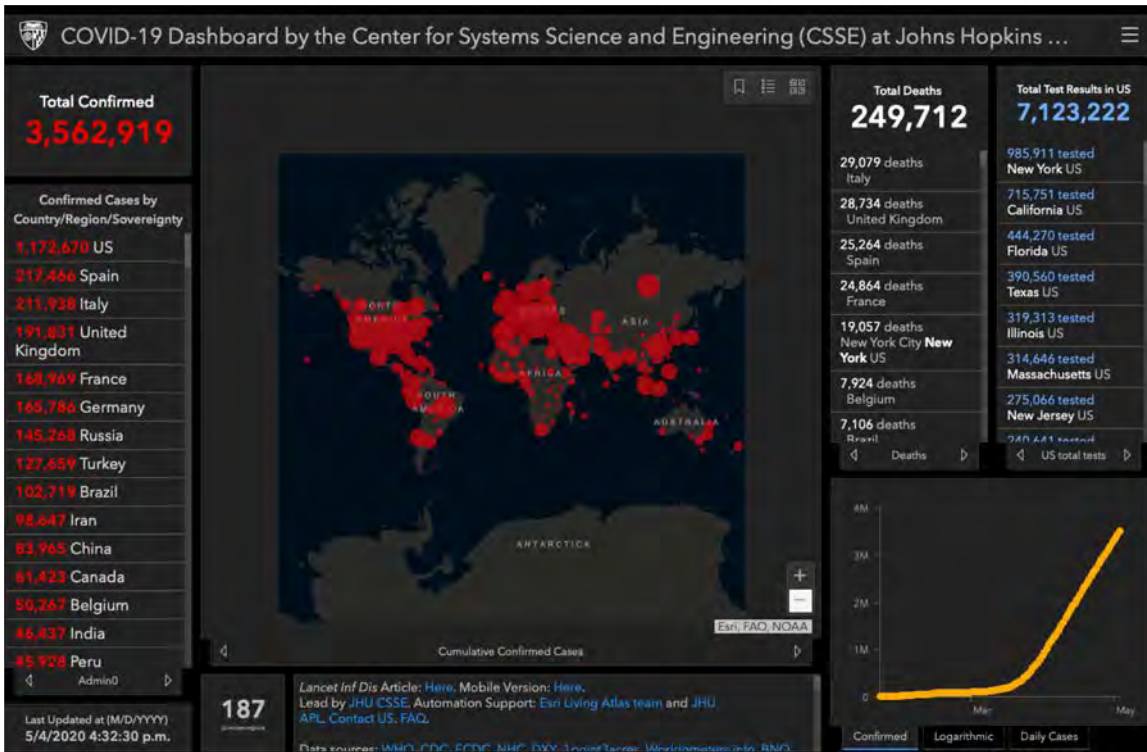
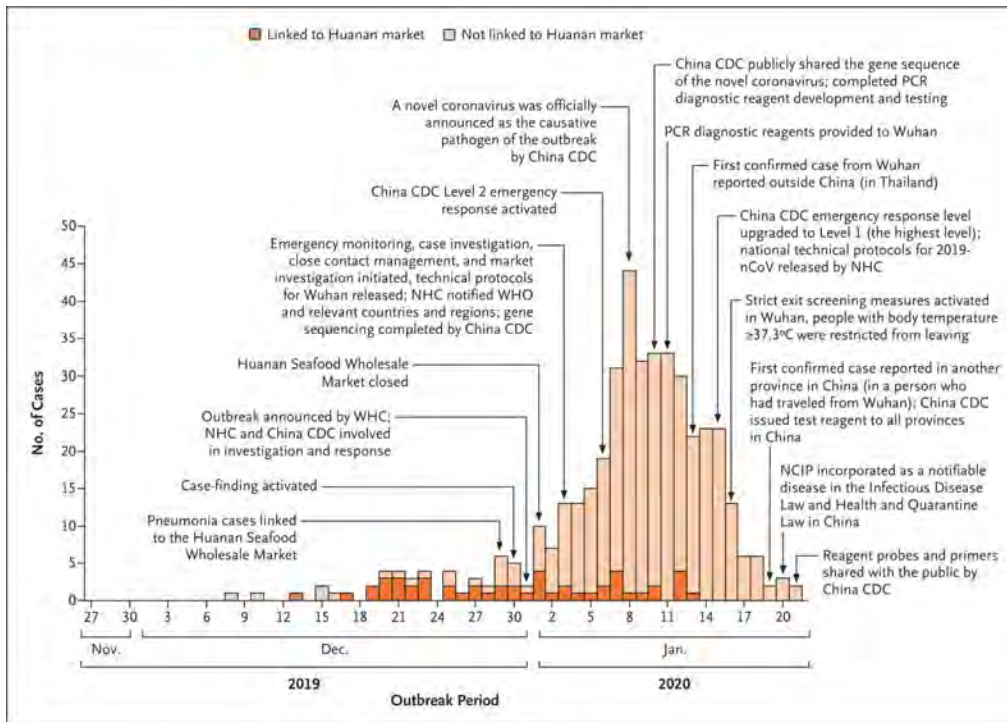


COVID-19 and Beyond - Knowns, Unknowns and Needs

Chris Walzer Wildlife Conservation Society



What do we know?



Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study



Nanshan Chen¹, Min Zhao¹, Xuan Deng¹, Junming Qu¹, Fengyan Gong, Yong Han, Yang Qiu, Jing Wang, Ying Liu, Yuan Wu, Guo Xia, Ting Yu, Xinyin Zhang, Li Zhang

Summary

Background In December, 2019, a pneumonia associated with the 2019 novel coronavirus (2019-nCoV) emerged in Wuhan, China. We aimed to further clarify the epidemiological and clinical characteristics of 2019-nCoV pneumonia.

Methods In this retrospective, single-centre study, we included all confirmed cases of 2019-nCoV in Wuhan Jinyintan Hospital from Jan 1 to Jan 20, 2020. Cases were confirmed by real-time RT-PCR and were analysed for epidemiological, demographic, clinical, and radiological features and laboratory data. Outcomes were followed up until Jan 25, 2020.

Findings Of the 99 patients with 2019-nCoV pneumonia, 49 (49%) had a history of exposure to the Huanan seafood market. The average age of the patients was 55.5 years (SD 13.1), including 67 men and 32 women. 2019-nCoV was detected in all patients by real-time RT-PCR. 50 (51%) patients had chronic diseases. Patients had clinical manifestations of fever (82 [83%] patients), cough (81 [82%] patients), shortness of breath (31 [31%] patients), muscle ache

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Science and Education Department (Y Han PhD) and

THE NEW ENGLAND JOURNAL OF MEDICINE

ORIGINAL ARTICLE

Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia

Qun Li, M.Med., Xuhua Guan, Ph.D., Peng Wu, Ph.D., Xiaoye Wang, M.P.H., Lei Zhou, M.Med., Yeqing Tong, Ph.D., Ruiqi Ren, M.Med., Kathy S.M. Leung, Ph.D., Eric H.Y. Lau, Ph.D., Jessica Y. Wong, Ph.D., Xuesen Xing, Ph.D., Nijuan Xiang, M.Med., Yang Wu, M.Sc., Chao Li, M.P.H., Qi Chen, M.Sc., Dan Li, M.P.H., Tian Liu, B.Med., Jing Zhao, M.Sc., Man Liu, M.Sc., Wenxiao Tu, M.Med., Chuding Chen, M.Sc., Lianmei Jin, M.Med., Rui Yang, M.Med., Qi Wang, M.P.H., Suhua Zhou, M.Med., Rui Wang, M.D., Hui Liu, M.Med., Yingbo Luo, M.Sc., Yuan Liu, M.Med., Ge Shao, B.Med., Huan Li, M.P.H., Zhongfa Tao, M.P.H., Yang Yang, M.Med., Zhiqiang Deng, M.Med., Boxi Liu, M.P.H., Zhitao Ma, M.Med., Yanping Zhang, M.Med., Guoqing Shi, M.P.H., Tommy T.Y. Lam, Ph.D., Joseph T. Wu, Ph.D., George F. Gao, D.Phil., Benjamin J. Cowling, Ph.D., Bo Yang, M.Sc., Gabriel M. Leung, M.D., and Zijian Feng, M.Med.

ABSTRACT



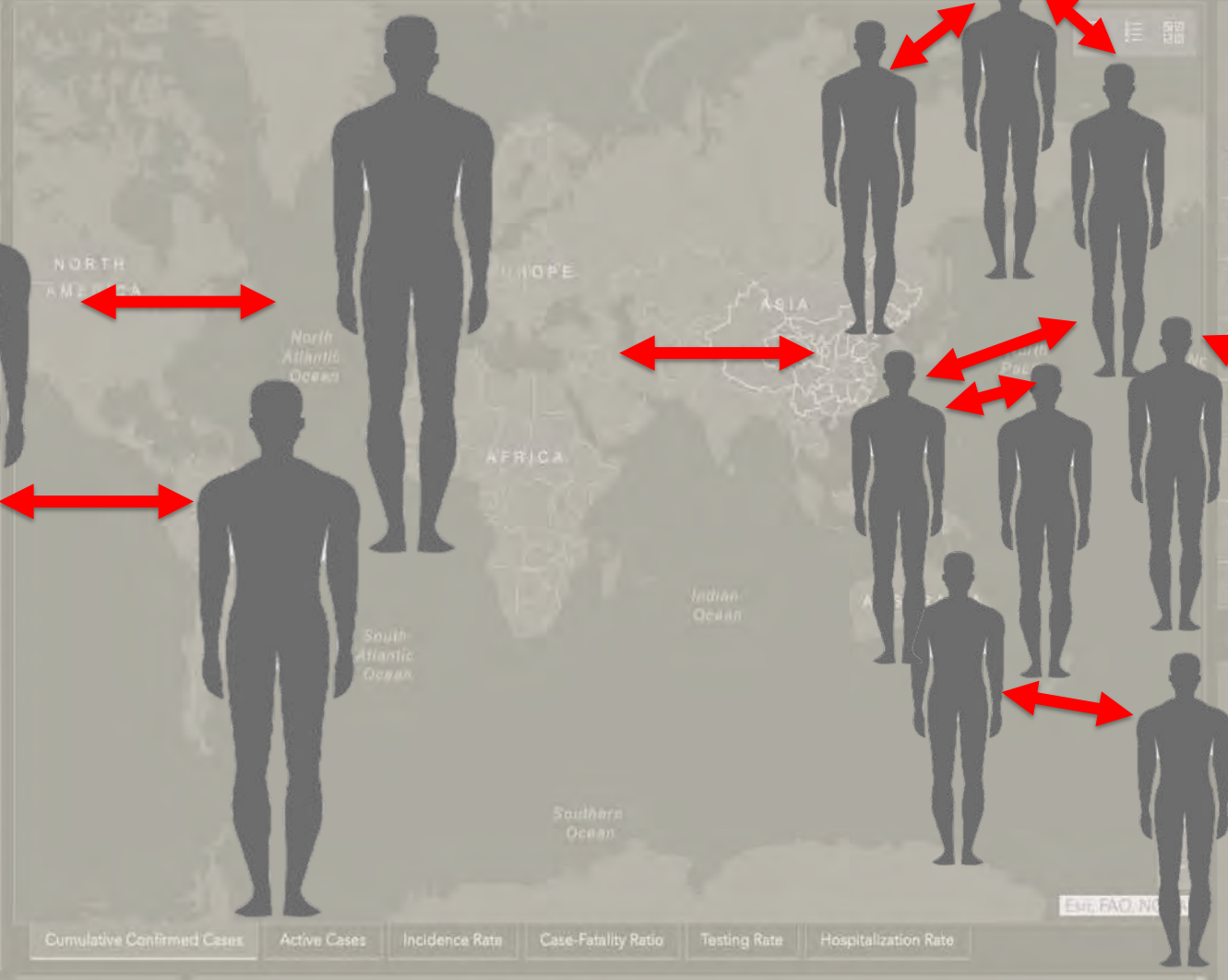
COVID-19 Dashboard by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU)

Total Confirmed

3,329,740

Confirmed Cases by Country/Region/Sovereign

- US
- Spain
- Italy
- United Kingdom
- France
- Germany
- Turkey
- Russia
- Iran
- Brazil
- China
- Canada
- Belgium
- Peru
- Netherlands
- India
- Switzerland



Total Deaths

237,647

- 28,236 deaths Italy
 - 27,510 deaths United Kingdom
 - 24,594 deaths France
 - 24,543 deaths New York US
 - 18,399 deaths New York US
 - 7,700 deaths Belgium
 - 6,670 deaths Germany
 - 6,329 deaths Brazil
- Deaths Recovered

4M
3M
2M
1M

Cumulative Confirmed Cases Active Cases Incidence Rate Case-Fatality Ratio Testing Rate Hospitalization Rate

Exp: FAO, NCD



What do we know?



Infection, Genetics and Evolution

journal homepage: www.elsevier.com/locate/meegid

Research paper

Genetic diversity of coronaviruses in bats in Lao PDR and Cambodia

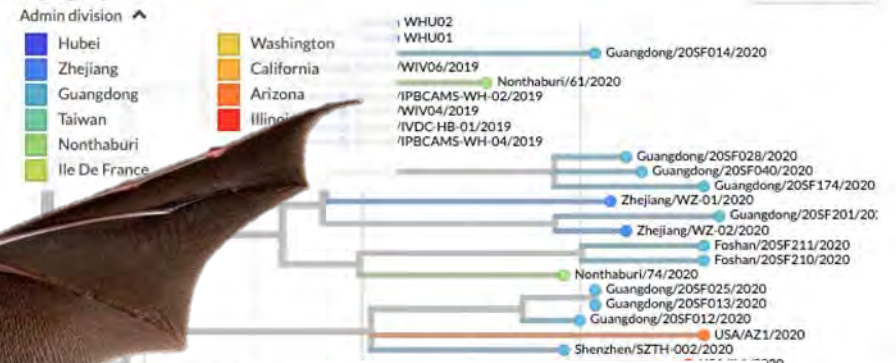
Audrey Lacroix^a, Veasna Duong^a, Vibol Hul^a, Sorn San^b, Hull Davun^b, Keo Omaliss^c, Sokha Chea^d, Alexandre Hassanin^e, Watthana Theppangna^f, Soubanh Silithammavong^{g,h}, Kongsy Khammvong^g, Sinpakone Singhalath^g, Zoe Creatorex^g, Amanda E. Fine^l, Tracey Goldstein^l, Sarah Olson^k, Damien O. Joly^{k,l}, Lucy Keatts^d, Philippe Dussart^a, Aneta Afelt^m, Roger Frutos^{n,o,*}, Philippe Buchy^{a,p,*}

^a Institut Pasteur du Cambodge, Virology Unit, Phnom Penh, Cambodia
^b National Veterinary Research Institute, Ministry of Agriculture Forestry and Fisheries, Cambodia
^c Forest Administration, Ministry of Agriculture Forestry and Fisheries, Cambodia
^d Wildlife Conservation Society, Cambodia



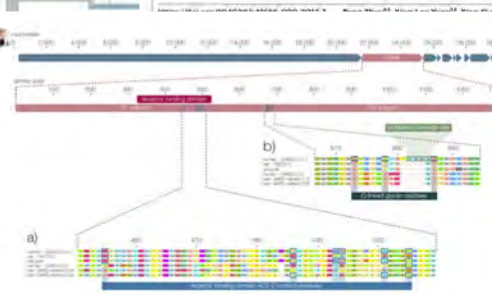
Showing 42 of 42 genomes sampled between Dec 2019 and Jan 2020.

Phylogeny



Article

A pneumonia outbreak associated with a new coronavirus of probable bat origin



*¹ Ben Hu¹, Lei Zhang¹, Wei Zhang¹, Hui-Dong Chen¹, Jing Chen¹, Yun Liu¹, Han¹, Xu-Rui Shen¹, Xi Wang¹, et al., Fu-Dong Lin¹, Liu-Lin Liu¹, Bing Yang¹, Song Li¹ et al.
 A number of severe acute respiratory (SARS-CoV-2) have been identified in their natural hosts that some of those bat SARS-CoV-2 we report the identification and phylogenetic analysis of SARS-CoV-2 which caused an epidemic of Wuhan, China. The epidemic, which started by respiratory-confirmed infections with six patients, sequences were obtained from the bat, are almost identical to each other and Furthermore, it was found that some level to a bat coronavirus. The conserved non-structural proteins show SARS-CoV-2. The SARS-CoV-2 was identified of a critically ill patient, which can be spontaneously, we have confirmed that this ACE2 as SARS-CoV-2.

'A/1/2020
 /DF0373/2020
 /DF0372/2020
 /2/2020
 /20
 /SFS207/2020
 ou/20SF206/2020

What do we know?

- Across 25 high-risk viral families, there are estimated to be **1.7M unknown viruses**
- About **700k of which** likely have the potential to infect humans
- For example, for every known coronavirus, there are thousands of unknown coronaviruses circulating in wildlife



Carroll et al. (2018) Science



INFECTIOUS DISEASES

The Global Virome Project

Expanded viral discovery can improve mitigation

By Dennis Carroll, Peter Daszak, Nathan D. Wolfe, George F. Gao, Carlos M. Morel, Subhash Morzaria, Ariel Pablos-Méndez, Oyewale Tomori, Jonna A. K. Mazet

causing the next great pandemic (1, 2). However, if these viruses are our enemy, we do not yet know our enemy very well. Around 263 viruses from 25 viral families are known to infect humans (3) (see the figure), and given

Scientists prepare to collect a blood sample from a *Rousettus* sp. fruit bat in Thailand to test for novel viruses. The Global Virome Project aims to identify and characterize the majority of currently unknown viruses in key wildlife groups, including rodents, nonhuman primates, and bats.

Other previous studies had begun to conduct targeted viral discovery in wildlife (9), and develop mitigation strategies for the emergence of avian flu, for example. However, the USAID Emerging Pandemic Threats (EPT) PREDICT project is the first global-scale coordinated program designed to conduct viral discovery in wildlife reservoir hosts, and characterize ecological and socioeconomic factors that drive their risk of spillover, to mitigate their emergence in people (10).

Working with local partners and governments, wildlife and domestic animals and at-risk human populations in geographic hotspots of disease emergence (1) are sampled, and viral discovery conducted. A strategy to identify which novel viruses are most at risk of spillover has been developed (11), and further work is conducted on these to characterize them prior to, or in the early stages of, spillover. Metadata on the ecology of wildlife-livestock-human transmission interfaces, and on human behavioral patterns in communities, are concurrently analyzed so that strategies to reduce spillover can be developed (supplementary text). To date,

Downloaded from <http://science.sciencemag.org/>



What do we not know?



health Food Fitness Wellness Running Year 2019 LIVE TV

Snakes could be the source of the Wuhan coronavirus outbreak

THE CONVERSATION By Haitao Guo, Guangxiang "George" Luo and Shou-Jiang Gao, The Conversation
Updated 3:41 PM ET, February 24, 2020

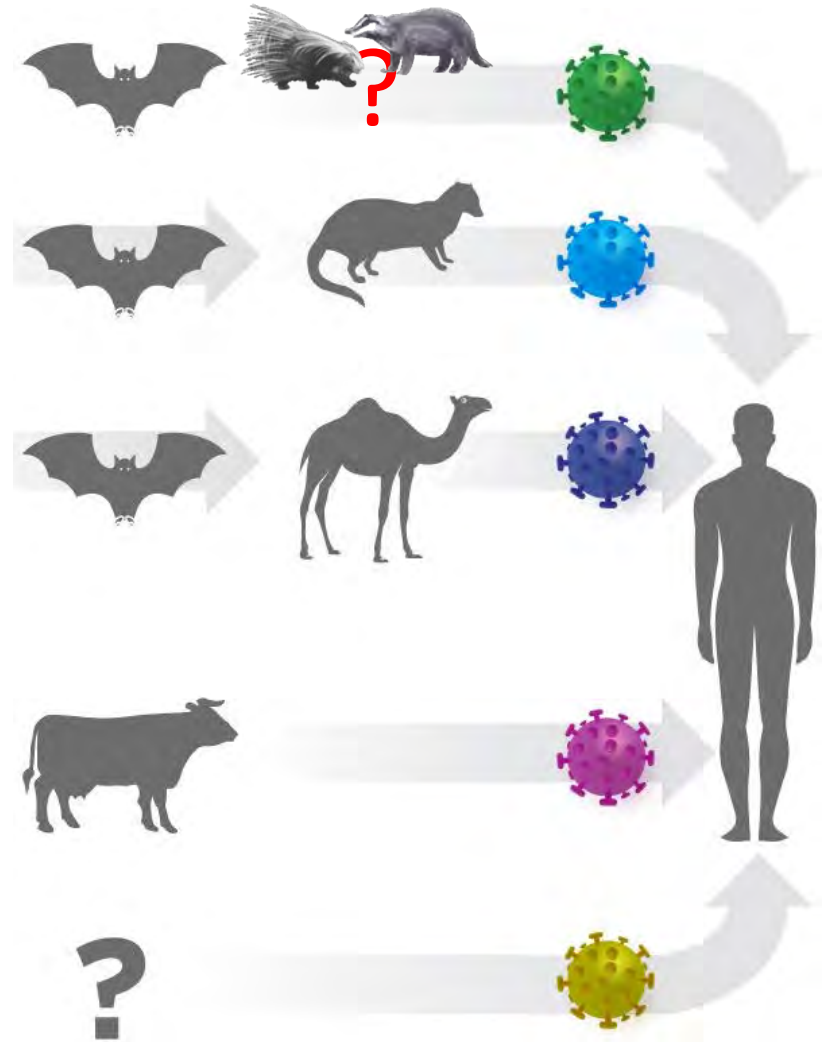


TUSK International Tusk Campaign

Coronavirus from Space?

A Heterologous Recombination of SARS-CoV-2 and a Novel Coronavirus from Chanda Virus Strain in the Lab

February 4, 2020 1 Comment



What do we know?

Furuse et al. *Virology Journal* 2010, 7:52
<http://www.virology.com/content/7/1/52>

SHORT REPORT

Origin of measles virus: divergence of rinderpest virus and measles virus

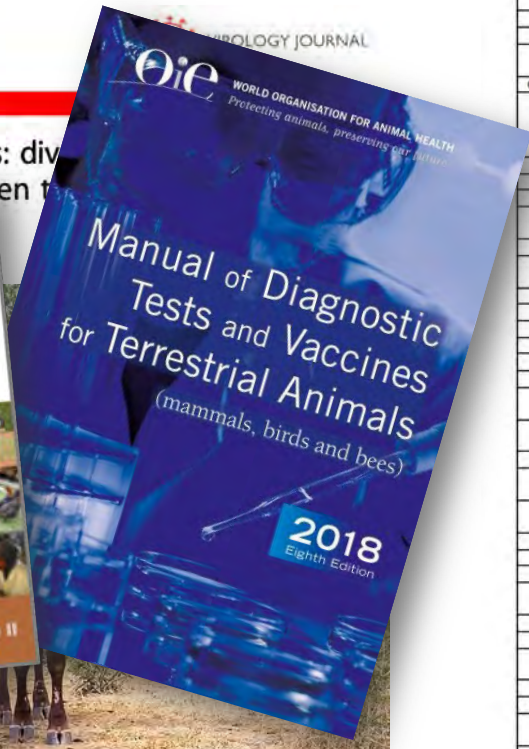
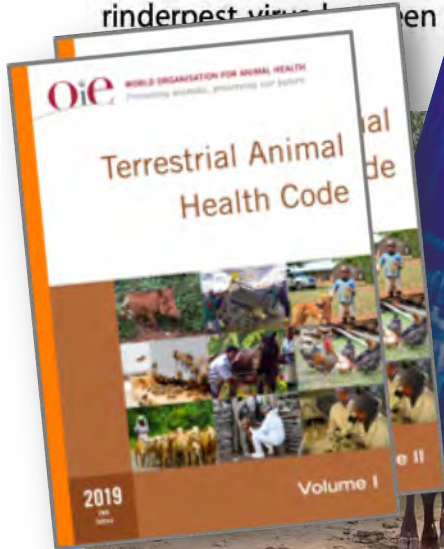
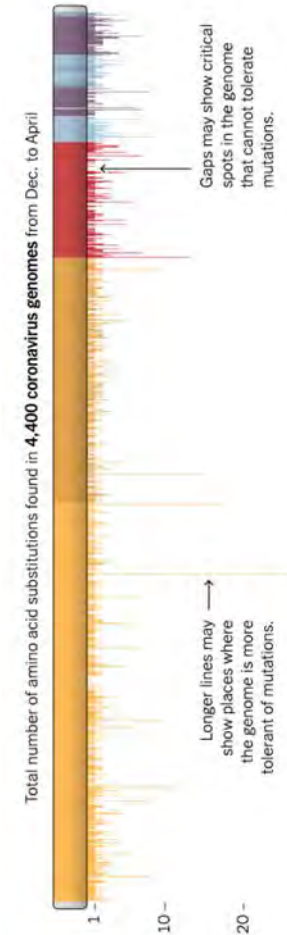


Table A: Extant knowledge about species sensitivity to SARS-CoV-2 from [17][30-32] N/A= not assessed yet

Species	In Vitro Viral Particle entry	Computer & molecular prediction of ACE2 receptor binding		In vivo experimental infection success (blank= no data yet)	Natural transmission (Human > Animal)
		From [17]	From [30,31]		
Horseshoe bat	YES	Likely	Very low (17/25)		
Daubenton's bat	NO	N/A			
Vampire bat	N/A	Likely (4/5)	Very low (13/25)		
Coquerel sifaka	N/A	N/A	High (24/25)		
Blue eyed black lemur	N/A	N/A	High (22/25)		
Cynomolgus monkey	YES	Likely (5/5)		Yes[33]	
Rhesus macaque	N/A	N/A	Very High (25/25)	Yes, and reinfection could not occur at T0+28 days new challenge	
Anubis baboon	N/A	Likely (5/5)	Very High (25/25)		
Orangutan	N/A	Likely (5/5)	Very High (25/25)		
Chimpanzee	N/A	Likely (5/5)	Very High (25/25)		
Gorilla	N/A		Very High (25/25)		
Swine	NO	Likely (5/5)	Low (19/25)	No: Failed to get positive PCR and seroconversion	
Cattle	NO	Likely (4/5)			
African elephant	N/A	Unlikely (3/5)	Low (18/25)		
Camel	N/A	N/A	Medium (21/25)		
Giraffe, Okapi	N/A	N/A	Medium (21/25)		
Hippopotamus	N/A	N/A	Medium (20/25)		
Alpaca	N/A	N/A	Medium (20/25)		
Reindeer	N/A	N/A	High (21/25)		
Giant anteater	N/A	N/A	High (21/25)		
Mouse	NO	Unlikely (2/5)	Very low (16/25)		
Rat	N/A	Unlikely (3/5)	Very low (16/25)		
Chinese hamster	NO	Likely (4/5)	High (22/25)		
Guinea pig	N/A	Unlikely (2/5)			
Dog	YES	Likely (3/5)	Low (19/25)	No positive PCR but seroconversion	Yes
Domestic cat	N/A	Likely (3/5)	Medium (21/25)	Yes + transmission to other cats	Yes
Tiger, Lion	N/A	N/A	Medium (21/25)		Yes
Puma	N/A	N/A	Medium (21/25)		
Ferret	YES	Likely	Very low (17/25)	Yes + transmission to other ferrets[23,24]	
American mink	N/A	N/A	Very low (14/25)		Yes
European mink	N/A	N/A	Very low (17/25)		
Meerkat	N/A	Unlikely (2/5)	Very low (15/25)		
Civet cat	N/A	Likely			
Masked palm civet	N/A	Very low	Very low (13/25)		
Raccoon	?	Unlikely (2/5)			
Fossa	N/A	N/A	Very low (16/25)		
Red panda	N/A	N/A	Very low (13/25)		
Sea otter	N/A	N/A	Low (17/25)		
Chicken	?	Unlikely (3/5)		No. Failed to get positive PCR and seroconversion	
Duck	?	?		No. Failed to get positive PCR and seroconversion	



NYT - April 2020

It is not about bat-soup,
civets or pangolins





What do we know?

Detection rates of coronaviruses

0.6 -



trade

large market

restaurant

Field rat value chain interface



- What do we not know?



Photo/Xinhua



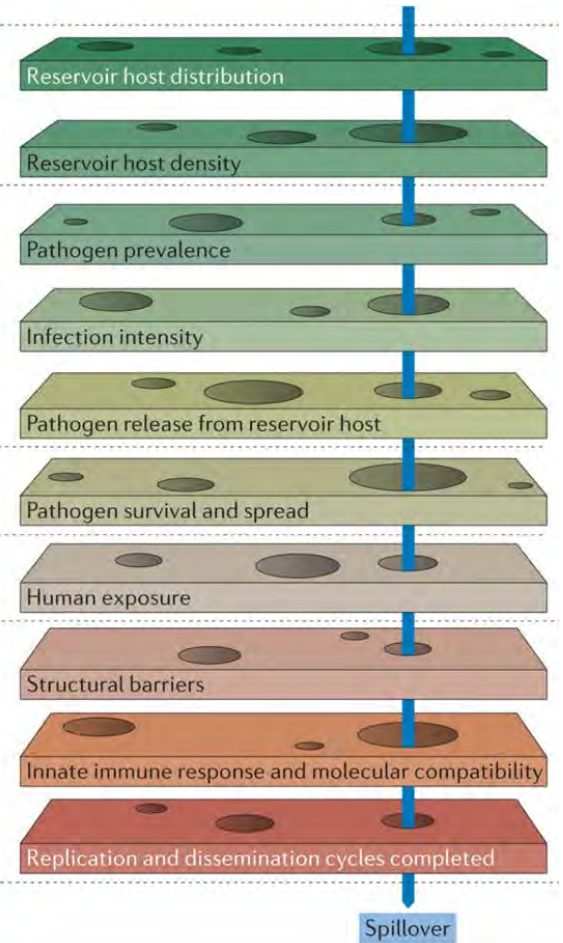
Animal ecology, population biology, biogeography, behavioural ecology, landscape ecology, agricultural sciences

Disease ecology, animal epidemiology, infectious disease dynamics, immunology, microbiology, veterinary medicine

Microbiology, disease ecology, vector ecology, epidemiology, spatial ecology, infectious disease dynamics

Human epidemiology, medical anthropology, vector ecology, social sciences, behavioural ecology, infectious disease dynamics

Microbiology, innate and adaptive immunology, cell biology of pathogen–host interactions, pathology, genetics, evolutionary biology



Barriers to spillover. This figure was adapted from Plowright et al. 2017

One Health History

- 2004 **One World, One Health** meetings with human public health, conservation and infectious disease experts were organized by WCS
 - **Manhattan Principles**
- **Berlin Principles 2019**



Congo Basin – Spillover Frontline

- Long-standing program: 3 main pillars
 - Carcass monitoring [Ebola virus community engagement targeted 6,600 IPLC living in northern RoC]
 - Community outreach and education
 - Research on EBV
- Developing field test kits to better understand causes of great ape mortality





What do we need to do now?

- Permanently ban the commercial trade in wildlife for consumption
- Strengthen efforts to combat trafficking of wild animals within countries and across borders
- Work to change dangerous wildlife consumption behaviors, especially in cities



WCS ISSUES POLICY ON REDUCING RISK OF FUTURE ZOOONOTIC PANDEMICS

MARCH 28, 2020



A NEW PARADIGM URGENTLY NEEDED:

To prevent future major viral outbreaks such as the COVID-19 outbreak, impacting human health, well-being, economies, and security on a global scale, WCS recommends stopping all commercial trade in wildlife for human consumption (particularly of birds and mammals) and

ENFERMEDADES ZOOONÓTICAS: QUÉ SON Y CÓMO LAS ACCIONES HUMANAS AUMENTAN SU POSIBILIDAD DE TRANSMISIÓN

¿Qué son las enfermedades zoonóticas?

- Son un grupo de enfermedades infecciosas transmitidas de animales a seres humanos (y viceversa).
- La transmisión puede darse por contacto directo con los animales (por ejemplo, al tocarlos, al comerlos o al estar cerca de sus heces, leche, sangre) o indirectamente a través de un intermediario (por ejemplo, un insecto o un animal que se alimenta de otro animal).

Algunas de las formas de enfermedades zoonóticas a nivel mundial en los últimos años:

- 60% de las enfermedades infecciosas emergentes en humanos son zoonóticas.
- 75% de las enfermedades infecciosas emergentes, que afectan al ser humano, son de origen animal.

Muchas de las enfermedades zoonóticas que afectan al ser humano son transmitidas por vectores (mosquitos, chicharras, etc.). Algunas de estas enfermedades son:

- Chikungunya
- Ebola
- Mal de Chagas
- etc.

¿Qué es el COVID-19?

- Es una enfermedad infecciosa causada por un nuevo tipo de coronavirus (SARS-CoV-2), que en humanos causa coronavirus respiratorio y también la muerte.
- Los primeros reportes del virus datan de diciembre de 2019, en un mercado de animales vivos en Wuhan, China. Se cree que el coronavirus pudo haberse propagado en otros países del mundo.
- Es transmitido como una pandemia debido a su propagación en otros países del mundo.

Condiciones que incrementan las posibilidades de transmisión de enfermedades zoonóticas:

- El mayor contacto entre humanos y animales silvestres es facilitado por actividades que reducen la diversidad de especies y aumentan la fragmentación y degradación de hábitats, tales como:
 - Deforestación
 - Degradación de los bosques
- Alteración de las distancias naturales por:
 - Deforestación
 - Degradación de los bosques
- Mixtura de hábitats silvestres sin parámetros de biodiversidad y su interacción con hábitats agrícolas.
- Explotación ilegal de especies silvestres de su hábitat natural (ej. comercio ilegal).

Los riesgos del comercio ilegal de fauna silvestre

Hay riesgo de transmisión de enfermedades zoonóticas en los lugares de extracción, zonas de tránsito y zonas de destino de los animales.

Comparar los costos reales, comerciales, para conservar o usar medicinalmente especies a los beneficios del comercio ilegal con patógenos que podrían causar enfermedades.

Al recordar de su ambiente natural, los visitantes silvestres pueden transportar y dispersar patógenos (bacterias, parásitos, hongos y virus) en nuevas zonas.

Los municipios que modera procesos planifican y silvestres en condiciones de hacinamiento o multitudinarios incrementan el riesgo de transmisión de enfermedades a las personas con las que entran en contacto, ya que estos pueden albergar y compartir patógenos.

Los esfuerzos de WCS para combatir el tráfico de vida silvestre en la región Andes, Amazonia y Orinoquía

ESTA REGIÓN ESTÁ CONFORMADA POR BOLIVIA, BRASIL, COLOMBIA, ECUADOR Y PERÚ.

- Producir y analizar información que mejore la comprensión de la dinámica del tráfico de vida silvestre.
- Sensibilizar a la sociedad civil e involucrarla en la reducción de la demanda de vida silvestre.
- Apoyar el desarrollo de políticas públicas.





What do we need to do now?

- Mainstream holistic One Health Approaches
 - Devise adaptive, holistic, and forward-looking approaches to the detection, prevention, monitoring, control, and mitigation of emerging/resurging diseases
- Link Economic recovery funding to support One Health
 - Increase cross-sectoral investment in the global human, livestock, wildlife, plant, and ecosystem health infrastructure and international funding mechanisms

We Stand for Wildlife™

