Chen-Hanson Ting SVFIG February 22, 2020

Wuhan Coronavirus can be cured by taking 10 grams of vitamin C every 4 hours, until diarrhea.

 Flucan be cured by taking 5 grams of vitamin C every 4 hours, until diarrhea.

- Wuhan Coronavirus is now named COVID-19, replacing SARS-CoV-2.
- The pandemic now exceeds the size and seriousness of SRAS in 2003.
- We still do not know its origin.

- Rumors have that it was manufactured in Wuhan P4 Lab.
- It is sequenced in many laboratories in many countries.
- It is suspected to evolve continually.

- It is suspected to have evolved in hosts like bats, snakes, and pangolins.
- Relations to other coronaviruses:
 - **SARS** 79%
 - Bat Coronavirus 80%
 - Bat RaTG13 96%

Compare Viral Genomes

- Have the best tools to compare genomes.
- My Exhaustive Pattern Search algorithm can be used to identify repeated sequences in two similar genomes.

Genomes of SARS-CoV-2

- I have the best tools to compare genomes.
- My Exhaustive Pattern Search algorithm can be used to identify repeated sequences in two similar genomes.

Genomes of COVID-19

ID	Matches	Differences
MN908947	29883	0
MN938384	29758	60
MN975262	29771	100
MN985325	29802	60
MN988668	29861	0
MN988669	29861	0
LC521925	29769	59
LR757995	29811	41
LR757996	29848	0
LR757998	29806	40
SARS-CoV	1618	28113
MERS-CoV	5	30023

Genomes of COVID-19

- COVID-19 genomes are very different from these of MERS-CoV and SARS-CoV.
- 3 COVID-19 are identical to the Reference Sequence.
- 20 differences are caused by 1 different nucleotide.
- 6 COVID-19 differ from the Reference Sequence by <6 nucleotides.

Genomes of CoVs

Name	ID	Length
Bat-sl-CoVZC45	MG772933	29802
Bat-sl-CoVZXC21	MG772934	29732
Bat-RaTG13	MN996532	29855
Human CoV-229E	NC_002645	27317
Human SARS-Cov	NC_004718	29751
Human CoV-NL63	NC_005831	27553
Human CoV-OC43	NC_006213	30741
Human CoV-HKU1	NC_006577	29926
Human MERS-CoV	NC_019843	30119
Human COVID-19	NC_045512	29903

Matches in CoV Genomes

Name	ZC45	ZXC21	RaTG13	229E	SARS	NL63	OC43	HKU1	MERS	COVID
ZC45	29782	19509	4593	13	2444	0	7	8	5	4741
ZXC21	19509	29712	4584	11	2563	0	13	7	2	4674
RaTG13	4587	4578	29835	4	1597	0	5	3	13	14946
229E	27	25	24	27297	25	85	24	5	4	24
SARS	2442	2561	1601	9	29731	1	7	5	1	1618
NL63	0	0	0	85	1	27533	4	14	2	1
OC43	9	15	13	12	11	4	30721	313	14	18
HKU1	8	7	3	5	5	14	313	29906	7	18
MERS	5	2	13	4	1	2	14	7	30099	1
COVID	4748	4681	14959	17	1627	1	23	18	1	29883

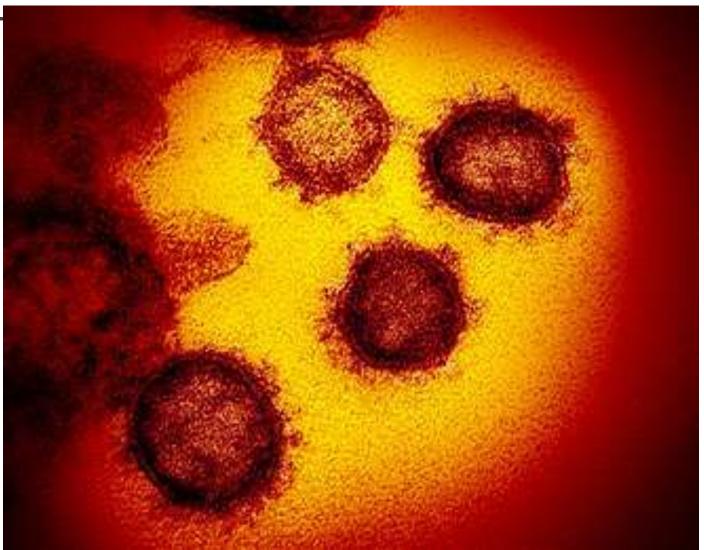
Matches in CoV Genomes

- COVID-19 genomes are very different from other coronaviruses.
- Best matches to COVID-19 sequences:
 - Bat RaTG13 14959
 - Bat CoVCZC45 4748
 - Bat CoVCZXC21 4681
 - Human SARS-CoV 1627

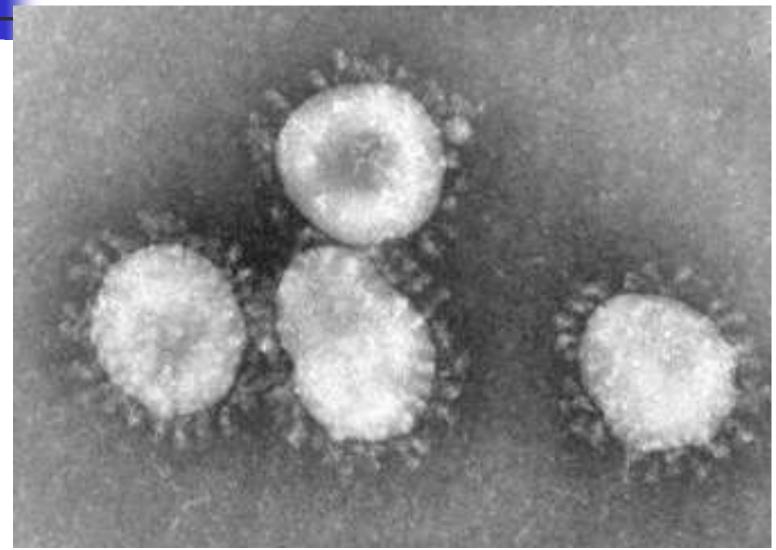
SARS-CoV-2 Engineered?

- COVID-19 genome is most closely related to Bat RaTG13.
- It is so much different from all other coronaviruses that it is unlikely to be engineered.
- It is difficult to prove either way unless we have the exact sources from which COVID-19 is assembled.

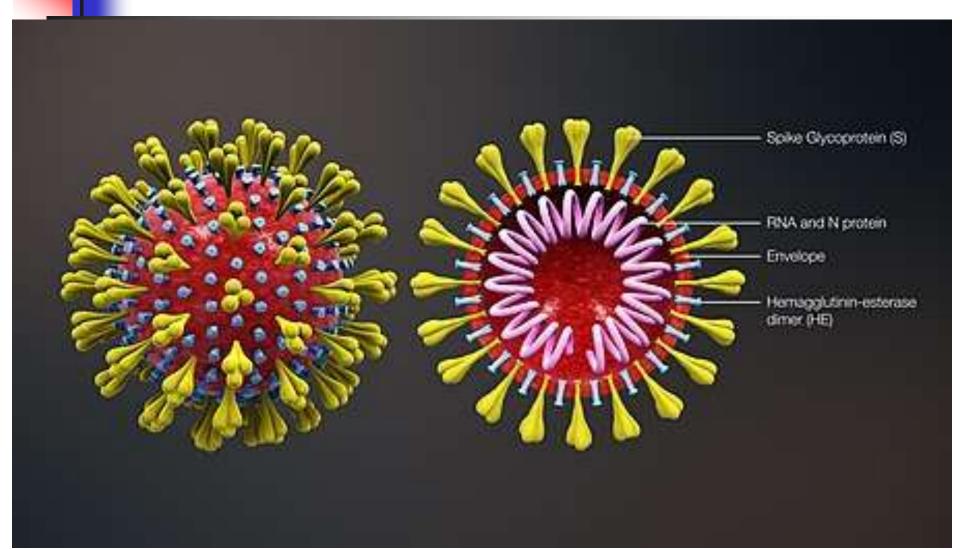
COVID-19

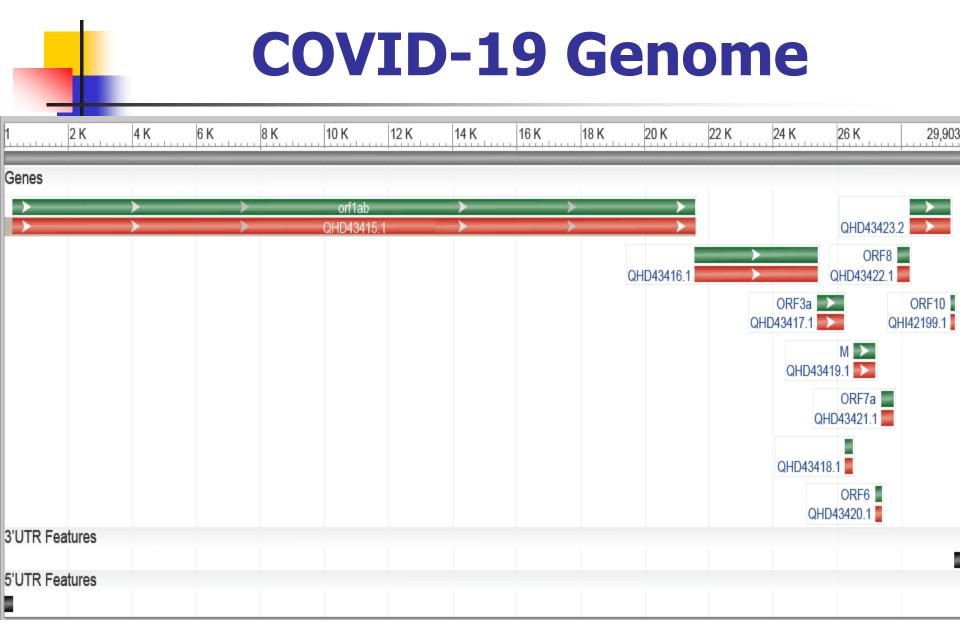


COVID-19



COVID-19

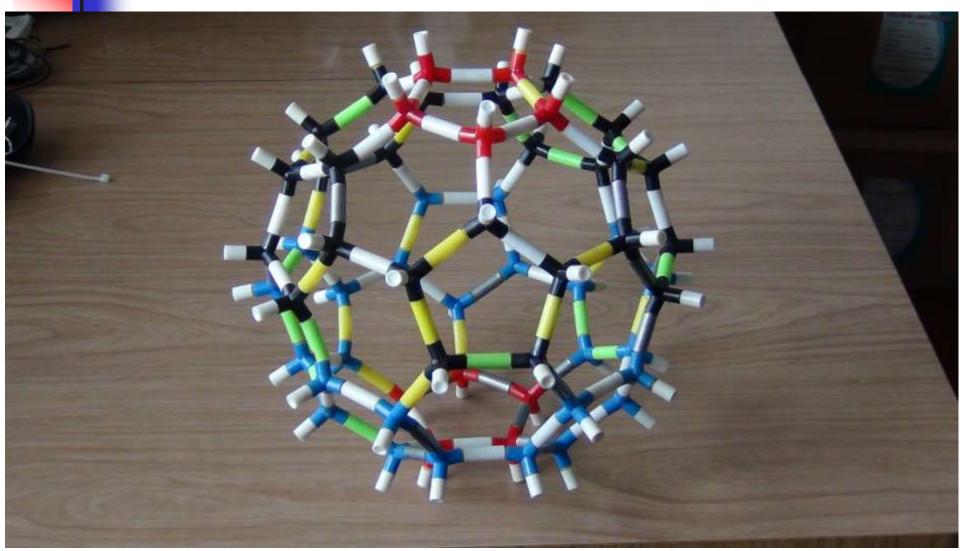


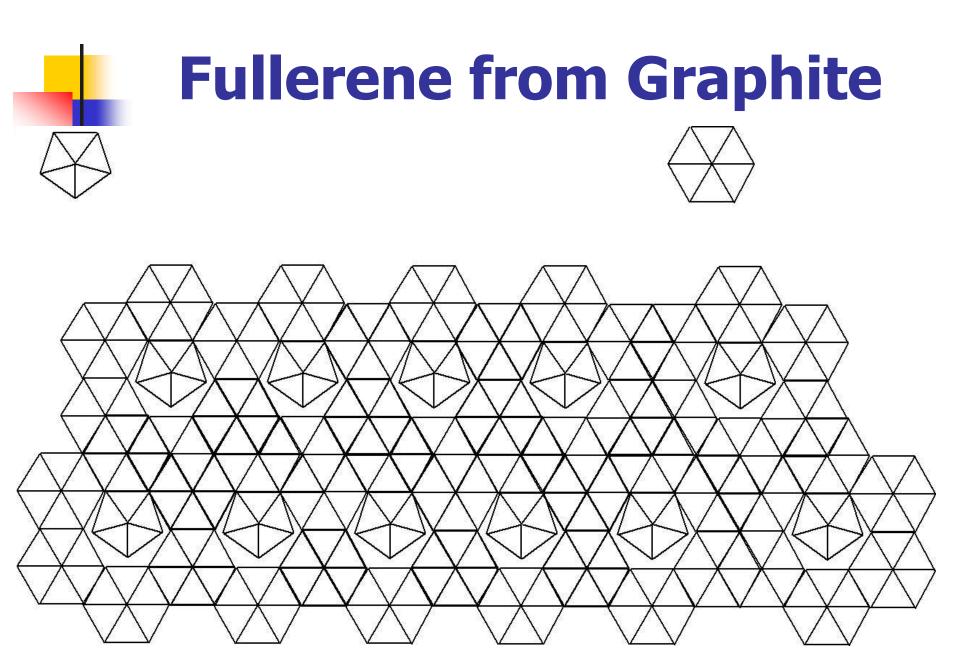


Structure of Coronavirus

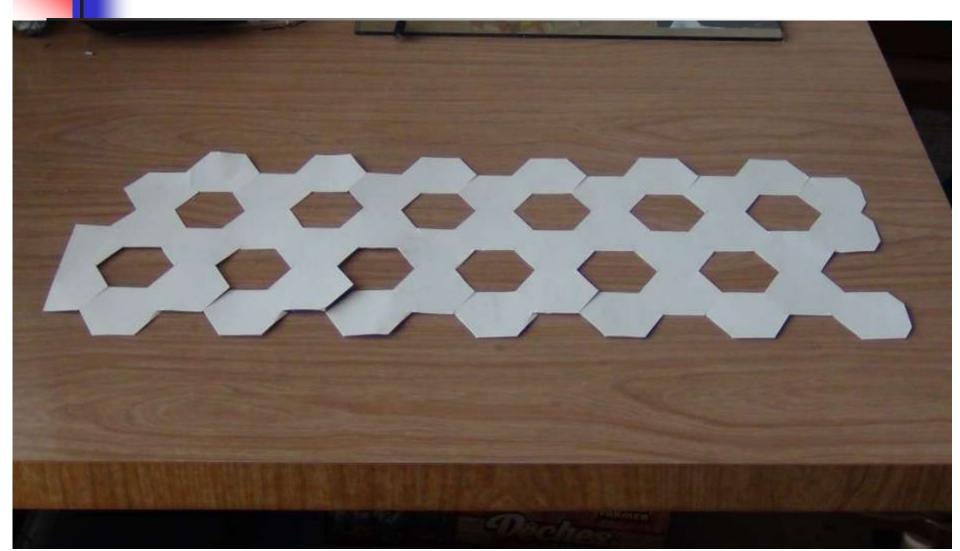
- It has the look of a C60 Fullerene or Buckminsterfullerene molecule.
- Fullerene is formed from graphite.
- A plain sheet of graphite buckled under heat to form a ball.

Fullerene

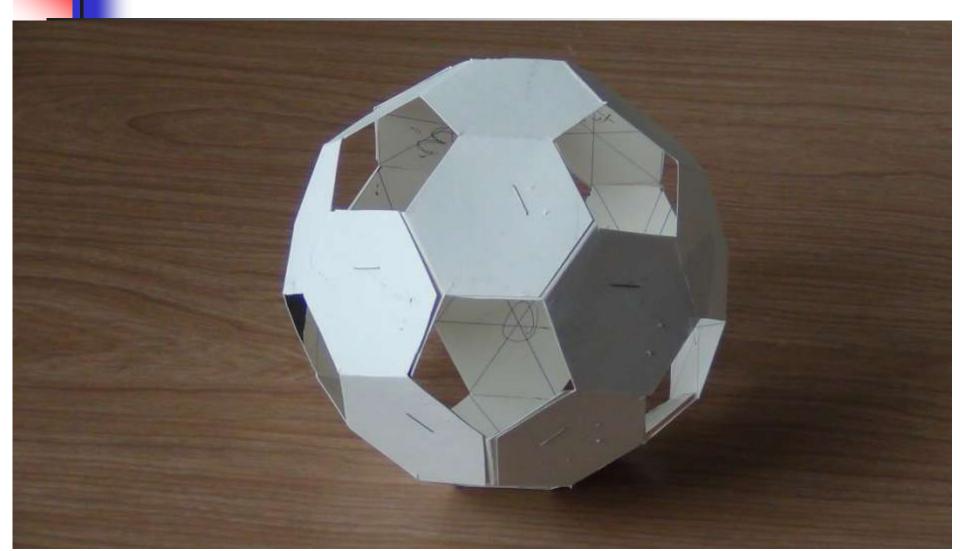




Fullerene



Fullerene

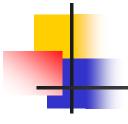




Folding a Fullerene

Coronavirus Genome

- It has the look of a C60 Fullerene or Buckminsterfullerene molecule.
- Fullerene is formed from graphite.
- A plain sheet of graphite buckled under heat to form a ball.



Questions?



Thank You!