Songbirds are mysteriously dying across the eastern U.S. Scientists are scrambling to find out why

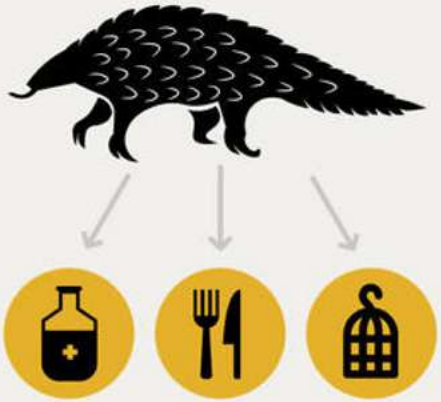
06 Jul 2021

HOW WILDLIFE MARKETS SPREAD DISEASE

WHERE DID THE COVID-19 CORONAVIRUS COME FROM?

The spread of zoonotic diseases – those pathogens that jump from the species that it evolved with to a new host – is exacerbated by wildlife trafficking, habitat destruction and climate change. These threats drive humans and animals closer together. Coronavirus is just one example of a string of pathogens that has come from wildlife trafficking, including SARS, Ebola, Bird Flu, and more. | #COVID19

1. WILDLIFE TRAFFICKING & POACHING



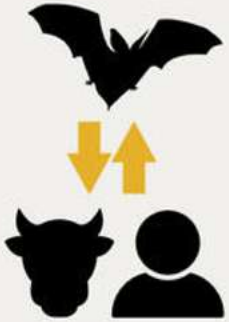
Animals are hunted, trapped and taken to markets to be sold for traditional medicine, food and the pet trade.

GLOBAL WILDLIFE CONSERVATION WCS

2. RESERVOIRS OF DISEASE

Wild animals that appear healthy can harbor diseases that can make other animals, including humans, sick. When animals are forced into markets, they can spread disease.

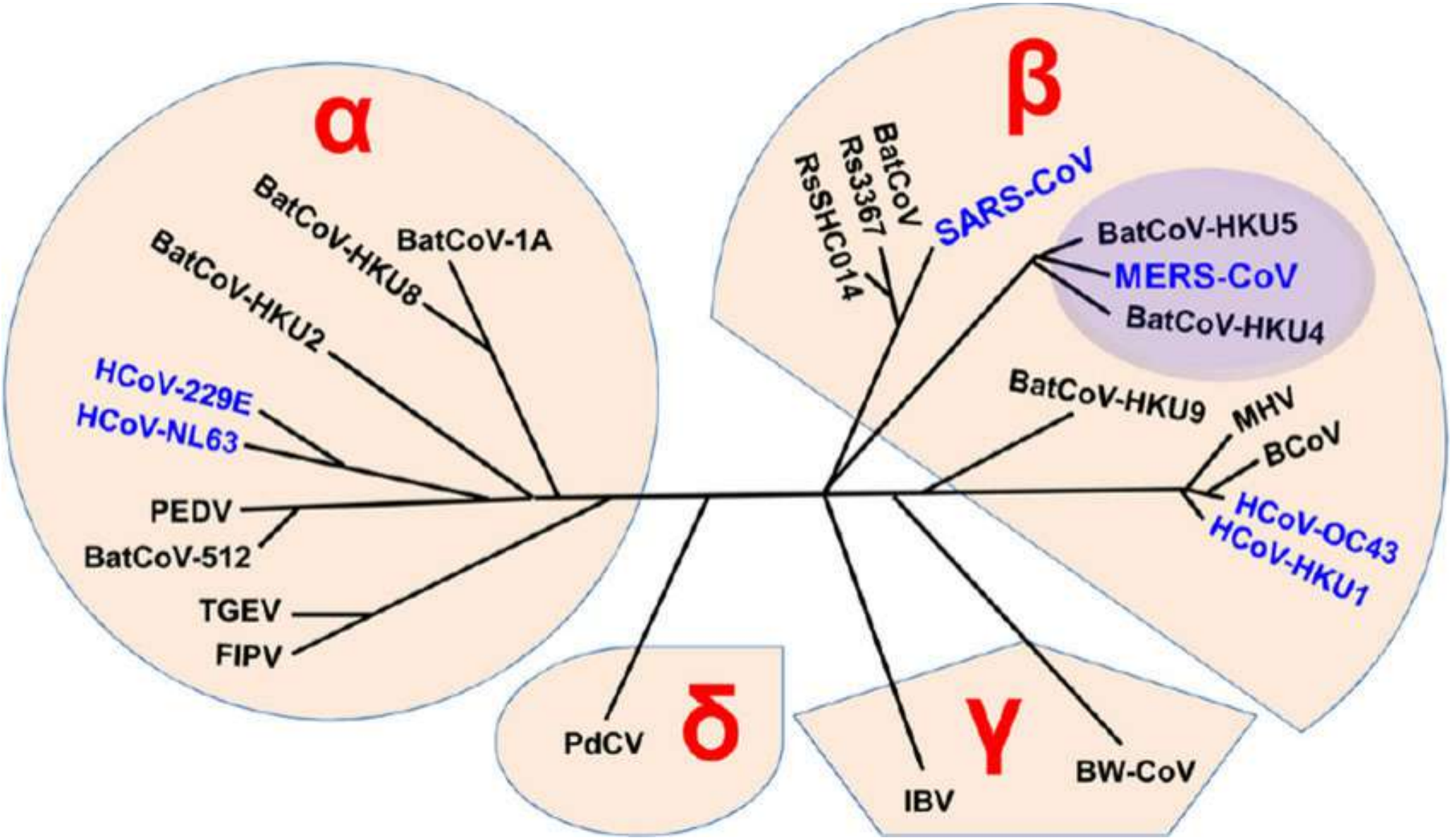
3. PATHOGEN EXCHANGE

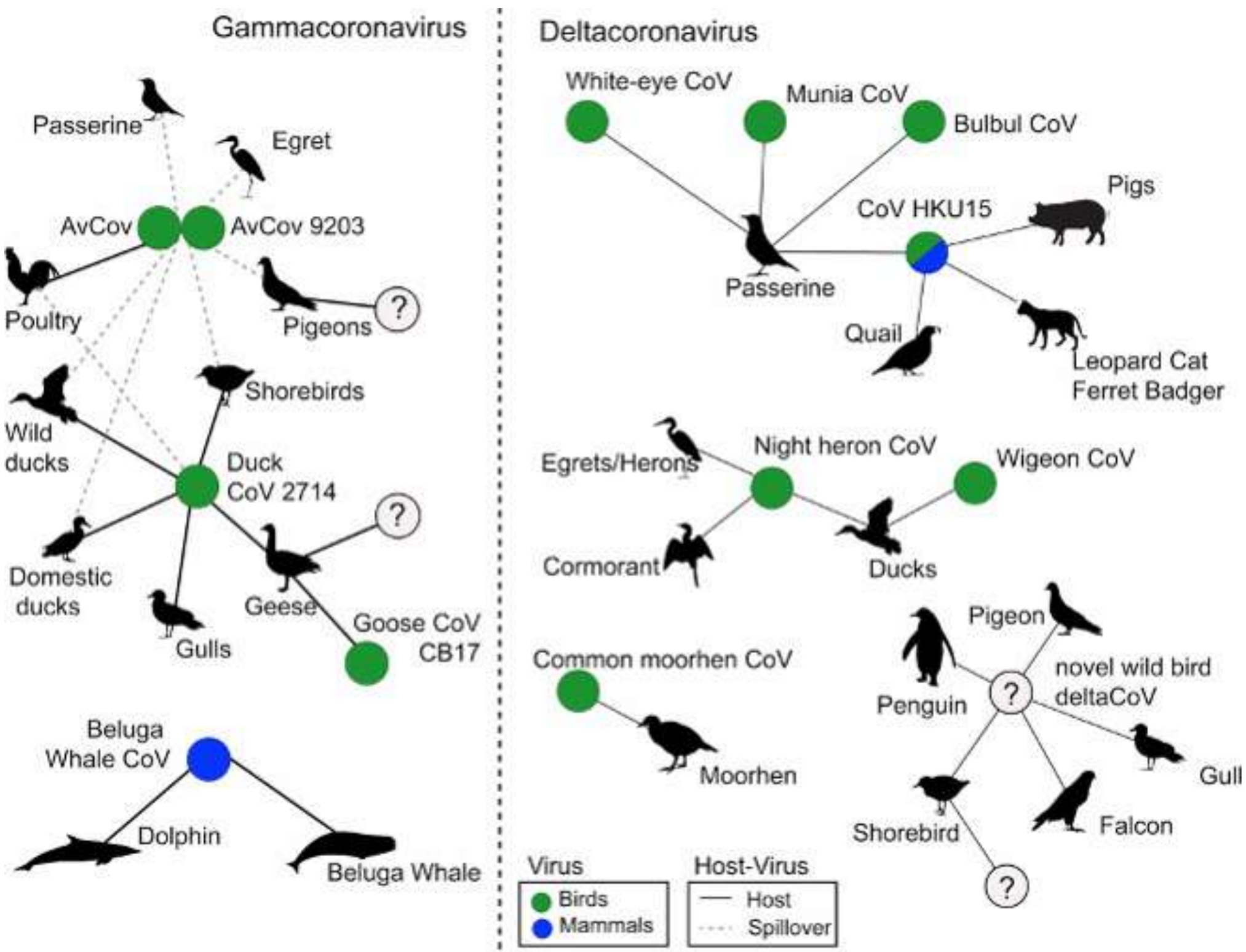


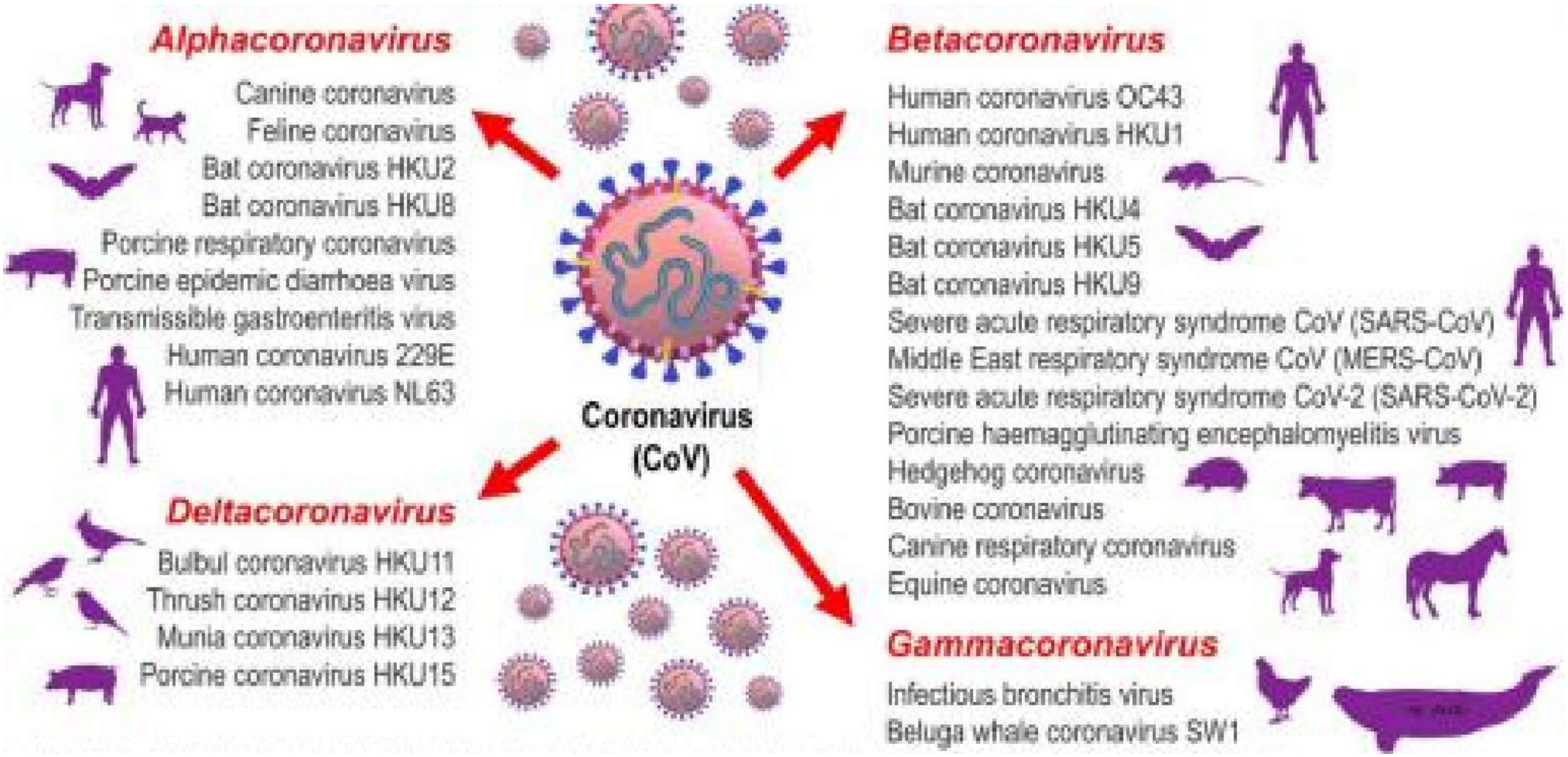
It's only when humans hunt wildlife or destroy their homes that these viruses and other pathogens jump species. We must combat trafficking of wild animals and change dangerous wildlife consumption behaviors, especially in cities.

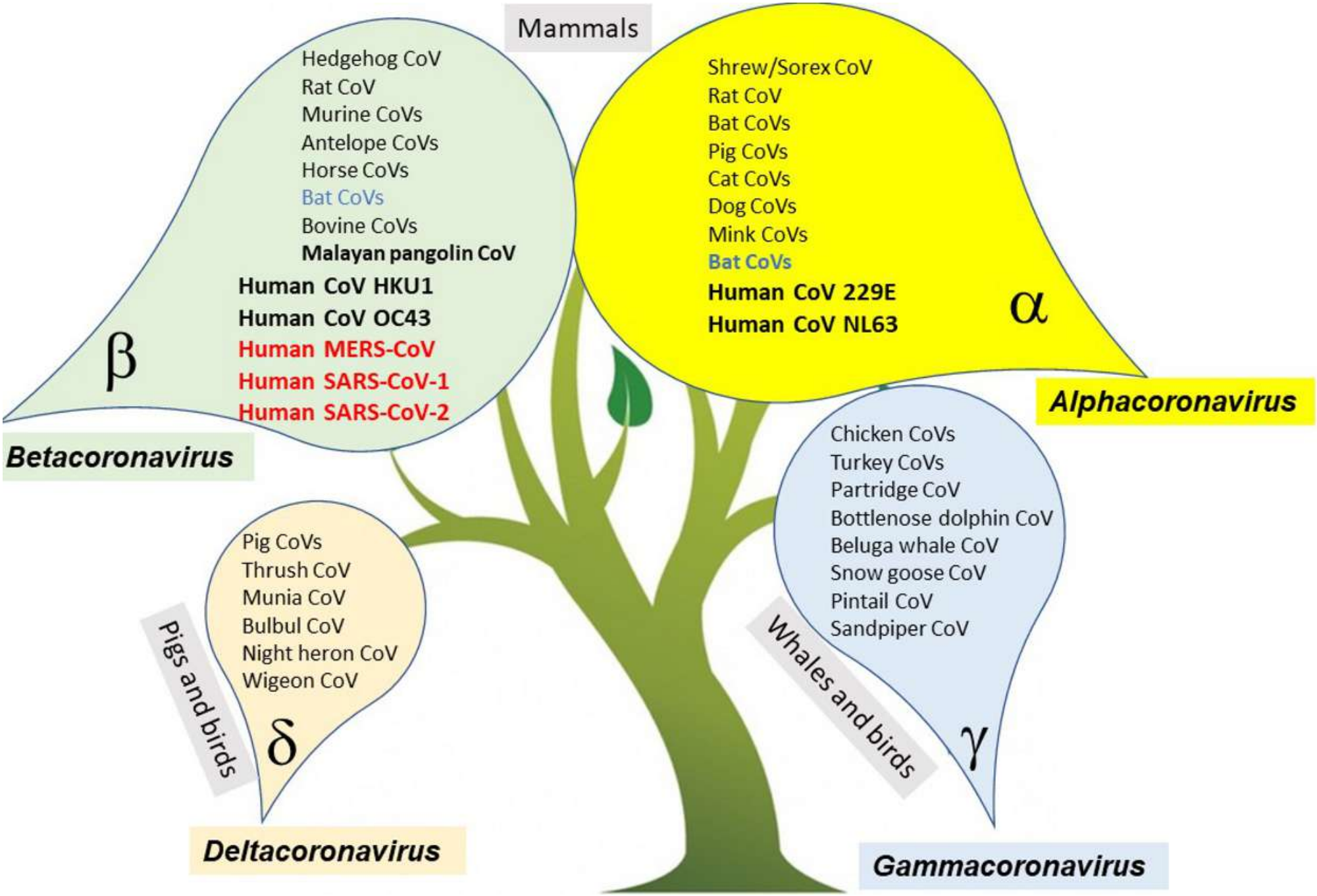
STOP THE SPREAD

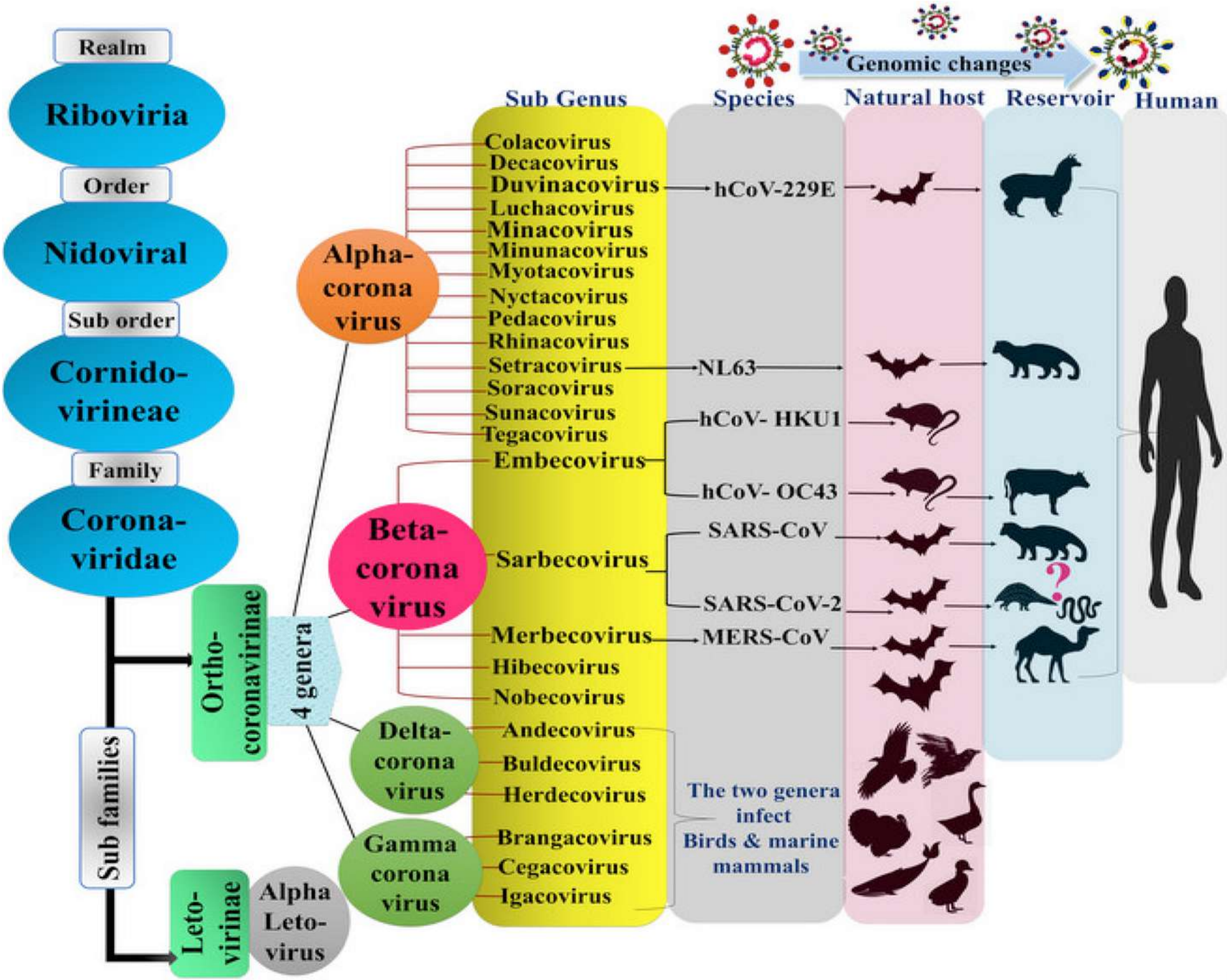
Ban live animal markets that trade in wildlife. Stop illegal trafficking and poaching of wild animals. Not only will this help prevent the spread of disease, it will address one of the major drivers of species extinction.

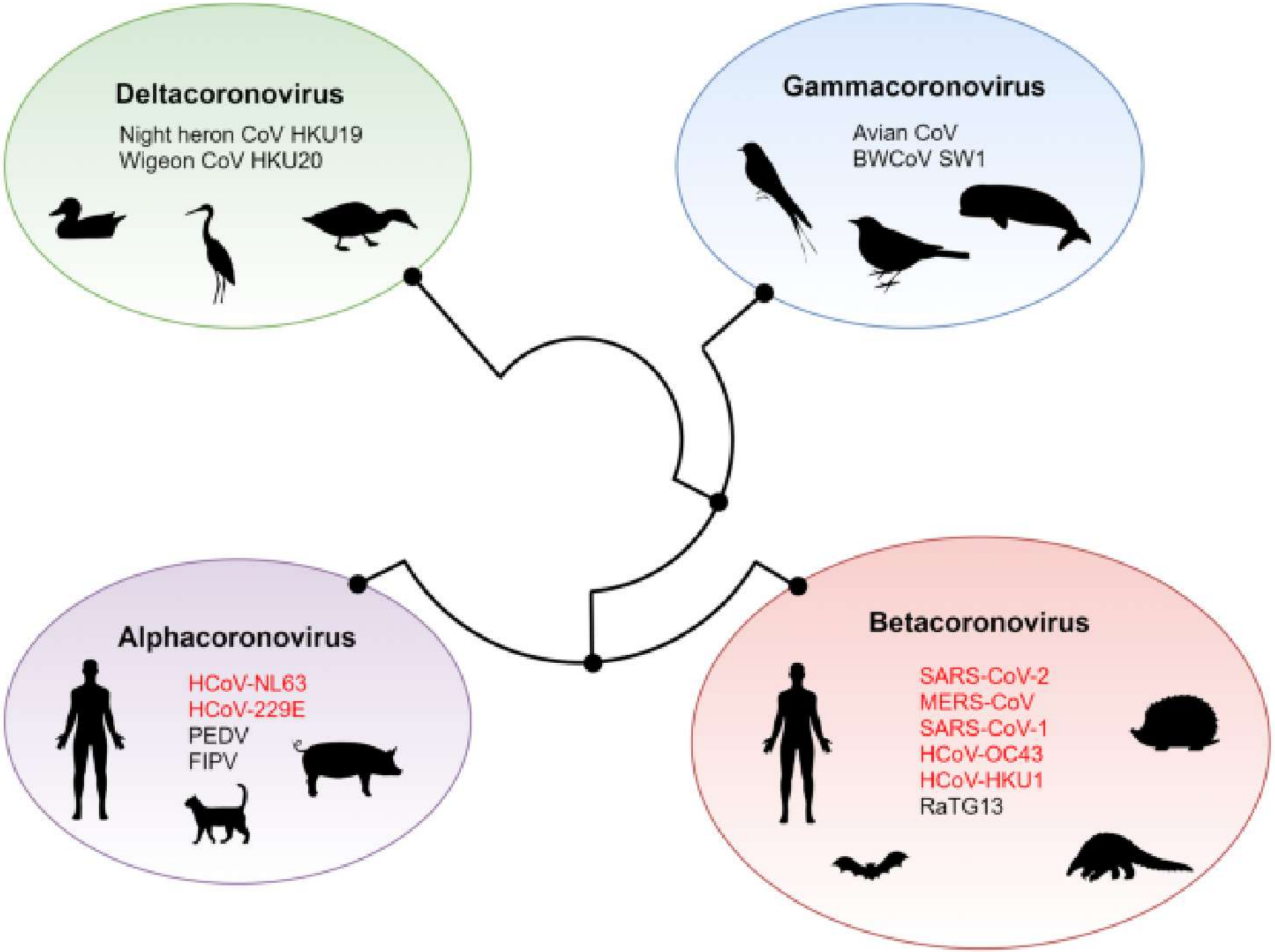

α
BatCoV-HKU8
BatCoV-1A
BatCoV-HKU2
HCoV-229E
HCoV-NL63
PEDV
BatCoV-512
TGEV
FIPV
β
BatCoV
Rs3367
RsSHC014
SARS-CoV
BatCoV-HKU5
MERS-CoV
BatCoV-HKU4
BatCoV-HKU9
MHV
BCoV
HCoV-OC43
HCoV-HKU1
δ
PdCV
γ
IBV
BW-CoV

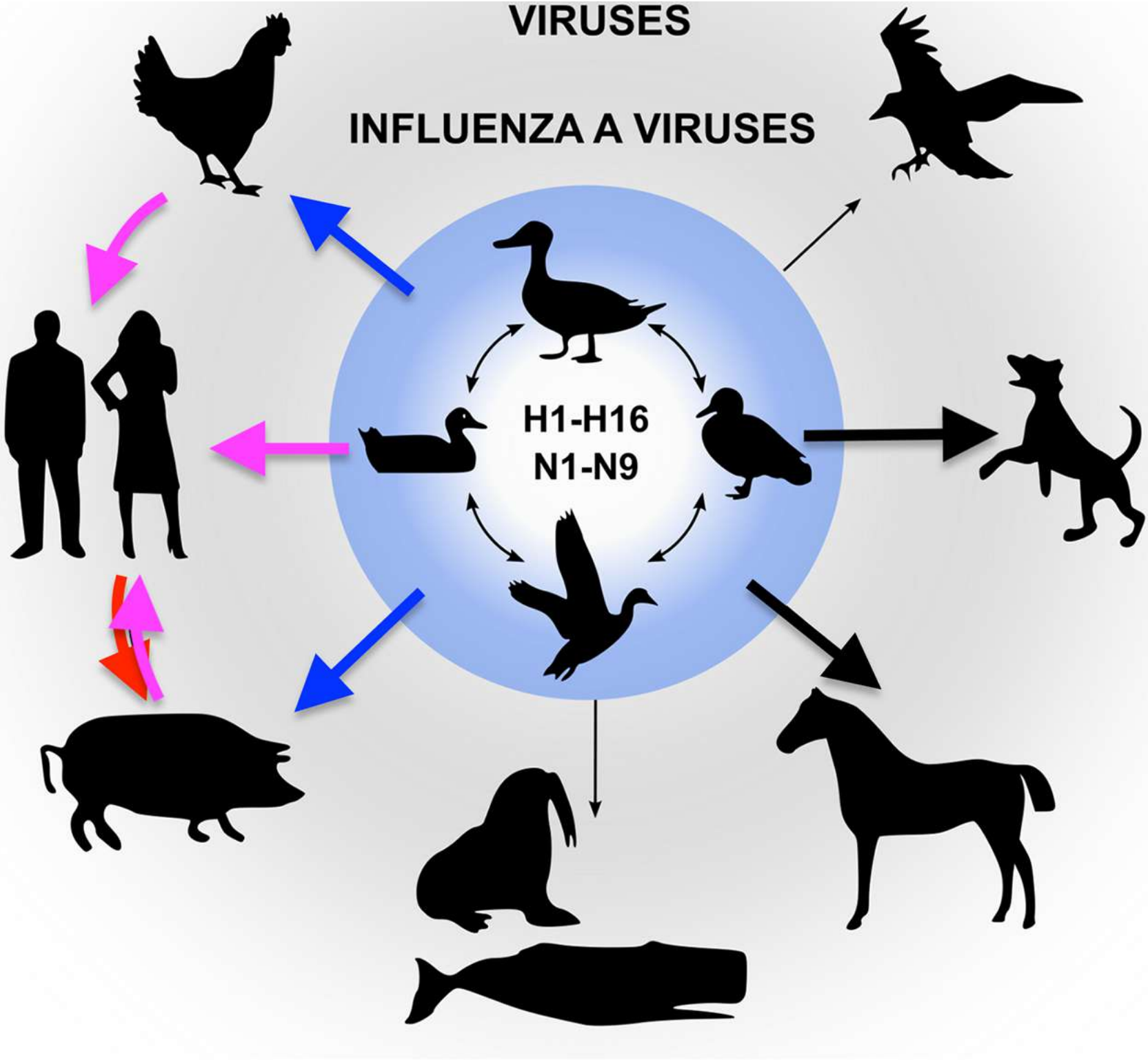

Gammacoronavirus
Passerine
Egret
AvCov
AvCov 9203
Poultry
Pigeons
?
Shorebirds
Wild ducks
Duck CoV 2714
?
Domestic ducks
Geese
Gulls
Goose CoV CB17
Beluga Whale CoV
Dolphin
Beluga Whale
Deltacoronavirus
White-eye CoV
Munia CoV
Bulbul CoV
Pigs
CoV HKU15
Passerine
Quail
Leopard Cat
Ferret Badger
Egrets/Herons
Night heron CoV
Wigeon CoV
Cormorant
Ducks
Common moorhen CoV
Moorhen
Pigeon
Penguin
?
novel wild bird deltaCoV
Gull
Shorebird
Falcon
?
Virus
Birds
Mammals
Host-Virus
Host
Spillover

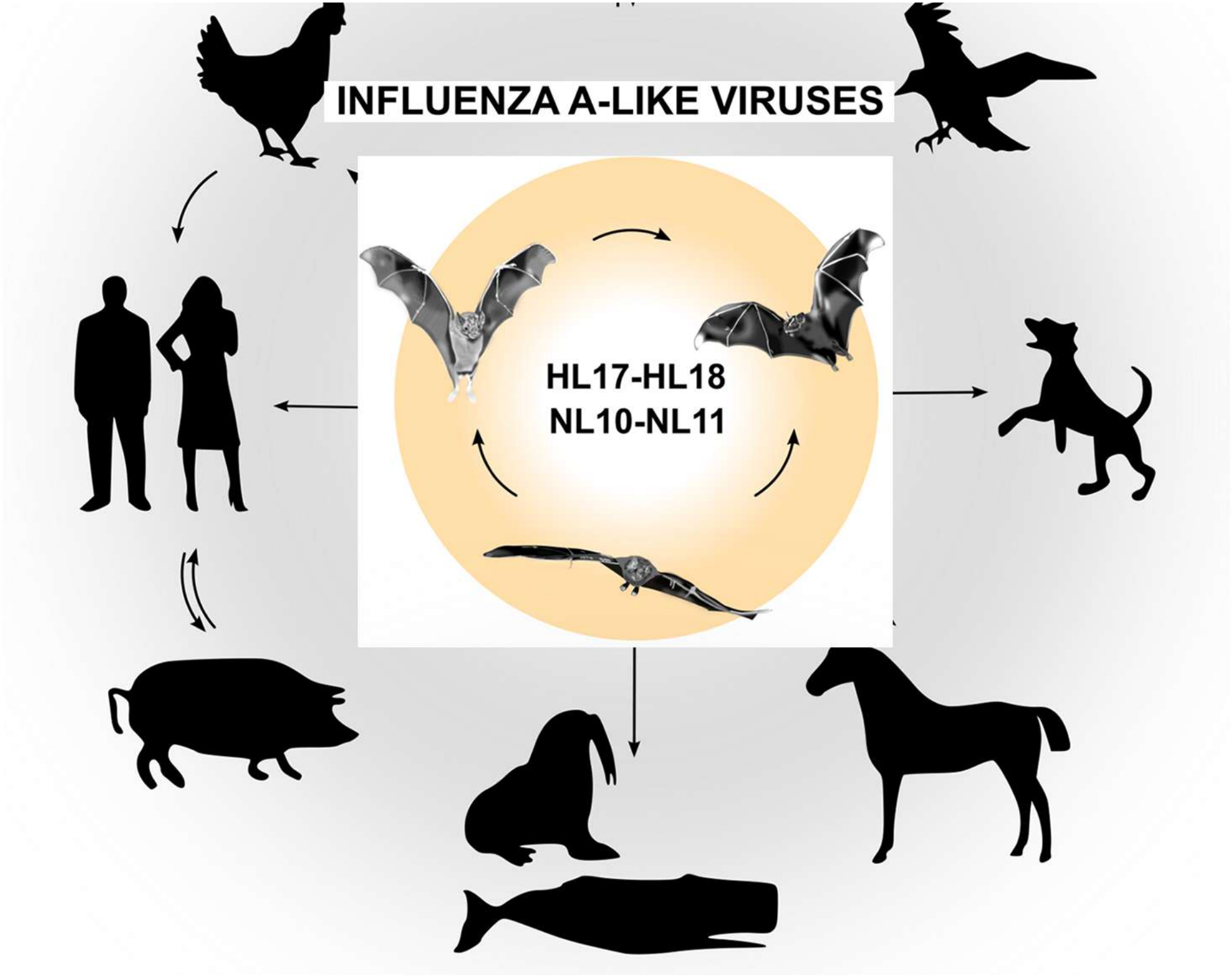

Alphacoronavirus
Canine coronavirus
Feline coronavirus
Bat coronavirus HKU2
Bat coronavirus HKU8
Porcine respiratory coronavirus
Porcine epidemic diarrhoea virus
Transmissible gastroenteritis virus
Human coronavirus 229E
Human coronavirus NL63
Deltacoronavirus
Bulbul coronavirus HKU11
Thrush coronavirus HKU12
Munia coronavirus HKU13
Porcine coronavirus HKU15
Coronavirus
(CoV)
Betacoronavirus
Human coronavirus OC43
Human coronavirus HKU1
Murine coronavirus
Bat coronavirus HKU4
Bat coronavirus HKU5
Bat coronavirus HKU9
Severe acute respiratory syndrome CoV (SARS-CoV)
Middle East respiratory syndrome CoV (MERS-CoV)
Severe acute respiratory syndrome CoV-2 (SARS-CoV-2)
Porcine haemagglutinating encephalomyelitis virus
Hedgehog coronavirus
Bovine coronavirus
Canine respiratory coronavirus
Equine coronavirus
Gammacoronavirus
Infectious bronchitis virus
Beluga whale coronavirus SW1


Mammals
Hedgehog CoV
Rat CoV
Murine CoVs
Antelope CoVs
Horse CoVs
Bat CoVs
Bovine CoVs
Malayan pangolin CoV
Human CoV HKU1
Human CoV OC43
Human MERS-CoV
Human SARS-CoV-1
Human SARS-CoV-2
β
Betacoronavirus
Shrew/Sorex CoV
Rat CoV
Bat CoVs
Pig CoVs
Cat CoVs
Dog CoVs
Mink CoVs
Bat CoVs
Human CoV 229E
Human CoV NL63
α
Alphacoronavirus
Pig CoVs
Thrush CoV
Munia CoV
Bulbul CoV
Night heron CoV
Wigeon CoV
Pigs and birds
δ
Deltacoronavirus
Chicken CoVs
Turkey CoVs
Partridge CoV
Bottlenose dolphin CoV
Beluga whale CoV
Snow goose CoV
Pintail CoV
Sandpiper CoV
Whales and birds
γ
Gammacoronavirus


Realm
Riboviria
Order
Nidoviral
Sub order
Cornido-virineae
Family
Corona-viridae
Sub families
Ortho-coronavirinae
Leto-virinae
4 genera
Alpha-corona virus
Beta-corona virus
Delta-corona virus
Gamma corona virus
Alpha Leto-virus
Sub Genus
Colacovirus
Decacovirus
Duvinacovirus
Luchacovirus
Minacovirus
Minunacovirus
Myotacovirus
Nyctacovirus
Pedacovirus
Rhinacovirus
Setracovirus
Soracovirus
Sunacovirus
Tegacovirus
Embecovirus
Sarbecovirus
Merbecovirus
Hibecovirus
Nobecovirus
Andecovirus
Buldecovirus
Herdecovirus
Brangacovirus
Cegacovirus
Igacovirus
Species
hCoV-229E
NL63
hCoV- HKU1
hCoV- OC43
SARS-CoV
SARS-CoV-2
MERS-CoV
The two genera infect Birds & marine mammals
Genomic changes
Natural host
Reservoir
Human


Deltacoronovirus
Night heron CoV HKU19
Wigeon CoV HKU20
Gammacoronovirus
Avian CoV
BWCoV SW1
Alphacoronovirus
HCoV-NL63
HCoV-229E
PEDV
FIPV
Betacoronovirus
SARS-CoV-2
MERS-CoV
SARS-CoV-1
HCoV-OC43
HCoV-HKU1
RaTG13


VIRUSES
INFLUENZA A VIRUSES
H1-H16
N1-N9


INFLUENZA A-LIKE VIRUSES
HL17-HL18
NL10-NL11

Les recombinants du coronavirus

1 **Une personne est infectée** au même moment **par deux virus différents.**

2 **Ces deux virus infectent une même cellule** et libèrent leur génome (ARN).

3 Le **noyau de la cellule réplique de nombreux ARN** viraux.

4 L'**ARN se recrée une enveloppe virale** dans la cellule infectée.

5 Le nouveau virus présente des **propriétés de ses deux « parents ».**

Durant la réplication, les génomes des deux virus se rencontrent et mutent pour former une nouvelle combinaison.

LP/INFOGRAPHIE, C.TÊCHE.

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OPEN ACCESS

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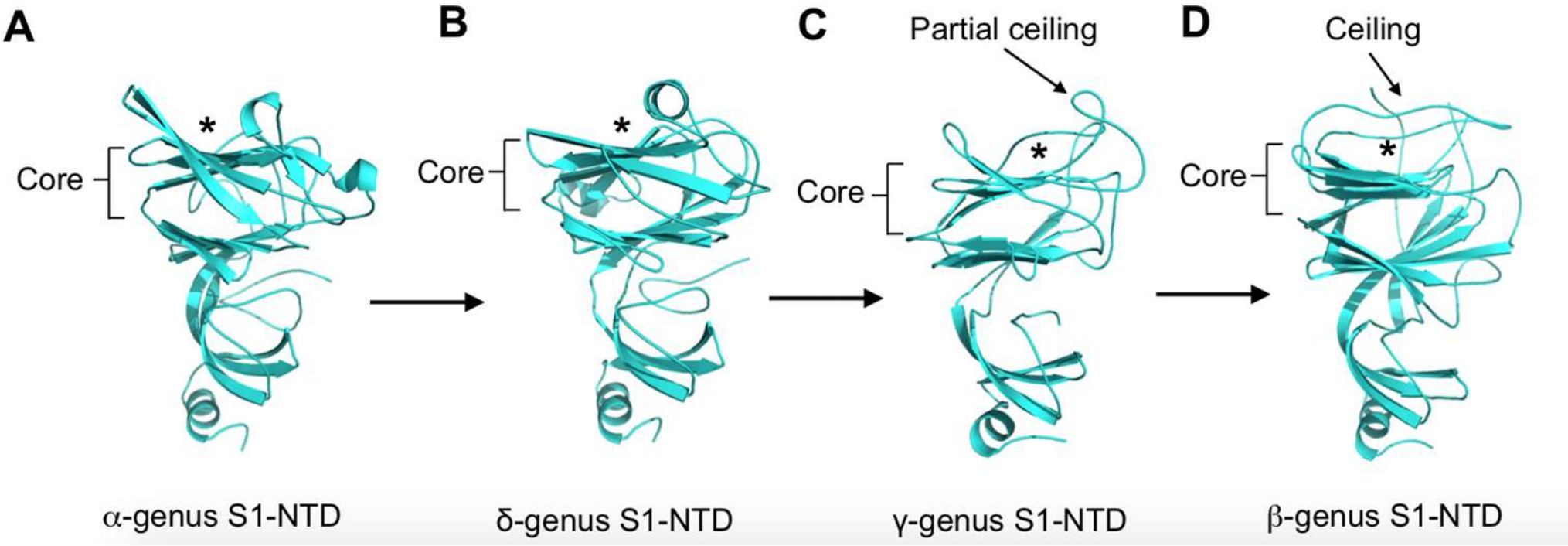
As cell-invading molecular machinery, coronavirus spike proteins pose an evolutionary conundrum due to their high divergence. In this study, we determined the cryo-EM structure of avian infectious bronchitis coronavirus (IBV) spike protein from the γ-genus. The trimeric IBV spike ectodomain contains three receptor-binding S1 heads and a trimeric membrane-fusion S2 stalk. While IBV S2 is structurally similar to those from the other genera, IBV S1 possesses structural features that are unique to different other genera, thereby bridging these diverse spikes into an evolutionary spectrum. Specifically, among different genera, the two domains of S1, the N-terminal domain (S1-NTD) and C-terminal domain (S1-CTD), diverge from simpler tertiary structures and quaternary packing to more complex ones, leading to different functions of the spikes in receptor usage and membrane fusion. Based on the above structural and functional comparisons, we propose that the evolutionary spectrum of coronavirus spikes follows the order of α-, δ-, γ-, and β-genus. This study has provided insight into the evolutionary relationships among coronavirus spikes and deepened our understanding of their structural and functional diversity.

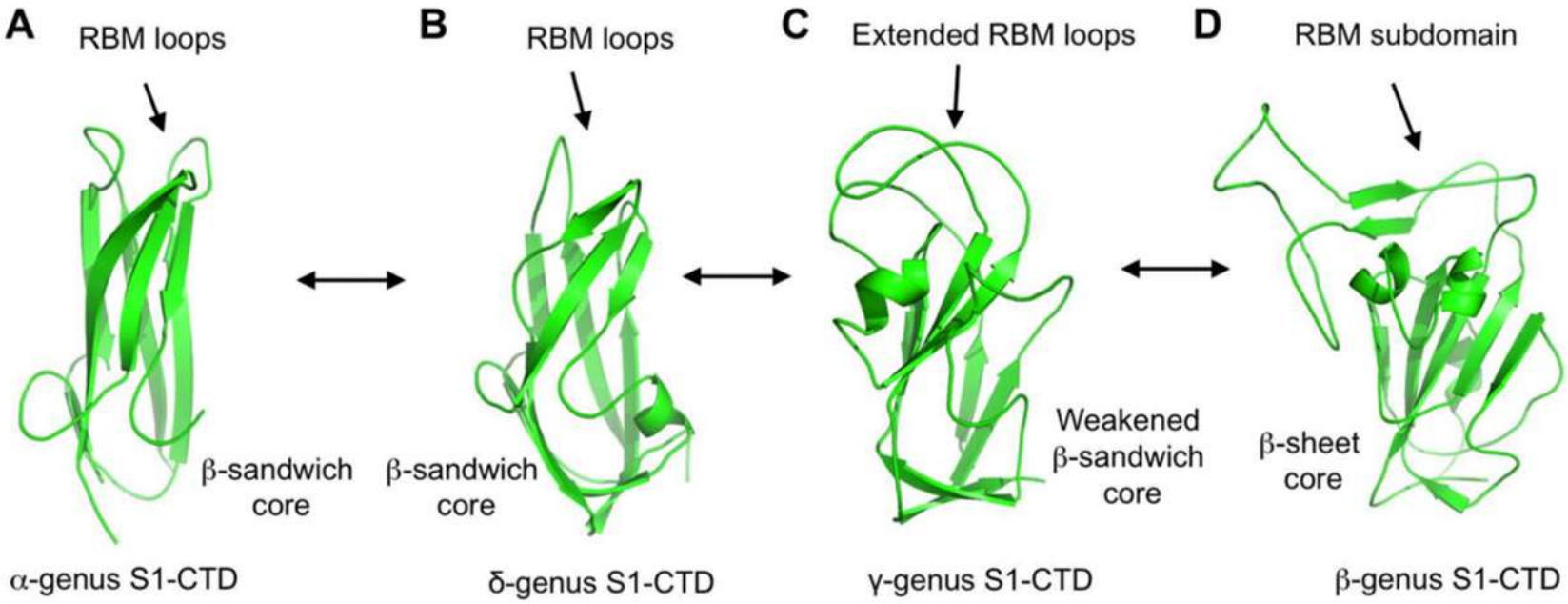
Cryo-EM structure of infectious bronchitis coronavirus spike protein reveals structural and functional evolution of coronavirus spike proteins

Fig 3

Structural comparisons of S1-NTDs from four coronavirus genera.

(A) Structure of S1-NTD from α-genus human coronavirus NL63 (PDB ID: 5SZS). Although each subunit of NL63 S1 contains two copies of S1-NTDs (i.e., S1-NTD1 and S1-NTD2), S1-NTD2 was used in structural comparisons with the S1-NTDs from the other genera because it occupies the same location as the S1-NTDs from the other genera in quaternary structures of the spikes (see Fig 5A). (B) Structure of S1-NTD from δ-genus porcine delta coronavirus (PdCoV) (PDB ID: 6B7N). (C) Structure of S1-NTD from γ-genus IBV. (D) Structure of S1-NTD from β-genus SARS coronavirus (PDB ID: 5X58). * indicates sugar-binding site or putative sugar-binding site in sugar-binding S1-NTDs from each genus. Core structure, partial ceiling, and extensive ceiling are labeled. Arrows from panels (A) to (D) indicate evolutionary direction. (E) Quantitative structural comparisons among S1-NTDs from different genera using software Dali [58]. Both Z-score and r.m.s.d. were calculated for each pair of the proteins. PDB IDs for NL63, PdCoV and SARS S1-NTDs are the same as in panels (A)-(D). PDB IDs for mouse hepatitis coronavirus (MHV) and MERS coronavirus are 3JCL and 5X5F, respectively. CEACAM1b (PDB ID: 5VST), whose β-sandwich fold is topologically different from that of coronavirus S1-NTDs [59], was used as a negative control. N.D.: no detectable structural similarity.





E

Z score/ rmsd (Å)	α-genus	β-genus			γ-genus	δ-genus	(-) control
	NL63	MHV	SARS	MERS	IBV	PdCoV	CEACAM1b
NL63		N.D.	N.D.	2.1/ 4.3	3.4/ 3.8	10.1/ 2.2	N.D.
MHV	N.D.		13.8/ 3.5	19.1/ 3.1	5.3/ 4.0	N.D.	N.D.
SARS	N.D.	13.8/ 3.5		14.2/ 3.2	4.7/ 3.7	2.9/ 4.4	N.D.
MERS	2.1/ 4.3	19.1/ 3.1	14.2/ 3.2		6.1/ 3.7	3.6/ 3.8	N.D.
IBV	3.4/ 3.8	5.3/ 4.0	4.7/ 3.7	6.1/ 3.7		7.1/ 3.5	N.D.
PdCoV	10.1/ 2.2	N.D.	2.9/ 4.4	3.6/ 3.8	7.1/ 3.5		N.D.
CEACAM1b	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	

Fig 4. Structural comparisons of S1-CTDs from four coronavirus genera. (A)-(D): Structures of S1-CTDs from different genera. Core structures and RBMs are labeled. (E) Quantitative structural comparisons among S1-CTDs from different genera. The PDB IDs are the same as those in Fig 3. Left right arrows from panels (A) to (D) indicate that evolution could go either way.

https://doi.org/10.1371/journal.ppat.1007009.g004

L’Europe s’engage à interdire l’élevage en cage des animaux d’ici 2027