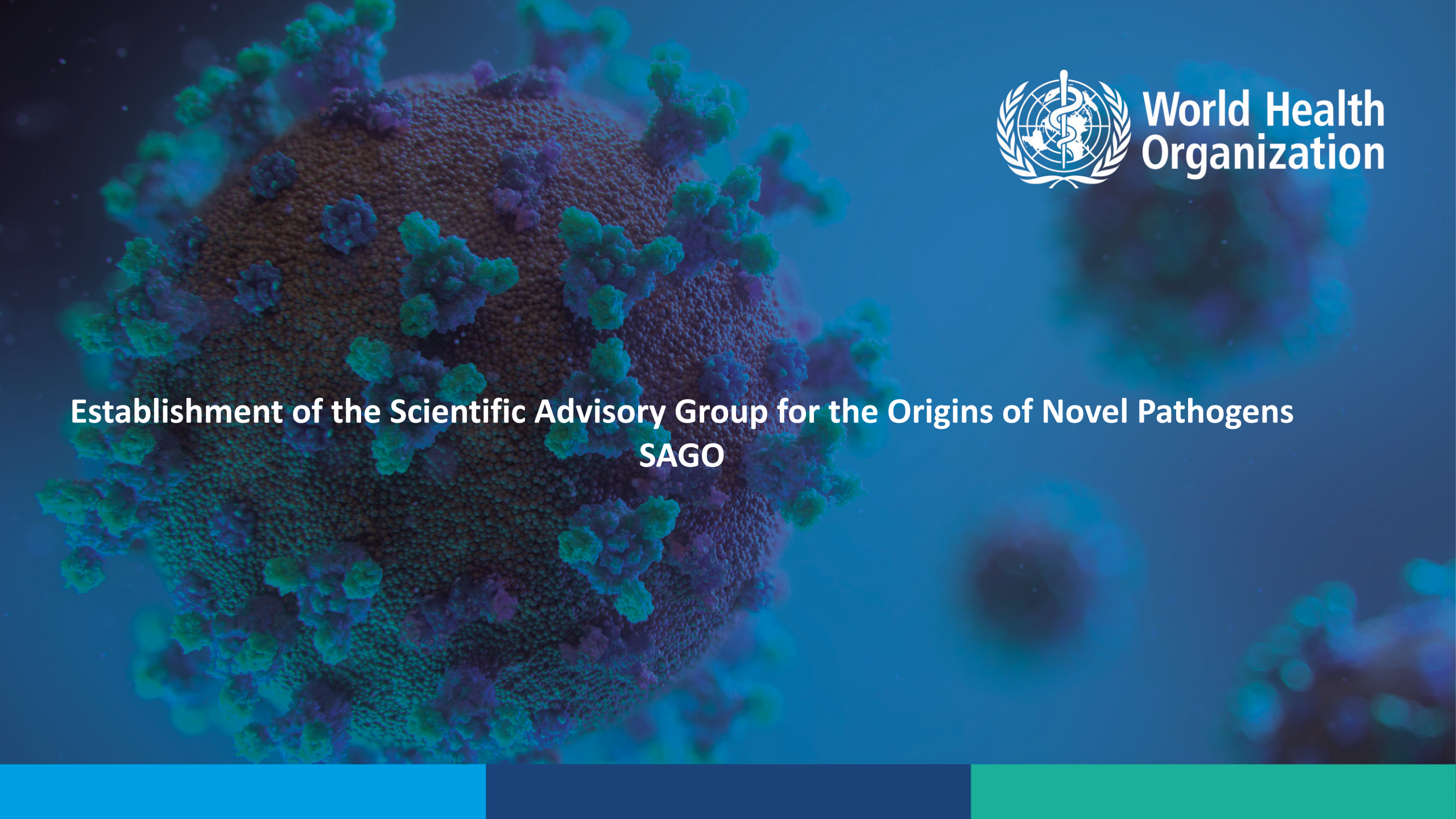
World Health Organization

Update from the Secretariat

Scientific Advisory Group for the Origins of Novel Pathogens

Update on studies into the origin of SARS-CoV-2



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Establishment of the Scientific Advisory Group for the Origins of Novel Pathogens SAGO

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LEGEND
Epidemic
Pandemic

MAJOR EPIDEMIC THREATS SINCE 2000

COVID-19
Ebola (DRC)
Yellow fever (Central Africa, Brazil)
Zika
H7N9
Ebola (West Africa)
H1N1
H5N1
MERS
SARS
Cholera (Haiti)
Cholera (Yemen)
Plague (Madagascar)

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020

INTERNATIONAL COLLABORATION EFFORTS TO FIGHT EPIDEMIC THREATS

GAVI

Gavi, the Vaccine Alliance, is an international organisation that was created in 2000 to improve access to new and underused vaccines for children living in the world's poorest countries.

GOARN

The **Global Outbreak Alert and Response Network (GOARN)** is a technical collaboration of existing institutions and networks who pool human and technical resources for the rapid identification, confirmation and response to outbreaks of international importance.

IHR (2005)

The **International Health Regulations (2005)** or IHR (2005) are an international law which helps countries work together to save lives and livelihoods caused by the international spread of diseases and other health risks. The IHR (2005) aim to prevent, protect against, control and respond to the international spread of disease while avoiding unnecessary interference with international traffic and trade.

PIP Framework

The **Pandemic Influenza Preparedness (PIP) Framework** brings together Member States, industry, other stakeholders and WHO to implement a global approach to pandemic influenza preparedness and response. Its key goals include:
- to improve and strengthen the sharing of influenza viruses with human pandemic potential; and
- to increase the access of developing countries to vaccines and other pandemic related supplies.

R&D Blueprint

R&D Blueprint is a global strategy and preparedness plan that allows the rapid activation of research and development activities during epidemics. Its aim is to fast-track the availability of effective tests, vaccines and medicines that can be used to save lives and avert large scale crises.

PIP Review

IHR Review

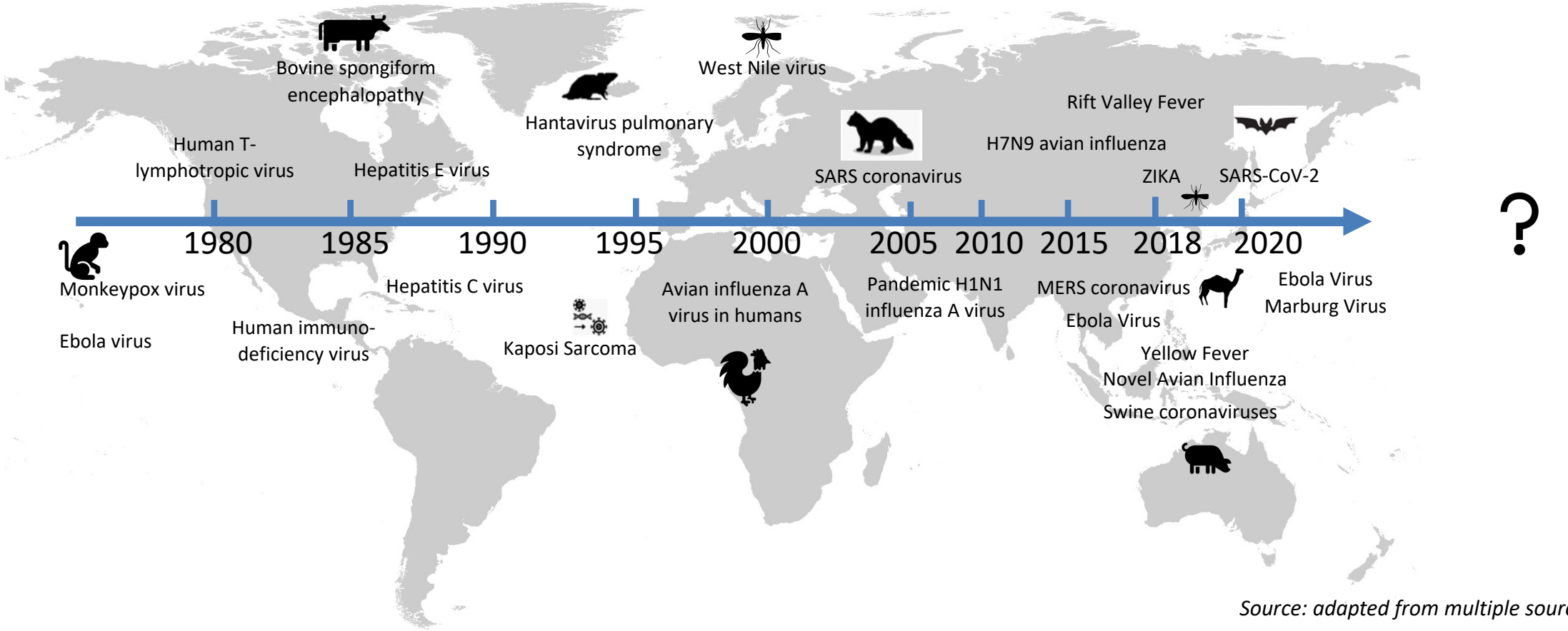
Access to COVID-19 Tools (ACT) Accelerator is a global collaboration to accelerate the development, production and equitable access to new COVID-19 diagnostics, therapeutics and vaccines.

ACT Accelerator

Timeline

Major infectious threats in the 21st Century & collaboration mechanisms to fight against them

The critical importance of a One Health approach



Source: adapted from multiple sources

Human health, animal health and the state of ecosystems are inextricably linked with 70-80% of emerging and re-emerging infectious diseases known to be of zoonotic origin

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Scientific Advisory Group on Novel Origins (SAGO)

In the context of the continued threat of the emergence or re-emergence of pathogens with epidemic and pandemic potential

The Need

- A global framework to study future emerging and re-emerging pathogens, including
  - Comprehensive and coordinated studies
  - A holistic approach to study the emergence of high threat zoonotic pathogens including the animal human interface, environmental safety, biosafety and biosecurity
  - An established framework for studying emerging pathogens where and when they emerge

Addressing a gap

- A scientific advisory group to advise WHO on technical and scientific considerations regarding origins of emerging and re-emerging pathogens:

The Scientific Advisory Group for the Origins of Novel Pathogens (SAGO)

Functions of the SAGO

1. To advise WHO on the development of a global framework to define and guide studies into the origins of emerging and re-emerging pathogens of epidemic and pandemic potential

2. To advise WHO on prioritizing studies and field investigations into the origins of emerging and re-emerging pathogens of epidemic and pandemic potential, in accordance with the framework described above

3. To advise WHO on the development of a detailed work plan of the SAGO

Functions of the SAGO (continued)

4. **In the context of SARS-CoV-2;**
   a) To provide the WHO Secretariat with an independent evaluation of all available scientific and technical findings from global studies on the origins of SARS-CoV-2;
   b) To advise the WHO Secretariat regarding developing, monitoring and supporting the next series of studies into the origins of SARS-CoV-2, including rapid advice on WHO's operational plans to implement the next series of global studies into the origins of SARS-CoV-2, as outlined in the Joint WHO-China Global Study of Origins of SARS-CoV-2: China Part report published on 30 March 2021, and advise on additional studies as needed; and

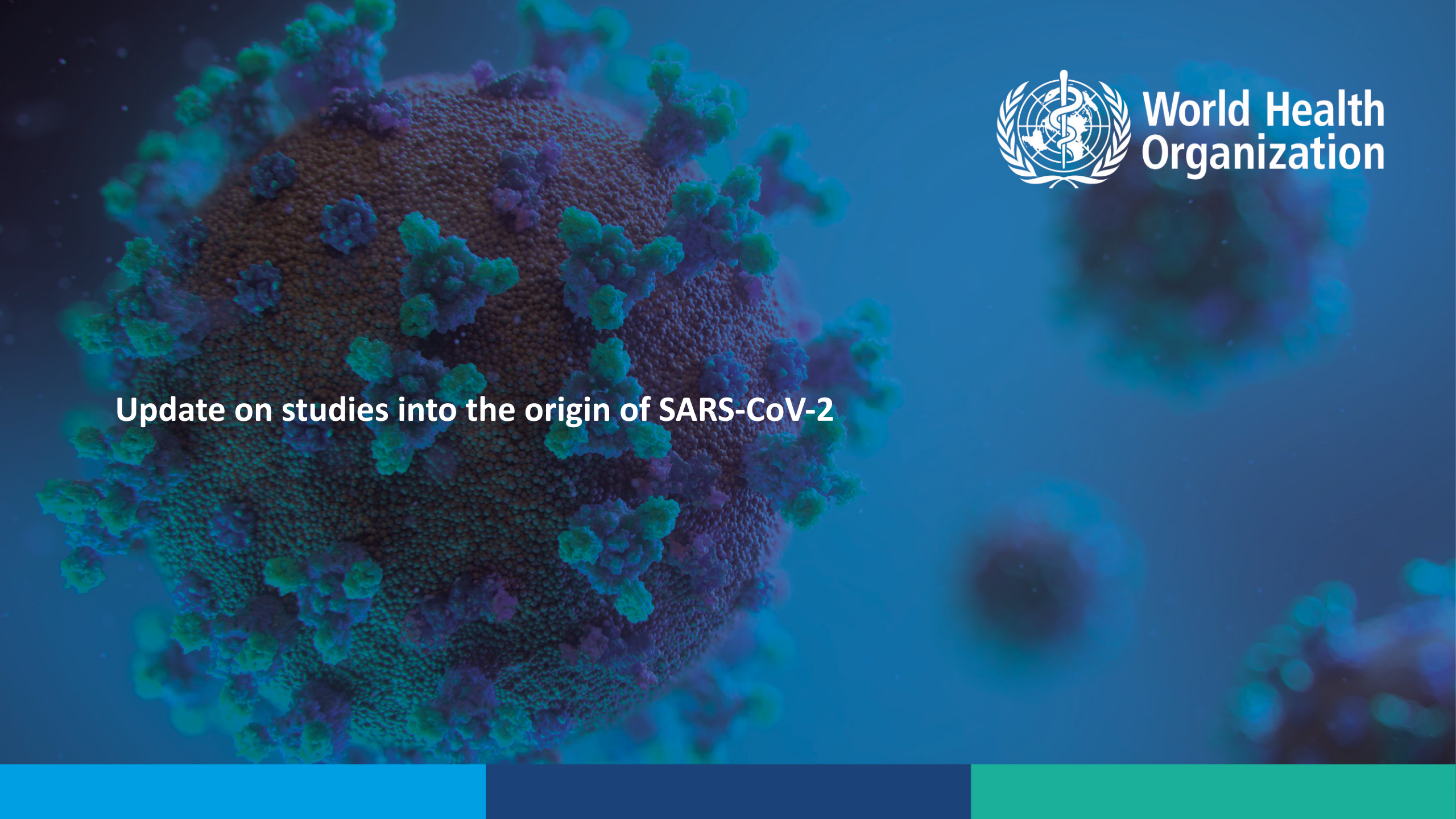
5. To provide additional advice and support to WHO, as requested by the WHO Secretariat, which may include participation in future WHO-international missions to study the origins of SARS-CoV-2 or for other emerging pathogens.

SAGO - Composition

- Up to 25 members
- Members must have significant expertise in one or more of the following technical disciplines:

  infectious disease epidemiology and conducting epidemiological studies, field research, virology, ecology, molecular epidemiology, sero-epidemiology, medicine, bioinformatics, outbreak analytics, health statistics, microbiology, veterinary medicine, food safety, bacteriology, environmental science, biosafety, biosecurity, occupational health and safety, or laboratory safety and security, ethics and social sciences, or other activities related to the emergence or re-emergence of pathogens of pandemic potential.

- Geographic representation, gender balance, declaration of interest
- Members of the SAGO shall be appointed to serve for a period of 2 years and shall be eligible for reappointment



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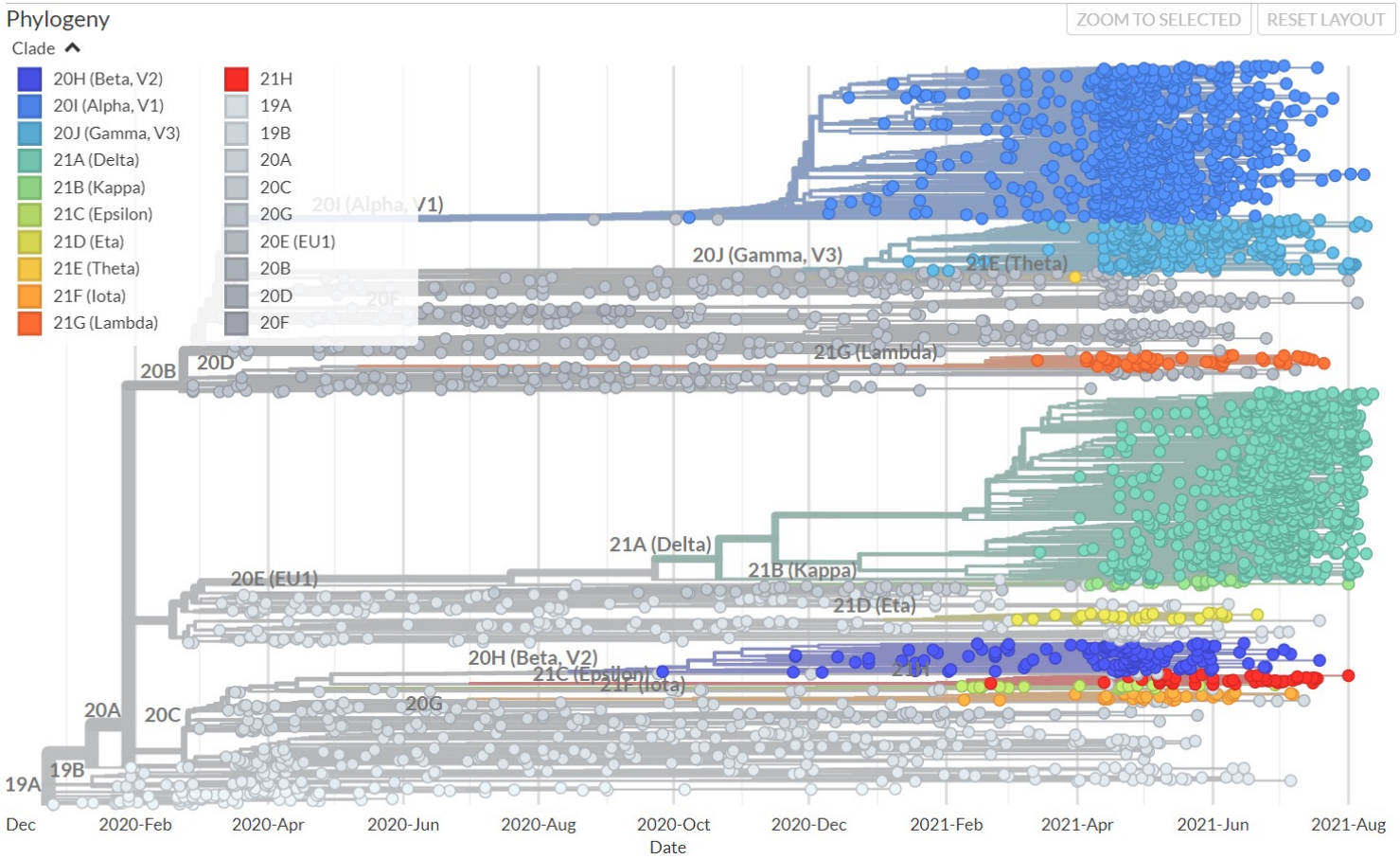
Update on studies into the origin of SARS-CoV-2

Global spread of SARS-CoV-2: findings from phylogenetic analyses



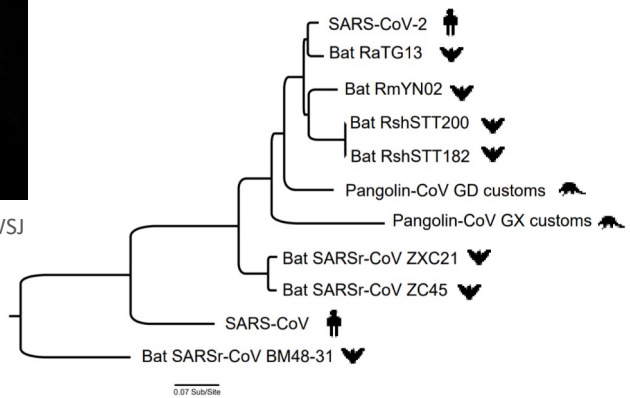
Source: Nextstrain.org

Current TMRCA estimates: November 2019 (95% credible interval October -December 2019)

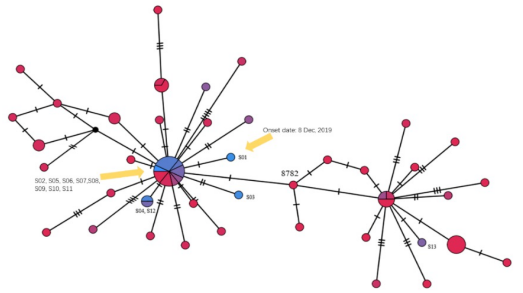
SARS-CoV-2 and other SARS- related CoVs

- SARS-CoV-2 is likely to be a coronavirus of bat origin, with the closest viral genome (RaTG13, 96.2% homology) found in *Rhinolophus affinis* bats in Yunnan, China
- Rhinolophus species are abundant and diverse in South China and across Asia, the Middle East, Africa and Europe; Apart from China, SARS-CoV-2 related coronaviruses have also been isolated from bats in Southeast Asia
- Two other closely-related coronaviruses with 85.5% to 92.4% sequence similarity to SARS-CoV-2 were sequenced from custom-seized trafficked Malayan pangolins that were housed in rehabilitation facilities in China
- Earliest market related cases in Wuhan already some diversity suggesting original spill over event to humans may not have happened at the market itself
- Several decades of evolutionary distance between most similar viruses from bats and SARS-CoV-2 suggests the need for search of intermediaries

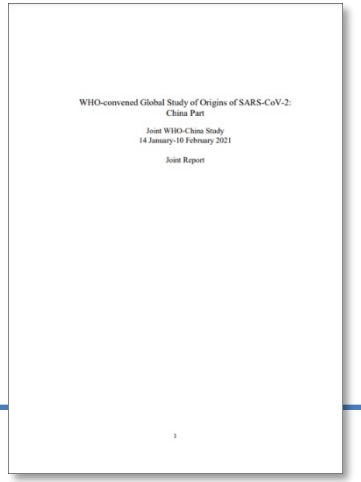
Photo: Minden Pictures; WSJ



Phylogenetic tree of SARS-CoV-2 and other coronaviruses in bats and pangolins



Sequences of cases with onset of illness in December

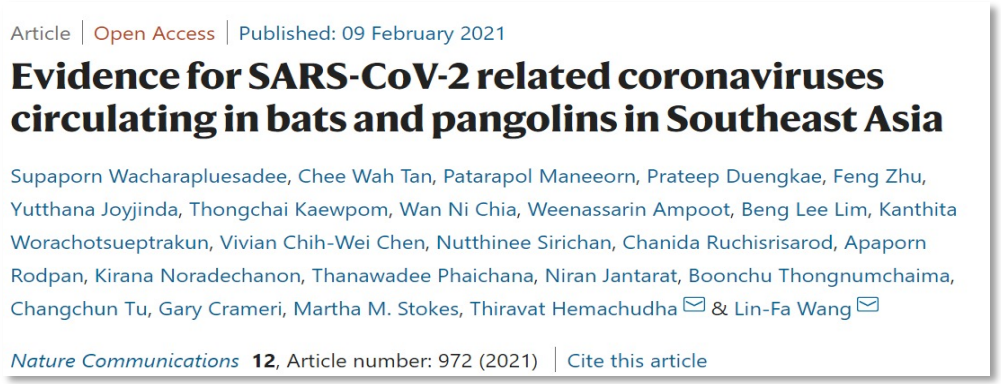


SARS-related coronaviruses found in different parts of Asia

NEWS | 23 November 2020 | Correction 29 November 2020 | Correction 17 December 2020

Coronaviruses closely related to the pandemic virus discovered in Japan and Cambodia

The viruses, both found in bats stored in laboratory freezers, are the first SARS-CoV-2 relatives to be found outside China.



Article | Open Access | Published: 09 February 2021

Evidence for SARS-CoV-2 related coronaviruses circulating in bats and pangolins in Southeast Asia

Supaporn Wacharapluesadee, Chee Wah Tan, Patarapol Maneeorn, Prateep Duengkae, Feng Zhu, Yutthana Joyjinda, Thongchai Kaewpom, Wan Ni Chia, Weenassarin Ampoot, Beng Lee Lim, Kanthita Worachotsueptrakun, Vivian Chih-Wei Chen, Nutthinee Sirichan, Chanida Ruchisrisarod, Apaporn Rodpan, Kirana Noradechanon, Thanawadee Phaichana, Niran Jantarat, Boonchu Thongnumchaima, Changchun Tu, Gary Crameri, Martha M. Stokes, Thiravat Hemachudha ✉ & Lin-Fa Wang ✉

Nature Communications **12**, Article number: 972 (2021) | Cite this article

New Results

Identification of a novel lineage bat SARS-related coronaviruses that use bat ACE2 receptor

Hua Guo, Ben Hu, Hao-rui Si, Yan Zhu, Wei Zhang, Bei Li, Ang Li, Rong Geng, Hao-Feng Lin, Xing-Lou Yang, Peng Zhou, Zheng-Li Shi

doi: https://doi.org/10.1101/2021.05.21.445091

Animals Positive for SARS-CoV-2: Globally by Species as of 16 August 2021

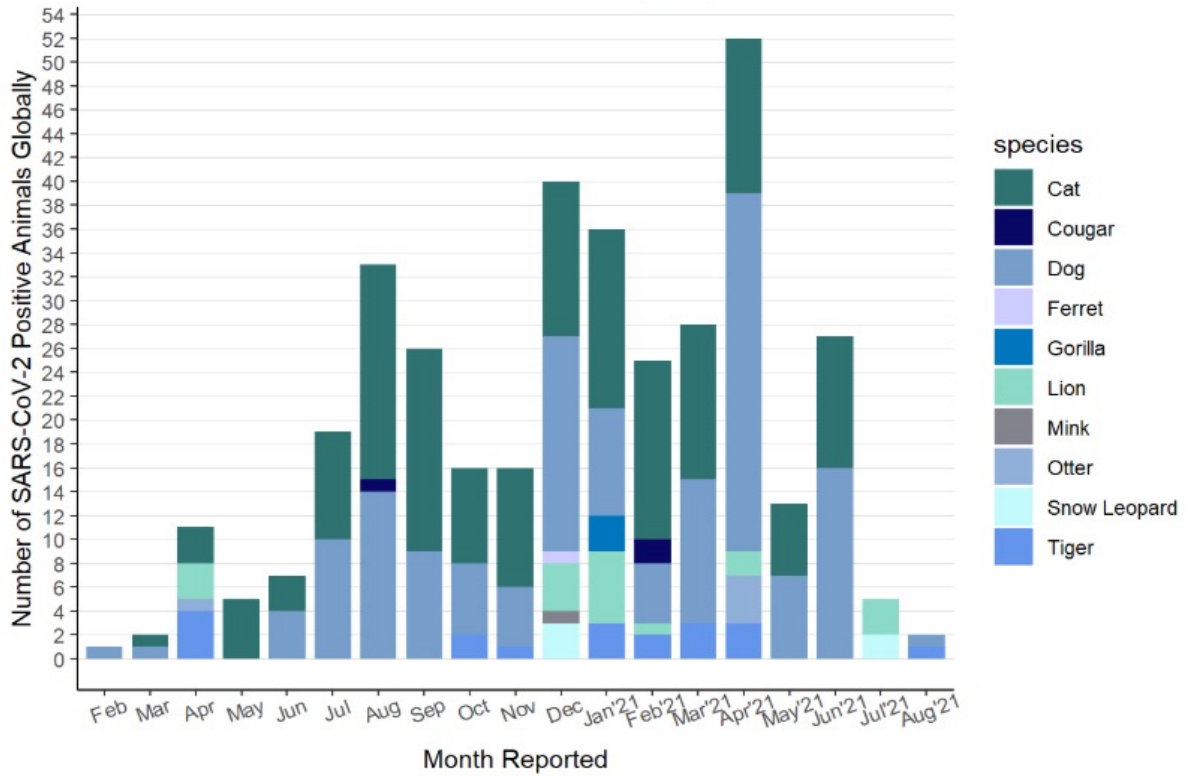
Susceptibility of several animal species to SARS-CoV-2 has been confirmed, including pets and (farmed) wildlife

366 animals from 27 countries*

- Cats: 161
- Dogs: 149
- Tigers: 19
- Lions: 19
- Asian small-clawed otters: 5
- Snow leopards: 5
- Cougar: 3
- Gorillas: 3
- Wild caught mink: 1
- Pet ferret: 1
- White tailed deer (30% sero+)

435 mink farms in 12 countries

**Does not include individual numbers of positive farmed mink*



Source: OIE, FAO, UDA APHIS

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Animal species experimentally infected with SARS-CoV-2

- Cats*
- Dogs
- Ferrets*
- Mink*
- Hamsters*†
- Deer mice*
- Rabbits
- Tree shrews
- Raccoon dogs*
- Cattle
- Non-human primates‡
- Egyptian fruit bats*
- White-tailed deer*
- Striped skunks
- Raccoons
- Bushy-tailed woodrats
- Bank voles
- Striped skunks
- Raccoons

* Transmission to other animals of the same species reported

†Hamster species include Chinese hamsters and golden Syrian hamsters

‡Non-human primate species include African green monkeys, baboons, common marmosets, cynomolgus macaques, pigtail macaques, rhesus macaques, and savanna monkeys

Source: OIE, FAO, References included in CDC's One Health Scientific Publication Tracker- One Health and Animal Studies

Animal Sales in Wuhan (Xiao et al 20201)

scientific reports

Check for updates

OPEN

Animal sales from Wuhan wet markets immediately prior to the COVID-19 pandemic

Xiao Xiao[1,2], Chris Newman[3,4], Christina D. Buesching[4,5], David W. Macdonald[3] & Zhao-Min Zhou[1,6]✉

Here we document 47,381 individuals from 38 species, including 31 protected species sold between May 2017 and November 2019 in Wuhan's markets. We note that no pangolins (or bats) were traded, supporting reformed opinion that pangolins were not likely the spillover host at the source of the current coronavirus (COVID-19) pandemic. While we caution against the misattribution of COVID-19's origins, the wild animals on sale in Wuhan suffered poor welfare and hygiene conditions and we detail a range of other zoonotic infections they can potentially vector. Nevertheless, in a precautionary response to COVID-19, China's Ministries temporarily banned all wildlife trade on 26th Jan 2020 until the COVID-19 pandemic concludes, and permanently banned eating and trading terrestrial wild (non-livestock) animals for food on 24th Feb 2020. These interventions, intended to protect human health, redress previous trading and enforcement inconsistencies, and will have collateral benefits for global biodiversity conservation and animal welfare.

Species on sale	Monthly mean (and SD) number of individuals sold	Price (mean ± SD) $ per individual
Mammals		
Raccoon dog (*Nyctereutes procyonoides*)[W,R,F,+]	38.33 ± 17.24 (n = 30)	63.32 ± 15.46 (n = 5)
Amur hedgehog (*Erinaceus amurensis*)[R,F,+]	332.14 ± 190.62 (n = 28)	2.66 ± 0.41 (n = 5)
Siberian weasel (*Mustela sibirica*)[W,R,F,+]	(10.06 ± 12.09, n = 31)	11.24 ± 3.07 (n = 5)
Hog badger (*Arctonyx albogularis*)[W,R,F,+]	(6.81 ± 5.37, n = 31)	72.79 ± 34.08 (n = 5)
Asian badger (*Meles leucurus*)[W,R,F,+]	12.24 ± 7.39 (n = 29)	59.77 ± 15.89 (n = 5)
Chinese hare (*Lepus sinensis*)[W,R,F,+]	168.96 ± 89.06 (n = 29)	16.87 ± 2.88 (n = 5)
Pallas's squirrel (*Callosciurus erythraeus*)[R,P,+]	16.52 ± 4.87 (n = 23)	25.74 ± 7.59 (n = 5)
Masked palm civet (*Paguma larvata*)[F,+]	10.69 ± 8.42 (n = 29)	62.73 ± 15.25 (n = 5)
Chinese bamboo rat (*Rhizomys sinensis*)[F,+]	42.76 ± 20.68 (n = 29)	18.64 ± 7.58 (n = 5)
Malayan porcupine (*Hystrix brachyura*)[F,+]	10.00 ± 0.00 (n = 29)	68.06 ± 14.23 (n = 5)
Chinese muntjac (*Muntiacus reevesi*)[F,+]	10.00 ± 0.00 (n = 29)	142.62 ± 49.67 (n = 5)
Coypu (*Myocastor coypus*)[F]	5.00 ± 0.00 (n = 29)	28.70 ± 5.08 (n = 5)
Marmot (*Marmota himalayana*)[F]	15.00 ± 4.29 (n = 20)	81.37 ± 11.70 (n = 5)
Red fox (*Vulpes vulpes*)[F,+]	30.00 ± 0.00 (n = 25)	60.96 ± 21.68 (n = 5)
Mink (*Neovison vison*)[F]	10.37 ± 1.92 (n = 27)	34.62 ± 14.78 (n = 5)
Red squirrel (*Sciurus vulgaris*)[R,P,+]	16.43 ± 9.51 (n = 28)	26.04 ± 8.14 (n = 5)
Wild boar (*Sus scrofa*)[W,R,F,*,+]	(4.17 ± 5.77, n = 29)	319.57 ± 55.95 (n = 5)
Complex-toothed Flying Squirrel (*Trogopterus xanthipes*)[F,P,+]	5.17 ± 27.85 (n = 29)	28.11 ± 9.64 (n = 5)
Birds		
Collared crow (*Corvus torquatus*)[R,P]	9.14 ± 20.18 (n = 29)	54.74 ± 8.43 (n = 5)
Spotted dove (*Spilopelia chinensis*)[R,F,+]	200.00 ± 0.00 (n = 29)	7.54 ± 1.10 (n = 5)
Eurasian magpie (*Pica pica*)[R,F,P,+]	21.54 ± 28.53 (n = 13)	10.21 ± 3.56 (n = 5)
Crested myna (*Acridotheres cristatellus*)[R,P,+]	60.34 ± 20.61 (n = 29)	15.39 ± 16.23 (n = 5)
Chukar partridge (*Alectoris chukar*)[F,+]	273.68 ± 45.24 (n = 19)	6.66 ± 1.38 (n = 5)
Ring-necked Pheasant (*Phasianus colchicus*)[F,+]	80.00 ± 0.00 (n = 26)	14.80 ± 5.44 (n = 5)
Peacock (*Pavo cristatus*)[F,P,*]	15.00 ± 0.00 (n = 15)	55.63 ± 20.33 (n = 5)
Guinea fowl (*Numida meleagris*)[F]	35.00 ± 15.81 (n = 10)	12.13 ± 5.17 (n = 5)
Reptiles		
Beauty rat snake (*Orthriophis taeniurus*)[R,F,+]	(7.00 ± 10.90, n = 28)	22.78 ± 15.36 (n = 5)
Red large-toothed Snake (*Dinodon rufozonatum*)[R,F,+]	(7.78 ± 11.56, n = 27)	10.06 ± 4.84 (n = 5)
Many-banded krait (*Bungarus multicinctus*)[R,F,+]	(3.18 ± 3.32, n = 27)	11.24 ± 3.41 (n = 5)
Ringed water snake (*Sinonatrix annularis*)[R,P,+]	(19.00 ± 39.21, n = 29)	3.25 ± 1.24 (n = 5)
Short-tailed pit viper (*Gloydius brevicaudus*)[R,F,+]	(5.96 ± 10.30, n = 27)	7.84 ± 1.93 (n = 5)
Chinese cobra (*Naja atra*)[R,F,+]	(59.04 ± 54.93, n = 28)	N/A
Monocled cobra (*Naja kaouthia*)[F,+]	(18.48 ± 48.50, n = 29)	20.42 ± 6.57 (n = 5)
Oriental rat snake (*Ptyas mucosa*)[F,+]	(11.76 ± 20.44, n = 29)	18.94 ± 3.21 (n = 5)
Sharp-nosed pit viper (*Deinagkistrodon acutus*)[F,+]	(3.69 ± 5.35, n = 26)	41.13 ± 16.65 (n = 5)
Siamese crocodile (*Crocodylus siamensis*)[F,*]	(2.07 ± 2.53, n = 27)	N/A
Big-eyed rat snake (*Ptyas dhumnades*)[R,F,+]	(121.10 ± 138.11, n = 29)	10.36 ± 2.09 (n = 5)
King rat snake (*Elaphe carinata*)[R,F,+]	(104.97 ± 85.07, n = 29)	N/A

SARS-CoV-2 testing in samples from 2019

- Literature screening and review (including preprints)
- Laboratory Reference Network discussions with experts
- WHO Lab Network – review of pre-pandemic testing of samples or referral of samples for confirmatory testing to external laboratories

Testing of pre-pandemic samples – negative results

Countries	Study period	Sample type	Population	Results for samples
Germany[1]	December 2019 – April 2020	Respiratory specimens	Patients with pneumonia	No positive results before March 2020 N=195
UK[2]	January 2020	Respiratory specimens	Patients with pneumonia	No positive results before February 2020. N=1,378
Scotland[3]	December 2019 – February 2020	Respiratory specimens	ICU admitted patients	No positive results before March 2020. N=148
US [4]	December 2019 – June 2020	Respiratory specimens	Patients, BAL samples, dept. defense	No positive samples found before January 2020. N=7,000
Italy[5]	November 2019 – March 2020	Respiratory specimens	Patients, SARI	No positive results. N=166
Italy[6]	December 2019 – March 2020	Respiratory specimens	Patients with respiratory symptoms	No positive results. N=906
Canada[7]	August 2019	Wastewater	NA	Negative
Netherlands[8]	February 2020	Wastewater	NA	Negative
US[9]	January – April 2020	Wastewater	NA	Negative

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1. Panning et al 2020 10.1007/s15010-020-01471-y;
2. Chappell et al 2020 10.1101/2020.08.18.20174623
3. Tomb et al 2020 10.1016/j.jinf.2020.06.022
4. Chapleau et al. 10.1101/2021.02.18.21251368
5. Capalbo et al IJERP 2020; 10.3390/ijerph17228461
6. Calderaro et al IJID 2020 10.1016/j.ijid.2020.09.1473
7. D'aoust et al. 10.1016/j.watres.2020.116560
8. WHO expert network communications
9. Sherchan et al. 10.1016/j.scitotenv.2020.140621

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Testing of pre-pandemic samples – positive results

Countries	Study Period	Sample type	Population	Results	Dates of positive samples
France[1]	December 2019 – January 2020	Respiratory sample	ICU admitted patients	1//14 tested positive (PCR)	December 2019
	November 2019 – January 2020	Serum	Blood donations	10/9144 tested positive (neutralization)	November – December 2019
US[2]	December 2019 – January 2020	Serum	Blood donations	84/7389 tested positive (neutralization)	December 2019 – January 2020
Italy[3,4,5,6]	[3]September 2019 – February 2020	Oropharyngeal	Measles-suspected patients	1/39 tested positive (in house PCR)	December 2019
	[4]August 2019 – February 2020	Oropharyngeal	Measles-suspected patients	11/44 tested positive (in house PCR) *	September-December 2019
	[5]November 2019	Dermatosis sample	Patients with skin manifestations	1 tested positive (in house assay)	November 2019
	[6] December 2019	Wastewater	-	Tested positive (PCR)	December 2019
Brazil[7]	October 2019 – March 2020	Wastewater	NA	Tested positive (PCR)	November, December 2019
Spain[8]	2019	Wastewater	NA	Tested positive but cannot be verified	March 2019
Italy[9]	September 2019 – March 2020	Serum	Cancer screening trials	Initially positive, negative upon re-testing 6/959 (neutralization)	October – December 2019

1. Deslandes et al., 2020; 10.1016/j.ijantimicag.2020.106006
2. Basavaraju et al., 2020; 10.1093/cid/ciaa1785
3. Amendola et al., 2020; 10.3201/eid2702.204632
4. Amendola et al., 2021; 10.2139/ssrn.3883274
5. Gianotti et al., 2021; 10.1111/bjd.19804
6. La Rosa et al., 2021, 10.1016/j.watres.2021.117104
7. Fongaro et al., 2021 10.1016/j.scitotenv.2021.146198
8. Chavarria-Miro et al. 10.1101/2020.06.13.20129627
9. Apolone et al. 10.1177/0300891620974755

*followed up

Collaborations and verification of early results

- Italy - after notification of a positive signal retrieved from a lung cancer screening trial in October-December 2019, a collaboration was established between researchers in Italy, the UK and the Netherlands

- Samples were shared with an external site from the WHO lab network - Erasmus Medical Centre in Netherlands for re-testing, the initial results have not been verified.

National Cancer Institute, Milan, Italy

Erasmus Medical Center, Rotterdam, The Netherlands

Summary of pre-pandemic sampling

- Many negative signals from retrospective studies testing respiratory and serum samples from Germany, France, Italy, UK and the US.

- Some serological and molecular evidence of SARS-CoV-2 circulation in late 2019 (France, US, Italy, Brazil), verification is ongoing.

- No study was able to generate a whole genome sequence from a 2019 sample thus far.

SAGO - Open Call & Selection Process

- Open call – circulation of open call to Member States, existing WHO networks, GOARN, and available on WHO website
- Interested individuals will be asked to register their interest to SAGO@who.int and include:
  - A cover letter
  - Curriculum vitae
  - A signed and completed Declaration of Interests (DOI) form for WHO Experts, available at https://www.who.int/about/ethics/declarations-of-interest
- All applications will be assessed by the WHO secretariat in accordance with the WHO procedures, based on their technical expertise, taking into consideration diverse perspectives from different regions, especially from low and middle-income countries, and for gender balance