Biology of SARS-CoV-2

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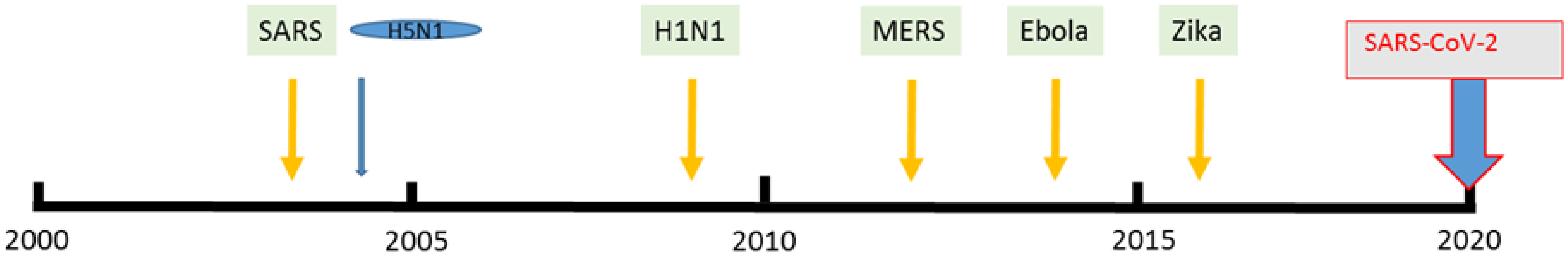
- Despite remarkable advances in medical science and treatment during 20th century, infectious diseases remain the leading cause of death worldwide
- ***Emerging*** *disease* is a disease that has never been recognized before.
    - During the last 20 years, at least 30 new infectious have emerged.

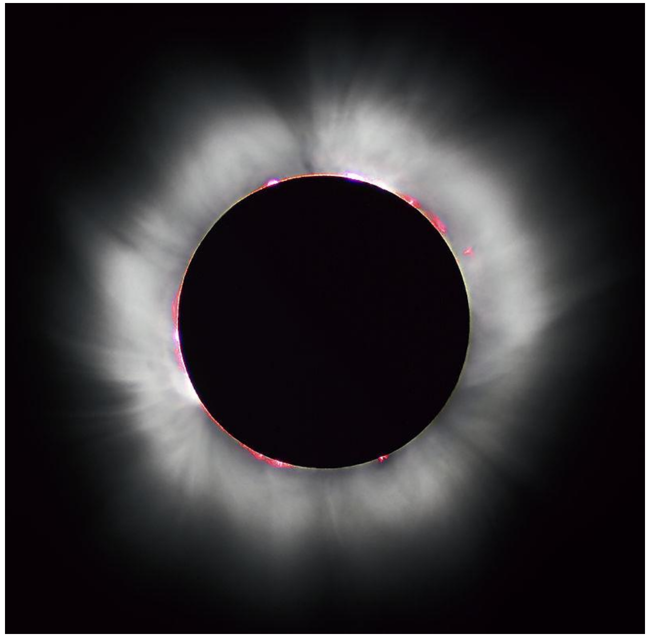
These diseases are the leading cause of death worldwide, claiming at least 17 million lives every year

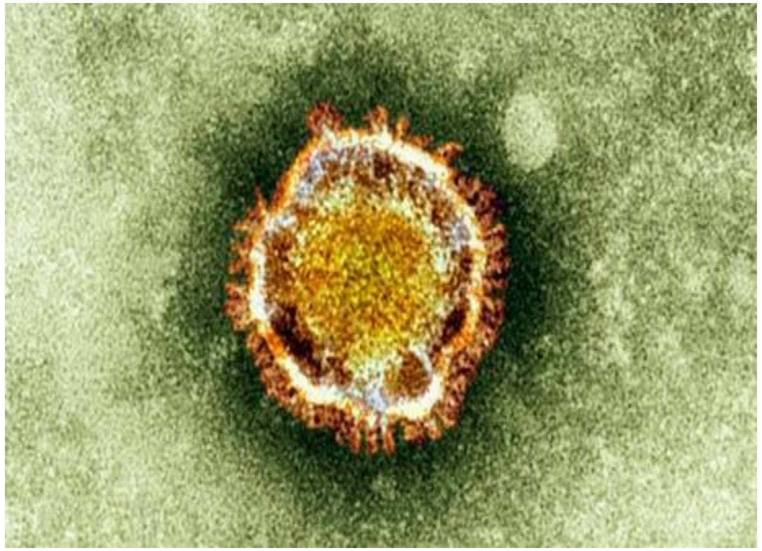


coronaviridae

Coronaviridae is a family of:
enveloped, positive-sense, single-stranded RNA viruses.
The viral genome is 26–32 kilobases in length.
Coronaviruses (CoVs) are characterized by club-shaped spike projections emanating from their surface of the virion, which in electron micrographs of spherical particles create an image reminiscent of the solar corona.

The structure of CoVs comprises the spike (S), envelope (E), membrane (M), and nucleocapsid (N).
The family *Coronaviridae* is organized in 2 sub-families, 5 genera, 23 sub-genera and about 40 species



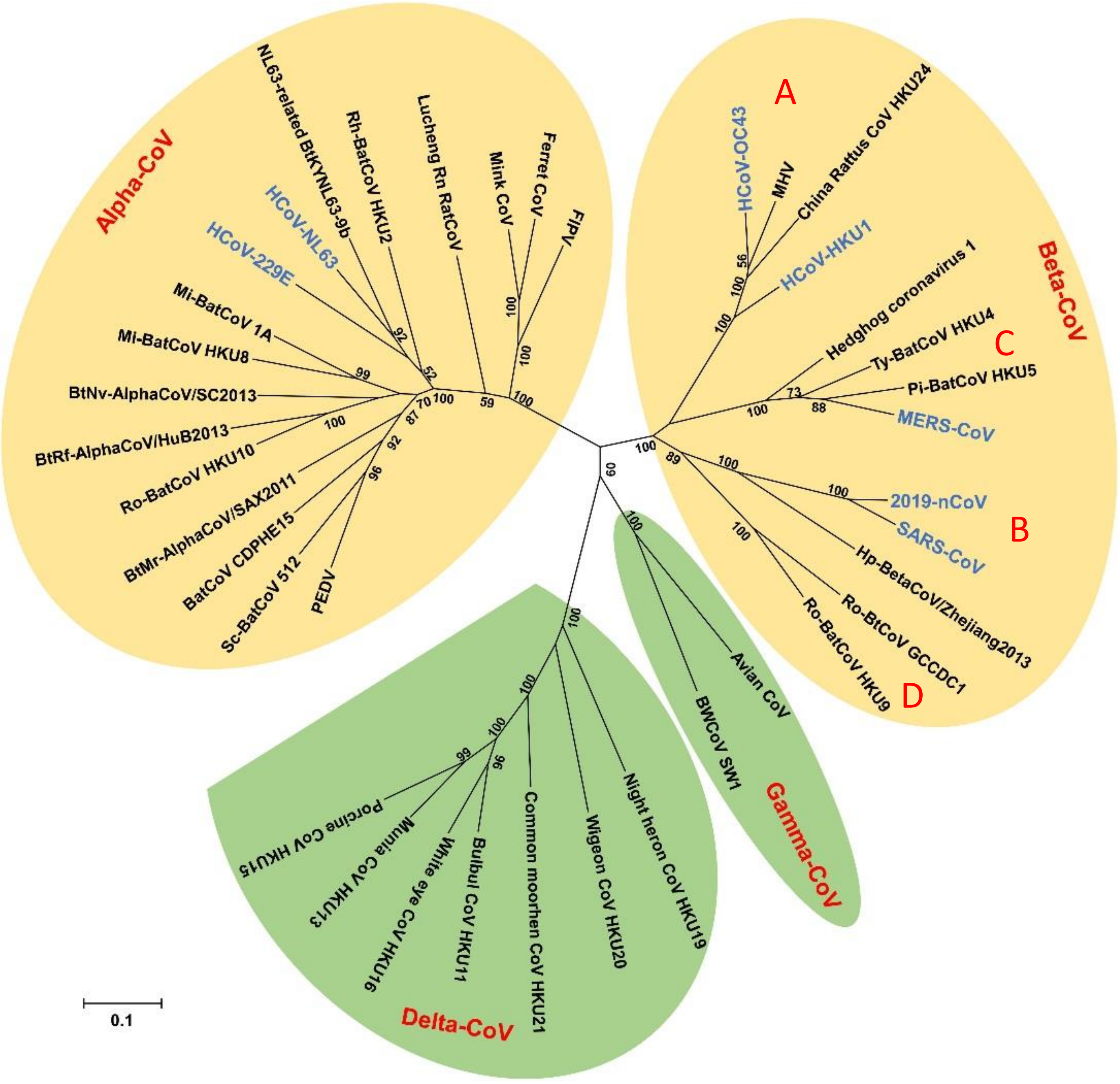


Why do we have new viruses in this family

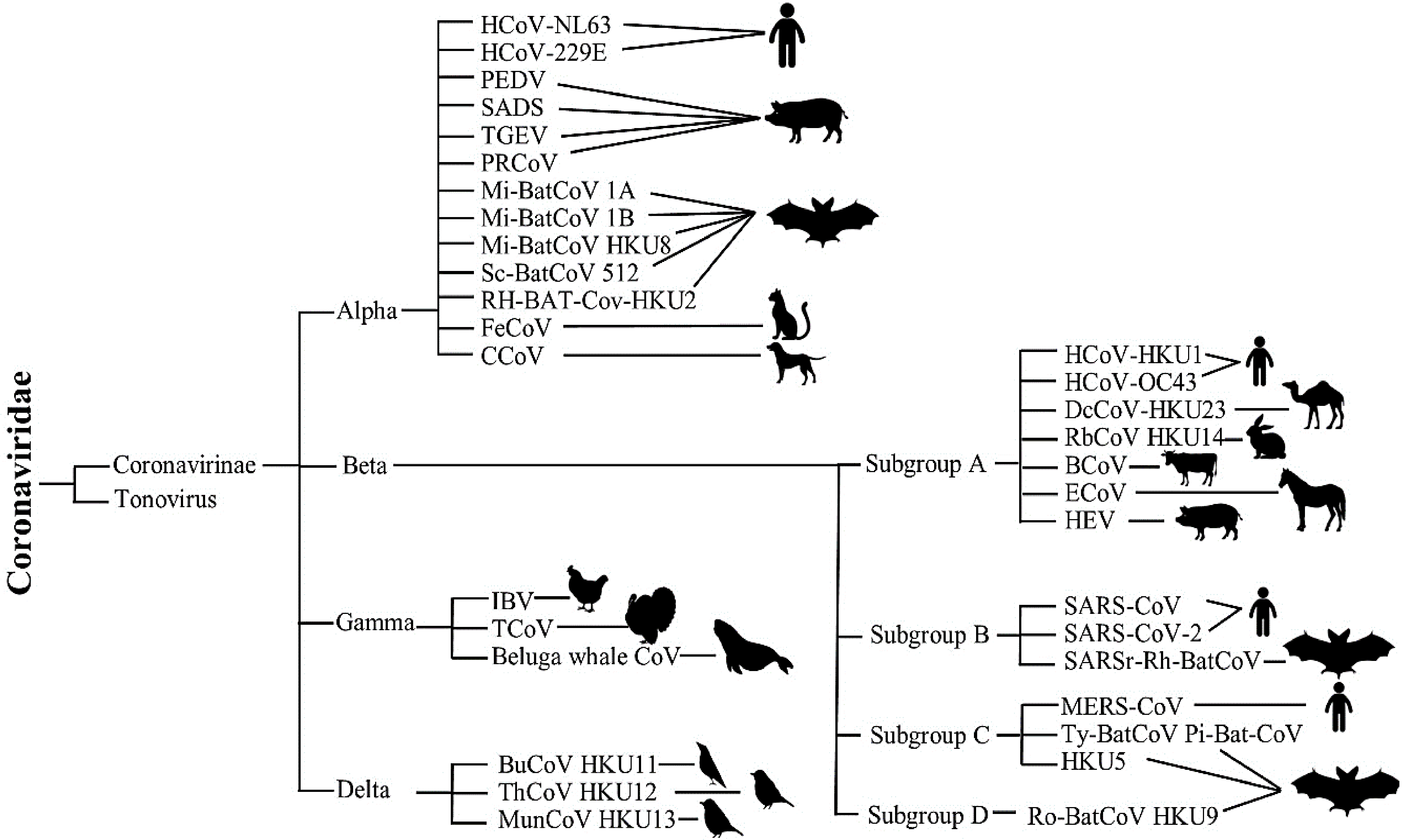
- Coronaviruses are zoonotic, meaning they are transmitted between animals and people. Several known coronaviruses are circulating in animals that have not yet infected humans.
- An unusually large RNA genome 26-32 kb , and In comparing with the genomes of all other RNA viruses have the largest genome. coronavirus genomes contain cis-acting RNA elements that ensure the specific replication of viral RNA
- Like other RNA viruses has the potential for mutation.

CORONAVIRUSES- CLASSIFICATION

- Coronaviruses are enveloped, positive-sense, single-stranded RNA viruses of ~30 kb.
- They infect a wide variety of host species.
- They are largely divided into four genera
  - α, β, γ, and δ based on their genomic structure.
  - α and β coronaviruses infect only mammals
    - Human coronaviruses such as 229E and NL63 are responsible for common cold and croup and belong to α coronavirus.
    - In contrast, SARSCoV, Middle East respiratory syndrome coronavirus (MERS-CoV) and SARS-CoV-2 are classified to β coronaviruses.



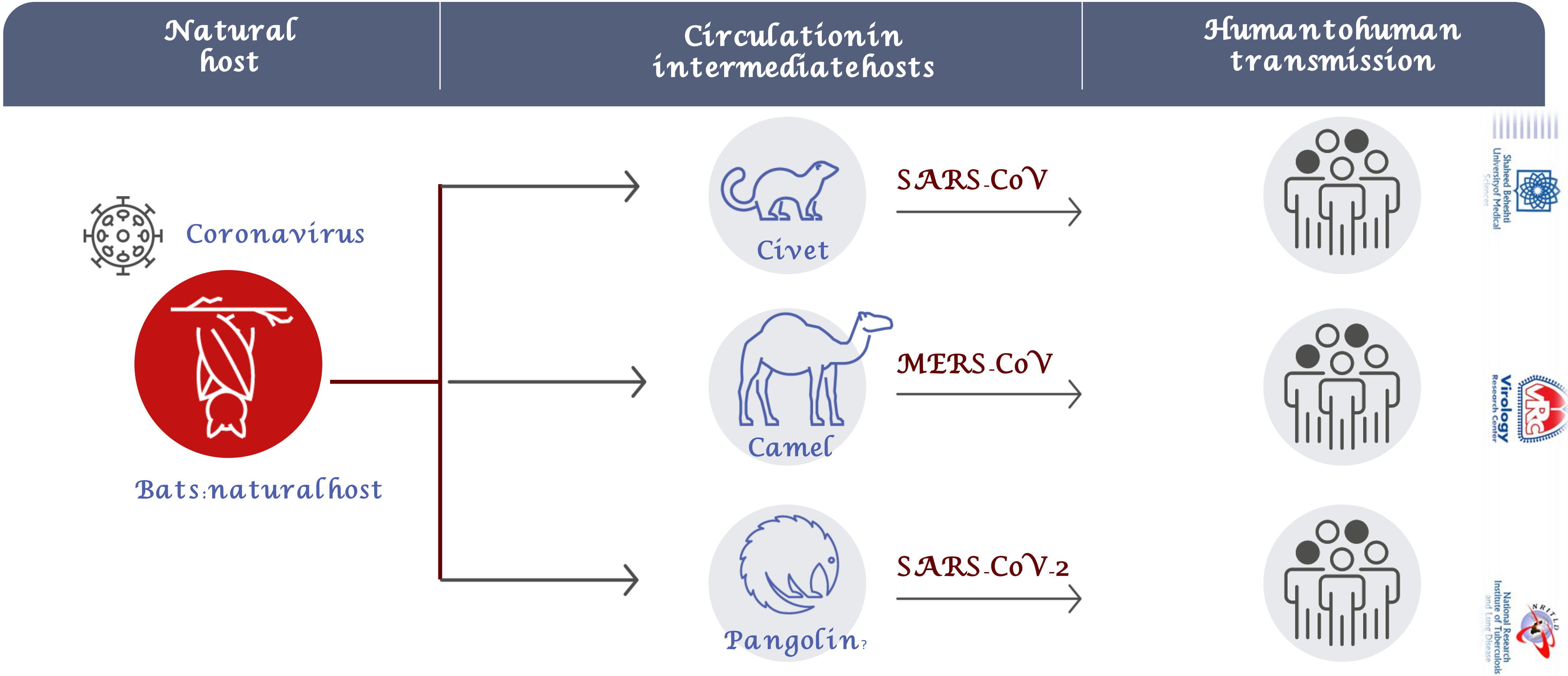
CORONAVIRUSES- HOST



Human Coronaviruses

Coronaviruses	Disease
SARS-CoV-2	COVID-19
SARS-CoV	Severe Acute Respiratory Syndrome (SARS)
MERS-CoV	Middle East Respiratory Syndrome (MERS)
HCoV – HKU1	Usually mild respiratory disease (10-15% of common colds caused by HCoVs) but can cause severe disease in vulnerable groups
HCoV – OC43	
HCoV – NL63	
HCoV - 229E	

Ecology of emerging coronaviruses SARS-CoV, MERS-CoV, and SARS-CoV-2 are all bat origin coronaviruses, which cause human infections after circulation in other animal hosts



Natural host	Circulation in intermediate hosts	Human to human transmission

Coronavirus

Bats: natural host

Civet — SARS-CoV →

Camel — MERS-CoV →

Pangolin? — SARS-CoV-2 →

Jin Y et al. Viruses. 2020 Mar 27;12(4). pii: E372. doi: 10.3390/v12040372.

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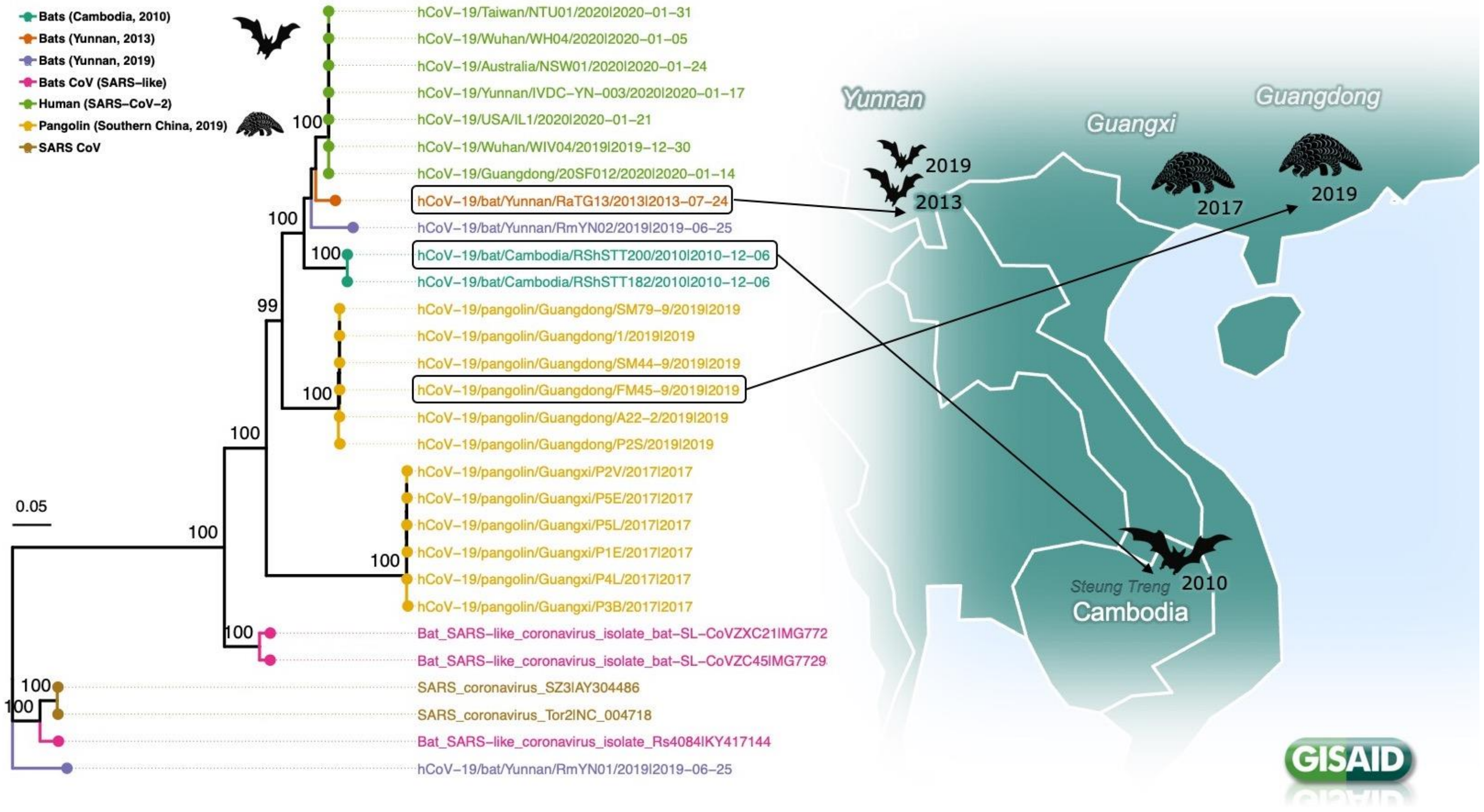
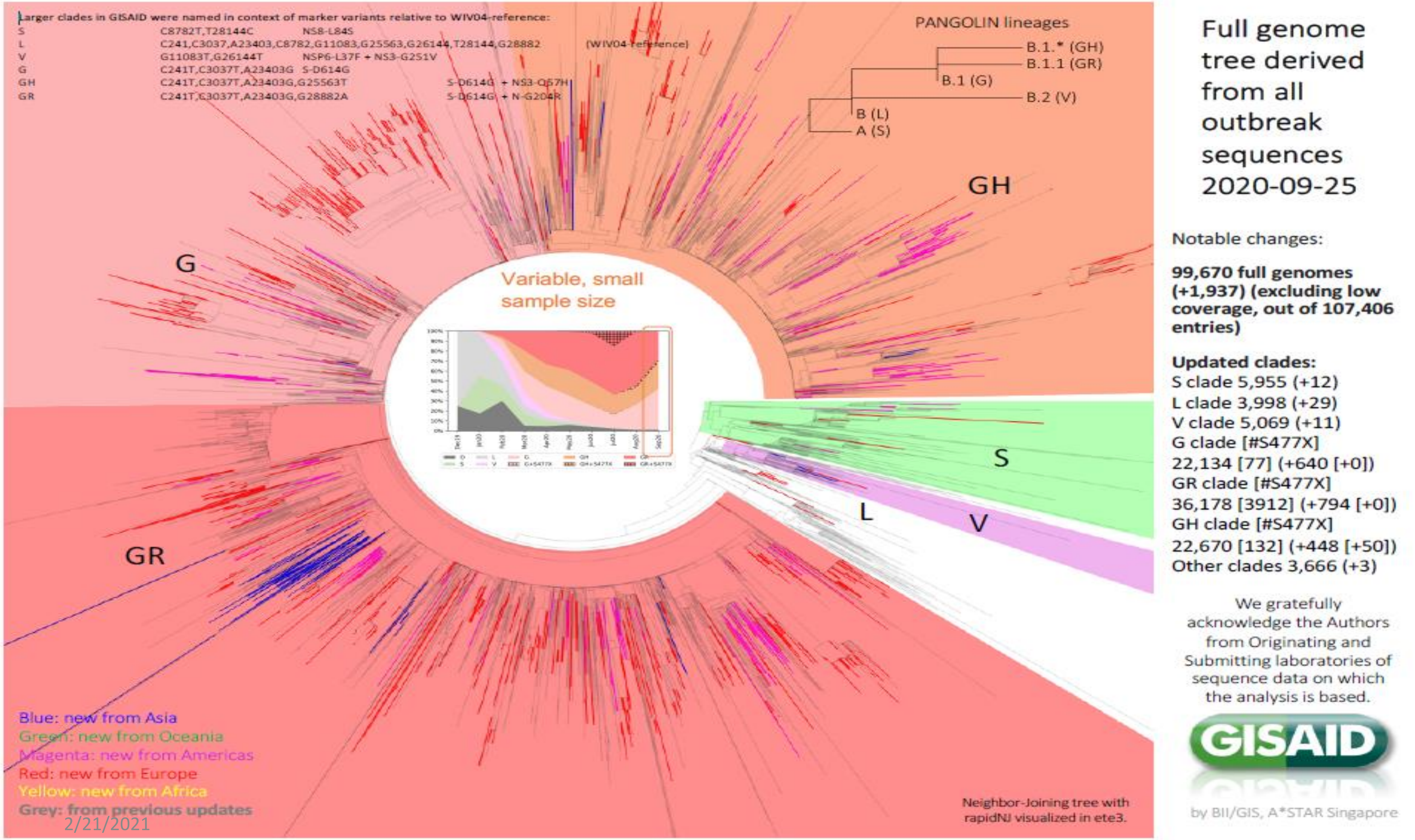
Additional closely related bat CoVs identified in Cambodia

The Virology Unit of the Institut Pasteur du Cambodge has recently submitted the full genome sequences for 2 bat coronaviruses from samples taken from bats in 2010 in the Steung Treng province of Cambodia; they appear to join the list of coronaviruses that are closely related to the current pandemic virus.

Other potential precursors known so far include bat coronaviruses from caves in Yunnan (Southern China), sampled in 2013 and 2019, and samples derived from pangolins in Southern China from 2017 and 2019.

see: Vibol Hul et al (2021) A novel SARS-CoV-2 related coronavirus in bats from Cambodia





Larger clades in GISAID were named in context of marker variants relative to WIV04-reference:

S	C8782T,T28144C	NS8-L84S
L	C241,C3037,A23403,C8782,G11083,G25563,G26144,T28144,G28882	(WIV04-reference)
V	G11083T,G26144T	NSP6-L37F + NS3-G251V
G	C241T,C3037T,A23403G	S-D614G
GH	C241T,C3037T,A23403G,G25563T	S-D614G + NS3-Q57H
GR	C241T,C3037T,A23403G,G28882A	S-D614G + N-G204R

Blue: new from Asia
Green: new from Oceania
Magenta: new from Americas
Red: new from Europe
Yellow: new from Africa
Grey: from previous updates

Neighbor-Joining tree with rapidNJ visualized in ete3.

Full genome tree derived from all outbreak sequences 2020-09-25

Notable changes:

99,670 full genomes (+1,937) (excluding low coverage, out of 107,406 entries)

Updated clades:
S clade 5,955 (+12)
L clade 3,998 (+29)
V clade 5,069 (+11)
G clade [#S477X]
22,134 [77] (+640 [+0])
GR clade [#S477X]
36,178 [3912] (+794 [+0])
GH clade [#S477X]
22,670 [132] (+448 [+50])
Other clades 3,666 (+3)

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GISAID

by BII/GIS, A*STAR Singapore

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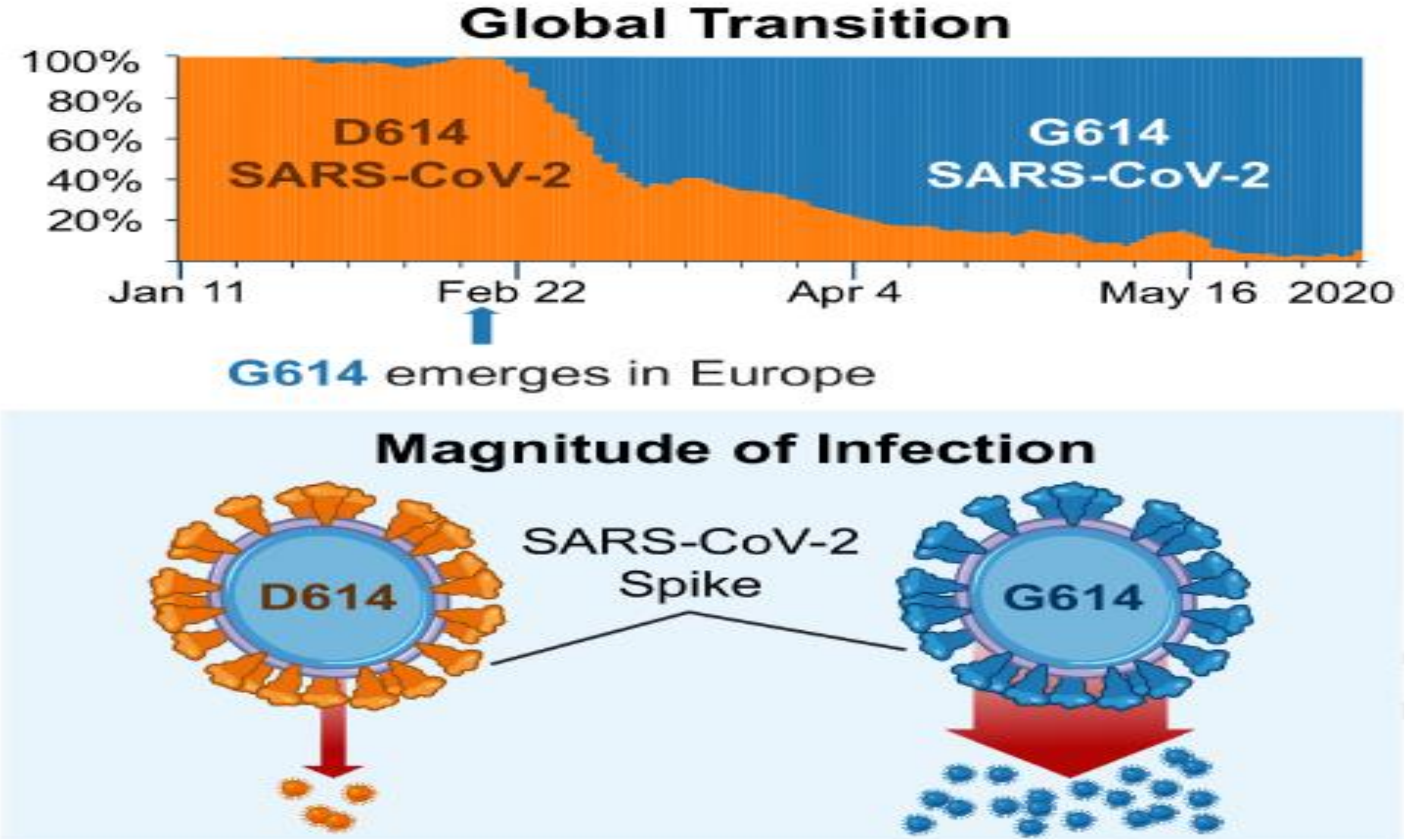
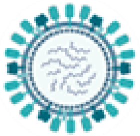
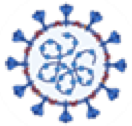
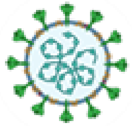
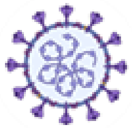

Global Transition
100%
80%
60%
40%
20%
D614
SARS-CoV-2
G614
SARS-CoV-2
Jan 11
Feb 22
Apr 4
May 16
2020
G614 emerges in Europe
Magnitude of Infection
D614
SARS-CoV-2
Spike
G614

Comparison between Flu, COVID-19, SARS and MERS

	FLU 	COVID-19 	SARS 	MERS 
R0	1.28[1]	2. – 2.5[3]	3[7]	0.29 – 0.8[10]
CFR	< 0.1%[2]	3.8%[3]	9.6 [8]	35%[12]
Incubation time	1 – 4 days	1 – 14 days[3]	2 – 10 days[9]	2-14 days[12]
Hospitalization rate	2%	20-30%[5]	Most cases	Most cases
global infected	≈ 1 billion cases Every year [4]	N/A (ongoing)	8,096 in cumulated (2003)[8]	2519 in Cumulated (since 2012) [13]

References are in the note.

Thank you

Question:

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