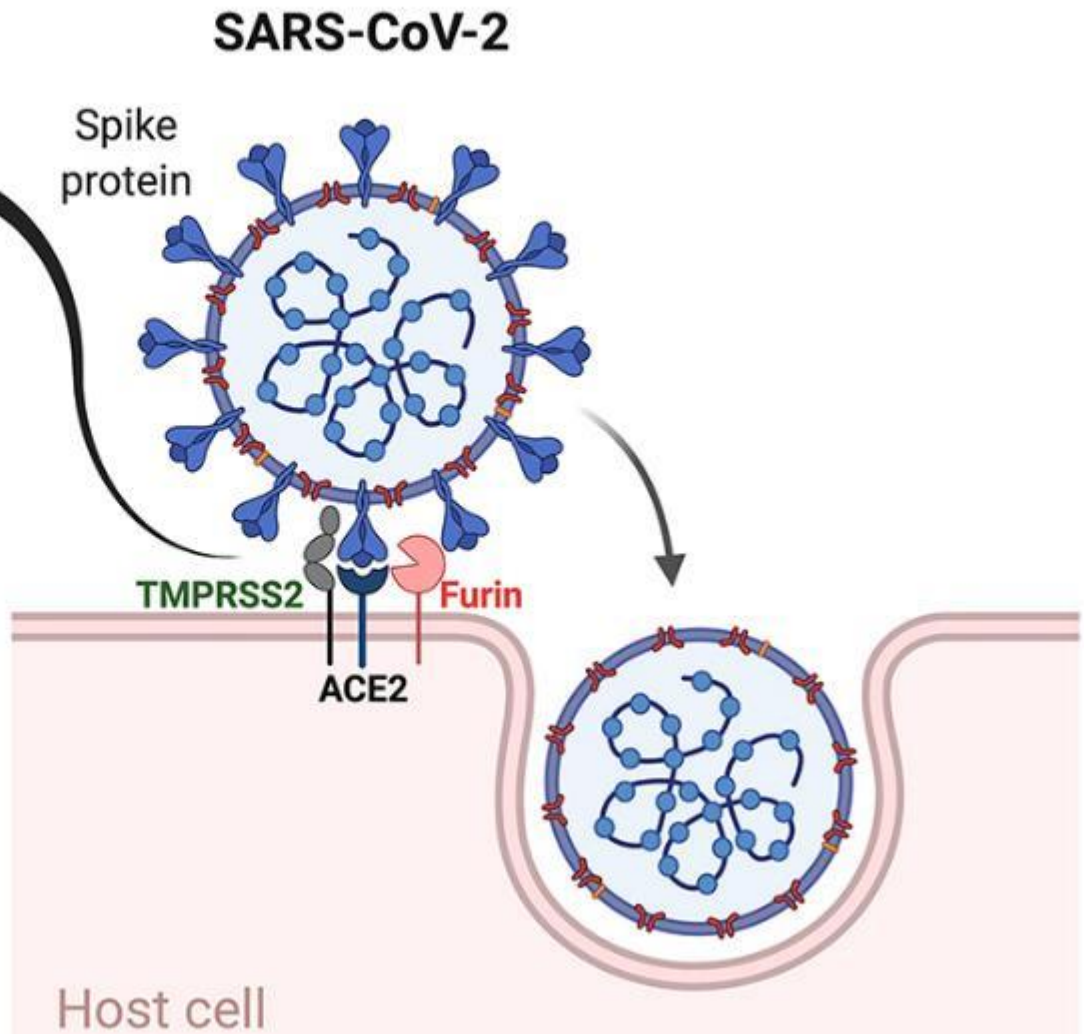
いずれも独立な事象

新型コロナウイルス感染のメカニズム

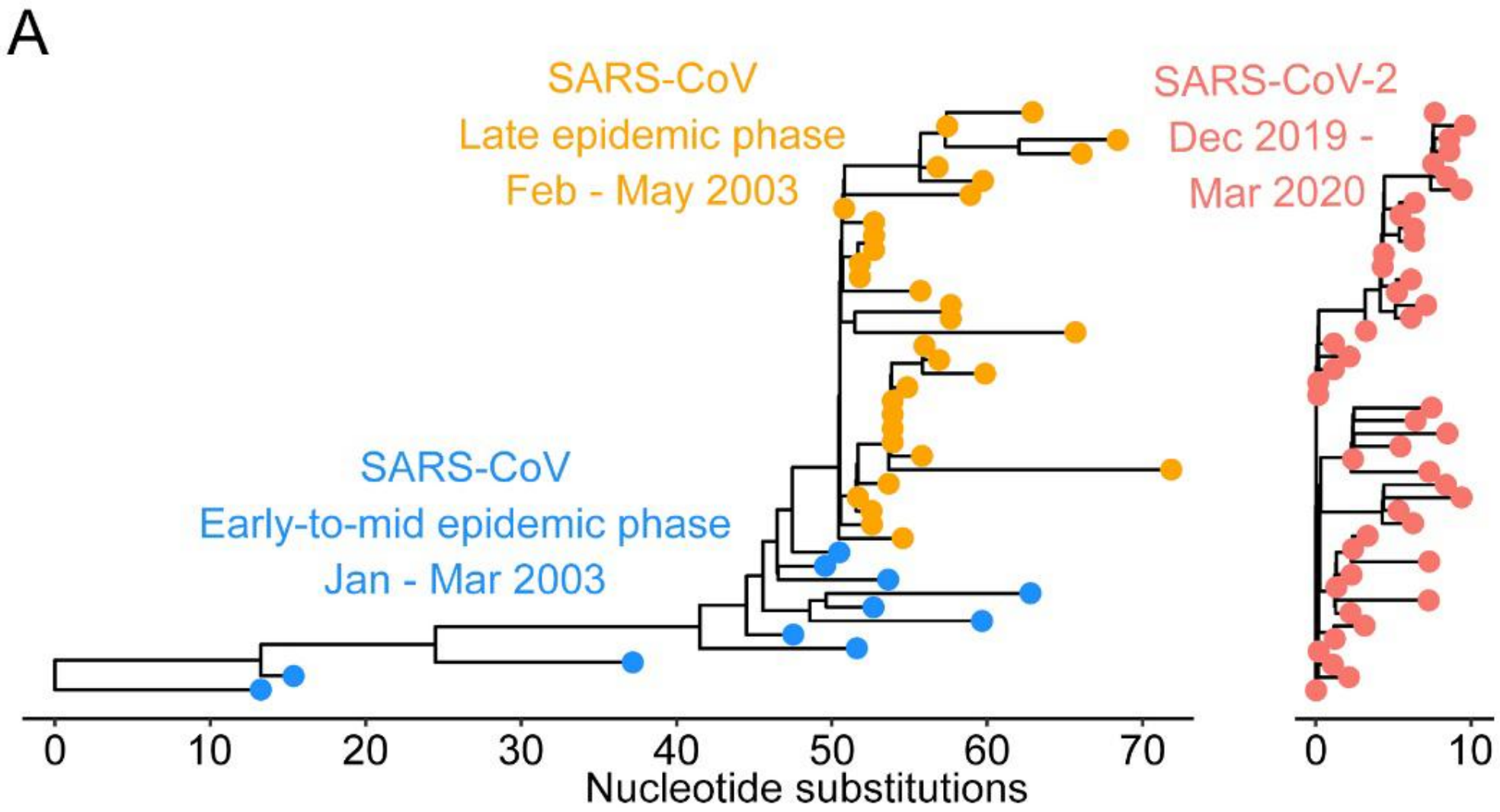
https://www.degruyter.com/document/doi/10.1515/cclm-2020-0727/html



S1/S2 subunits cleavage by furin and SARS-CoV-2 genomes penetrate into the host cell



流行初期からのヒトACE2受容体結合力の最適化



https://www.biorxiv.org/content/10.1101/2020.05.01.073262v1

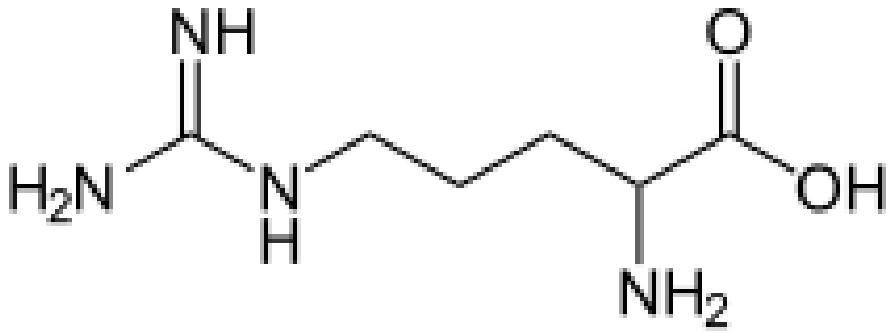
Species	ΔGeqn1 (kcal/mol)	ΔGMMPBSA (kcal/mol)	SARS-Cov-2 infectivity
Homo sapiens (human)	− 52.8	− 57.6 ± 0.25	Permissive, high infectivity, severe disease in 5-10%,
Manis javanica (pangolin)	− 52.0	− 56.3 ± 0.4	Permissive
Canis luparis (dog)	− 50.8	− 49.5	Permissive, low/mod infectivity, no overt disease
Macaca fascicularis (monkey)	− 50.4	− 50.8	Permissive, high infectivity, lung disease
Mesocricetus auratus (hamster)	− 49.7	− 50.0	Permissive, high infectivity, lung disease
Mustela putorius furo (ferret)	− 48.6	− 49.2	Permissive, moderate infectivity, no overt disease
Felis catus (cat)	− 47.6	− 48.9	Permissive, high infectivity, lung disease
Panthera tigris (tiger)	− 47.3	− 42.5	Permissive, overt disease, RNA positive
Rhinolophus sinicus (bat)	− 46.9	− 50.1 ± 1.0	Not permissive
Paguma larvata (civet)	− 45.1	− 46.1	No reported infection
Equus ferus caballus (horse)	− 44.1	− 49.2	No naturally occurring infections
Bos taurus (cow)	− 43.6	− 42.5	No naturally occurring infections
Ophiophagus hannah (king cobra)	− 39.5	− 40.7 ± 1.2	No reported infection
Mus musculus (mouse)	− 38.8	− 39.4	Resistant to infection

https://www.nature.com/articles/s41598-021-92388-5

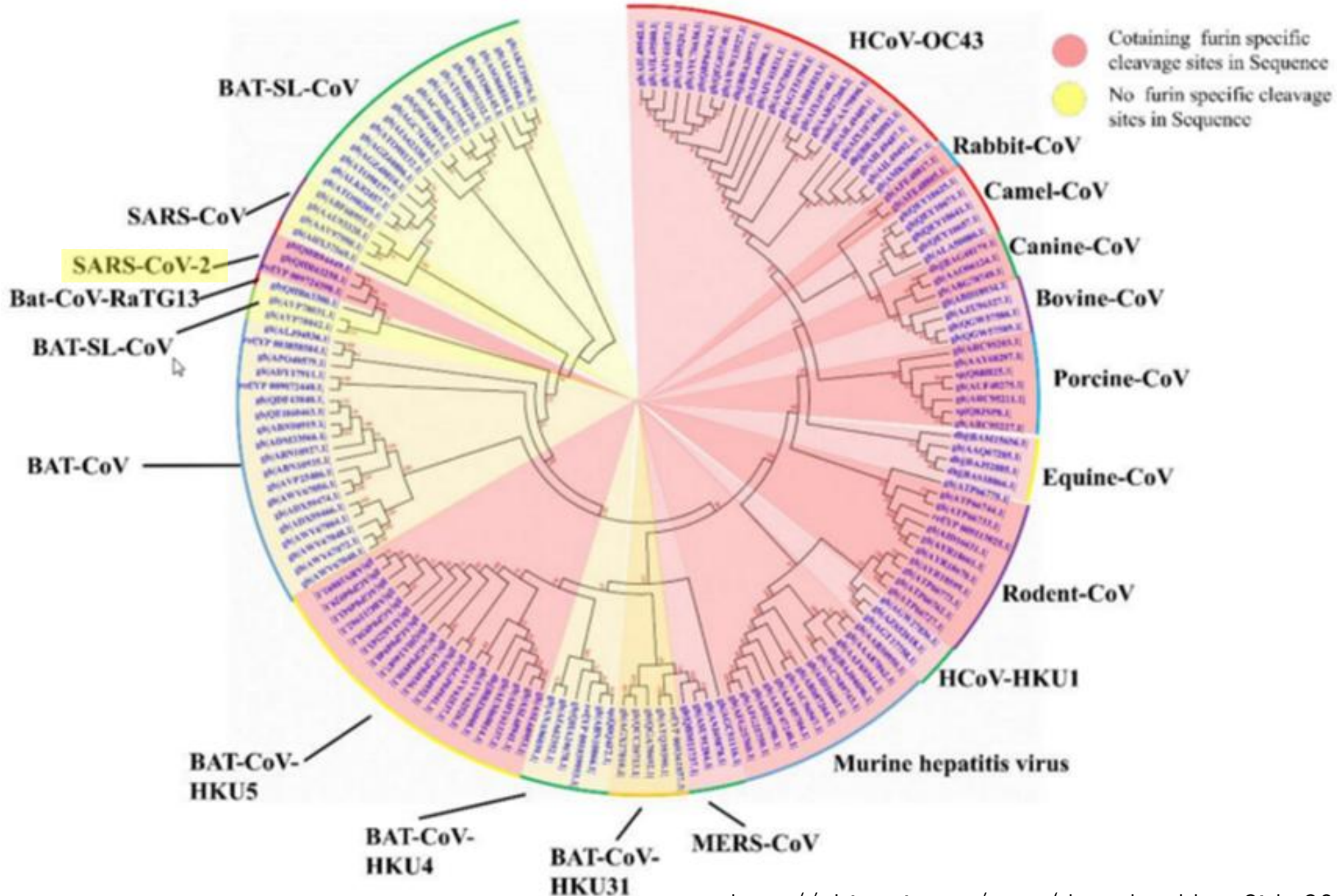
フーリン切断部位（FCS）の挿入

Furin cuts proteins in strictly defined places, namely after an RxxR sequence (that is, Arg-X-X-Arg, where X can be any amino acid). Moreover, if arginine is also in the second or third place (that is, RRxR or RxRR), then the cleavage efficiency is significantly increased.

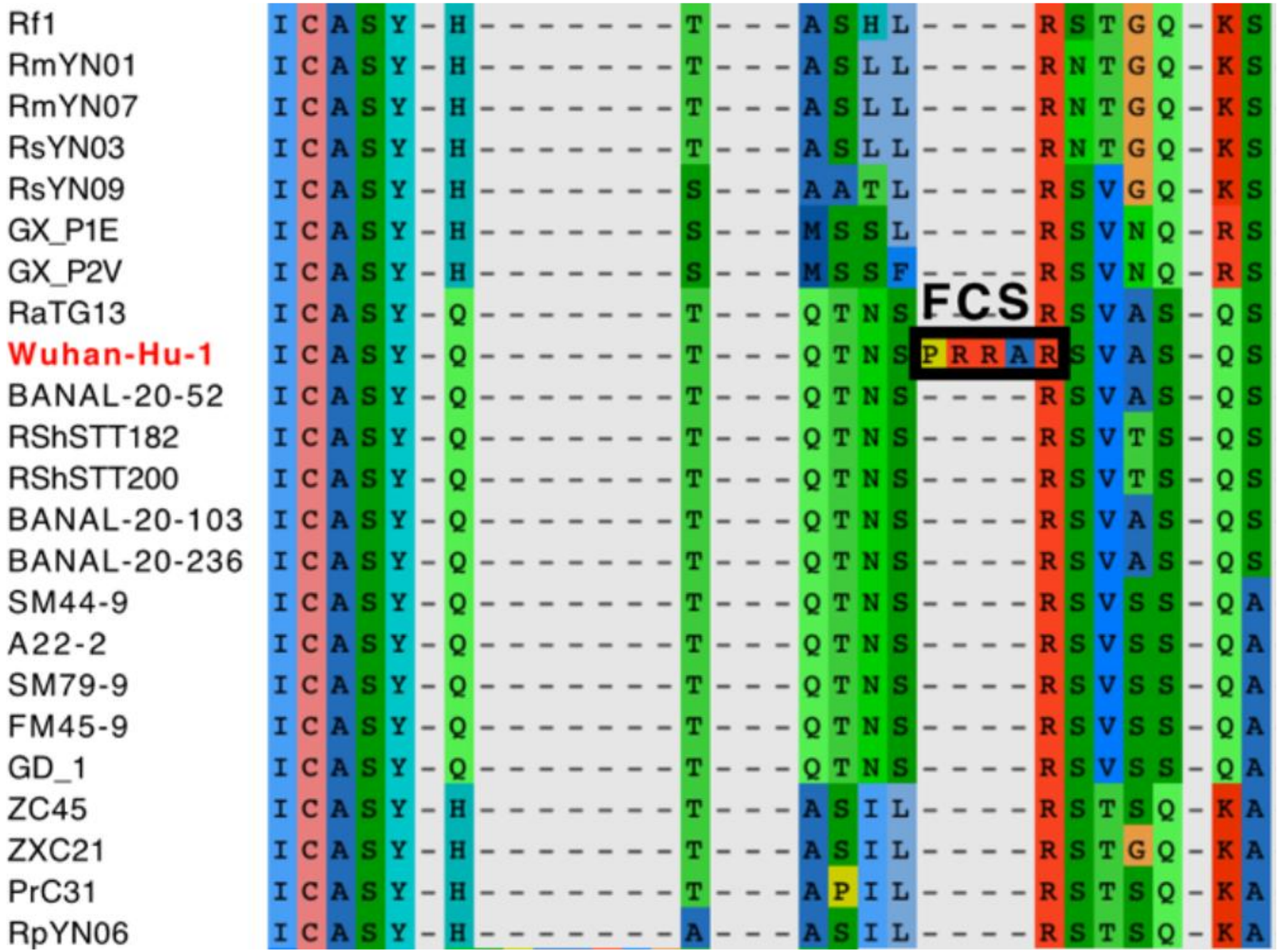
Arginine



https://medium.com/@yurideigin/lab-made-cov2-genealogy-through-the-lens-of-gain-og-function-researh-f96dd7413748



http://chinaxiv.org/user/download.htm?id=30223

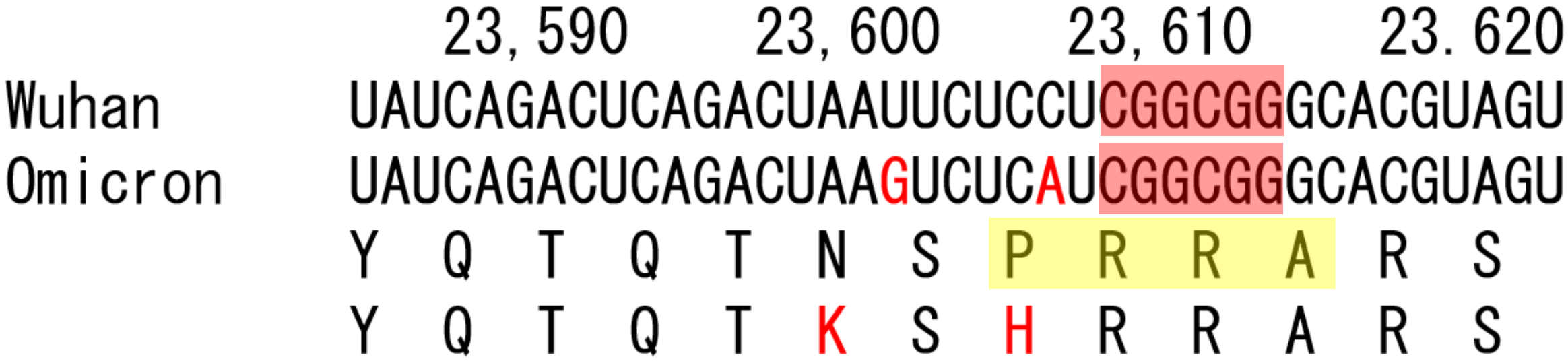


https://academic.oup.com/mbe/advance-article/doi/10.1093/molbev/msab327/6426085

First Position	Second Position: U		Second Position: C		Second Position: A		Second Position: G		Third Position
	code	amino acid	code	amino acid	code	amino acid	code	amino acid	
U	UUU	phe	UCU	ser	UAU	tyr	UGU	cys	U
	UUC		UCC		UAC		UGC		C
	UUA	leu	UCA		UAA	STOP	UGA	STOP	A
	UUG		UCG		UAG	STOP	UGG	trp	G
C	CUU	leu	CCU	pro	CAU	his	CGU	arg	U
	CUC		CCC		CAC		CGC		C
	CUA		CCA		CAA	gln	CGA		A
	CUG		CCG		CAG		CGG		G
A	AUU	ile	ACU	thr	AAU	asn	AGU	ser	U
	AUC		ACC		AAC		AGC		C
	AUA		ACA		AAA	lys	AGA	arg	A
	AUG	met START	ACG		AAG		AGG		G
G	GUU	val	GCU	ala	GAU	asp	GGU	gly	U
	GUC		GCC		GAC		GGC		C
	GUA		GCA		GAA	glu	GGA		A
	GUG		GCG		GAG		GGG		G

https://nerdhaspower.weebly.com/ratg13-is-fake.html

フーリン切断部位の塩基配列



CGGはサルベコウイルスで最も稀なコドン

制限酵素切断部位の人工合成に好都合な配置

Endonuclease fingerprint indicates a synthetic origin of SARS-CoV-2

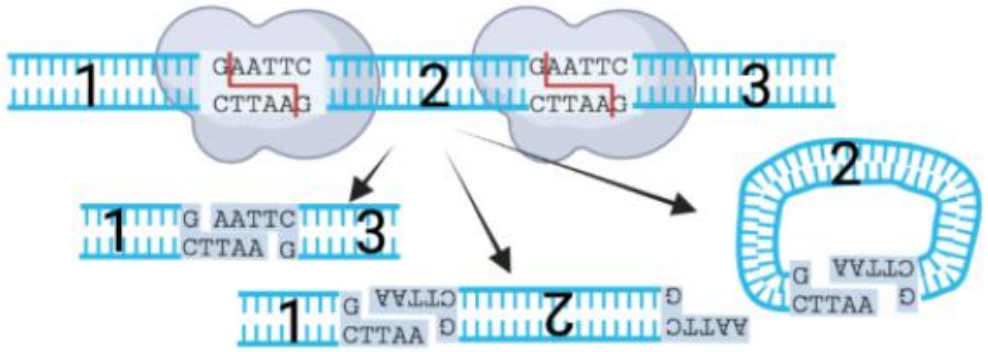
Valentin Bruttel[1,*], Alex Washburne[2,*,+], and Antonius VanDongen[3,*]

[1]Department for Obstetrics and Gynecology, University Clinics of Würzburg, Germany
[2]Selva Analytics, Bozeman, Montana, USA
[3]Department of Pharmacology and Cancer Biology, Duke University, Durham, NC, USA

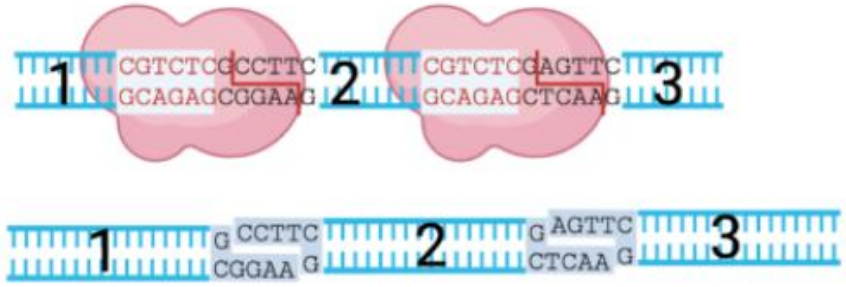
[*]all authors contributed equally to this work
[+]corresponding author alex.washburne@joinselva.com

How to synthesize a virus

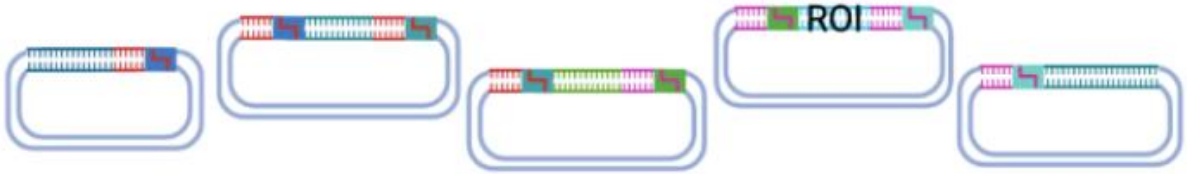
A) same type II RE



B) same type II**S** RE

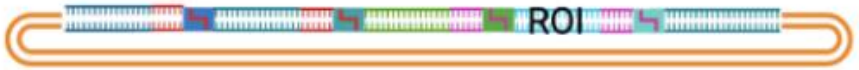


C) fragment amplification in plasmids

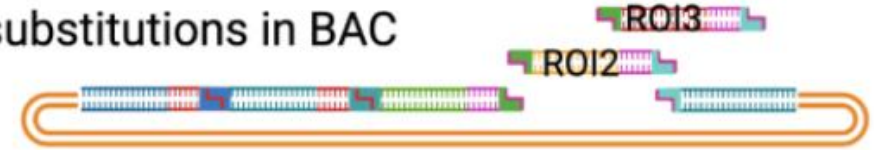


D) digestion via type IIS RE and purification

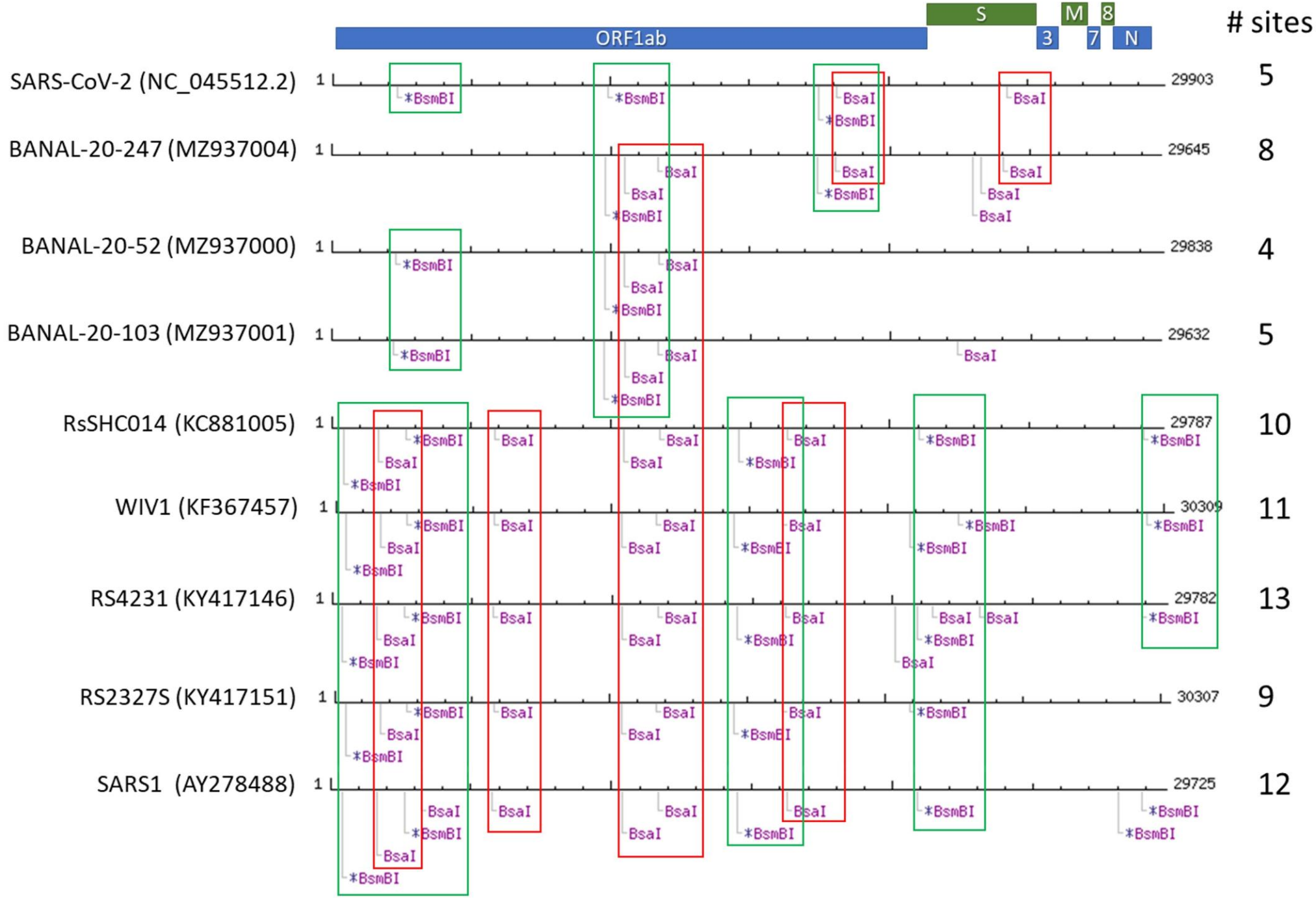
E) directed assembly via unique sticky ends in BAC



F) ROI substitutions in BAC



G) resulting genomic type IIs recognition site pattern


ORF1ab
S
3
M
7
8
N
sites
SARS-CoV-2 (NC_045512.2)
1
29903
5
BANAL-20-247 (MZ937004)
1
29645
8
BANAL-20-52 (MZ937000)
1
29838
4
BANAL-20-103 (MZ937001)
1
29632
5
RsSHC014 (KC881005)
1
29787
10
WIV1 (KF367457)
1
30309
11
RS4231 (KY417146)
1
29782
13
RS2327S (KY417151)
1
30307
9
SARS1 (AY278488)
1
29725
12
*BsmBI
BsaI

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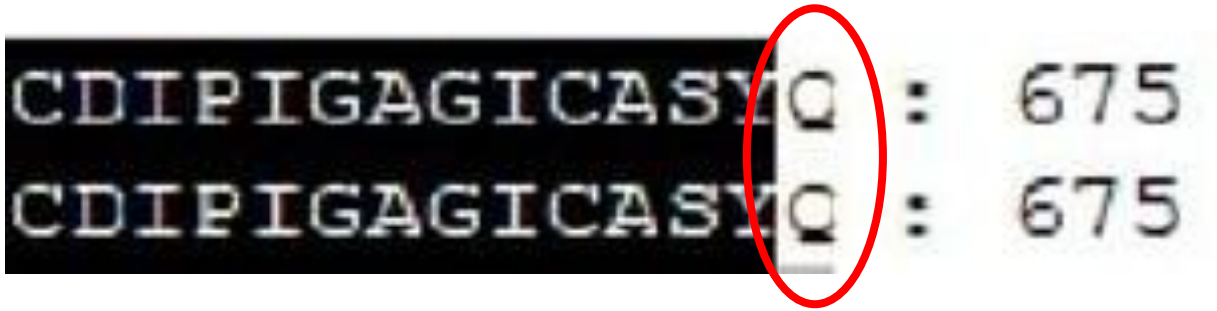
中国の研究者による情報隠蔽

- 武漢ウイルス研究所は2019年9月より、それまで公開していた22,000のウイルスのデータを見られないようにしている
- 2020年2月Natureに発表したSARS-CoV-2に最も近いウイルスRaTG-13の論文で、フーリン切断部位の直前でデータをカット



https://www.nature.com/articles/s41586-020-2012-7

Correspondence | Published: 17 March 2020

The proximal origin of SARS-CoV-2

Kristian G. Andersen ✉, Andrew Rambaut, W. Ian Lipkin, Edward C. Holmes & Robert F. Garry

Nature Medicine **26**, 450–452 (2020) | Cite this article

SARS-CoV-2 is the seventh coronavirus known to infect humans; SARS-CoV, MERS-CoV and SARS-CoV-2 can cause severe disease, whereas HKU1, NL63, OC43 and 229E are associated with mild symptoms. Here we review what can be deduced about the origin of SARS-CoV-2 from comparative analysis of genomic data. We offer a perspective on the notable features of the SARS-CoV-2 genome and discuss scenarios by which they could have arisen. Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus.

AndersenからFauciに宛てたメール

From: Kristian G. Andersen (b) (6)>
Sent: Friday, January 31, 2020 10:32 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Cc: Jeremy Farrar (b) (6)>
Subject: Re: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Hi Tony,

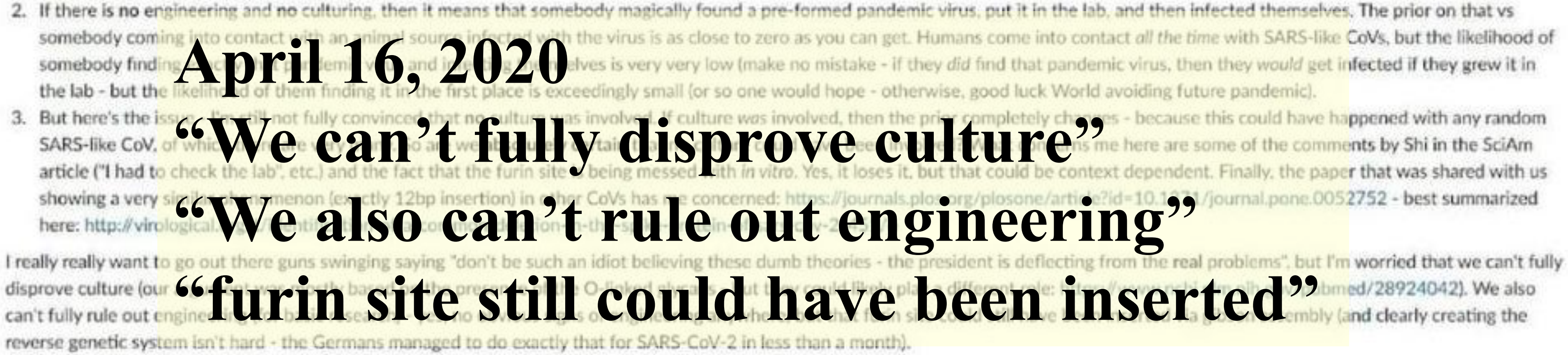
Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered.

We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory. But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

Best,
Kristian

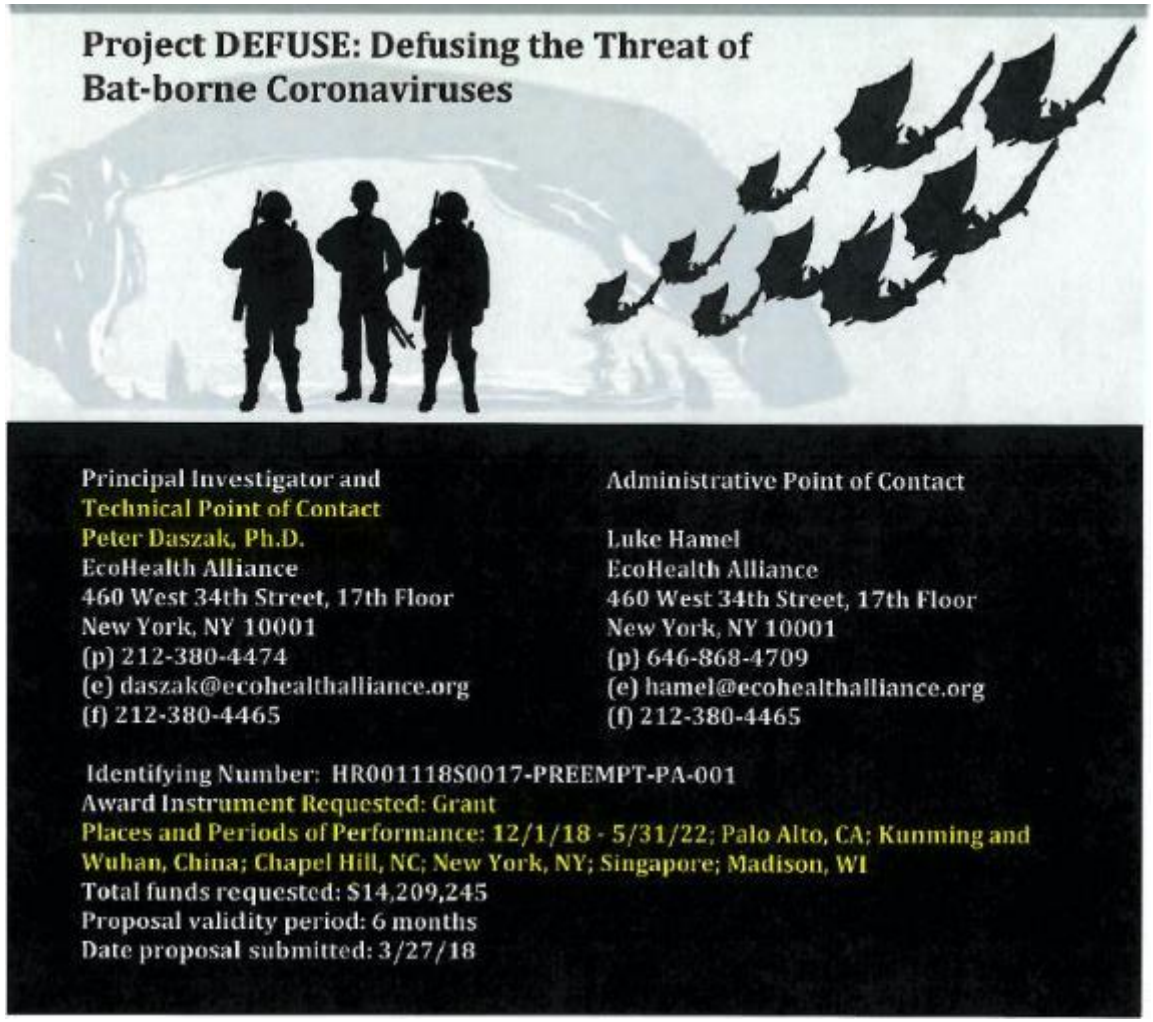
US House Hearing (July 11, 2023)

Kristian Andersen and Robert Garry testified under oath. They testified they changed their minds after the FOIA'ed email. After the testimony, their private Slack messages were uncovered, whey Andersen wrote he thought lab leak was likely even after the publication of the paper.



https://www.science.org/content/article/politicians-scientists-spar-over-alleged-nih-cover-up-using-covid-19-origin-paper

Project DEFUSE
DARPAへの研究予算申請書(2018)



Project DEFUSE: Defusing the Threat of Bat-borne Coronaviruses

Principal Investigator and Technical Point of Contact
Peter Daszak, Ph.D.
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New York, NY 10001
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(e) daszak@ecohealthalliance.org
(f) 212-380-4465

Administrative Point of Contact
Luke Hamel
EcoHealth Alliance
460 West 34th Street, 17th Floor
New York, NY 10001
(p) 646-868-4709
(e) hamel@ecohealthalliance.org
(f) 212-380-4465

Identifying Number: HR001118S0017-PREEMPT-PA-001
Award Instrument Requested: Grant
Places and Periods of Performance: 12/1/18 - 5/31/22; Palo Alto, CA; Kunming and Wuhan, China; Chapel Hill, NC; New York, NY; Singapore; Madison, WI
Total funds requested: $14,209,245
Proposal validity period: 6 months
Date proposal submitted: 3/27/18

- 米国の機関、大学、武漢ウイルス研究所が共同で申請
  →不採択
- 2021年9月に内部告発で流出
  「新型コロナの設計図」
  多くの学者が研究所起源支持に
  ウイルス学者は反論
- 2023年末に申請書のドラフト版をUS Right to Knowが情報公開請求で米国地質調査所から入手・公開

DEFUSEの研究計画内容

to use human ACE2 and grow in human cells. *S2 Proteolytic Cleavage and Glycosylation Sites:* After receptor binding, a variety of cell surface or endosomal proteases[68-71] cleave the SARS-CoV S glycoprotein causing massive changes in S structure [72] and activating fusion-mediated entry[64,73]. We will analyze all SARSr-CoV S gene sequences for appropriately conserved proteolytic cleavage sites in S2 and for the presence of potential furin cleavage sites[74,75]. SARSr-CoV S with mismatches in proteolytic cleavage sites can be activated by exogenous trypsin or cathepsin L. Where clear mismatches occur, we will introduce appropriate human-specific cleavage sites and evaluate growth potential in Vero cells and HAE cultures. In SARS-CoV, we

SARS系統のウイルス
にフーリン切断部位を
人工的に挿入する計画

ウイルス学者の反論

DEFUSE計画書について

- 実験は米国でやると書いている。中国とは書いていない
- フーリン切断部位をS1／S2の間に挿入とは書いていない
- フーリン切断部位のPRRARの配列は標準的でない

Bruttel et al. 論文について

- そんな作り方はしない
  Andersen「幼稚園の分子生物学だ」

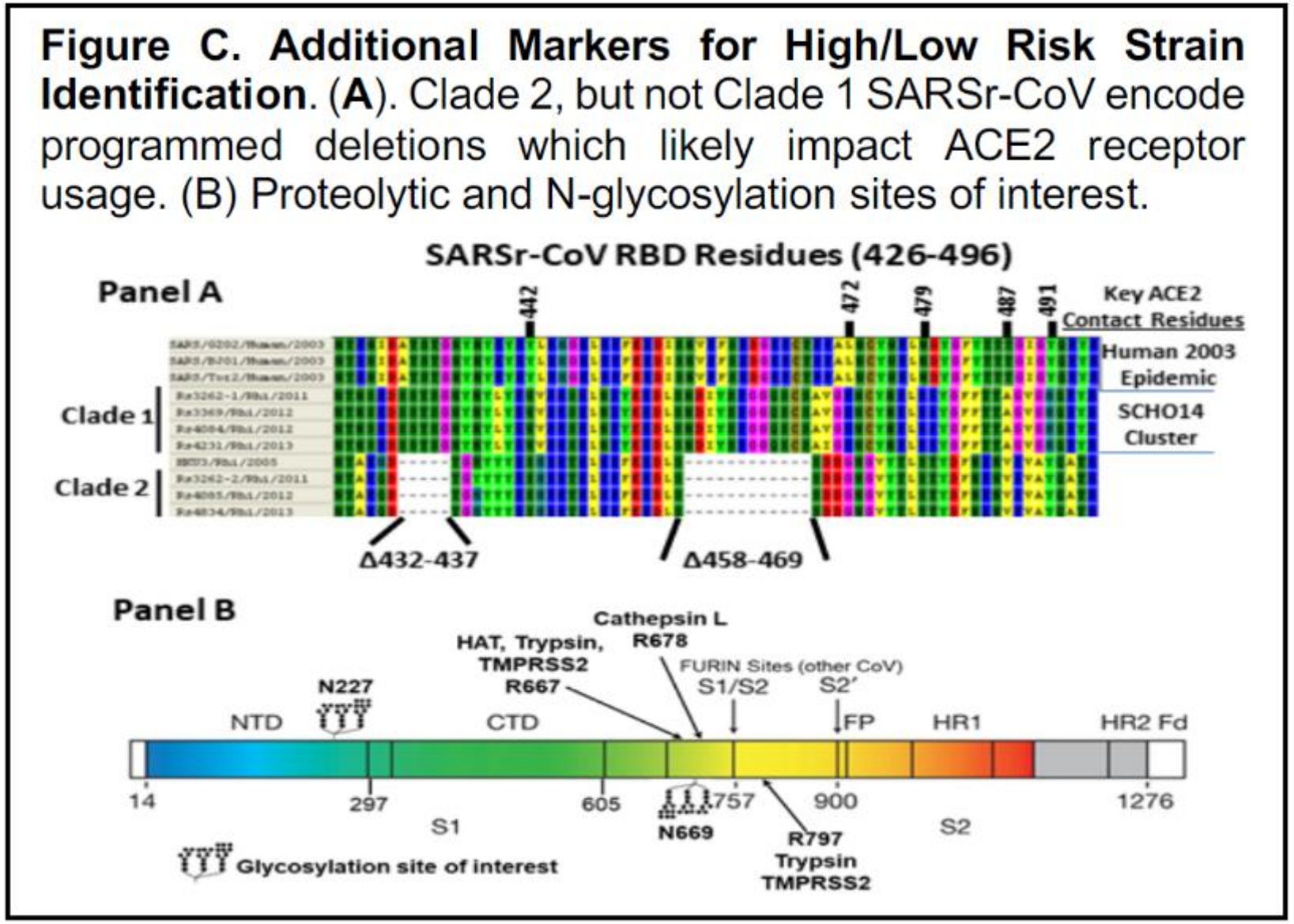
DEFUSEの草稿

DaszakとBaricは申請書には実験を米国でやると書いて、実際は武漢でやろうとコメントしていた。

DARPAが心配しないように、全ての仕事はラルフによって行われることにしておいて、予算を獲得したらどこでどの仕事をするか割り振ろう。実際には多くの分析は武漢で行われることになると私は思っている。

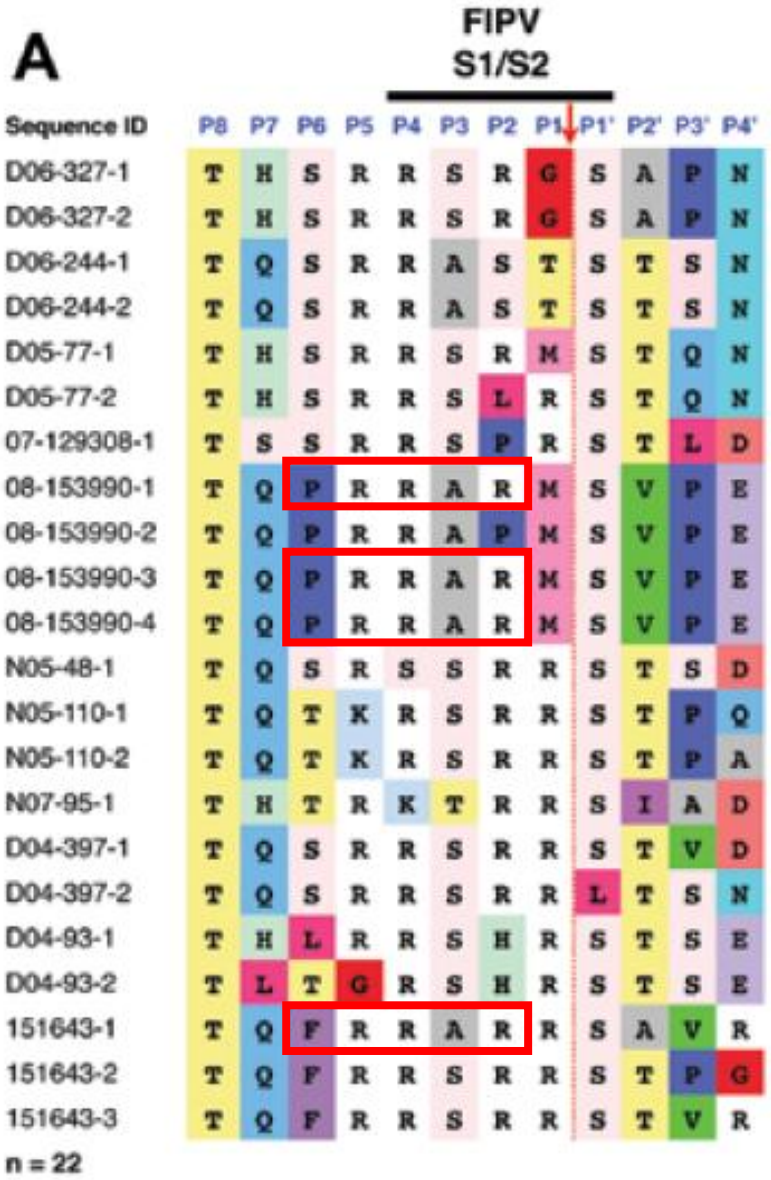
米国では、ヒトの細胞に結合して増える組換えSARSウイルスの研究はBSL2ではなくBSL3の実験室で行われる。武漢ではBSL2で行われるだろう。米国の研究者はそれを知ったら驚くぞ。

DEFUSEの草稿



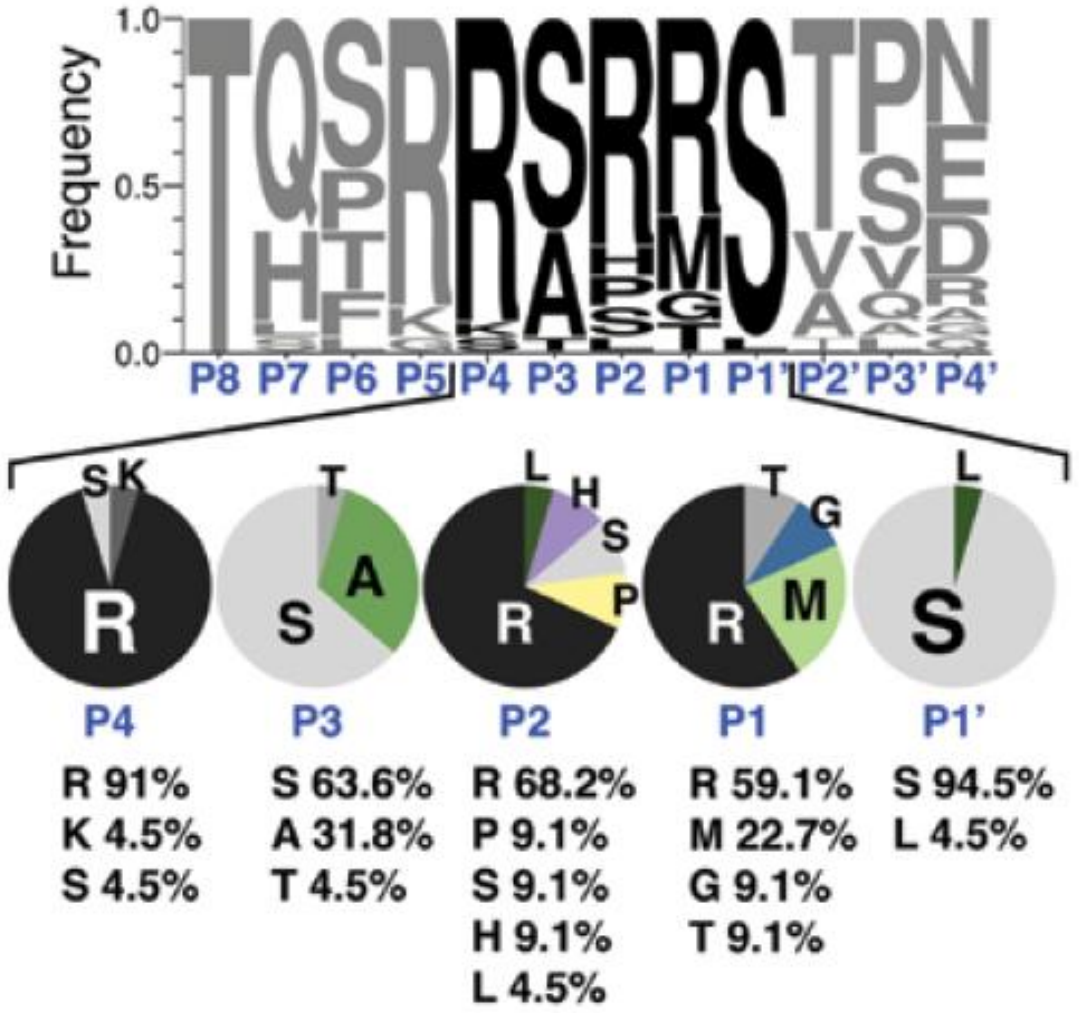
フーリン切断部位を入れるより具体的な計画を記載。

Baricは議会の聴取で、FCS挿入はネコのコロナウイルスを参考にしたと供述



B

https://wwwnc.cdc.gov/eid/article/19/7/12-1094_article



DEFUSE草稿にあった決定的証拠

「６つのセグメントで合成」「BsmBIの購入」

PMC2583659, PMC3791741). We will identify the best consensus candidate and synthesize the genome using commercial vendors (e.g., BioBasic, etc.), as six contiguous cDNA pieces linked by unique restriction endonuclease sites that do not disturb the coding sequence, but allow for full length genome assembly. Full length genomes will be transcribed into RNA and electoration is used to recovery full length recombinant viruses (PMC3977350, PMC240733). Using the full length genomes, we will re-evaluate virus growth in primary human airway epithelial cells at low and high multiplicity of infections and in vivo in hACE2 transgenic mice, testing whether backbone genome sequence alters full length SARSr-CoV pre-epidemic or pathogenic potential in models of human infection. All experiments are performed in triplicate and the data provided to the Modeling

MATEI

Item	Manufacturer	Number/Descr	Unit Price
Restriction Enzymes small tubes	NE BIO LABS	R0580S	$72.00
Restriction Enzymes large tubes	NE BIO LABS	R0580L	$292.00
SuperScript™ III Reverse Transcriptase	FISHER	18-080-051	$460.00
T4 DNA Polymerase - 750 units	NE BIO LABS	M0203L	$268.00
Antarctic DNA Phosphatase - 1000 units	NE BIO LABS	M0289S	$68.00
T4 DNA Ligase	NE BIO LABS	M0202L	$256.00

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情報機関の分析

COVID-１９の起源

- 天然起源なら科学の問題→６年経っても中間宿主を発見できず
- 研究所起源ならForensicの問題→捜査機関・情報機関の仕事

FBI: 中確信度で研究所起源

CIA, エネルギー省: 低確信度で研究所起源

MI-6: 早期に研究所起源と分析し首相に報告

BND（ドイツ）：2020年に80～95%で研究所起源と分析
→メルケル首相が握りつぶす

2023年6月の報道

2019年11月最初にCOVID-19に感染した武漢ウイルス研究所の研究員3名の氏名が公表。

いずれも、同研究所で新型コロナウイルスに極めて近いウイルスの遺伝子を人工的に改変する研究に従事していた。

PUBLIC

First People Sickened By COVID-19 Were Chinese Scientists At Wuhan Institute Of Virology, Say US Government Sources

The three scientists were engaged in "gain-of-function" research on SARS-like coronaviruses when they fell ill

MICHAEL SHELLENBERGER, MATT TAIBBI, AND ALEX GUTENTAG
JUN 13, 2023

Share

Ben Hu, one of three Chinese researchers who U.S. government sources fell ill, in a 2017 video by Chinese state-run television, watching a lab worker handle specimens. Neither are wearing protective gear.

https://twitter.com/shellenberger/status/1668660948532625410

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考察１

気候変動問題との類似性

- 高校の知識でウソと見破れる
  - 再エネのダメさ（エネルギー密度の低さ）は高校の物理と化学の知識で容易に計算可能
  - 「コロナの起源」の書評で進化生物学者の青木重幸氏は新型コロナウイルスは「高校レベルの分子生物学の知識があれば、遺伝子操作を疑わないほうが変」とコメント
- 科学者がお金（研究費）のために平気でウソをつく

考察２

形而上学的価値の喪失
（神、真実、正義など）
c.f. 人権・民主主義の起源
米共和党議員の特徴

唯物論、唯我論の台頭
（マルクス主義、
実存主義、
ポストモダン）
→実在論の否定

Jordan Peterson（キリスト教）　Mat Ridley（啓蒙主義者）

https://www.youtube.com/watch?v=FEh5JyZC218

Jay Bhattacharya（現NIH所長）の言葉

私の人生の目的は賞をもらうことではありません。私はキリスト教徒です。信仰者です。自分の命を犠牲にして他人を救えるなら、それは充実した人生です。私にとって自分の地位は重要ではありません。「価値のある人生を送ったか？他人のために生きたか？」が重要なのです。もちろん、自らのキャリアの評価を落として嬉しいとは思いませんし、それを望んでもいません。それでも、私は自分のしたことを振り返ってこう言うことができます。「私は自分がすべきことをしたんだ。人生の本当の目的のために働いたんだ」と。私の人生の目的は自分の履歴書にもう1行追加することではありません。真の目的を成すことが最も大事なんだと。私には自分を愛してくれる家族がいます。NIHのトップに『異端者』と呼ばれてようとも、私は自分がすべきことをしているのです。

https://www.youtube.com/watch?v=PusXRm-mSd0