

# Presentation to Member States COVID-19 Information sessions

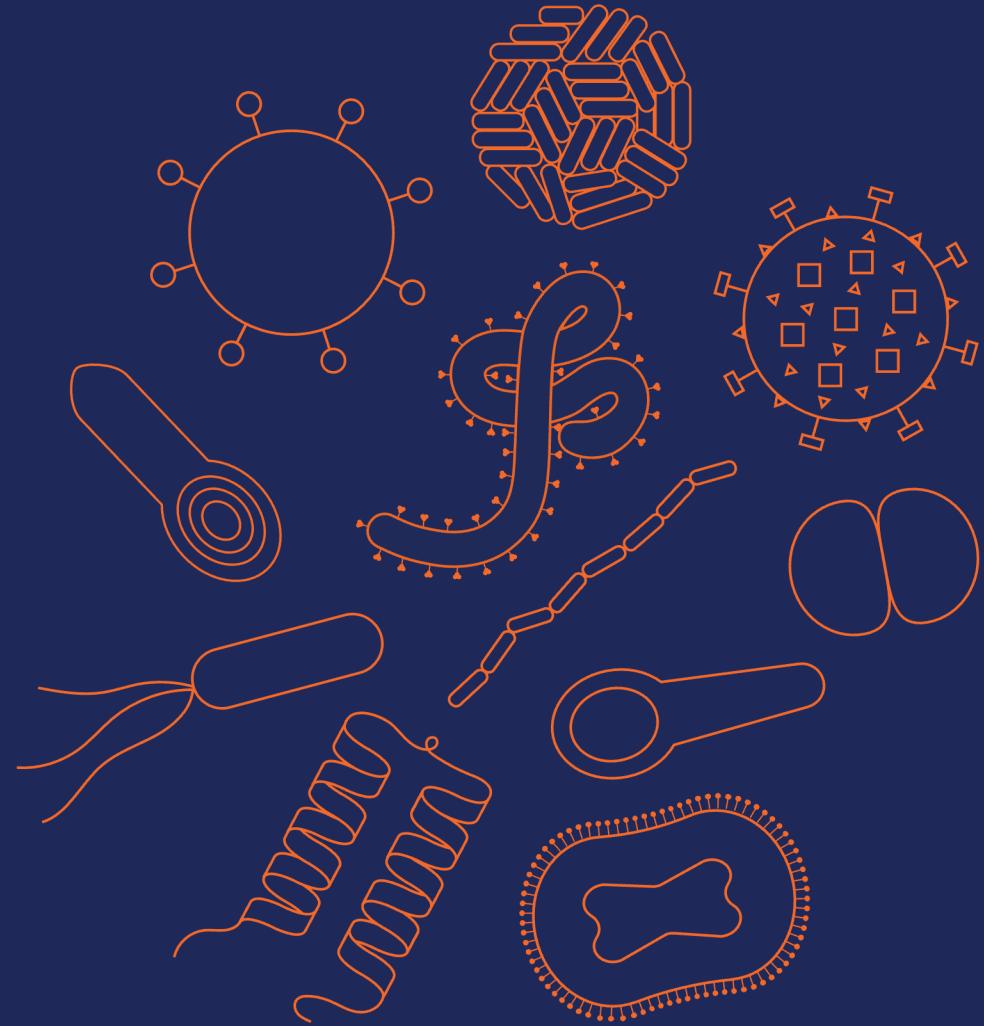
30 March 2023

**SAGO**

Scientific  
Advisory Group  
for the Origins  
of Novel Pathogens



SAGO, an advisory group to WHO



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

**SAGO has been formed 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)**

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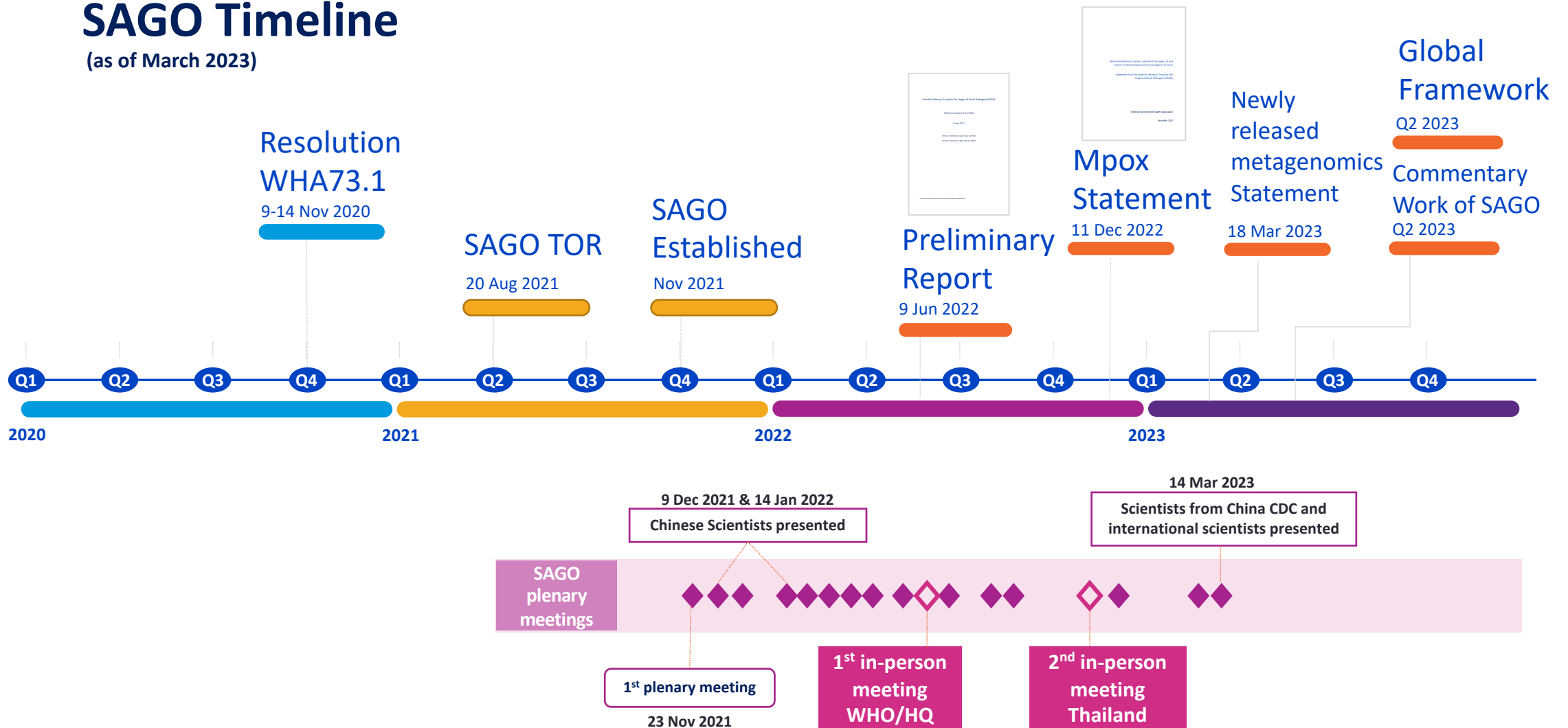
# Terms of Reference of the SAGO

In its capacity as an advisory body to WHO, the SAGO will follow the [terms of reference](#) as initially outlined and shall have the following functions:

1. To advise WHO on the development of a WHO global framework
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 WHO global framework
3. In the context of SARS-CoV-2 origins:
  - a. To provide 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
4. 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 Timeline

(as of March 2023)



# WHO Global Framework for Emerging and Re-emerging Diseases

- Rationale
  - Prior to SAGO - lack of a unified and structured approach to standardize origins investigations globally
  - Global framework to study origins of emerging and re-emerging pathogens using a One Health approach
- Significance of the Framework



Improve the understanding of the pathogen's origins.



Improve the global preparedness and response to emerging pathogens of similar origin



Improve the speed, quality, consistency, coordination, and comprehensiveness of investigations



Foreground the commitment of international health regulations (IHR)



Consider the diverse specializations and expertise via a participatory and integrative approach

# WHO Global Framework for Emerging and Re-emerging Diseases

## 6 Critical Elements & Timeline

Early investigations  
following the emergence

Human studies:  
epidemiology

Human/Animal Interface  
studies

Environmental/Ecological  
studies

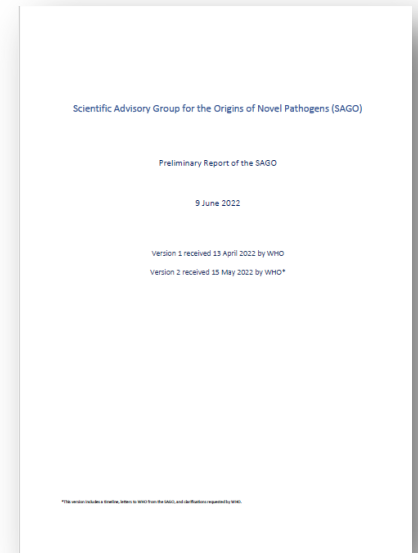
Genomics/Phylogenetics

Biosafety/Biosecurity

# SAGO first preliminary report – includes assessment of origins of SARS-CoV-2

Published June 2022

- **Note:** SAGO recommendations are based on published evidence and presentations from invited scientists.
- **Epidemiological and sequencing data:**
  - Ancestral strains to SARS-CoV-2 have a zoonotic origin, with the closest genetically related viruses being beta coronaviruses, identified in Rhinolophus bats in China 2013 (96.1%) and Laos in 2020 (96.8%).
- **Early investigations:**
  - Huanan Seafood Market played an important role in amplifying the pandemic, with several of the early cases first detected in December 2019 being linked to the market and environmental samples from the market testing positive for SARS-CoV-2.



Published June 2022

[Link to SAGO Preliminary Report](#)

# SAGO recommendations on studies to better understand Mpox emergence

Published December 2022

- Recommendations to better understand the monkeypox virus and its re-emergence, includes:
  - Clinical and epidemiological retrospective studies,
  - Reviewing clinical, and laboratory records in affected locations,
  - Sequencing and phylogenetic analysis of new and historical strains
  - One Health studies, investigate animal reservoirs in endemic countries and new locations, risk of reverse zoonoses
  - Environmental, anthropological, behavioural and social science studies.
- These are organised into technical elements consistent with the Global Framework (unpublished).
- These studies will help identify human-to-human and animal-to-human transmission dynamics, viral mutation patterns, and associated factors that drive the emergence and re-emergence of mpox.



Published December 2022

[Link to SAGO Mpox statement](#)



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# SAGO's latest assessment of evidence regarding the origins of SARS-CoV-2

Based on findings presented to SAGO on 14 March 2023 from China CDC and independent researchers

- **Background:**
  - 12 March 2023: WHO made aware of new SARS-CoV-2 sequences and metagenomics data on public database associated with samples collected in the Huanan Seafood Wholesale Market, *Wuhan, China*, from January 2020.
  - 14 March 2023: SAGO meeting, invited scientists from China CDC and international scientists to present their latest analysis of the data.
- **Data source:**

Data basis for an expected update to [Liu et al. 2022 preprint](#), being re-submitted for publication to *Nature* by China CDC. This included metagenomic data of environmental samples from various stalls and wastewater collection sites at the Market collected as early as January 2020.
- **Findings:**

Environmental samples from market positive for SARS-CoV-2 sequences, also contains human DNA, and mitochondrial DNA of several animal species; Some known to be susceptible to SARS-CoV-2, e.g. wild raccoon dogs, Malaysian porcupine, and bamboo rats, and palm Civets.
- **Possible interpretations:**

Findings indicate live susceptible animals were present at the market shortly before the market had been cleared on 1 January 2020, as part of the public health measures by Chinese authorities.

These results provide potential leads to identifying intermediate hosts of SARS-CoV-2 and potential sources of human infections in the market.

[SAGO Statement on 18 March 2023](#)

# Recent SARS-CoV-2 origins findings

ChinaXiv  
中国科学技术论文预发布平台

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**Surveillance of SARS-CoV-2 at the Huanan Seafood Market**

作者: William J. Liu (1); Peipei Liu (1); Wenwen Lei (1); Zhiyuan Jia (1); Xiaozhou He (1); Weifeng Shi (2); Yun Tan (3); Shumei Zou (1); Gary Wong (4); Ji Wang (1); Feng Wang (1); Gang Wang (1); Kun Qin (1); Rongbao Gao (1); Jie Zhang (1); Min Li (1); Wenling Xiao (1.5); Yuanyuan Guo (1); Ziqian Xu (1); Yingze Zhao (1); Jingdong Song (1); Jing Zhang (1); Wei Zhen (1); Wenting Zhou (1); Beiwai Ye (1); Juan Song (1); Mengjie Yang (1); Weimin Zhou (1); Yuting Dai (3); Gang Lu (3); Yuhai Bi (6); Wenjie Tan (1); Jun Han (1); George F. Gao (1.6); Guizhen Wu (1);

“evidence of the prevalence of SARS-CoV-2 in the Huanan Seafood Market during the early stage of COVID-19 outbreak.”

Update: Metagenomic data including human and animal DNA in SARSCO2 positive samples.

Note: WHO has requested reports and underlying data from the United States governmental agencies, but has yet to receive the requested information.

Genetic evidence of susceptible wildlife in SARS-CoV-2 positive samples at the Huanan Wholesale Seafood Market, Wuhan: Analysis and interpretation of data released by the Chinese Center for Disease Control

Crits-Christoph, Alex; Gangavarapu, Karthik; Pekar, Jonathan E.; Moshiri, Niema; Singh, Reema; Levy, Joshua I.; Goldstein, Stephen A.; Suchard, Marc A.; Popescu, Saskia; Robertson, David L.; Lemey, Philippe; Wertheim, Joel O.; Garry, Robert F.; Rasmussen, Angela L.; Andersen, Kristian G.; Holmes, Edward C.; Rambaut, Andrew; Worobey, Michael; Débarre, Florence

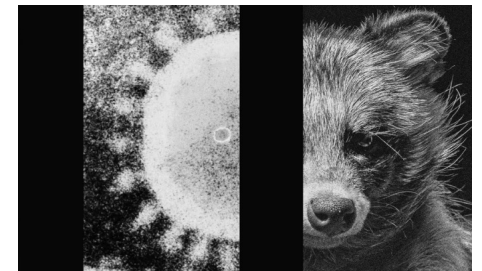
“Metagenomic data on GISAID: Animal DNA (raccoon dogs, bamboo rats, palm civets) in environmental swabs from the Huanan Seafood Market in Wuhan, China, linked to the origin of the COVID-19 pandemic.”

**SAGO statement on newly released SARS-CoV-2 metagenomics data from China CDC on GISAID**

18 March 2023 | Statement | Reading time: 3 min (781 words)

On 12 March 2023, WHO was made aware of new SARS-CoV-2 sequences and metagenomics data associated with samples collected in the Huanan Seafood Wholesale Market, Wuhan, China, from January 2020, that became available on GISAID for a short period of time. The data had subsequently been downloaded by a number of researchers from several countries. Access was restricted shortly after, apparently to allow further data updates by China CDC. WHO then immediately reached out to China CDC and to the Chair and Vice-Chair of SAGO. Upon discussions between WHO and Chinese colleagues, it was explained that the genomic data are the basis for an expected update to the existing Liu et al. 2022 preprint (1), which is in the process of being re-submitted for publication to Nature by China CDC.

Evidence of susceptible live animals in the market and clues into possible intermediate hosts but still no clear answer on the “origins” of those animals and where a zoonotic event may have occurred.



Alphotographic / Getty

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# SAGO's next assessment of the origins of SARS-CoV-2

Publication plan on further assessments

- SAGO continues its independent assessment of SARS-CoV-2 origins based on emerging evidence
- Two papers are in the pipeline:
  - SAGO Commentary for *Nature* – *What is the importance of SAGO*
  - SAGO Commentary on assessing the current understanding of SARS-CoV-2 origins
- SAGO further engages stakeholders to collaborate:
  - Request that all sequencing and metagenomic data to be made public on GISAID or any other sequence database, and pre-prints posted
  - Encourages researchers using this data to collaborate and engage with Chinese researchers.

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# Summary Slide

Updated March 2023

- Currently, unable to make final conclusions about the origins of the COVID-19 pandemic
- Key information is not yet available from recommended studies
- Update on recommended studies provided by Chinese scientists:
  - molecular epidemiology studies; blood bank serosurvey, animal and environmental studies and cold-chain transmission of SARS-CoV-2 in the Huanan market.
- Available epidemiological and sequencing data suggest ancestral strains of SARS-CoV-2 originate from zoonotic source:
  - Closest genetically related beta coronaviruses, identified in Rhinolophus bats in China and Laos.
  - Virus progenitors; the natural/intermediate hosts or spill-over event to humans has not yet been identified.
  - Newly released metagenomics data –suggest leads on possible intermediate hosts at Huanan Seafood Market.
- No new findings or access to information regarding potential breaches in biosafety and biosecurity related to laboratory or research activities surrounding SARS-CoV-2 related viruses.
  - WHO requested reports and underlying data from the United States governmental agencies-not yet granted.
- Still some outstanding results from the recommended studies as outlined in the report.
- The SAGO will remain open to all scientific evidence that becomes available in the future to allow for comprehensive testing of all reasonable hypotheses.



27 Members with significant and diverse expertise

Chair and vice-chair

2 Observers FAO/OIE