Food and Agriculture Organization of the United Nations

ISSN 0254-6019

Exposure of humans or animals to SARS-CoV-2 from wild, livestock, companion and aquatic animals

Qualitative exposure assessment

FAO ANIMAL PRODUCTION AND HEALTH / **PAPER 181**

FAO ANIMAL PRODUCTION AND HEALTH / **PAPER 181**

Exposure of humans or animals to SARS-CoV-2 from wild, livestock, companion and aquatic animals

Qualitative exposure assessment

Authors

Ihab El Masry, Sophie von Dobschuetz, Ludovic Plee, Fairouz Larfaoui, Zhen Yang, Junxia Song, Wantanee Kalpravidh, Keith Sumption
Food and Agriculture Organization for the United Nations (FAO), Rome, Italy

Dirk Pfeiffer
City University of Hong Kong, Hong Kong SAR, China

Sharon Calvin
Canadian Food Inspection Agency (CFIA), Science Branch, Animal Health Risk Assessment Unit, Ottawa, Canada

Helen Roberts
Department for Environment, Food and Rural Affairs (Defra), Equines, Pets and New and Emerging Diseases, Exotic Disease Control Team, London, United Kingdom of Great Britain and Northern Ireland

Alessio Lorusso
Istituto Zooprofilattico dell'Abruzzo e Molise, Teramo, Italy

Casey Barton-Behravesh
Centers for Disease Control and Prevention (CDC), One Health Office, National Center for Emerging and Zoonotic Infectious Diseases, Atlanta, United States of America

Zengren Zheng
China Animal Health and Epidemiology Centre (CAHEC), China Animal Health Risk Analysis Commission, Qingdao City, China

Food and Agriculture Organization of the United Nations
Rome, 2020

Required citation:
El Masry, I., von Dobschuetz, S., Plee, L., Larfaoui, F., Yang, Z., Song, J., Pfeiffer, D., Calvin, S., Roberts, H., Lorusso, A., Barton-Behravesh, C., Zheng, Z., Kalpravidh, W. & Sumption, K. 2020. *Exposure of humans or animals to SARS-CoV-2 from wild, livestock, companion and aquatic animals: Qualitative exposure assessment.* FAO animal production and health, Paper 181. Rome, FAO. https://doi.org/10.4060/ca9959en

The designations employed and the presentation of material in this information product do not imply the expression of any opinion whatsoever on the part of the Food and Agriculture Organization of the United Nations (FAO) concerning the legal or development status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. The mention of specific companies or products of manufacturers, whether or not these have been patented, does not imply that these have been endorsed or recommended by FAO in preference to others of a similar nature that are not mentioned.

The views expressed in this information product are those of the author(s) and do not necessarily reflect the views or policies of FAO.

ISSN 0254-6019 (print)
eISSN 2664-5165 (online)
ISBN 978-92-5-133008-1
© FAO, 2020

Some rights reserved. This work is made available under the Creative Commons Attribution-NonCommercial-ShareAlike 3.0 IGO licence (CC BY-NC-SA 3.0 IGO; https://creativecommons.org/licenses/by-nc-sa/3.0/igo/legalcode).

Under the terms of this licence, this work may be copied, redistributed and adapted for non-commercial purposes, provided that the work is appropriately cited. In any use of this work, there should be no suggestion that FAO endorses any specific organization, products or services. The use of the FAO logo is not permitted. If the work is adapted, then it must be licensed under the same or equivalent Creative Commons licence. If a translation of this work is created, it must include the following disclaimer along with the required citation: "This translation was not created by the Food and Agriculture Organization of the United Nations (FAO). FAO is not responsible for the content or accuracy of this translation. The original English edition shall be the authoritative edition."

Disputes arising under the licence that cannot be settled amicably will be resolved by mediation and arbitration as described in Article 8 of the licence except as otherwise provided herein. The applicable mediation rules will be the mediation rules of the World Intellectual Property Organization http://www.wipo.int/amc/en/mediation/rules and any arbitration will be conducted in accordance with the Arbitration Rules of the United Nations Commission on International Trade Law (UNCITRAL).

Third-party materials. Users wishing to reuse material from this work that is attributed to a third party, such as tables, figures or images, are responsible for determining whether permission is needed for that reuse and for obtaining permission from the copyright holder. The risk of claims resulting from infringement of any third-party-owned component in the work rests solely with the user.

Sales, rights and licensing. FAO information products are available on the FAO website (www.fao.org/publications) and can be purchased through publications-sales@fao.org.
Requests for commercial use should be submitted via: www.fao.org/contact-us/licence-request.
Queries regarding rights and licensing should be submitted to: copyright@fao.org

Cover photo: Wilson Chong

Communication and design: Natasha Little and Enrico Masci

Contents

Summary 1

Background and introduction 5

Exposure assessment 7

- Methodology for qualitative risk assessment and uncertainties 7
- Risk questions assessed 9
- Main assessment (key considerations and likelihoods of exposure) 11

Consequence assessment 21

Recommended studies to fill outstanding knowledge gaps 23

- One Health investigation studies (short-term priority) 23
- Targeted field investigation studies (short- and medium-term priority) 24
- Laboratory studies (short- and medium-term priority) 25
- Anthropological studies (medium- and long-term priority) 25
- Seasonality studies (long-term priority) 26

Suggested approaches for targeted field investigations in animals 27

Mitigation measures available 29

References 31

Glossary (for the purpose of this exposure assessment) 45

ANNEX 1
Figures illustrating the key steps that would be required if exposure to an animal or animal product infected or contaminated with SARS-CoV-2 were to pose a risk to humans or animals 49

ANNEX 2
Information and evidence considered for assessing likelihood levels for each risk question 53

ANNEX 3
Progressive approach to investigate SARS-CoV-2 wildlife reservoir(s) or intermediate host(s) 69

ANNEX 4
Prioritization of animal species to be investigated further through field surveillance 71

Summary

The objective of this qualitative exposure assessment is to provide:

I. assessment of the risk of human or animal exposure to SARS-CoV-2 through contact with, handling or consumption of wild, domestic and aquatic animal species◆ or their products;
II. identification of current knowledge gaps regarding the zoonotic origin or animal-human spillover of SARS-CoV-2 and recommendations for priority studies;
III. summary of available evidence for SARS-CoV-2 susceptibility of different animal species;
IV. evidence-based recommendations on how to prioritize animal species for targeted field investigations or research studies;
V. recommendations for targeted One Health investigations and epidemiological, laboratory, anthropological or seasonality studies to fill critical knowledge gaps evidenced by this exposure assessment.

Any measures implemented or strengthened at country level to mitigate the risk of exposure of humans and animals to SARS-CoV-2 from susceptible wild, livestock, companion and aquatic animals, should be based on the results of **country-specific risk assessment and critical review** of local animal husbandry and marketing practices, using the current knowledge outlined in this document. Risk assessments should be performed according to international guidance (e.g. OIE, 2019; FAO, 2011; FAO and WHO, 2007).

Likelihood of human or animal **infection** (post-exposure) is **not** assessed in this document and requires consideration of a variety of additional factors that are not presented here. Following exposure, human or animal infection may or may not occur. It is also important to note that during the current COVID-19 pandemic the primary source of human infection is human-to-human transmission.

The likelihood of **exposure of humans or animals** to SARS-CoV-2 **in COVID-19 affected areas** through:

1. Contact with **wild animals** is considered:

- **Low, i.e. unlikely to occur,** for **wild felines, old world monkeys, new world monkeys (family *Callitrichidae*), species of the family *Mustelidae*, species of the family *Cricetidae*, tree shrews of the family *Tupaiidae***, **bats of families *Rhinolophidae* and *Pteropodidae*, and pangolins** kept **in congregation areas, markets, wildlife ranches, wildlife farms, zoo and circus facilities**.
- **Very low, i.e. very unlikely to occur,** for the above-mentioned species in their **natural habitat in Southeast Asia and sub-Saharan Africa**, and **negligible, i.e. extremely unlikely to occur,** for these species in their natural habitat **in other areas of the world and for wild swine and wild birds** in general.

◆ The source of infection for the assessed animal species may have been a human COVID-19 case (reverse zoonosis), another infected animal or a contaminated environment.

- **Likelihood of exposure cannot currently be assessed**[•] for **other live mammalian wildlife species, reptiles or predatory invertebrates** as the information available is limited[■] to their angiotensin converting enzyme 2 (ACE2) binding affinity to SARS-CoV-2 receptor binding domain (RBD).

2. **Contact** with **livestock** is considered:
   - **Negligible, i.e. extremely unlikely to occur,** for **live pigs and poultry** in general.
   - **Likelihood of exposure cannot currently be assessed**[•] for **live ovine, caprine, bovine, camelid, rabbit and equine species** as the information available is limited[■] to their ACE2 binding affinity to SARS-CoV-2 RBD.
3. **Contact** with **live companion animals** is considered**:**
   - **Moderate, i.e. potentially occurring,** for **cats, ferrets and hamsters, and susceptible uncommon exotic pets such as monkeys and bats owned by or in contact with COVID-19 patient(s)**, infected animals or environments known to be contaminated with SARS-CoV-2; and **low, i.e. unlikely to occur,** for these species **in other sites** with unknown infection or contamination status (including live cats kept in markets as food and stray cats).
   - **Low, i.e. unlikely to occur,** for **companion dogs owned by or in contact with COVID-19 patient(s)**, infected animals or environments known to be contaminated with SARS-CoV-2; and **very low, i.e. very unlikely to occur,** for dogs **in other sites** with unknown infection or contamination status (including live dogs kept in markets as food and stray dogs).
   - **Negligible, i.e. extremely unlikely to occur,** for **companion birds** in general.
   - **Likelihood of exposure cannot currently be assessed**[•] **for exotic pets of other mammals or reptiles** as the information available is limited[■] to their ACE2 binding affinity to SARS-CoV-2 RBD.
4. **Contact** with **aquatic animals** is considered**:**
   - **Negligible, i.e. extremely unlikely to occur,** for **all aquatic mammals** (except captive dolphins), **fish, amphibians, molluscs and crustaceans.**
   - **Likelihood of exposure cannot currently be assessed**[•] for **captive dolphin** as the information available is limited[■] to their ACE2 binding affinity to SARS-CoV-2 RBD.
5. **Handling or consumption** of **animal carcasses, meat/organs, body fluids and excretions** is considered:
   - **Low, i.e. unlikely to occur,** for **products originating from felines, old world monkeys, new world monkeys (family *Callitrichidae),* species of the families *Mustelidae* and *Cricetidae*, tree shrews of the family *Tupaiidae,* bats of the families *Rhinolophidae* and *Pteropodidae*, pangolins and dogs,** processed and/or sold as raw product in markets or retail shops **in any condition**.
   - **Low, i.e. unlikely to occur,** for **raw products originating from any other animal species (wild, domestic or aquatic),** processed and/or sold in markets or retail shops **in conditions not meeting the Codex Alimentarius food hygiene**

• Likelihoods for conditions that cannot be assessed could be any level between negligible and high.

■ Once information from ex-vivo cell or experimental animal infection studies, or evidence from comprehensive epidemiological or animal pathology studies becomes available, likelihood of exposure for these species will be assessed in future updates of this document.

standards (CAC, 2009), where cross contamination from the environment, hitherto unidentified animal hosts or a SARS-CoV-2 infected human **is likely to have occurred**.

- **Negligible, i.e. extremely unlikely to occur,** for **sufficiently heat-treated products originating from any animal species (wild, domestic or aquatic)** as long as there is no opportunity for cross-contamination after heat-treatment in addition to **raw products of poultry, pigs and aquatic animals** if processed and/or sold in markets or retail shops **in conditions meeting the Codex Alimentarius food hygiene standards (CAC, 2009)**.
- **Likelihood of exposure cannot currently be assessed**• for **raw products originating from other mammalian wildlife species, reptiles or predatory invertebrates or from most livestock species (other than pigs and poultry) in any condition** because the information available is only limited■ to their ACE2 binding affinity to SARS-CoV-2 RBD.

In the assessment, the uncertainty of the different levels of likelihood generally remains medium (small sample data set(s), fair correlation/good fit; reliable method) to high (lack of data, limited data, or lack of conclusive data; weak correlation or crude speculation) due to the information gaps outlined.

Specifying the name of some animal species in this assessment does not imply a role in SARS-CoV-2 zoonotic spillover and the results of this assessment do not justify any measures that may subject these species to unnecessary stress, impact their trade or affect their conservation status.

A direct precursor virus has not been detected in any wild animal species to date, thus it is unknown if the precursor virus is still circulating in the original reservoir or intermediate host. However, the ongoing pandemic involves millions of human cases shedding high levels of virus and is thus creating new contaminated environments other than the original natural reservoir. This has been taken into account in the assessment together with evidenced susceptibility of different animal species.

At this early stage, when available data is not sufficient to draw specific conclusions, **FAO discourages sampling surveys as part of active surveillance for SARS-CoV-2 in animal species** that would distract time and resources away from other responsibilities of veterinary services. Instead, FAO encourages public health, veterinary and wildlife authorities, and forestry and natural resources management to work closely together with a One Health approach to investigate SARS-CoV-2 transmission between animals and humans, provided conditions and resources allow. A suggested approach for field investigation in animals is provided**.**

From a risk management perspective, it is important to consider that yet another zoonotic pathogen, of probable bat-origin and able to infect multiple animal species, was able to jump the species barrier and cause a pandemic in humans of unprecedented proportion. A process of country assessment and review – which includes reduction of contact

• Likelihoods for conditions that cannot be assessed could be any level between negligible and high.

■ Once information from ex-vivo cell or experimental animal infection studies, or evidence from comprehensive epidemiological or animal pathology studies becomes available, likelihood of exposure for these species will be assessed in future updates of this document.

Capturing bats for research, Democratic Republic of the Congo

between humans or domestic animals, and bats or other susceptible wild animals that might act as bridge species – will lead to evidence-based actions which reduce the likelihood and impact of future emergence and spillover of zoonotic pathogens with pandemic potential. Maintenance of strict biosecurity measures, respecting standards of the Codex Alimentarius basic texts on food hygiene (CAC, 2009), wildlife trade controls and restrictions, with bans on illegal trade, and/or behaviour change in consumers and traders would require additional medium- to long-term engagement. Such measures, as informed by national risk assessment, should take into account impact on livelihoods and food security. The assessment is based upon information available up to 30 June 2020 and will be revised as circumstances change and new information becomes available.

Background and introduction

Coronaviruses (CoVs) are responsible for respiratory and intestinal infections in animals and humans. Four genera of CoVs can be distinguished: *alphacoronavirus*, *betacoronavirus*, *gammacoronavirus* and *deltacoronavirus*. Generally, *alpha*- and *betacoronaviruses* infect only mammals, whereas *gamma*- and *deltacoronaviruses* infect mainly birds; however, some *deltacoronaviruses* have also been shown to infect mammals (Cui *et al.* 2019). One *alpha*- and two *gammacoronaviruses* have been detected in marine mammals (Schütze, 2016). In the past 20 years two *betacoronaviruses* have already caused public health emergencies, namely Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS). Before the emergence of SARS-CoV, only two human CoVs (HCoVs) were known (the *Alphacoronavirus HCoV-229E* and the *Betacoronavirus HCoV-OC43)*. Increased interest in HCoVs following the SARS epidemic lead to the discovery of two additional viruses, the *Alphacoronavirus* HCoV-NL63 and the *Betacoronavirus* HCoV-HKU1. All four HCoVs mostly cause mild infections in immunocompetent people with symptoms similar to a common cold (Lorusso *et al.*, 2020). Based upon available genomic sequences, bats are thought to be the animal host from which *Alphacoronaviruses* HCoV-NL63 and HCoV-229E were introduced into the human population and rodents for the *Betacoronaviruses* HCoV-OC43 and HKU1. Some of these CoVs infect intermediate mammalian hosts which enables spillover to infect humans: dromedary camels for HCoV-229E (Corman *et al.*, 2016), cattle for HCoV-OC43, marketed masked palm civets for SARS-CoV, and dromedary camels for MERS-CoV (Cui *et al.* 2019).

However, the newly emerged SARS-CoV-2, a *betacoronavirus*, is genetically different from any other human coronavirus discovered so far. The name SARS-CoV-2 was chosen because this new virus genetically clusters with hundreds of CoVs within the species SARS-related CoVs, subgenus *Sarbecovirus*, genus *betacoronavirus* (Gorbalenya *et al.* 2020). These related viruses, mostly detected through genetic sequencing of samples collected from humans and bats, all have names derived from SARS-CoV. However, only isolates from the 2002–2003 epidemic have been confirmed to cause SARS in humans. Phylogenetic analysis shows that SARS-CoV-2 is not a descendent of SARS-CoV but constituted an independent new introduction (Gorbalenya *et al.* 2020).

SARS-CoV-2 has a genome similarity of 96 percent to a SARS-related bat coronavirus (Zhou *et al.*,2020a) and of between 85.5 and 92.4 percent to a pangolin coronavirus sampled months before the first detection of SARS-CoV-2 in humans (Lam *et al.*, 2020a), demonstrating the circulation of a very close ancestral strain. Furthermore, analysis of the spike proteins of SARS-CoV-2 and the SARS-related bat and pangolin coronaviruses shows that the SARS-CoV-2 spike protein may have optimized its binding affinity to human-like ACE2 during natural selection in an animal host before zoonotic transfer (Andresen *et al.*, 2020). One Health collaboration – involving coordination between public, animal and environmental health sectors to address health threats at the human-animal-environment interface – is required to effectively tackle this emerging zoonotic disease threat.

A SARS-related coronavirus has been detected in pangolins

FAO received several requests from member countries to provide advice on surveillance or testing for SARS-CoV-2 in animals which led to the review of available information on SARS-CoV-2 and betacoronaviruses in animals. This qualitative exposure assessment aims to support One Health partners, including veterinary services and research institutions, in prioritizing animal species for targeted field investigations or research studies aimed at generating data and knowledge on potential SARS-CoV-2 animal host(s) and their role in maintenance and/or spread of the virus. The assessment is based upon review of information available up to 30 June 2020 and will be revised as circumstances change and new information becomes available. The reader should note that the uncertainty in the assessment of the different levels of likelihood remains generally medium to high since there is a need for a better understanding of SARS-CoV-2 characteristics and the epidemiology of infection to provide a more precise assessment.

It is important to note that at the time of preparation of this document (30 June 2020), the COVID-19 pandemic is propagated by human-to-human transmission and the reader is referred to WHO for information regarding all public health aspects.

While occurrence of zoonotic spillover events from animals to humans during the current pandemic has only been reported on one occasion, in a Dutch mink farm (Rijksoverheid, 2020a) and is subject to further investigation, exposure and infection of animals (felids, dogs and/or mink) sharing the same space with SARS-CoV-2 infected humans has been confirmed in Asia, Europe and the the United States of America as described in the considerations for this assessment. FAO, the World Organisation for Animal Health (OIE) and partners collaborate in providing evidence-based advice to veterinary authorities and the veterinary community on all SARS-CoV-2 related animal health issues.

Exposure assessment

This qualitative exposure assessment was prepared in response to a request for guidance on SARS-CoV-2 investigations in animals, as expressed to FAO by its Members and several research institutions. The methodology draws on previous FAO qualitative risk assessments addressing Zaire Ebolavirus Outbreaks (2018) and Chinese-origin H7N9 avian influenza (2019).

METHODOLOGY FOR QUALITATIVE RISK ASSESSMENT AND UNCERTAINTIES

The risk questions assessed consider likelihoods of SARS-CoV-2 exposure (of humans or animals) from different animal species◆, domestic and wild. Following exposure, human or animal infection may or may not occur. The reader should note that **likelihood of human or animal infection, post-exposure, is not assessed in this document** and needs to consider a variety of additional factors that are not presented here.

This exposure assessment defines the likelihood of human or animal exposure to SARS-CoV-2 released directly from infected animal hosts or indirectly from their products, from highest to lowest levels as follows:

- **High** (highly likely to occur/result in exposure);
- **Moderate** (potential to occur/result in exposure);
- **Low** (unlikely to occur/result in exposure);
- **Very low** (very unlikely to occur/result in exposure); and
- **Negligible** (extremely unlikely to occur/result in exposure).

A full list of considerations and evidence used to answer each risk assessment question can be found in Information and Evidence Considered (Annex 2).

The assessment considers the level of uncertainty when interpreting the available data, to reflect data quality and quantity.

Definition of uncertainty levels used:

- **High** uncertainty **(H)**: lack of data, limited data, or lack of conclusive data; weak correlation or crude speculation;
- **Medium** uncertainty **(M)**: small sample data set(s), fair correlation/good fit; reliable method;
- **Low** uncertainty **(L)**: large sample data set(s); known fact, event known to occur, or exact measure.

The reader should note that due to the limited availability of field studies and investigations on SARS-CoV-2 in different animal species at the time of the assessment **the overall uncertainty in the exposure assessment is generally medium to high**. The exposure assessment will be updated once new relevant information becomes available.

◆ The source of infection for the assessed animal species may have been a human COVID-19 case (reverse zoonosis), another infected animal or a contaminated environment.

Effort was made to include mainly peer-reviewed articles related to SARS-CoV-2 in the considerations. However, where important novel or unique information was made available online through rapid pre-print releases, government reports and official press releases, it has been included, despite not being peer-reviewed.

The figures in Annex 1 illustrate key steps that would be required for exposure to an animal or animal product infected or contaminated with SARS-CoV-2 to pose a risk to humans or animals.

Assessment of human exposure to SARS-CoV-2 from animals or their products not only considers the public, such as consumers or live animal market visitors, but also occupationally exposed individuals, including those frequently involved in hunting, farming, transportation, processing and marketing of wild or domestic animals.

The exposure assessment underwent two major review processes and includes input from the following FAO staff, FAO Reference Centres and subject matter experts identified based on their expertise in coronavirus virology, zoonotic disease epidemiology, local hunting, production, marketing and trade practices, food safety and/or qualitative risk assessment:

Internal reviewers:

- Emmanuel Kabali, Ryan Aguanno, Holy Akwar, Etienne Bonbon, Cristian De Battisti, Alejandro Dorado-Garcia, Alice Green, Bin Hao, Gael Lamielle, Francesca Latronico, Jeffrey Lejeune, Markus Lipp, Brett Mackinnon, Samia Metwally, Claudia Pittiglio, Sandra Ratiarison, Melba Reantaso, Xavier Roche, Kristina Rodina, Cristina Rojo, Sean Shadomy (Food and Agriculture Organization of the United Nations – FAO, Rome, Italy)
- Filip Claes (FAO Regional Office for Asia and the Pacific, Bangkok, Thailand)
- Garba Maina Ahmed, Scott Newman, Mamadou Niang, Ismaila Seck (FAO Regional Office for Africa, Accra, Ghana)
- Friederike Mayen (FAO Regional Office for the Near East and North Africa, Cairo, Egypt)
- Markos Tibbo (FAO Subregional Office for the Gulf Cooperation Council States and Yemen, Abu Dhabi, United Arab Emirates)
- Charles Bebay, Joshua Kimutai (FAO Subregional Office for Eastern Africa, Nairobi, Kenya)
- Serge Nzietchueng (FAO Representation Office in Congo, Brazzaville, Republic of the Congo)
- Pawin Padungtod (FAO Country Office in Viet Nam, Hanoi, Viet Nam)

External reviewers:

- Paolo Calistri (Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale" Campo Boario, Teramo)
- Giovanni Cattoli (Joint FAO/IAEA Division for Nuclear Applications in Food and Agriculture, Seibersdorf, Austria)
- Peter Daszak (EcoHealth Alliance, New York, United States of America)
- Stephane De La Rocque (World Health Organization – WHO, Health Emergencies Programme, Geneva, Switzerland)
- Anwar Mohamad Hadi Hashem (King Abdulaziz University, Jeddah, Saudi Arabia)
- Louise Kelly (Animal and Plant Health Agency – APHA, Weybridge, United Kingdom of Great Britain and Northern Ireland)
- Marion Koopmans (Viroscience Department, Erasmus Medical Centre, Rotterdam The Netherlands)

- Sophie Lepoder (Agence Nationale de Sécurité Sanitaire de l'Alimentation, de l'Environnement et du Travail – ANSES, Maisons-Alfort, France)
- Malik Peiris (School of Public Health, The University of Hong Kong, Hong Kong, P.R. China)
- Francisco Reviriego Gordejo (Directorate-General for Health and Food Safety, European Commission, Brussels, Belgium)
- Francois Roger (Centre de Coopération Internationale en Recherche Agronomique pour le Développement – CIRAD, Montpellier, France)
- Suminder Sawhney (Canadian Food Inspection Agency – CFIA, Ottawa, Canada)
- Changchun Tu (Changchun Veterinary Research Institute – CVRI, Chinese Academy of Agricultural Sciences – CAAS, Changchun, China)
- Linfa Wang (Duke-NUS Medical School, Singapore)
- Cristobel Zepeda (United States Department for Agriculture Animal and Plant Health Inspection Service – USDA APHIS, Brasília, Brazil)

RISK QUESTIONS ASSESSED

1. What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of **wild animals** or their products?
2. What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of **livestock** or their products?
3. What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with or handling of **companion animal species** or handling or consumption of **dog and cat products***?
4. What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of **aquatic animals** or their products?

Important notes:

- Specifying the name of some animal species in this assessment **does not imply a role in SARS-CoV-2 zoonotic spillover.** At this early point, with the limited data available at the date of publishing, we attempt to assess the potential role of animal species (wild or domestic) in exposing humans or animals to SARS-CoV-2 with the aim of supporting the research community in targeting or prioritizing studies to investigate potential SARS-CoV-2 reservoir or intermediate host(s). See Annexes 3 and 4 for a suggested progressive approach to investigating potential SARS-CoV-2 wildlife reservoir(s) or intermediate host(s). **Results of this assessment do not justify any measures that may subject any species to unnecessary stress, impact their trade or affect their conservation status.**
- At this early stage when available data is not sufficient to draw specific conclusions, **FAO discourages sampling surveys as part of active surveillance for**

* As per Glossary, products are defined as carcass, raw meat (including offal), tissue, milk and other fluids and excretions of animals

Men cutting meat in a butchery, Addis Ababa, Ethiopia

SARS-CoV-2 in animal species that would distract time and resources away from other responsibilities of veterinary services. FAO encourages public health, veterinary, forestry and natural resources management and wildlife authorities to work closely together under the One Health approach to systematically investigate SARS-CoV-2 infected humans for history of contact with animals and animal products and conduct targeted, robust epidemiological investigations coupled with laboratory testing for animal species potentially linked with COVID-19 human cases, provided conditions and resources allow (see Suggested Approaches for Field Investigations in Animals).

- Increased relative exposure risk should be considered for occupational risk groups (including hunters, butchers, market middlemen, retailers, farmers and veterinarians) handling certain animal species when compared to the general public, owing to increased frequency and intensity of contact with animals.
- Likelihood of a reverse zoonotic event happening, where SARS-CoV-2 is transmitted from humans to animals, is not addressed in this assessment. However, reverse zoonosis (either by direct contact with infected humans or indirectly through environments contaminated by infected humans) is indirectly considered in the steps required that would lead to an animal species being infected or its products being contaminated and thus pose SARS-CoV-2 exposure risk for humans or animals.
- Exposure of humans to the virus during the current pandemic is predominantly through human-to-human transmission by respiratory droplets from coughing, sneezing, and talking (CDC, 2020). Human-to-human transmission is likely to occur in households, workplaces, or health care centres (WHO, 2020a).

MAIN ASSESSMENT
key considerations and likelihoods of exposure

Risk question 1: What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of wild animals or their products?

See Annex 1 for illustration of key steps that would be required for exposure to an animal or animal product infected or contaminated with SARS-CoV-2 to pose a risk to humans or animals. See Annex 2 for a full list of considerations with respective references.

Key considerations used to assign likelihood estimates for live wild mammals

- Local hunting and captive farming of wild mammals for trade and consumption purposes mainly occurs in Southeast Asia and to a lesser extent in some countries in sub-Saharan Africa.
- Extensive trafficking of these mammals occurs in Southeast Asia as well as sub-Saharan Africa.
- Experimentally infected ferrets of the family *Mustelidae*, hamsters of the family *Cricetidae*, Egyptian fruit bats of the family *Pteropodidae*, tree shrews of the family *Tupaiidae* and some species of old world monkeys and new world monkeys of the family *Callitrichidae* have demonstrated susceptibility to SARS-CoV-2 infection.
- Experimentally SAR-CoV-2 infected hamsters, ferrets and Egyptian fruit bats transmitted infection to naïve co-housed animals of the same species in experimental settings.
- Natural SARS-CoV-2 infection in captive tiger and lion in a zoo in the United States of America as a result of human-to-animal transmission has been confirmed, with likely onwards animal-to-animal transmission.
- Natural SARS-CoV-2 infection in captive farmed mink in the Netherlands as a result of human-to-animal transmission has been confirmed, with likely onwards animal-to-animal and animal-to-human transmission.
- There is evidence of coronaviruses such as SARS-CoV-2, Feline Coronavirus (FCoV) and MERS-CoV affecting different species of the same animal family.
- Sustained and robust SARS-CoV-2 replication has been observed in intestinal organoid cultures derived from horseshoe bats (*Rhinolophus sinicus*) of the family R*hinolophidae*.
- A high affinity of ACE2 receptors has been found in certain wildlife species (primates, family *Cricetidae*) to bind RBD of SARS-CoV-2.
- Pangolin coronaviruses have been identified with 92.4 percent full genome sequence similarity to SARS-CoV-2, and 97.4 percent amino acid sequence similarity to SARS-CoV-2 RBD supporting the hypothesis that pangolins might host SARS-CoV-2 virus or a recent common ancestor, and could be a potential source for human and animal exposure regardless if they are infected in their natural habitat or acquired infection in a contaminated environment owing to anthropogenic activities.
- No susceptibility of pigs (a member of the family Suidae) to SARS-CoV-2 after experimental infection has been demonstrated.
- Lessons have been learned from SARS-CoV in China, where direct or indirect accidental animal-to-animal infection is thought to have occurred in traditional markets, including cross-species transmission.

SARS-CoV-2 transmission to tigers from their caretaker was confirmed in Bronx Zoo, New York

- There is serological evidence of exposure to SARS-related CoVs in market traders or people living in the vicinity of bat caves in Southeast Asia.

Key considerations used to assign the likelihood estimate for live wild birds:

- Only *gamma-* and *deltacoronaviruses* are commonly detected in wild birds. No evidence of *betacoronavirus* detection was reported, except for one study from Brazil detecting *betacoronavirus* RNA in wild birds preying on bats and another study in China detecting SARS-CoV RNA in a greylag goose (*Anser anser*) sampled in a traditional market – however environmental contamination of the samples could not be excluded.
- Analysis of key amino acid residues of ACE2 of 79 wild birds demonstrated very low likelihood of binding SARS-CoV-2 RBD; except for a few studies supporting the hypothesis of a likely binding affinity favouring SARS-CoV-2 infection in some (nine) wild bird species, contradicting, however, results generated by other studies.
- Chicken, ducks, geese, turkey and quail demonstrated no susceptibility to SARS-CoV-2 after experimental infection.

Key considerations used to assign likelihood estimates for handling or consumption of wild mammal and wild bird carcasses, raw meat/organs, body fluids and excretions:

- Human-to-human transmission is of pandemic proportion and environmental contamination occurs in areas where COVID-19 patients are present or have visited, therefore surface contamination of food products is possible where food hygiene standards do not meet those described in the Codex Alimentarius (CAC, 2009).
- There is evidence of SARS-CoV-2 isolation from environmental samples collected in traditional markets.
- SARS-CoV-2 is stable in different pH conditions and on different surfaces.
- Viability of SARS-CoV-2 is preserved for longer periods on different surfaces in the presence of protein substance.
- SARS-CoV-2 RNA has been detected in blood and lungs of experimentally infected monkeys.
- SARS-related CoV has been detected in the blood and lungs of naturally infected pangolin.
- SARS-CoV-2 RNA has been detected in several internal organs of experimentally infected Egyptian fruit bats, tree shrews and ferrets.

TABLE 1

Assessed likelihood levels (and associated uncertainty) for exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of wild animals or their products

Exposure type	Animals and products	Site/ condition	Region/ countries	Likelihood estimate* (uncertainty **low**, **medium** or **high****)
Contact	• live wild felines • live old world monkeys • live new world monkeys (family *Callitrichidae*) • live species of the family *Mustelidae* • live species of the family *Cricetidae* • live tree shrews of family *Tupaiidae* • live bats of families *Rhinolophidae* and *Pteropodidae* • live pangolins	• congregation areas • markets • wildlife ranches • wildlife farms • zoo and circus facilities	all	**Low (M)**
		natural habitat	Southeast Asia, sub-Saharan Africa	**Very low (H)**
			other areas of the world	**Negligible (H)**
	live wild suids	all	all	**Negligible (M)**
	live wild birds	all	all	**Negligible (M)**
Handling or consumption	carcasses, meat/organs, body fluids and excretions of wild felines, old world monkeys, new world monkeys (family *Callitrichidae*), species of the families *Mustelidae*, *Cricetidae* and *Tupaiidae*, bats of the families *Rhinolophidae* and *Pteropodidae*, and pangolins	processed and/or sold as raw product in markets or retail shops in any condition	all	**Low (H)**
		sufficiently heat-treated, with no opportunity for cross-contamination after heat-treatment	all	**Negligible (L)**
	Other wildlife carcasses, meat/organs, body fluids and excretions (including those of mammals and birds)	processed and/or sold as raw product in markets or retail shops in conditions not meeting the Codex Alimentarius food hygiene standards (CAC, 2009), where cross-contamination from the environment, unidentified animal hosts or a SARS-CoV-2 infected human is likely to have occurred	all	**Low (H)**
		sufficiently heat-treated, with no opportunity for cross-contamination after heat-treatment	all	**Negligible (L)**
Contact, handling or consumption	other live wildlife species (including reptiles and predatory invertebrates)	likelihood of exposure cannot currently be assessed•: information available is limited▪ to ACE2 binding affinity to SARS-CoV-2 RBD		
	carcasses, meat/organs, body fluids and excretions of these species	sufficiently heat-treated, with no opportunity for cross-contamination after heat-treatment	all	**Negligible (L)**

* Definition of likelihood levels used: **High** = highly likely to occur/result in exposure; **Moderate** = potentially occurring/ resulting in exposure; **Low** = unlikely to occur/result in exposure; **Very low** = very unlikely to occur/result in exposure; and **Negligible** = extremely unlikely to occur/result in exposure.

** Definition of uncertainty levels used: **High** uncertainty **(H)**: lack of data, limited data, or lack of conclusive data; weak correlation or crude speculation; **Medium** uncertainty **(M)**: small sample data set(s), fair correlation/ good fit; reliable method; **Low** uncertainty **(L)**: large sample data set(s); known fact, event known to occur, or exact measure.

• Likelihoods for conditions that cannot be assessed could be any level between negligible and high.

▪ Once information from ex-vivo cell or experimental animal infection studies, or evidence from comprehensive epidemiological or animal pathology studies becomes available, likelihood of exposure for these species will be assessed in future updates of this document.

Important notes:

- The estimates for likelihood levels do not take into account the disease control measures adopted in Southeast Asian countries and other regions since January 2020 (i.e. market closure, market decontamination, movement restrictions, etc.). However, as seen after the SARS outbreak in 2002–2003, such measures may not be permanent. Maintenance of strict biosecurity measures, wildlife trade bans or restrictions and/or behaviour change in consumers and traders would require additional medium to long-term engagement.
- There is no evidence of natural pangolin or bat infection with SARS-CoV-2 to date. However, identification of pangolin and intermediate horseshoe bat coronaviruses with 92.4 percent and 96.2 percent full genome sequence similarity with SARS-CoV-2, respectively, suggests that these species might host SARS-CoV-2 virus or a recent common ancestor and could be a potential source for human exposure – whether infected in their natural habitat or a contaminated environment owing to anthropogenic activities.

Risk question 2: What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of livestock or their products?

See Annex 1 for illustration of key steps that would be required for exposure to an animal or animal product infected or contaminated with SARS-CoV-2 to pose a risk to humans or animals. See Annex 2 for a full list of considerations with respective references.

Key considerations used to assign likelihood estimates for live livestock:

- Pigs, chickens, ducks, geese, turkey and quail have demonstrated no susceptibility to SARS-CoV-2 after experimental infection.
- ACE2 receptors of bovine, ovine, caprine and rabbit were were predicted by some studies to have good affinity to bind SARS-CoV-2 RBD while studies addressing camelid and equine report contradictory findings of either good or poor affinity. However, further studies are still needed to confirm or deny these predictions and investigate whether any of these species is able to amplify and shed infectious virus.
- Only *gamma-* and *deltacoronaviruses* have been detected in poultry, whereas no infection with *betacoronaviruses* has been reported so far.

Key considerations used to assign likelihood estimates for handling or consumption of livestock carcasses, raw meat/organs, body fluids and excretions:

- Human-to-human transmission is of pandemic proportion and environmental contamination occurs in areas where COVID-19 patients are present or have visited, therefore surface contamination of food products is possible where food hygiene standards do not meet those described in the Codex Alimentarius (CAC, 2009).
- There is evidence of SARS-CoV-2 isolation from environmental samples collected in traditional markets.
- Viability of SARS-CoV-2 is preserved for longer periods on different surfaces in the presence of protein substance.
- SARS-CoV-2 is stable in different pH conditions and on different surfaces.

TABLE 2

Assessed likelihood levels (and associated uncertainty) for exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of livestock or their products

Exposure type	Animals and products	Site/ condition	Region/ countries	Likelihood estimate* (uncertainty **low**, **medium** or **high****)
Contact	live pigs	all	all	**Negligible (M)**
	live poultry	all	all	**Negligible (M)**
	live ovine, caprine, bovine, camelids, rabbit and equine species	likelihood of exposure cannot currently be assessed•: information available is limited▪ to their ACE2 binding affinity to SARS-CoV-2 RBD		
Handling or consumption	livestock carcasses, meat/organs, body fluids and excretions	processed and/or sold as raw product in markets or retail shops in conditions not meeting the Codex Alimentarius food hygiene standards (CAC, 2009), where cross contamination from the environment, unidentified animal hosts or a SARS-CoV-2 infected human is likely to have occurred	all	**Low (H)**
		processed and/or sold as raw product in markets or retail shops in hygienic conditions (i.e. meeting the Codex Alimentarius food hygiene standards (CAC, 2009)	all	**Negligible (M)** if originating from poultry and pigs
			likelihood of exposure cannot currently be assessed• for livestock species other than poultry and pigs: information available is limited▪ to their ACE2 binding affinity to SARS-CoV-2 RBD	
		sufficiently heat-treated, with no opportunity for cross-contamination after heat-treatment	all	**Negligible (L)**

* Definition of likelihood levels used: **High** = highly likely to occur/result in exposure; **Moderate** = potentially occurring/ resulting in exposure; **Low** = unlikely to occur/result in exposure; **Very low** = very unlikely to occur/result in exposure; and **Negligible** = extremely unlikely to occur/result in exposure.

** Definition of uncertainty levels used: **High** uncertainty **(H)**: lack of data, limited data, or lack of conclusive data; weak correlation or crude speculation; **Medium** uncertainty **(M)**: small sample data set(s), fair correlation/ good fit; reliable method; **Low** uncertainty **(L)**: large sample data set(s); known fact, event known to occur, or exact measure.

• Likelihoods for conditions that cannot be assessed could be any level between negligible and high.

▪ Once information from ex-vivo cell or experimental animal infection studies, or evidence from comprehensive epidemiological or animal pathology studies becomes available, likelihood of exposure for these species will be assessed in future updates of this document.

Risk question 3: What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with or handling of companion animal species or handling or consumption of dog and cat products*?

See Annex 1 for illustration of key steps that would be required for exposure to an animal or animal product infected or contaminated with SARS-CoV-2 to pose a risk to humans or animals. See Annex 2 for a full list of considerations with respective references.

Key considerations used to assign likelihood estimates for live companion animals and stray dogs and cats:

- Experimentally infected cats, ferrets and hamsters have demonstrated susceptibility to SARS-CoV-2 infection and ability to infect other animals of the same species in experimental settings.
- Natural SARS-CoV-2 infection of pet cats owned by or in contact with COVID-19 patients has been confirmed.
- There is evidence of natural infection and seroconversion of dogs owned by or in contact with COVID-19 patients. However in one case, a second dog living in the same household tested negative with polymerase chain reaction (PCR).
- Experimentally inoculated dogs did not transmit the virus to other co-housed naïve dogs in experimental settings.
- Contact between humans and pets is close and mutual exposure to respiratory and oral secretions is likely to occur in the household.

Key considerations used to assign likelihood estimates for handling or consumption of dog and cat products*:

- Human-to-human transmission is of pandemic proportion and environmental contamination occurs in areas where COVID-19 patients are present or have visited, therefore surface contamination of food products by direct contamination or cross-contamination is possible where food hygiene standards are not meeting those described in the Codex Alimentarius (CAC, 2009).
- There is evidence of SARS-CoV-2 isolation from environmental samples collected in traditional markets.
- SARS-CoV-2 is stable in different pH conditions and on different surfaces.
- Viability of SARS-CoV-2 is preserved for longer periods on different surfaces in the presence of protein substance.
- There is evidence of natural infection in cats and SARS-CoV-2 RNA has been isolated from the lung, trachea and tonsils of experimentally infected cats.
- There is evidence of natural infection and seroconversion of dogs owned by or in contact with COVID-19 patients. However in one case, a second dog living in the same household tested negative with polymerase chain reaction (PCR).
- SARS-CoV-2 was isolated from a naturally infected dog.

* As per Glossary, products are defined as carcass, raw meat (including offal), tissue, milk and other fluids and excretions of animals

TABLE 3

Assessed likelihood levels (and associated uncertainty) for exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with or handling of companion animal species or handling or consumption of dog and cat products

Exposure type	Animals and products	Site/ condition	Region/ countries	Likelihood estimate* (uncertainty **low**, **medium** or **high****)
Contact	• live companion cat • live companion ferret • live companion hamster • uncommon exotic pets belonging to susceptible species such as live monkeys and bats	owned by or in contact with COVID-19 patient(s), infected animals or environments known to be contaminated with SARS-CoV-2	all	**Moderate (M)**
		other sites, with unknown infection or contamination status (including live cats intended for use as food)	all	**Low (H)**
	live companion birds	all	all	**Negligible (M)**
	live companion dog	owned by or in contact with COVID-19 patient(s), infected animals or environments known to be contaminated with SARS-CoV-2	all	**Low (M)**
		other sites, with unknown infection or contamination status (including live dogs intended for use as food)	all	**Very low (H)**
	other exotic live mammalian or reptilian pets	likelihood of exposure cannot currently be assessed•: information available is limited▪ to their ACE2 binding affinity to SARS-CoV-2 RBD		
	live stray cat	all (including live cats intended for use as food)	all	**Low (H)**
	live stray dog	all (including live dogs intended for use as food)	all	**Very Low (H)**
Handling or consumption	dog and cat carcasses, meat/organs, body fluids and excretions	processed and/or sold as raw product in markets or retail shops in any condition	all	**Low (H)**
		sufficiently heat-treated, with no opportunity for cross-contamination after heat-treatment	all	**Negligible (L)**

* Definition of likelihood levels used: **High** = highly likely to occur/result in exposure; **Moderate** = potentially occurring/ resulting in exposure; **Low** = unlikely to occur/result in exposure; **Very low** = very unlikely to occur/result in exposure; and **Negligible** = extremely unlikely to occur/result in exposure.

** Definition of uncertainty levels used: **High** uncertainty **(H)**: lack of data, limited data, or lack of conclusive data; weak correlation or crude speculation; **Medium** uncertainty **(M)**: small sample data set(s), fair correlation/ good fit; reliable method; **Low** uncertainty **(L)**: large sample data set(s); known fact, event known to occur, or exact measure.

• Likelihoods for conditions that cannot be assessed could be any level between negligible and high.

▪ Once information from ex-vivo cell or experimental animal infection studies, or evidence from comprehensive epidemiological or animal pathology studies becomes available, likelihood of exposure for these species will be assessed in future updates of this document.

Risk question 4: What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of aquatic animals or their products?

See Annex 1 for illustration of key steps that would be required for exposure to an animal or animal product infected or contaminated with SARS-CoV-2 to pose a risk to humans or animals. See Annex 2 for a full list of considerations with respective references.

Key considerations used to assign likelihood estimates for live aquatic animals:

- Only *alpha*- and *gammacoronaviruses* have been found to infect aquatic animals, whereas none of the *betacoronaviruses* have been found to infect them.
- Although analysis of ACE2 receptors of cetacean species predicted high binding affinity to SARS-CoV-2 RBD, it is extremely unlikely for humans and animals to be exposed to these species in their natural habitat.
- Analysis of key amino acid residues of 82 fish and four amphibian species supported the hypothesis of very low affinity to bind SARS-CoV-2 RBD, only one study supported the hypothesis of a binding energy favourable for SARS-CoV-2 infection for ten fish species, contradicting, however, results of another study.

Key considerations used to assign likelihood levels for handling or consumption of aquatic animal products:

- Human-to-human transmission is of pandemic proportion and environmental contamination occurs in areas where COVID-19 patients are present or have visited, therefore surface contamination of food products is possible where food hygiene standards do not meet those described in the Codex Alimentarius (CAC, 2009).
- There is evidence of SARS-CoV-2 isolation from environmental samples collected in traditional markets where aquatic animals were sold.
- SARS-CoV-2 is stable in different pH conditions and on different surfaces.
- Viability of SARS-CoV-2 is preserved for longer periods on different surfaces in the presence of protein substance.

TABLE 4

Assessed likelihood levels (and associated uncertainty) for exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of aquatic animals

Exposure type	Animals and products	Site/ condition	Region/ countries	Likelihood estimate* (uncertainty **low**, **medium** or **high****)
Contact	live dolphins	captive	likelihood of exposure cannot currently be assessed•: information available is limited▪ to their ACE2 binding affinity to SARS-CoV-2 RBD	
		natural habitat	all	**Negligible (M)**
	other live aquatic mammals	all	all	**Negligible (M)**
	live fish, molluscs, crustacean and amphibians	all	all	**Negligible (M)**
Handling or consumption	aquatic animal carcasses, meat/ organs, body fluids and excretions	processed and/or sold as raw products in markets or retail shops in conditions not meeting the Codex Alimentarius food hygiene standards (CAC, 2009), where cross contamination from the environment, unidentified animal hosts or a SARS-CoV-2 infected human is likely to have occurred	all	**Low (H)**
		processed and/or sold in markets or retail shops in hygienic conditions (i.e. meeting the Codex Alimentarius food hygiene standards (CAC, 2009))	all	**Negligible (M)**
		sufficiently heat-treated, with no opportunity for cross-contamination after heat-treatment	all	**Negligible (L)**

* Definition of likelihood levels used: **High** = highly likely to occur/result in exposure; **Moderate** = potentially occurring/ resulting in exposure; **Low** = unlikely to occur/result in exposure; **Very low** = very unlikely to occur/result in exposure; and **Negligible** = extremely unlikely to occur/result in exposure.

** Definition of uncertainty levels used: **High** uncertainty **(H)**: lack of data, limited data, or lack of conclusive data; weak correlation or crude speculation; **Medium** uncertainty **(M)**: small sample data set(s), fair correlation/ good fit; reliable method; **Low** uncertainty **(L)**: large sample data set(s); known fact, event known to occur, or exact measure.

• Likelihoods for conditions that cannot be assessed could be any level between negligible and high.

▪ Once information from ex-vivo cell or experimental animal infection studies, or evidence from comprehensive epidemiological or animal pathology studies becomes available, likelihood of exposure for these species will be assessed in future updates of this document.

Consequence assessment

SARS-CoV-2 exposure of humans or animals from different animal species has been assessed to range from negligible, i.e. extremely unlikely to occur, to moderate, i.e. potentially occurring, depending on the animal species involved. Increased relative exposure risk should be considered for occupational risk groups (including hunters, market middlemen, retailers, farmers and veterinarians) when compared to the general public, owing to their increased frequency and intensity of contact with animals. In occupational settings exposure risk from animals can be reduced by personnel following standard personal protection measures such as wearing gloves and masks as well as frequent cleaning and disinfection of equipment, areas and surfaces.

Information on recommended measures for livestock market chain settings (in the context of human-to-human spread) are included in FAO Guidelines to mitigate the impact of the COVID-19 pandemic on livestock production and animal health (2020) and the FAO Policy brief: Food Safety in the time of COVID-19 (2020), while applicable food hygiene standards are outlined in the Codex Alimentarius Basic Texts on Food Hygiene (2009).

Since a direct precursor virus has not been detected in any wild animal species to date, it is unknown if the virus is still circulating in the original reservoir or intermediate host/s. Spillover from the original animal reservoir or intermediate hosts to human populations may be considered a rare event, unless future evidence suggests that this is happening more frequently than currently thought. However, the ongoing pandemic involves millions of human cases shedding high levels of virus and is thus creating new contaminated environments other than the original natural reservoir. This has been taken into account in the assessment together with evidenced susceptibility of different animal species. From a risk management perspective, it is important to consider that yet another zoonotic pathogen, of probable bat-origin and able to infect multiple animal species, was able to jump the species barrier and cause a pandemic in humans of unprecedented proportion. COVID-19 has demonstrated that the public health impact and wide-reaching socio-economic consequences of such spillover, when it occurs, are devastating and long lasting.

A process of country assessment and review – which includes reduction of contact between humans or domestic animals, and bats or other susceptible wild animals that might act as bridge species – will lead to evidence-based actions which reduce the likelihood and impact of future emergence and spillover of zoonotic pathogens with pandemic potential. Maintenance of strict biosecurity measures, respecting requirements of the Codex Alimentarius basic texts on food hygiene (CAC, 2009), wildlife trade controls and restrictions, with bans on illegal trade, and/or behaviour change in consumers and traders would require additional medium- to long-term engagement. Such measures, informed by national risk assessment, should take into account impact on livelihoods and food security.

Original SARS-CoV-2 animal reservoir or intermediate hosts are still unknown. Should a livestock species be identified as natural reservoir of SARS-CoV-2, additional burden will be

Increased relative exposure risk should be considered for occupational risk groups when compared to the general public

placed on the human, logistical and financial resources of veterinary services. Consequently, drawbacks on funding and continuity of prevention and control measures for other priority animal diseases may be expected. In some countries, following extensive media coverage on presumed susceptibility of cats and dogs, people abandoned their pets. Such action, albeit unjustified, is posing an enormous threat to animal welfare and health. The relatively low impact of potential occasional zoonotic transmission from farmed/captive animals to their caretakers (evidenced in the Netherlands on a mink farm) or a pet to its owner (even though not evidenced to date), has to be seen within the larger context of the pandemic and the vast number of cases resulting from human-to-human transmission.

Since surface contamination of food products, including those of animal origin, is possible where food hygiene standards do not meet those described in the Codex Alimentarius (CAC, 2009), consumer misinformation or negative propaganda may result in unjustified consumer behaviour, such as avoidance of certain animals or animal products.

Recommended studies to fill outstanding knowledge gaps

To reduce uncertainty of the assessment, understanding of COVID-19 epidemiology and involvement of animals needs to be enhanced. It is important to note that the uncertainty associated with each of the likelihood levels in this assessment is generally medium to high because of significant outstanding knowledge gaps. As this is a rapidly evolving situation with many unknowns, the assessment will need to be revisited as more information becomes available.

Based on information gaps evidenced by the assessment we recommend a list of priority studies.

ONE HEALTH INVESTIGATION STUDIES (SHORT-TERM PRIORITY)

- Investigate human COVID-19 cases using a One Health approach and document events that indicate human exposure to SARS-CoV-2 from animal source(s):
  - Develop molecular studies involving advanced virus characterization to identify direction of infection, from animal to human or by reverse zoonosis. Collect information on settings or factors that may increase the risk of human exposure from animals.
  - Conduct field studies, including case-control studies, to test susceptible and potentially susceptible animals and exposed communities and occupations at the human-animal interface using serological assays specific to SARS-CoV-2 once available.
- Investigate human COVID-19 cases using a One Health approach and document events that implicate exposure of companion, captive wild or livestock animals to SARS-CoV-2, to investigate the potential of further zoonotic spillover as well as consequences for animal health:
  - Conduct timely[1] molecular studies for SARS-CoV-2 RNA detection in companion, captive wild or livestock animals (excluding non-susceptible species such as birds and pigs) in contact with COVID-19 patients, perform advanced virus characterization and investigate animal health consequences as well as further zoonotic spillover potential.
  - Conduct serological studies to investigate exposure of companion, captive wild or livestock animals using serological assays specific to SARS-CoV-2 once available.

[1] Late intervention (≥seven days) following confirmation of human infection may result in missing the virus shedding window in animals.

TARGETED FIELD INVESTIGATION STUDIES (SHORT- AND MEDIUM-TERM PRIORITY)

- Conduct field investigation studies to identify potential reservoir and intermediate host species and relationships between different host populations that may facilitate SARS-CoV-2 spillover or have facilitated its evolution and adaptation:
  - Target animal species (wild or domestic) that were identified by field investigations or laboratory studies as most relevant and that have ACE2 receptors compatible with SARS-CoV-2 RBD for comprehensive epidemiological and animal pathology studies.
  - Target bats (particularly families *Rhinolophidae* and *Pteropodidae)*, primates (those with ACE2 receptors compatible with SARS-CoV-2 RBD, see supplementary tables), wild felines, wild animals of the families *Tupaiidae*, *Cricetidae* and *Mustilidae* and pangolins worldwide, either in captive conditions or their wild habitat, to identify the diversity of SARS-CoV-like and other CoVs in these species, increase knowledge of their role as CoV-reservoirs and inform risk reduction strategies. It is highly likely that ancestral strains of future SARS- or MERS-like coronavirus outbreaks will originate from bats, and the probability of spillover is increased in countries where extensive wildlife habitat encroachment (e.g. due to economic activity) and illegal trade in wildlife takes place. Extensive studies performed over the past decades have helped identify a range of pathogens in bat populations. These efforts need to continue and expand to widely map diversity and distribution of potentially zoonotic pathogens in bats and allow for detection of early warning signs, which can help minimize the impact of future human outbreaks. Although there is no evidence of natural pangolin or bat infection with SARS-CoV-2 to date, identification of pangolin and intermediate horseshoe bat coronaviruses with 92.4 percent and 96.2 percent sequence similarity with SARS-CoV-2, respectively, may suggest that these species host SARS-CoV-2 virus or a recent common ancestor and could be a potential source for human exposure. Identification of the viral ancestor of SARS-CoV-2 may further support ongoing vaccine research efforts, as well as considerations for measures to reduce future spillover risk for humans and animals.

Detailed investigation of SARS-CoV-2 transmission mechanisms between humans and animals is a research priority

  - Target animal species, particularly mammals such as wild or stray cats, monkeys and raccoons, known to prey on bats or pangolins, to investigate if they play any role in the amplification of SARS-CoV-2 or zoonotic adaptation of its recent ancestor(s).
- Conduct studies to investigate SARS-CoV-2 presence and viability in the immediate environment of locations where target animal species are held, sold or slaughtered, including after different meat processing or disinfection methods; tracing of animal DNA in positive environmental samples would help in hypothesizing potential animal host species which can then be targeted in further field studies.
- Target additional animal species as needed if new evidence suggests potential involvement in SARS-CoV-2 epidemiology and transmission.
- Sites to prioritize for sampling include animal markets, natural habitats and/or commercial farms (including farmed wildlife). For more details related to prioritizing wildlife species for sampling please see Annex 4.
- Screen recent historical samples or RNA banks from wildlife (and domestic animals assessed to be susceptible or potentially susceptible) for presence of SARS-CoV-2 or its precursor viruses, especially in Southeast Asian and sub-Saharan African regions.

LABORATORY STUDIES (SHORT- AND MEDIUM-TERM PRIORITY)

- Conduct laboratory studies on ex-vivo tissue explants of different animal species or experimental animal infection studies to investigate potential animal hosts and confirm or deny findings from studies of ACE2 binding affinity to SARS-CoV-2 RBD.
- Develop and validate real-time PCR protocols for RNA detection of SARS-CoV-2 and SARS-related CoVs in wild and domestic animals, given that real-time PCR protocols currently employed for SARS-CoV-2 may not efficiently detect CoVs circulating in animals that are related to SARS-CoV-2 but not identical.
- Develop and validate of serologically assays to screen sera of animal species for exposure to SARS-CoV-2. This would enable targeted testing of serologically positive species with molecular tests, such as coronavirus family PCR, and further targeted testing of those that test positive, with a specific SARS-CoV-2 PCR assay.

ANTHROPOLOGICAL STUDIES (MEDIUM- AND LONG-TERM PRIORITY)

- Identify likely transmission pathways between animals, humans and involving the environment.
- Understand human behaviour that may lead to increased exposure risk and conduct case-control studies.
- Understand value chains and related drivers for wildlife and wild meat demand, marketing and supply to urban centres, or internationally for wildlife species susceptible to SARS-CoV-2.
- Understand how to better manage risks associated with the trade of wildlife and wild meat.
- Understand the consequences of market closures (local or national; daily, weekly, or monthly) and wildlife trade restrictions (local, national, regional or global; temporary or permanent) as well as if and how such measures could be maintained longer-term.

A traditional market selling wild meat, Indonesia

SEASONALITY STUDIES (LONG-TERM PRIORITY)

- If sustained infection in animal populations is confirmed, any effects of environmental factors, e.g. humidity, temperature, seasonal activities, on the epidemiology of COVID-19 should then be explored. A recent paper by Kissler *et al.* 2020 has projected the transmission dynamics of SARS-CoV-2 in humans during the post-pandemic period up to 2025, taking into consideration the impact of different environmental conditions on control measures implemented at different latitudes. Similar may be considered for the disease in animals, if sustained.

For additional data gaps see the recommendations of the expert meeting held by WHO, Geneva, 11-12 February 2020.

Suggested approaches for targeted field investigations in animals

FAO discourages haphazard or random surveys in animals as part of active surveillance efforts. However, given that scientific evidence for involvement of animal species (wild or domestic) in SARS-CoV-2 epidemiology is scarce to date, developing a systematic approach to target investigations remains a challenge.

The following approaches are suggested, based on the knowledge available at the time of publication:

- **Investigation of potential SARS-CoV-2 animal reservoir(s) and intermediate host(s):** veterinary services and research partners should use a risk-based approach targeting high-risk areas, e.g. those where previous spillover of zoonotic pathogens occurred, critical value chain nodes and susceptible and potentially susceptible animal species as identified in this exposure assessment. For details on a progressive approach for wildlife and domestic animal species prioritization, see Annexes 3 and 4. It would be valuable to start by investigating the potential SARS-CoV-2 animal reservoir(s) where the first zoonotic spillover is thought to have taken place, as well as other countries with extensive wildlife and domestic animal trade (either formal or informal). International wildlife trade and value chains and associated national and international trade networks have to be characterized and surveillance conducted at key points that are epidemiologically relevant.
- **Investigation of reverse zoonotic spillover events from humans to animals:** In countries affected by COVID-19, One Health investigations of companion, captive wild and livestock animals in close contact with affected humans may be undertaken. The number of cases to be investigated will depend on local capacities and available resources. Animal species identified to be susceptible or potentially susceptible should be targeted for investigation (see Annexe 4).
- **Samples to take from live animals:** Deep nasal, throat and rectal swab samples should be taken from live animals. Ideally, blood samples should be collected in parallel with swab samples. Even if serological assays are not validated yet, these sera can be stored frozen at -20 °C until a targeted serological assay is available and validated.
- **Samples to take from carcasses:** Tissue samples from nasal turbinates, trachea or lungs and respiratory lymph nodes should be collected from animal carcasses. In addition, specimens from intestinal tissues (particularly from bats) and other lymphoid tissues can be considered if resources allow.
- **Samples to take from traditional market environments:** Swabs from chopping or slaughtering boards, processing tables, cages or baskets holding animals, waste

bins, scales and tables for display may give higher chances of detecting the virus if it is present.

- Banked animal or environmental samples taken in China and the Southeast Asia and sub-Saharan Africa regions, especially from the second half of 2019, may be tested retrospectively.
- **Laboratory testing:**
  - When available, test serum samples with a validated enzyme linked immunosorbent assay (ELISA) that is specific for SARS-CoV-2, or use SARS-CoV-2 or SARS-CoV-2 pseudotyped virus in a relevant virus neutralization assay.
  - Screen swabs or tissue samples with real-time PCR protocol(s) targeting SARSr-CoV and/or SARS-CoV-2 (depending on the study objectives), followed by a full genomic characterization on positive samples for phylogenetic analysis to determine the relatedness to SARS-CoV-2.
- **Interpretation of positive laboratory results:** Any positive laboratory results should be interpreted with care before incriminating an animal as SARS-CoV-2 reservoir or intermediate host. Some atypical animal hosts might accidentally become infected due to anthropogenic activities (i.e. production or marketing practices) or exposed to SARS-CoV-2 RNA in a contaminated environment, however they may not play a role in virus amplification, spread or zoonotic spillover. Some real life examples include the detection of sporadic case(s) of influenza A/H5N1 RNA in donkeys (Abdel-Moneim *et al.*, 2010), MERS-CoV RNA in cattle, sheep, goat and donkeys (Kandeil *et al.*, 2019), and SARS-CoV RNA in a Greylag goose (Wang *et al.*, 2005). Specifying the name of some animal species in this assessment does not imply a role in SARS-CoV-2 zoonotic spillover. Confirmation of animal infection by virus isolation and/or serology is essential, beyond positive PCR. Additional evidence that an animal species could act as SARS-CoV-2 reservoir or intermediate host includes demonstration of high-level RNA shedding and the detection of SARS-CoV-2 RNA and/or anti-SARS-CoV-2 antibodies in other animals of the same species in their natural habitat or commercial production settings. The reader is referred to the OIE Considerations for sampling, testing and reporting of SARS-CoV-2 in animals, for further details (OIE, 2020a).
- SARS-CoV-2 positive findings in animals that comply with the OIE case definition should be reported to the OIE as an 'emerging disease' in accordance with the OIE Terrestrial Animal Health Code, including information about the species, diagnostic tests used, and relevant epidemiological information.

Acknowledging that veterinary services around the world currently have other priorities to handle, for example, animal health emergencies such as African swine fever or avian influenza, research partners such as universities and One Health institutions may be involved to support field studies, investigations and research for SARS-CoV-2 in animals or the environment. However, veterinary services are encouraged to play an active role in the technical planning and coordination of SARS-CoV-2 operational research at national and regional levels to ensure complementarity of activities, and to promote progressive steps toward better understanding of SARS-CoV-2 infection in animals.

Mitigation measures available

In addition to the latest FAO COVID-19 key messages and FAO COVID-19 resources on risk mitigation:

- **Results of this assessment are expected to assist Members, One Health partners, the research community and interested organizations/institutions in conducting country-specific risk assessments, targeted epidemiological investigations and research studies, aiming to epidemiological investigations and research studies aiming to better understand SARS-CoV-2 infection in animals, and do not justify any measures that may subject animal species to unnecessary stress, impact their trade or affect their conservation status.**
- Carrying out country-specific risk assessment and critical review of animal husbandry, food hygiene and marketing practices, using the current knowledge outlined in this document, will allow for evidence-based measures to be put in place or strengthened, which mitigate the risk of exposure of humans and animals to SARS-CoV-2 from susceptible wild, livestock, companion and aquatic animals. Risk assessments should be performed according to international guidance (e.g. OIE, 2019; FAO, 2011; FAO and WHO, 2007).
- A process of country assessment and review – which includes reduction of contact between humans or domestic animals, and bats or other susceptible wild animals that might act as bridge species – will lead to evidenced-based actions which reduce the likelihood and impact of future emergence and spillover of zoonotic pathogens with pandemic potential.
- Maintenance of strict biosecurity measures, wildlife trade controls and restrictions, with bans on illegal trade, and/or behaviour change in consumers and traders would require additional medium- to long-term engagement. Such measures, informed by national risk assessment, should take into account impact on livelihoods and food security.
- Countries should consider promoting and reinforcing generic biosecurity and biosafety interventions along the animal market chain including:
  - All-in, all-out strategies on farms
  - Species segregation and distancing in farms and markets
  - Good hygienic standards (CAC, 2009) during preparation and selling of raw animal products
  - Daily cleaning of markets, no overnight rules and regular market rest days
  - Review and critical assessment of national measures or controls on wildlife trade or farming, and their enforcement or strengthening if necessary.[2]

[2] At the time of publication, China and Viet Nam are taking steps to institutionalize bans on wildlife trade and consumption, implemented in response to COVID-19, through a review of national laws with the aim to strengthen their enforcement, promote behaviour change through communication campaigns, and support wildlife farmers in the transition to other agricultural practices.

Codex Alimentarius food hygiene standards should be followed to prevent contamination of food products

Biosecurity guidance for specific settings can be found in FAO and partners' publications.

- Veterinary services and wildlife authorities should raise awareness of the importance of biosecurity measures in livestock and wildlife farming, and marketing facilities to protect human health.
- Veterinary services and public health authorities should advise people who are sick with suspected or confirmed COVID-19 to restrict contact with animals (including companion animals), just like you would with people. Until more is known about this virus, people sick with COVID-19 should avoid contact with pets and other animals.
- Veterinary services should ensure appropriate diagnostic capacities for the detection of SARS-CoV-2.
- Governments are encouraged to strengthen border controls (including veterinary, food safety, trade, etc.) on illegal wildlife trade.
- Veterinary services and public health authorities should advise occupational risk groups about standard personal protection measures that can reduce exposure risk from animals, e.g. wearing gloves and masks as well as frequent cleaning and disinfection of equipment, areas and surfaces.

FAO has published Guidelines to mitigate the impact of the COVID-19 pandemic on livestock production and animal health (2020) that include practical recommendations to reduce human-to-human transmission in livestock market settings. These Guildelines are for farmers, traders, animal health workers, policy makers and other stakeholders and aim to reduce the impact of disruptions along the livestock market chain, and maintain essential control and prevention of animal diseases – in order to safeguard and strengthen food systems and One Health. Information on recommended food safety measures are outlined in the FAO Policy brief Food Safety in the time of COVID-19 (2020), while generally applicable food hygiene standards are outlined in the Codex Alimentarius Basic Texts on Food Hygiene (2009).

For additional information on COVID-19 information and guidance please refer to the WHO, FAO and OIE dedicated webpages.

References

Abdel-Moneim, A.S., Abdel-Ghany, A.E. & Shany, S.A. 2010. Isolation and characterization of highly pathogenic avian influenza virus subtype H5N1 from donkeys. *Journal of Biomedical Science,* 17, 25.

Ancillotto, L., Serangeli, M.T. & Russo, D. 2013. Curiosity killed the bat: domestic cats as bat predators. *Mammalian Biology,* 78: 369–373.

Andersen, K.G., Rambaut, A., Lipkin, W.I., Holmes, E.C., Garry, R.F. 2020. The proximal origin of SARS-CoV-2. *Nature Medicine*, 26(4): 450–452.

Asian Canine Protection Alliance (ACPA). 2013. Risk assessment - the risk the dog meat trade poses to rabies transmission and the ASEAN plus 3 countries' pledge to eliminate rabies by 2020. (available at http://www.acpagroup.org/images/resources/Risk%20Assessment_TheIllegalTradeinDogsandRabiesTransmission_ACPA.pdf)

Bao, L., Deng, W., Gao, H., Xiao, C., Liu, J., Xue, J., Lv Q., Liu, J., Yu, P., Xu, Y., Qi, F., Qu, Y., Li, F., Xiang, Z., Yu, H., Gong, S., Liu, M., Wang, G., Wang, S., Song, Z., Zhao, W., Han, Y., Zhao, L., Liu, X., Wei, Q., Qin, C. 2020. Reinfection could not occur in SARS-CoV-2 infected rhesus macaques. *bioRxiv* doi: 10.1101/2020.03.13.990226

Boinski, S. and Timm, R. 1985**.** Predation of squirrel monkey and double toothed kites on tent-making bats. *American Journal of Primatology,* 9: 121–127.

Bondad-Reantaso, M., Mackinnon, B., Bin, H., Jie, H., Tang-Nelson, K., Surachetpong, W., Alday Sanz, V., Salman, M., Brun, E., Karunasagar, I, Hanson, L., Sumption, K., Barange, M., Lovatelli, A., Sunarto, A., Fejzic, N., Subasinghe, R., Mathiesen, A., Shariff, M. 2020. Viewpoint: SARS-CoV-2 (the cause of COVID-19 in humans) is not known to infect aquatic food animals nor contaminate their products. *Asian Fisheries Science,* 33: 74–78.

Bondad-Reantaso, M.G., McGladdery, S.E., East, I. & Subasinghe, R.P. 2001. Asia diagnostic guide to aquatic animal diseases. *FAO Fisheries Technical Paper* No. 402/2.

Bosco-Lauth, B., Hartwig, A., Porter, S., Gordy, P., Nehring, M., Byas, A., VandeWoude, S., Ragan, I., Maison, R., Bowen, R. 2020. Pathogenesis, transmission and response to re-exposure of SARS-CoV-2 in domestic cats *bioRxiv* 2020.05.28.120998; doi: https://doi.org/10.1101/2020.05.28.120998

Bossart, G.D. and Schwartz, J.C. 1990. Acute necrotizing enteritis associated with suspected coronavirus infection in three harbor seals (Phoca vitulina). *Journal of Zoo and Wildlife Medicine,* 21(1): 84–87.

CAC. 2009. Food hygiene (Basic texts), Fourth edition. Codex Alimentarius Commission, *ISBN 978-92-5-105913-5*.

Castanheira De Matos, R.E. and Morrisey, J.K. 2006. Common procedures in the pet ferret. *Veterinary Clinics of North America: Exotic Animal Practice,* 9(2): 347–65, vii.

Cawthorn, D.M. and Hoffman, L.C. 2015. The bushmeat and food security nexus: a global account of the contributions, conundrums and ethical collisions. *Food Research International,* 76: 906–25.

CDC and USDA. 2020**.** Confirmation of COVID-19 in two pet cats in New York. Media statement, 22 April 2020. (available at https://www.cdc.gov/media/releases/2020/s0422-covid-19-cats-NYC.html)

CDC. 2003. Prevalence of IgG antibody to SARS-associated coronavirus in animal traders --- Guangdong Province, China, 2003. *Morbidity and Mortality Weekly Report,* 52(41): 986–987.

CDC. 2020. How COVID-19 spreads. Updated: 13 April 2020. (available at https://www.cdc.gov/coronavirus/2019-ncov/prevent-getting-sick/how-covid-spreads.html)

Chaber, A.-L., Gaubert, P., Green, H., Garigliany, M., Renault, V., Busoni, V., Dieudonné, M., Saegerman, C. 2020. Report on the illegal importation of meat, including bushmeat, seized at Zaventem Airport - 2017/2018**.** *World Wide Fund for Nature Report*. (available at https://wwf.be/assets/IMAGES-2/CAMPAGNES/COVID-19/REPORTONTHEILLEGALIMPORTATIONOFMEATFinal.pdf)

Chacón-Madrigal, E. and Barrantes, G. 2004. Blue-crowned motmot (Momotus momota) predation on a long-tongued bat (*Glossophaginae*). *The Wilson Bulletin*, 116(1): 108–110.

Challender, D and Waterman, C. 2017. Implementation of CITES decisions 17.239 b) and 17.240 on pangolins (*Manis spp.*). Prepared by International Union for the Conservation of Nature for the CITES Secretariat. (available at https://cites.org/sites/default/files/eng/com/sc/69/E-SC69-57-A.pdf)

Challender, D. 2011. Asian pangolins: increasing affluence driving hunting pressure. *TRAFFIC Bulletin,* 23(3).

Chan, J.F., Zhang, A.J., Yuan, S., Poon, V.K., Chan, C.C., Lee, A.C., Chan, W.M., Fan, Z., Tsoi, H.W., Wen, L., Liang, R., Cao, J., Chen, Y., Tang, K., Luo, C., Cai, J.P., Kok, K.H., Chu, H., Chan, K.H., Sridhar, S., Chen, Z., Chen, H., To, K.K., Yuen, K.Y. 2020. Simulation of the clinical and pathological manifestations of Coronavirus Disease 2019 (COVID-19) in golden Syrian hamster model: implications for disease pathogenesis and transmissibility. *Clinical Infectious Diseases.* doi: 10.1093/cid/ciaa325.

Chin, A., Chu, J., Perera, M., Hui, K., Yen, H., Chan, M., Peiris, M., Poon, L. 2020. Stability of SARS-CoV-2 in different environmental conditions. *The Lancet, Correspondence,* 1(1), e10. doi: 10.1016/S2666-5247(20)30003-3.

Chomel, B.B. and Sun, B. 2011. Zoonoses in the bedroom. *Emerging Infectious Diseases,* 17(2): 167–72.

Chomel, B.B., Belotto, A., Meslin, F.X. 2007. Wildlife, exotic pets, and emerging zoonoses. *Emerging Infectious Diseases,* 13(1): 6–11.

Choudhury, A. and Mukherjee, S. 2020. In silico studies on the comparative characterization of the interactions of SARS-CoV-2 spike glycoprotein with ACE-2 receptor homologs and human TLRs. (Advance online publication: 8 May 2020.) *Journal of Medical Virology,* doi: 10.1002/jmv.25987.

Chu, H., Chan, J., Yuen, T., Shuai, H., Yuan, S., Wang, Y., Hu, B., Yip, C., Tsang, J., Huang, X., Chai, Y., Yang, D., Hou, Y., Chik, K., Zhang, X., Fung, A., Tsoi, H., Cai, J., Chan, W., Daniel, J., Chu, A., Zhou, J., Lung, D., Kok, K., To, K., Tsang, O., Chan, K., Yuen, K. 2020. Comparative tropism, replication kinetics, and cell damage profiling of SARS-CoV-2 and SARS-CoV with implications for clinical manifestations, transmissibility, and laboratory studies of COVID-19: an observational study. *The Lancet Microbe*, 1(1): 14-23.

Coggins, C. 2002. The tiger and the pangolin: nature, culture, and conservation in China. *University of Hawaii Press, 2003*

Corman, V.M., Eckerle, I., Memish, Z.A., Liljander, A.M., Dijkman, R., Jonsdottir, H., Juma Ngeiywa, K.J., Kamau, E., Younan, M., Al Masri, M., Assiri, A., Gluecks, I., Musa, B.E., Meyer, B., Müller, M.A., Hilali, M., Bornstein, S., Wernery, U., Thiel, V., Jores, J., Drexler, J.F., Drosten, C. 2016. Link of a ubiquitous human coronavirus to dromedary camels. *Proceedings of the National Academy of Sciences of the United States of America,* 113(35): 9864–9.

Cui, J., Li, F., Shi, Z.L. 2019. Origin and evolution of pathogenic coronaviruses. *Nature Reviews Microbiology,* 17: 181–192

Cupertino, M., Resende, M., Mayer, N., Carvalho, L., Siqueira-Batista, R. 2020. A systematic review of the role of wild animals with a focus on public health impact. *Emerging and re-emerging human infectious diseases*, 13(3): 99–106.

Czajkowski, C. 2014. Dog meat trade in South Korea: a report on the current state of the trade and efforts to eliminate it. *Animal Law Review, Lewis & Clark Law School,* 21(29): 30–64.

Damas, J., Hughes, G., Keough, K., Painter, C., Persky, N., Corbo, M., Hiller, M., Koepfli, K., Pfenning, A., Zhao, H., Genereux, D., Swofford, R., Pollard, K., Ryder, O., Nweeia, M., Lindblad-Toh, K., Teeling, E., Karlsson, E., Lewin, H. 2020. Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. *bioRxiv.* doi: 10.1101/2020.04.16.045302.

David, D., Rotenberg, D., Khinich, E., Erster, O., Bardenstein, S., van Straten, M., Okba, N.M.A., Raj, S.V., Haagmans, B.L., Miculitzki, M., Davidson, I. 2018. Middle East respiratory syndrome coronavirus specific antibodies in naturally exposed Israeli llamas, alpacas and camels. *One Health,* 5: 65–68.

De Noronha, J., Battirola, L., Júnior, A., De Miranda, R., De Sá Carpanedo, R., Rodrigues, D. *2015.* Predation of bat (*Molossus molossus: Molossidae*) by the centipede scolopendra viridicornis (*Scolopendridae*) in Southern Amazonia. *Acta Amazonica*, 45(3): 333–336.

Decaro, N. and Lorusso, A. 2020. Novel human coronavirus (SARS-CoV-2): a lesson from animal coronaviruses. *Veterinary microbiology,* 244, 108693.

Del Rio, C. and Malani, P.N. 2020. 2019 novel coronavirus - important information for clinicians. *Journal of the American Medical Association,* 323(11): 1039–1040. doi:10.1001/jama.2020.1490.

Delpietro, H., Konolsaisen, F., Marchevsky, N., Russo, G. 1994. Domestic cat predation on vampire bats (*Desmodus rotundus*) while foraging on goats, pigs, cows and human beings. *Applied Animal Behaviour Science,* 39(2): 141–150.

Deng, J., Jin, Y., Liu, Y., Sun, J., Hao, L., Bai, J., Huang, T., Lin, D., Jin, Y., Tian, K. 2020b. Serological survey of SARS-CoV-2 for experimental, domestic, companion and wild animals excludes intermediate hosts of 35 different species of animals. *Transboundry and Emerging Diseases.* doi:10.1111/tbed.13577.

Deng, W., Bao, L., Gao, H., Xiang, Z., Qu, Y., Song, Z., Gong, S., Liu, J., Liu, J., Yu, P., Qi, F., Xu, Y., Li, F., Xiao, C., Lv, Q., Xue, J., Wei, Q., Liu, M., Wang, G., Wang, S., Yu, H., Liu, X., Zhao, W., Han, Y., Qin, C. 2020. Ocular conjunctival inoculation of SARS-CoV-2 can cause mild COVID-19 in Rhesus macaques. *bioRxiv.* doi: 10.1101/2020.03.13.990036.

Devaux, C., Pinault, L., Osman, I., Raoult, D. 2020. Can ACE2 receptor polymorphism predict species susceptibility to SARS-CoV-2?, *Research Square*. doi: 10.21203/rs.3.rs-25753/v1

Durães-Carvalho, R., Caserta, L.C., Barnabé, A.C., Martini, M.C., Ferreira, H.L., Felippe, P.A., Santos, M.B., Arns, C.W. 2015. Coronaviruses detected in Brazilian wild birds reveal close evolutionary relationships with *beta*- and *deltacoronaviruses* isolated from mammals. *Journal of Molecular Evolution,* 81(1–2): 21–23. doi: 10.1007/s00239-015-9693-9.

Eberli, P., Gebhardt-Henrich, S., Steiger, A. 2011. The influence of handling and exposure to a ferret on body temperature and running wheel activity of golden hamsters (*Mesocricetus auratus*). *Applied Animal Behaviour Science,* 131(3–4): 131–137

EIA. 2017. Cultivating demand: the growing threat of tiger farms. *Environmental Investigation Agency technical report*. (available at https://eia-international.org/report/cultivating-demand-growing-threat-tiger-farms)

Esbérard, C. and Vrcibradic, D. 2007. Snakes preying on bats: new records from Brazil and a review of recorded cases in the Neotropical Region. *Revista Brasileira De Zoologia,* 24(3). doi: 10.1590/S0101-81752007000300036

FAO and WHO. 2007. Food Safety Risk Analysis. *FAO Food and Nutrition Paper 87*.

FAO. 1994. Definition and classification of commodities. (available at http://www.fao.org/waicent/faoinfo/economic/faodef/fdef16e.htm)

FAO. 2011. A value chain approach to animal diseases risk management – Technical foundations and practical framework for field application. *FAO Animal Production and Health Guidelines. No. 4.* Rome.

FAO. 2014. Meat quality. Updated: 25 November 2014. (available at http://www.fao.org/ag/againfo/themes/en/meat/backgr_composition.html)

FAO. 2015. Wildlife farming in Viet Nam, Southern Viet Nam's wildlife farm survey report in a glance. (available at http://www.fao.org/3/a-az118e.pdf)

Fischer, E., Munin, R.L., Longo, J.M., Fischer, W., Souza, P.R. 2010. Predation on bats by great kiskadees. *Journal of Field Ornithology,* 81(1): 17–20.

Forman, D., Liles, G., Barbe, P. 2004. Evidence of lesser horseshoe bat (*Rhinolophus hipposideros*) predation by otter (*Lutra lutra*) in a Welsh cave system. *Lutra,* 47 (1): 53–56.

Frank, H., Enard, D., Boyd, S. 2020. Exceptional diversity and selection pressure on SARS-CoV and SARS-CoV-2 host receptor in bats compared to other mammals. *bioRxiv.* doi: 10.1101/2020.04.20.051656.

Fur Europe. 2015. Annual report 2014. (available at https://www.fureurope.eu/wp-content/uploads/2015/09/Fur_Europe_Annual_Report_September_2015_smallsize.pdf)

Goodpaster, W. and Hoffmeister, D. 1950. Bats as prey for mink in Kentucky cave. *Journal of Mammalogy,* 31(4): 457.

Gorbalenya, A., Baker, S., Baric, R., de Groot, R., Drosten, C., Gulyaeva, A., Haagmans, B., Lauber, C., Leontovich, A., Neuman, B., Penzar, D., Perlman, S., Poon, L., Samborskiy, D., Sidorov, I., Sola, I. & Ziebuhr, J. 2020. The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2. *Nat Microbiol* 5, 536–544 (2020). https://doi.org/10.1038/s41564-020-0695-z

Gray, T.N.E., Hughes, A.C., Laurance, W.F. Long B., Lynam A., O'Kelly H., Ripple W., Seng T., Scotson L., Wilkinson N. 2018. The wildlife snaring crisis: an insidious and pervasive threat to biodiversity in Southeast Asia. *Biodiversty and Conservation,* 27: 1031–1037.

Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen,

K.Y., Peiris, J.S., Poon, L.L. 2003. Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China. *Science (New York, N.Y.),* 302(5643): 276–278.

Guo, Z.D., Wang, Z.Y., Zhang, S.F., Li, X., Li, L., Li, C., Cui, Y., Fu, R.B., Dong, Y.Z., Chi, X.Y., Zhang, M.Y., Liu, K., Cao, C., Liu, B., Zhang, K., Gao, Y.W., Lu, B., Chen, W. 2020. Aerosol and surface distribution of severe acute respiratory syndrome coronavirus 2 in hospital wards, Wuhan, China. *Emerging Infectious Diseases,* 26(7). doi: 10.3201/eid2607.200885.

Halfmann, P.J., Hatta, M., Chiba, S., Maemura, T., Fan, S., Takeda, M., Kinoshita, N., Hattori, S.I., Sakai-Tagawa, Y., Iwatsuki-Horimoto, K., Imai, M., Kawaoka, Y. 2020. Transmission of SARS-CoV-2 in domestic cats. *New England Journal of Medicine, correspondence.* doi: 10.1056/NEJMc2013400

Haramoto, E., Malla, B., Thakali, O., Kitajima, M. 2020. First environmental surveillance for the presence of SARS-CoV-2 RNA in wastewater and river water in Japan. *medRxiv* 2020.06.04.20122747; doi: https://doi.org/10.1101/2020.06.04.20122747

Hartman, A., Nambulli, S., McMillen, C., White, A., Tilston-Lunel, N., Albe, J., Cottle, E., Dunn, M., Frye, J., Gilliland, T., Olsen, E., O'Malley, K., Schwarz, M., Tomko, J., Walker, R., Xia, M., Hartman, M., Klein, E., Scanga, C., Flynn, J., Klimstra, W., McElroy, A., Reed, D., Duprex, W. 2020. SARS-CoV-2 infection of African green monkeys results in mild respiratory disease discernible by PET/CT imaging and prolonged shedding of infectious virus from both respiratory and gastrointestinal tracts . *bioRxiv* 2020.06.20.137687; doi: https://doi.org/10.1101/2020.06.20.137687

Haydon, D.T., Cleaveland, S., Taylor, L.H., Laurenson, M.K. 2002. Identifying reservoirs of infection: a conceptual and practical challenge. *Emerging Infectious Disease,* 8(12): 1468–73.

He, Z., Liu, B., Tao, Y., Li, C., Xia, M., Zhong, W., Jiang, X., Liu, H., & Tan, M. 2017. Norovirus GII.17 Natural Infections in Rhesus Monkeys, China. *Emerging infectious diseases*, 23(2): 316–319.

Heinrich, S., Wittman, T., Ross, J., Shepherd, C., Challender, D., Cassey, P. 2017. The global trafficking of pangolins: seizures and trafficking routes from 2010–2015. *Traffic.* (available at https://www.traffic.org/publications/reports/the-global-trafficking-of-pangolins/)

Huang, C,, Wang, Y., Li, X., Ren, L., Zhao, J., Hu, Y., Zhang, L., Fan, G., Xu, J., Gu, X., Cheng, Z., Yu, T., Xia, J., Wei, Y., Wu, W., Xie, X., Yin, W., Li, H., Liu, M., Xiao, Y., Gao, H., Guo, L., Xie, J., Wang, G., Jiang, R., Gao, Z., Jin, Q., Wang, J., Cao, B. 2020a. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet.* 395(10223): 497–506.

Huang, Y., Vanlandingham, D., Bilyeu, A., Sharp, H., Hettenbach, S., Higgs, S. 2020b. SARS-CoV-2 and mosquitoes: an extreme challenge. Research Square, doi: 10.21203/rs.3.rs-32261/v1

Hui, E.K. 2006. Reasons for the increase in emerging and re-emerging viral infectious diseases. *Microbes and Infection,* 8(3): 905–16.

Hunt, T.D., Ziccardi, M.H., Gulland, F.M., Yochem, P.K., Hird, D.W., Rowles, T., Mazet, J.A. 2008. Health risks for marine mammal workers. *Diseases of Aquatic Organisms,* 81(1): 81–92.

Hutterer, R., Ivanova, T., Meyer-Cords, C., Rodrigues, L. 2005. Bat migrations in Europe - a review of banding data and literature. *Naturschutz und Biologische Vielfalt*, 28: 180

Ibanez, C., Ramo, C., Busto, B. 1992. Notes on food habits of the black and white owl. *The Condor,* 94: 529–531

Jákl, J. 2019**.** Pangolin, Rāma, and the garden in Laṅkā in the 9th century CE: a few notes on a symbolically powerful "anteater". *The journal Archipel*, (97): 69–86.

Johnson, P.T., Stanton, D.E., Preu, E.R., Forshay, K.J., Carpenter, S.R. 2006. Dining on disease: how interactions between infection and environment affect predation risk. *Ecology,* 87(8): 1973–1980.

Kan, B., Wang, M., Jing, H., Xu, H., Jiang, X., Yan, M., Liang, W., Zheng, H., Wan, K., Liu, Q., Cui, B., Xu, Y., Zhang, E., Wang, H., Ye, J., Li, G., Li, M., Cui, Z., Qi, X., Chen, K., Du, L., Gao, K., Zhao, Y.T., Zou, X.Z., Feng, Y.J., Gao, Y.F., Hai, R., Yu, D., Guan, Y., Xu, J. 2005. Molecular evolution analysis and geographic investigation of severe acute respiratory syndrome coronavirus-like virus in palm civets at an animal market and on farms. *Journal of Virology,* 79(18): 11892–11900.

Kandeil, A., Gomaa, M., Shehata, M., El-Taweel, A., Kayed, A.E., Abiadh, A., Jrijer, J., Moatasim, Y., Kutkat, O., Bagato, O., Mahmoud, S., Mostafa, A., El-Shesheny, R., Perera, R.A., Ko, R.L., Hassan, N., Elsokary, B., Allal, L., Saad, A., Sobhy, H., McKenzie, P.P., Webby, R.J., Peiris, M., Ali, M.A., Kayali, G. 2019. Middle East respiratory syndrome coronavirus infection in non-camelid domestic mammals. *Emerging Microbes and Infections,* 8(1): 103–108.

Karesh, W.B., Cook, R.A., Bennett, E.L., Newcomb, J. 2005**.** Wildlife trade and global disease emergence. *Emerging Infectious Diseases,* 11(7): 1000–1002.

Kennedy, M., Citino, S., McNabb, A.H., Moffatt, A.S., Gertz, K., Kania, S. 2002. Detection of feline coronavirus in captive *Felidae* in the United States of America. *Journal of Veterinary Diagnostic Investigation,* 14(6): 520–522.

Kim, Y.I., Kim, S.G., Kim, S.M., Kim, E.H., Park, S.J., Yu, K.M., Chang, J.H., Kim, E.J., Lee, S., Casel, M.A.B., Um, J., Song, M.S., Jeong, H.W., Lai, V.D., Kim, Y., Chin, B.S., Park, J.S., Chung, K.H., Foo, S.S., Poo, H., Mo, I.P., Lee, O.J., Webby, R.J., Jung, J.U., Choi, Y.K. 2020. Infection and Rapid Transmission of SARS-CoV-2 in Ferrets. *Cell Host Microbe,* 27(5): 704–709.e2.

Kissler, S.M., Tedijanto, C., Goldstein, E., Grad, Y.H., Lipsitch, M. 2020. Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period. *Science (New York, N.Y.),* 368(6493): 860–868.

Lam, S.D., Bordin, N., Waman, V.P., Scholes, H.M., Ashford, P., Sen, N., Van Dorp, L., Rauer, C., Dawson, N.L., Pang, C.S.M., Abbasian, M., Sillitoe, I., Edwards, S.J.L., Fraternali, F., Lees, J.G., Santini, J.M., Orengo, C.A. 2020b. SARS-CoV-2 spike protein predicted to form stable complexes with host receptor protein orthologues from mammals. *bioRxiv.* 2020.05.01.072371; doi: https://doi.org/10.1101/2020.05.01.072371

Lam, T.T., Shum, M.H., Zhu, H.C., Tong, Y.G., Ni, X.B., Liao, Y.S., Wei, W., Cheung, W.Y., Li, W.J., Li, L.F., Leung, G.M., Holmes, E.C., Hu, Y.L., Guan, Y. 2020a. Identifying SARS-CoV-2 related coronaviruses in Malayan pangolins. *Nature.* doi: 10.1038/s41586-020-2169-0.

Lau, S.K.P., Li, K.S.M., Luk, H.K.H., He, Z., Teng, J.L.L., Yuen, K.Y., Wernery, U., Woo, P.C.Y. 2020. Middle East respiratory syndrome coronavirus antibodies in Bactrian and Hybrid camels from Dubai. *mSphere,* 5(1): e00898-19.

Lee, T.M., Sigouin, A., Pinedo-Vasquez, M., Nasi, R. 2014. The harvest of wildlife for bushmeat and traditional medicine in East, South and Southeast Asia: current knowledge base, challenges, opportunities and areas for future research. *Center for International Forestry Research, Bogor, Indonesia: Occasional Paper 115.* (available at: http://www.cifor.org/publications/pdf_files/OccPapers/OP-115.pdf)

Lefevre, K. 2005. Predation of a bat by American crows, *Corvus brachyrhynchos*. *The Canadian Field-Naturalist,* 119(3): 443–444.

Li, H.Y., Zhu, G.J., Zhang, Y.Z., Zhang, L.B., Hagan, E.A., Martinez, S., Chmura, A.A., Francisco, L., Tai, H., Miller, M., Daszak, P. 2020b. A qualitative study of zoonotic risk among rural communities in Southern China. *International Health,* 12(2): 77–85.

Li, J., Li, J., Xie, X., Cai, X., Huang, J., Tian, X., Zhu, H. 2020a. Game consumption and the 2019 novel coronavirus. *Lancet Infectious Diseases,* 20(3): 275–276.

Li, P., Sun, J., Yu, D. 2017. Dog "meat" consumption in China: a survey of the controversial eating habit in two cities. *Society & Animals,* 25(6): 513–532.

Liu, Y., Hu, G., Wang, Y., Zhao, X., Ji, F., Ren, W., Gong, M., Ju, X., Li, X., Hong, J., Zhu, Y., Cai, X., Wu, J., Lan, X., Xie, Y., Wang, X., Yuan, Z., Zhang, R., Ding, Q. 2020. Functional and genetic analysis of viral receptor ACE2 orthologs reveals broad potential host range of SARS-CoV-2. *bioRxiv.* doi: 10.1101/2020.04.22.046565.

Liu, Z., Jiang, Z., Fang, H., Li, C., Mi, A., Chen, J., Zhang, X., Cui, S., Chen, D., Ping, X., Li, F., Li, C., Tang, S., Luo, Z., Zeng, Y., Meng, Z. 2016. Perception, price and preference: consumption and protection of wild animals used in traditional medicine. *PLoS One,* 11(3): e0145901.

Livingstone, E., Gomez, L., Bouhuys, J. 2018. A review of bear farming and bear trade in Lao People's Democratic Republic. *Global Ecology and Conservation,* 13, e00380.

Lorusso, A., Calistri, P., Petrini, A., Savini, G., Decaro, N. 2020. Novel coronavirus (SARSCoV2) epidemic: a veterinary perspective. *Veterinaria Italiana,* 56(1): 5–10.

Lu, S., Zhao, Y., Yu, W., Yang, Y., Gao, J., Wang, J., Kuang, D., Yang, M., Yang, J., Ma, C., Xu, J., Qian, X., Li, H., Zhao, S., Li, J., Wang, H., Long, H., Zhou, J., Luo, F., Ding, K., Wu, D., Zhang, Y., Dong, Y., Liu, Y., Zheng, Y., Lin, X., Jiao, L., Zheng, H., Dai, Q., Sun, Q., Hu, Y., Ke, C, Liu, H., Peng, X. 2020. Comparison of SARS-CoV-2 infections among 3 species of non-human primates. *bioRxiv.* doi: 10.1101/2020.04.08.031807.

Luan, J., Jin, X., Lu, Y., & Zhang, L. 2020a. SARS-CoV-2 spike protein favors ACE2 from *Bovidae* and *Cricetidae*. *Journal of medical virology*. doi: 10.1002/jmv.25817.

Luan, J., Lu, Y., Jin, X., Zhang, L. 2020b. Spike protein recognition of mammalian ACE2 predicts the host range and an optimized ACE2 for SARS-CoV-2 infection. *Biochemical and Biophysical Research Communications,* 526(1): 165–169. doi: 10.1016/j.bbrc.2020.03.047.

McAlpine, D.F., Vanderwolf, K.J., Forbes, G.J., Malloch, D. 2011. Consumption of bats (*Myotis spp.*) by raccoons (*Procyon lotor*) during an outbreak of white-nose syndrome in New Brunswick, Canada: implications for estimates of bat mortality. *The Canadian Field Naturalist,* 125(3): 257–260.

Melin, A., Janiak, M., Marrone, F., Arora, P., Higham, J. 2020. Comparative ACE2 variation and primate COVID-19 risk. *bioRxiv.* doi: 10.1101/ 2020.04.09.034967.

Mikula, P. 2015. Fish and amphibians as bat predators. *European Journal of Ecology,* 1(1): 71–80.

Mikula, P., Morelli, F., Lucan, R.K., Jones, D.N., Tryjanowski, P. 2016. Bats as prey of diurnal birds: a global perspective. *Mammalian Review, 46: 160–174.*

Milano, M.Z. and Monteiro-Filho, E.L.A. 2009. Predation on small mammals by capuchin monkeys, *Cebus cay*. *Neotropical Primates,* 16(2): 78–80.

Mihindukulasuriya, A., Wu, G., St Leger, J., Nordhausen, W., & Wang, D. 2008. Identification of a novel coronavirus from a beluga whale by using a panviral microarray. *Journal of virology*, 82(10): 5084–5088.

Molinari, J., Gutierrez, E.E., De Ascencao, A.A., Nassar, J.M., Arends, A., Marquez, R.J., 2005. Predation by giant centipedes, *Scolopendra gigantea*, on three species of bats in a Venezuelan cave. *Caribbean Journal of Science,* 41: 340–346.

Nyffeler, M. and Knörnschild, M. 2013. Bat predation by spiders. *PLoS One,* 8(3): e58120.

OIE. 2015. Biological threat reduction strategy. *OIE Global Conference on Biological Threat Reduction, Paris, France*. (available at: https://www.oie.int/fileadmin/Home/eng/Our_scientific_expertise/docs/pdf/EN_FINAL_Biothreat_Reduction_Strategy_OCT2015.pdf)

OIE. 2019. Terrestrial Animal Health Code. (available at: https://www.oie.int/en/standard-setting/terrestrial-code/access-online/)

OIE. 2020a. Considerations for sampling, testing, and reporting of SARS-CoV-2 in animals. Version 1, 7 May 2020. (available at https://www.oie.int/fileadmin/Home/eng/Our_scientific_expertise/docs/pdf/COV-19/Sampling_Testing_and_Reporting_of_SARS-CoV-2_in_animals_final_7May_2020.pdf)

OIE. 2020b. Questions and answers on COVID-19. Update: 18 May 2020. (available at https://www.oie.int/en/scientific-expertise/specific-information-and-recommendations/questions-and-answers-on-2019novel-coronavirus/)

OIE. 2020c. Animal and environmental investigations to identify the zoonotic source of the COVID-19 virus. (available at https://www.oie.int/fileadmin/Home/eng/Our_scientific_expertise/docs/pdf/COV-19/1st_call_COVID19_21Feb.pdf)

OIE. 2020d. World animal health information system. *Follow Up Report No. 1 from USDA-APHIS, United States Department of Agriculture, Washington, United States of America, on SARS-CoV-2 infection of big cats in a zoo.* (available at https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=34054)

OIE. 2020e. Wildlife trade and emerging zoonotic diseases. *Statement of the OIE Wildlife Working Group, April 2020*. (available at https://www.oie.int/fileadmin/Home/eng/Our_scientific_expertise/docs/pdf/COV-19/A_OIEWildlifeTradeStatement_April2020.pdf)

OIE. 2020f. World animal health information system, immediate report from Hong Kong Special Administrative Region Government on cat infection with SA*RS-CoV-2*. (available at https://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=33832)

Ong, S.W.X., Tan, Y.K., Chia, P.Y., Lee, T.H., Ng, O.T., Wong, M.S.Y., Marimuthu, K. 2020. Air, surface environmental, and personal protective equipment contamination by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) from a symptomatic patient. *Journal of the American Medical Association,* 323(16): 1610–1612.

Oreshkova, N., Molenaar, J., Vreman, S., Harders, F., Oude, B., Hakze-van, R., Gerhards, N., Tolsma, P., Bouwstra, R., Sikkema, R., Tacken, M., de Rooij, M., Weesendorp, E., Engelsma, M., Bruschke, C., Smit L., Koopmans, M., van der Poel, W., Stegeman, A. 2020. SARS-CoV-2 infection in farmed minks, the Netherlands. *Eurosurveillance.* 25(23):pii=2001005. https://doi.org/10.2807/1560-7917.ES.2020.25.23.2001005

Pastorino, B., Touret, F., Gilles, M., De Lamballeries, X., Charrel, R. 2020. Prolonged viability of SARS-CoV-2 in fomites. *Preprint.* doi: 10.31219/osf.io/7etga.

Pach, S., Nguyen, T., Trimpert, J., Kunec, D., Osterrieder, N., Wolber, G. 2020. ACE2-Variants Indicate Potential SARS-CoV-2-Susceptibility in Animals: An Extensive Molecular Dynamics Study. bioRxiv 2020.05.14.092767; doi: https://doi.org/10.1101/2020.05.14.092767

Pietersen, D., McKechnie, A., Jansen, R. 2014. A review of the anthropogenic threats faced by Temminck's ground pangolin, *Smutsia temminckii*, in southern Africa. *South African Journal of Wildlife Research, 24-month delayed open access,* 44: 167–178.

Piplani, S., Singh, P., Winkler, D., Petrovsky, N. 2020. In silico comparison of spike protein-ACE2 binding affinities across species; significance for the possible origin of the SARS-CoV-2 virus. *arXiv,* eprint: 2005.06199.

Pizo, M., Silva, W., Galetti, M., Laps, R. 2002. Frugivory in cotingas of the Atlantic Forest of southeast Brazil. *Ararajuba,* 10(2): 177–185.

Plowright, R.K., Eby, P., Hudson, P.J., Smith, I.L., Westcott, D., Bryden, W.L., Middleton, D., Reid, P.A., McFarlane, R.A., Martin, G., Tabor, G.M., Skerratt, L.F., Anderson, D.L., Crameri, G., Quammen, D., Jordan, D., Freeman, P., Wang, L.F., Epstein, J.H., Marsh, G.A., Kung, N.Y., McCallum, H. 2015. Ecological dynamics of emerging bat virus spillover. *Proceedings of the Royal Society B: Biological Sciences,* 282:20142124.

Plowright, R.K., Parrish, C.R., McCallum, H., Hudson, P.J., Ko, A.I., Graham, A.L., Lloyd-Smith, J.O. 2017. Pathways to zoonotic spillover. *Nature Reviews Microbiology,* 15(8): 502–510.

Porter, L. and Lai, H. 2017. Marine mammals in Asian societies; trends in consumption, bait, and traditional use. *Frontiers in Marine Science, 4: 47*. doi: 10.3389/fmars.2017.00047.

Praharaj, M., Garg, P., Khan, R., Sharma, S., Panigrahi, M., Mishra, B.P., Mishra, B., Kumar, G., Gandham, R., Singh, R., Majumdar, S., Mohapatra, T. 2020. Prediction analysis of SARS-CoV-2 entry in livestock and wild animals. *bioRxiv.* doi: 10.1011/2020.05.08.084327.

Qiu, Y., Wang, Q., Li, J., Liao, C., Zhou, Z., Ge, X. 2020a. Receptor utilization of angiotensin converting enzyme 2 (ACE2) indicates a narrower host range of SARS-CoV-2 than that of SARS-CoV. *bioRxiv* 2020.06.13.149930; doi: https://doi.org/10.1101/2020.06.13.149930

Qiu, Y., Zhao, Y.B., Wang, Q., Li, J.Y., Zhou, Z.J., Liao, C.H., Ge, X.Y. 2020b. Predicting the angiotensin converting enzyme 2 (ACE2) utilizing capability as the receptor of SARS-CoV-2 (preprint 19 March 2020). *Microbes and Infection.* doi: 10.1016/j.micinf.2020.03.003.

Quick, H. 1951. Notes on the ecology of weasels in Gunnison County, Colorado. *Journal of Mammalogy,* 32(3): 281–290.

Reusken, C.B., Schilp, C., Raj, V.S., De Bruin, E., Kohl, R.H., Farag, E.A., Haagmans, B.L., Al-Romaihi, H., Le Grange, F., Bosch, B.J., Koopmans, M.P. 2016. MERS-CoV infection of alpaca in a region where MERS-CoV is endemic. *Emerging Infectious Diseases,* 22(6): 1129–1131.

Rhyan, J.C. and Spraker, T.R. 2010. Emergence of diseases from wildlife reservoirs. *Veterinary Pathology,* 47(1): 34–39.

Richard, M., Kok, A., De Meulder, D., Bestebroer, T., Lamers, M., Okba, N., Van Vlissingen, M., Rockx, B., Haagmans, B., Koopmans, M., Fouchier, R., Herfst, S. 2020. SARS-CoV-2 is transmitted via contact and via the air between ferrets. *bioRxiv.* doi: 10.1011/2020.04.16.044503.

Rijksoverheid (Government of the Netherlands). 2020a. New Covid-19 research results at mink farms. *News release 19 May 2020.* (available at https://www.rijksoverheid.nl/ministeries/ministerie-van-landbouw-natuur-en-voedselkwaliteit/nieuws/2020/05/19/nieuwe-onderzoeks-resultaten-covid-19-bij-nertsenbedrijven)

Rijksoverheid (Government of the Netherlands). 2020b. COVID-19 detected on two mink farms. *News release 26 April 2020.* (available at https://www.rijksoverheid.nl/actueel/nieuws/2020/04/26/covid-19-geconstateerd-op-twee-nertsenbedrijven)

Rijksoverheid (Government of the Netherlands). 2020c. Cabinet follows advice: clean up contaminated mink farms. *News release 3 June 2020.* (available at https://www.rijksoverheid.nl/actueel/nieuws/2020/06/03/kabinet-volgt-advies-besmette-nertsenbedrijven-ruimen).

Roch, R. 2015. Look what the cat dragged in: *Felis silvestris catus* as predators of insular bats and instance of predation on the endangered *Pipistrellus maderensis*. *Barbastella, 8(1): 18–21*.

Rockx, B., Kuiken, T., Herfst, S., Bestebroer, T., Lamers, M.M., Oude Munnink, B.B., De Meulder, D., Van Amerongen, G., Van Den Brand, J., Okba, N.M.A., Schipper, D., Van Run, P., Leijten, L., Sikkema, R., Verschoor, E., Verstrepen, B., Bogers, W., Langermans, J., Drosten, C., Fentener van Vlissingen, M., Fouchier, R., De Swart, R., Koopmans, M., Haagmans, B.L. 2020. Comparative pathogenesis of COVID-19, MERS, and SARS in a nonhuman primate model. *Science,* 368: 1012–1015.

Ryan, K., Bewley, K., Fotheringham, S., Brown, P., Hall, Y., Marriott, A., Tree, J., Allen, L., Aram, M., Brunt, E., Buttigieg, K., Cavell, B., Carter, D., Cobb, R., Coombes, N., Godwin, K., Gooch, K., Gouriet, J., Halkerston, R., Harris, D., Humphries, H., Hunter, L., Ho, C., Kennard, C., Leung, S., Ngabo, D., Osman, K., Paterson, J., Penn, E., Pullan, S., Rayner, E., Slack, G., Steeds, K., Taylor, I., Tipton, T., Thomas, S., Wand, N., Watson, R., Wiblin, N., Charlton, S., Hallis, B., Hiscox, J., Funnelly, S., Dennis, M., Whittaker, C., Catton, M., Druce, J., Salguero, F., Carroll, M. 2020. Dose-dependent response to infection with SARS-CoV-2 in the ferret model: evidence of protection to re-challenge. *bioRxiv* 2020.05.29.123810; doi: https://doi.org/10.1101/2020.05.29.123810

Schlottau, K., Rissmann, M., Graaf, A., Schön, J., Sehl, J., Wylezich, C., Höper, D., Mettenleiter, T., Balkema-Buschmann, A., Harder, T., Grund, C., Hoffmann, D., Breithaupt, A., Beer, M. 2020. SARS-CoV-2 in fruit bats, ferrets, pigs, and chickens: an experimental transmission study. *The Lancet Preprint.* doi: 10.2139/ssrn.3578792

Schütze, H. 2016. Coronaviruses in aquatic organisms. *Aquaculture virology,* 327–335. doi: 10.1016/B978-0-12-801573-5.00020-6

Scrimgeour, J., Beath, A., Swanney, M. 2012. Cat predation of short-tailed bats (*Mystacina tuberculata rhyocobia)* in Rangataua Forest, Mount Ruapehu, Central North Island, New Zealand. *New Zealand Journal of Zoology,* 39(3): 257–260.

Sharif, S., Ikram, A., Khurshid, A., Salman, M., Mehmood, N., Arshad, Y., Ahmad, J., Angez, M., Alam, M., Rehman, L., Mujtaba, G., Hussain, J., Ali, J., Akthar, R., Malik, M., Baig, Z., Rana, M., Usman, M., Ali, M., Ahad, A., Badar, N., Umair, M., Tamim, S., Ashraf, A., Tahir, F., Ali, N. 2020. Detection of SARS-Coronavirus-2 in wastewater, using the existing environmental surveillance network: An epidemiological gateway to an early warning for COVID-19 in communities. *medRxiv* 2020.06.03.20121426; doi: https://doi.org/10.1101/2020.06.03.20121426

Shi, J., Wen, Z., Zhong, G., Yang, H., Wang, C., Huang, B., Liu, R., He, X., Shuai, L., Sun, Z., Zhao, Y., Liu, P., Liang, L., Cui, P., Wang, J., Zhang, X., Guan, Y., Tan, W., Wu, G., Chen, H., Bu, Z. 2020. Susceptibility of ferrets, cats, dogs, and other domesticated animals to SARS-coronavirus 2. *Science (New York, N.Y.),* 368(6494): 1016–1020.

Sia, S.F., Yan, L.M., Chin, A.W.H., Fung, K., Choy, K.T., Wong, A.Y.L., Kaewpreedee, P., Perera, R.A.P.M., Poon, L.L.M., Nicholls, J.M., Peiris, M., Yen, H.L. 2020. Pathogenesis and transmission of SARS-CoV-2 in golden hamsters. *Nature,* advance publication. *doi:* 10.1038/s41586-020-2342-5.

Sit, T.H.C., Brackman, C.J., Ip, S.M., Tam, K.W.S., Law, P.Y.T., To, E.M.W., Yu, V.Y.T., Sims, L.D., Tsang, D.N.C., Chu, D.K.W., Perera, R.A.P.M., Poon, L.L.M., Peiris, M. 2020. Infection of dogs with SARS-CoV-2. *Nature.* doi: 10.1038/s41586-020-2334-5

Singh, D., Ganatra, S., Singh, B., Cole, J., Alfson, K., Clemmons, E., Gazi, M., Gonzalezy, O., Escobedo, R., Lee, T., Chatterjee, A., Goez-Gazi, Y., Sharan, R., Thippeshappa, R., Gough, M., Alvarez, C., Blakley, A., Ferdin, J., Bartley, C., Staples, H., Parodi, L., Callery, J., Mannino, A., Klaffke, B., Escareno, P., Platt, R., Hodara, V., Scordo, J., Oyejide, A., Ajithdoss, D., Copin, R., Baum, A., Kyratsous, C., Alvarez, X., Rosas, B., Ahmed, M., Goodroe, A., Dutton, J., Hall-Ursone, S., Frost, P., Voges, A., Ross, C., Sayers, K., Chen, C., Hallam, C., Khader, S., Mitreva, M., Anderson, T., Martinez-Sobrido, L., Patterson, J., Turner, J., Torrelles, J., Dick, E., Brasky, K., Schlesinger, L., Giavedoni, L., Carrion, R., Kaushal, D. 2020. SARS-CoV-2 infection leads to acute infection with dynamic cellular and inflammatory flux in the lung that varies across nonhuman primate species. *bioRxiv* 2020.06.05.136481; doi: https://doi.org/10.1101/2020.06.05.136481

Sorenson, J. and Matsuoka, A. 2019. Dog's best friend?: rethinking canid-human relations. *McGill-Queen's University Press*. doi: 10.2307/j.ctvscxt9m.

Souza, L.L., Ferrari, S.F., Pina, A.L. 1997. Feeding behaviour and predation of a bat by *Saimiri sciureus* in a semi-natural Amazonian environment. *Folia Primatol; international journal of primatology,* 68(3–5): 194–198.

Sparks, D., Simmons, M., Gummer, C., Duchamp, J. 2003. Disturbance of roosting bats by woodpeckers and raccoons. *Northeastern Naturalist,* 10(1): 105–108.

Srbek-Araujo, A., Nogueira, M., Lúcio, A. 2012. Predation by the centipede Scolopendra viridicornis (*Scolopendromorpha, Scolopendridae*) on roof-roosting bats in the Atlantic forest of southeastern Brazil. *Chiroptera Neotropical,* 18(2): 1128–1131.

Suarez, D., Pantin-Jackwood, M., Swayne, D., Lee, S., DeBlois, S., Spackman, E. 2020. Lack of susceptibility of poultry to SARS-CoV-2 and MERS-CoV. *bioRxiv* 2020.06.16.154658; doi: https://doi.org/10.1101/2020.06.16.154658

Sun, J., He, W., Wang, L., Lai, A., Ji, X., Zhai, X., Li, G., Suchard, M., Tian, J., Zhou, J., Veit, M., Su, S. 2020. COVID-19: epidemiology, evolution, and cross-disciplinary perspectives. *Trends in Molecular Medicine,* 26(5): 483–495.

Tagliamonte, M., Abid, N., Chillemi, G., Salemi, M., Mavian, C. 2020. Re-insights into origin and adaptation of SARS-CoV-2. *bioRxiv.* doi: 10.1011/2020.03.30.015685.

Tang, Y., Li, Y., Sun, J., Zhang, H., Wang, T., Sun, M., Yang, Y., Hu, X., Zhao, J., Cai, X. 2020. Cell entry of SARS-CoV-2 conferred by angiotensin-converting enzyme 2 (ACE2) of different species. *bioRxiv* 2020.06.15.153916; doi: https://doi.org/10.1101/2020.06.15.153916

Tapanes, E., Detwiler, K.M., Cords, M. 2016. Bat predation by cercopithecus monkeys: implications for zoonotic disease transmission. *EcoHealth,* 13: 405–409.

TRAFFIC. 2020. Wildlife trade, COVID-19 and zoonotic disease risks: Shaping the response. *Traffic briefing paper*, 6 April 2020. (available at: https://www.traffic.org/publications/reports/wildlife-trade-covid-19-and-zoonotic-disease-risks-shaping-the-response/)

USDA. 2020. USDA statement on the confirmation of COVID-19 in a tiger in New York. *News release 13 May 2020.* (available at https://www.aphis.usda.gov/aphis/newsroom/news/sa_by_date/sa-2020/ny-zoo-covid-19)

Van Doremalen, N., Bushmaker, T., Morris, D.H., Holbrook, M.G., Gamble, A., Williamson, B.N., Tamin, A., Harcourt, J.L., Thornburg, N.J., Gerber, S.I., Lloyd-Smith, J.O., De Wit, E., Munster, V.J. 2020. Aerosol and surface stability of SARS-CoV-2 as compared with SARS-CoV-1. *New England Journal of Medicine,* 382(16): 1564–1567.

Viana, M., Mancy, R., Biek, R., Cleaveland, S., Cross, P.C., Lloyd-Smith, J.O., Haydon, D.T. 2014. Assembling evidence for identifying reservoirs of infection. *Trends Ecology and Evolution,* 29(5): 270–279.

Wacharapluesadee, S., Sintunawa, C., Kaewpom, T., Khongnomnan, K., Olival, K. J., Epstein, J., Rodpan, A., Sangsri, P., Intarut, N., Chindamporn, A., Suksawa, K., Hemachudha, T. 2013. Group C *betacoronavirus* in bat guano fertilizer, Thailand. *Emerging Infectious Diseases,* 19(8): 1349–1352.

Wang, K., Chen, W., Zhou, Y., Lian, J., Zhang, Z., Du, P., Gong, L., Zhang, Y., Cui, H., Geng, J., Wang, B., Sun, X., Wang, C., Yang, X., Lin, P., Deng, Y., Wei, D., Yang, X., Zhu, Y., Zhang, K., Zheng, Z., Miao, J., Guo, T., Shi, Y., Zhang, J., Fu, L., Wang, Q., Bian, H., Zhu, P., Chen, Z. 2020. SARS-CoV-2 invades host cells via a novel route: CD147-spike protein *bioRxiv* 2020.03.14.988345; doi: https://doi.org/10.1101/2020.03.14.988345

Wang, M., Jing, H.Q., Xu, H.F., Jiang, X.G., Kan, B., Liu, Q.Y., Wan, K.L., Cui, B.Y., Zheng, H., Cui, Z.G., Yan, M.Y., Liang, W.L., Wang, H.X., Qi, X.B., Li, Z.J., Li, M.C., Chen, K., Zhang, E.M., Zhang, S.Y., Hai, R., Yu, D.Z., Xu, J.G. 2005. Surveillance on severe acute respiratory syndrome associated coronavirus in animals at a live animal market of Guangzhou in 2004. *Zhonghua Liu Xing Bing Xue Za Zhi,* 26(2): 84–87.

Wang, N., Li, S.Y., Yang, X.L., Huang, H.M., Zhang, Y.J., Guo, H., Luo, C.M., Miller, M., Zhu, G., Chmura, A.A., Hagan, E., Zhou, J.H., Zhang, Y.Z., Wang, L.F., Daszak, P., Shi, Z.L. 2018. Serological evidence of bat SARS-related coronavirus infection in humans, China. *Virologica Sinica,* 33(1): 104–107. doi: 10.1007/s12250-018-0012-7.

Wang, Y., Ma, G., Lu, C., Wen, H. 2006. Detection of canine coronaviruses genotype I and II in raised canidae animals in China. *Berl Munch Tierarztl Wochenschr,* 119(1–2): 35–39.

WHO. 2020a. Questions and answers on coronaviruses. Last update: 17 April 2020. (available at https://www.who.int/news-room/q-a-detail/q-a-coronaviruses)

WHO. 2020b. Surveillance strategies for COVID-19 human infection. Interim guidance 10 May 2020. (available at https://www.who.int/publications-detail/surveillance-strategies-for-covid-19-human-infection)

WHO. 2020c. Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19). (available at https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-covid-19-final-report.pdf)

WHO. 2020d. WHO recommendations to reduce risk of transmission of emerging pathogens from animals to humans in live animal markets. (available at https://www.who.int/health-topics/coronavirus/who-recommendations-to-reduce-risk-of-transmission-of-emerging-pathogens-from-animals-to-humans-in-live-animal-markets)

Wildlife Conservation Society (WCS). 2020. Bronx Zoo tigers and lions recovering from COVID-19. News release 22 April 2020. (available at https://newsroom.wcs.org/News-Releases/articleType/ArticleView/articleId/14084/Update-Bronx-Zoo-Tigers-and-Lions-Recovering-from-COVID-19.aspx)

Woo, P.C., Lau, S.K., Lam, C.S., Lau, C.C., Tsang, A.K., Lau, J.H., Bai, R., Teng, J.L., Tsang, C.C., Wang, M., Zheng, B.J., Chan, K.H., Yuen, K.Y. 2012. Discovery of seven novel mammalian and avian coronaviruses in the genus *deltacoronavirus* supports bat coronaviruses as the gene source of *alphacoronavirus* and *betacoronavirus* and avian coronaviruses as the gene source of *gammacoronavirus* and *deltacoronavirus*. *Journal of Virology, 86(7): 3995–4008*.

Woo, P.C., Lau, S.K., Lam, C.S., Tsang, A.K., Hui, S.W., Fan, R.Y., Martelli, P., Yuen, K.Y. 2014. Discovery of a novel bottlenose dolphin coronavirus reveals a distinct species of marine mammal coronavirus in *gammacoronavirus*. *Journal of Virology,* 88(2): 1318–1331.

Woolsey, C., Borisevich, V., Prasad, A., Agans, K., Deer, D., Dobias, N., Heymann, J., Foster, S., Levine, C., Medina, L., Melody, K., Geisbert, J., Fenton, K., Geisbert, T., Cross, R. 2020. Establishment of an African green monkey model for COVID-19*. bioRxiv.* doi: 10.1011/2020.05.17.100289.

Wu, C., Zheng, M., Yang, Y., Li, M., Liu, Y., Zhang, P., Wang, Y., Wang, Q., Xu, Y., Chen, L., Li, H. 2020b. In silico analysis of intermediate hosts and susceptible animals of SARS-CoV-2. *ChemRxiv*, preprint. doi: 10.26434/chemrxiv.12057996.v1

Wu, F., Zhao, S., Yu, B., Chen, Y.M., Wang, W., Song, Z.G., Hu, Y., Tao, Z.W., Tian, J.H., Pei, Y.Y., Yuan, M.L., Zhang, Y.L., Dai, F.H., Liu, Y., Wang, Q.M., Zheng, J.J., Xu, L., Holmes, E.C., Zhang, Y.Z. 2020a. A new coronavirus associated with human respiratory disease in China. *Nature,* 579(7798): 265–269.

Xu, L., Guan, J., Lau, W., Xiao, Y. 2016. An overview of pangolin trade in China. *Traffic. (available at: https://www.traffic.org/site/assets/files/10569/pangolin-trade-in-china.pdf)*

Zhai, X., Sun, J., Yan, Z., Zhang, J., Zhao, J., Zhao, Z., Gao, Q., He, W., Veit, M., Su, S. 2020. Comparison of SARS-CoV-2 spike protein binding to human, pet, farm animals, and putative intermediate hosts ACE2 and ACE2 receptors. *bioRxiv.* doi: 10.1011/2020.05.08.084061.

Zhang, L. and Yin, F. 2014. Wildlife consumption and conservation awareness in China: a long way to go. *Biodiversity and Conservation,* 23(9): 2371–2381.

Zhang, L., Zhu, G., Jones, G., Zhang, S. 2009. Conservation of bats in China: problems and recommendations. *Cambridge University Press,* 43(2): 179–182.

Zhang, Q., Zhang, H., Huang, K., Yang, Y., Hui, X., Gao, J., He, X., Li, C., Gong, W., Zhang, Y., Peng, C., Gao, X., Chen, H., Zou, Z., Shi, Z., Jin, M. 2020. SARS-CoV-2 neutralizing serum antibodies in cats: a serological investigation. *bioRxiv.* doi: 10.1011/2020.04.01.021196.

Zhao, X., Chen, D., Szabla, R., Zheng, M., Li, G., Du, P., Zheng, S., Li, X., Song, C., Li, R., Guo, J., Junop, M., Zeng, H., Lin, H. 2020b. Broad and differential animal ACE2 receptor usage by SARS-CoV-2. *bioRxiv.* doi: 10.1011/2020.04.19.048710.

Zhao, Y., Wang, J., Kuang, D., Xu, J., Yang, M., Ma, C., Zhao, S., Li, J., Long, H., Ding, K., Gao, J., Liu, J., Wang, H., Li, H., Yang, Y., Yu, W., Yang, J., Zheng, Y., Wu, D., Lu, S., Liu, H., Peng, X. 2020a. Susceptibility of tree shrew to SARS-CoV-2 infection. *bioRxiv.* doi: 10.1101/2020.04.30.029736.

Zhigalin, A. 2019. Siberian weasel Mustela sibirica Pallas, 1773 predatism on bats during winter period. *Subterranean biology,* 32: 111–117.

Zhong, M., Lin, B., Gao, H., Young, A., Wang, X., Liu, C., Wu, K., Liu, M., Chen, J., Huang, J., Lee, L., Qi, C., Ge, L., Wang, L. 2020. Significant expression of FURIN and ACE2 on oral epithelial cells may facilitate the efficiency of SARS-CoV-2 entry. *bioRxiv.* doi: 10.1011/2020.04.18.047951

Zhou, J., Li, C., Liu, X., Chiu, M. C., Zhao, X., Wang, D., Wei, Y., Lee, A., Zhang, A. J., Chu, H., Cai, J. P., Yip, C. C., Chan, I. H., Wong, K. K., Tsang, O. T., Chan, K. H., Chan, J. F., To, K. K., Chen, H., & Yuen, K. Y. 2020b. Infection of bat and human intestinal organoids by SARS-CoV-2. *Nature Medicine,* advance publication. doi: 10.1038/s41591-020-0912-6.

Zhou, P., Yang, X.L., Wang, X.G., Hu, B., Zhang, L., Zhang, W., Si, H.R., Zhu, Y., Li, B., Huang, C.L., Chen, H.D., Chen, J., Luo, Y., Guo, H., Jiang, R.D., Liu, M.Q., Chen, Y., Shen, X.R., Wang, X., Zheng, X.S., Zhao, K., Chen, Q.J., Deng, F., Liu, L.L., Yan, B., Zhan, F.X., Wang, Y.Y., Xiao, G.F., Shi, Z.L. 2020a. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature,* 579: 270–273.

Glossary *for the purpose of this exposure assessment*

Amplifying host: see Reservoir host.

Aquatic animals: All life stages (including eggs and gametes) of fish, molluscs, crustaceans and amphibians originating from aquaculture establishments or removed from the wild for farming purposes, for release into the environment, for human consumption or for ornamental purposes (Bondad-Reantaso *et al.*, 2001). Aquatic birds are excluded here (please refer to 'Wild birds' instead).

Bridge species: See Intermediate host.

Captive wild animal: An animal whose phenotype is not significantly affected by human selection but that is captive or otherwise lives under direct human supervision or control, including zoo animals and pets (OIE, 2019), or wild animal species in circus facilities and wildlife farms/ranches.

Companion animals: Dogs, cats, birds, reptiles and rodents kept as pets. Service or working dogs (e.g. guide dogs, police or military working dogs) and less common exotic pets (for instance ferrets, bats and monkeys) are included here. Horses are excluded here and assessed under 'livestock' instead.

Congregation areas: Places where animals or animal products are assembled from different sources prior to dispatching them to various markets.

Contact with live animals: Physically touching live animals or their excretions during caring, cleaning, feeding, petting, hunting, slaughtering, transporting or other activities.

Contamination: The introduction or occurrence of a contaminant in food or food environment (CAC, 2009).

COVID-19 (coronavirus disease 2019): Name of the disease caused by the virus SARS-CoV-2.

COVID-19 affected areas: A country, province, district or lower administrative division (i.e. community) where infection with SARS-CoV-2 is confirmed in at least one human and/or animal.

COVID-19 patient: A person with laboratory confirmation of COVID-19 infection, irrespective of clinical signs and symptoms (WHO, 2020b).

Exposure: A host comes into contact with viable SARS-CoV-2. Exposure may or may not lead to infection.

Food hygiene: see Hygienic conditions.

Handling and consumption of animal products: Physically touching, eating or drinking animal products.

Hygienic conditions: All conditions and measures necessary to ensure the safety and suitability of food at all stages of the food chain (CAC, 2009).

Incidental host: Dead-end host; an animal species that could be infected with SARS-CoV-2 after being in contact with infected animals or humans, but which cannot amplify the virus or transmit it further.

Infection: Exposure followed by active replication of the virus in the host leading to immune response (e.g. the production of antibodies); with or without clinical signs.

Intermediate host: An animal species that harbours a recent common ancestor of SARS-CoV-2 and played a role in the natural selection/adaptation of the virus before its spillover to humans.

Livestock: Domestic animals belonging to poultry, rabbit, ovine, caprine, bovine, equine, camelid and swine species (FAO, 1994).

Maintenance host: see Reservoir host.

Meat: All parts of an animal that are intended for human consumption (FAO, 2014), including offal such as liver, lung, intestine and other edible organs.

Naïve: Not having previously been infected with or exposed to SARS-CoV-2.

Natural infection: Infection with SARS-CoV-2 under natural circumstances (as opposed to 'laboratory infection/inoculation').

One Health: A collaborative, multidisciplinary, and multisectoral approach that can address urgent, ongoing, or potential health threats at the human-animal-environment interface at sub-national, national, global, and regional levels (FAO-OIE-WHO, 2019).

Poultry: Chicken, duck, turkey, guinea fowl, geese and other domesticated birds including pigeon and ostrich kept for the purpose of production or breeding (OIE, 2019).

Products: Carcass, raw meat (including offal), tissue, milk and other fluids and excretions of animals. Only raw and heat-treated products are assessed in this document. Products of animal origin that underwent processing (salting, pickling, smoking, etc.) are not included in the assessment.

Reservoir host: The habitat in which the virus normally survives (see Maintenance host) and multiplies (see Amplifying host) without requiring repeat introduction from another species. Possible reservoir hosts include humans and wild or domestic animal species.

Reverse zoonosis: Spread of infectious disease from human to animal (OIE, 2015).

SARS-CoV-2: Name of the virus causing coronavirus disease 2019 (COVID-19).

SARS-related coronavirus (SARSr-CoV): Virus species belonging to the subgenus *Sarbecovirus*, genus *Betacoronavirus*, including SARS-CoV, SARS-CoV-2 and SARS-related coronaviruses of Rhinolophus bats, masked palm civets, racoon dogs and pangolins.

Spillover: Transmission of a virus from its original animal host species to another animal species or a human.

Susceptible animals: Animals that can be infected by SARS-CoV-2, shed virus or harbour it in their tissues after efficient virus replication, regardless of showing clinical signs or not.

Traditional market: A market where food is sold, including items such as fresh produce, dry foods, raw and preserved animal products. This may include the selling of live animals or fresh animal products, and slaughtering of animals may happen on the premises.

Wild animal: A terrestrial or aquatic animal that is not domesticated (antonym of "Livestock"), lives independent of direct human supervision and control, and whose phenotype is not significantly affected by human selection (OIE, 2019).

Wild birds: Wild, migratory and aquatic birds.

Wildlife: Captive wild animals and wild animals having a phenotype unaffected by human selection and living independently of direct human supervision or control (OIE, 2019).

ANNEX 1

Figures illustrating the key steps that would be required if exposure to an animal or animal product infected or contaminated with SARS-CoV-2 were to pose a risk to humans or animals

FIGURE 1

Key steps required to expose humans or animals to SARS-CoV-2 from livestock, wildlife or aquatic animals, or their products

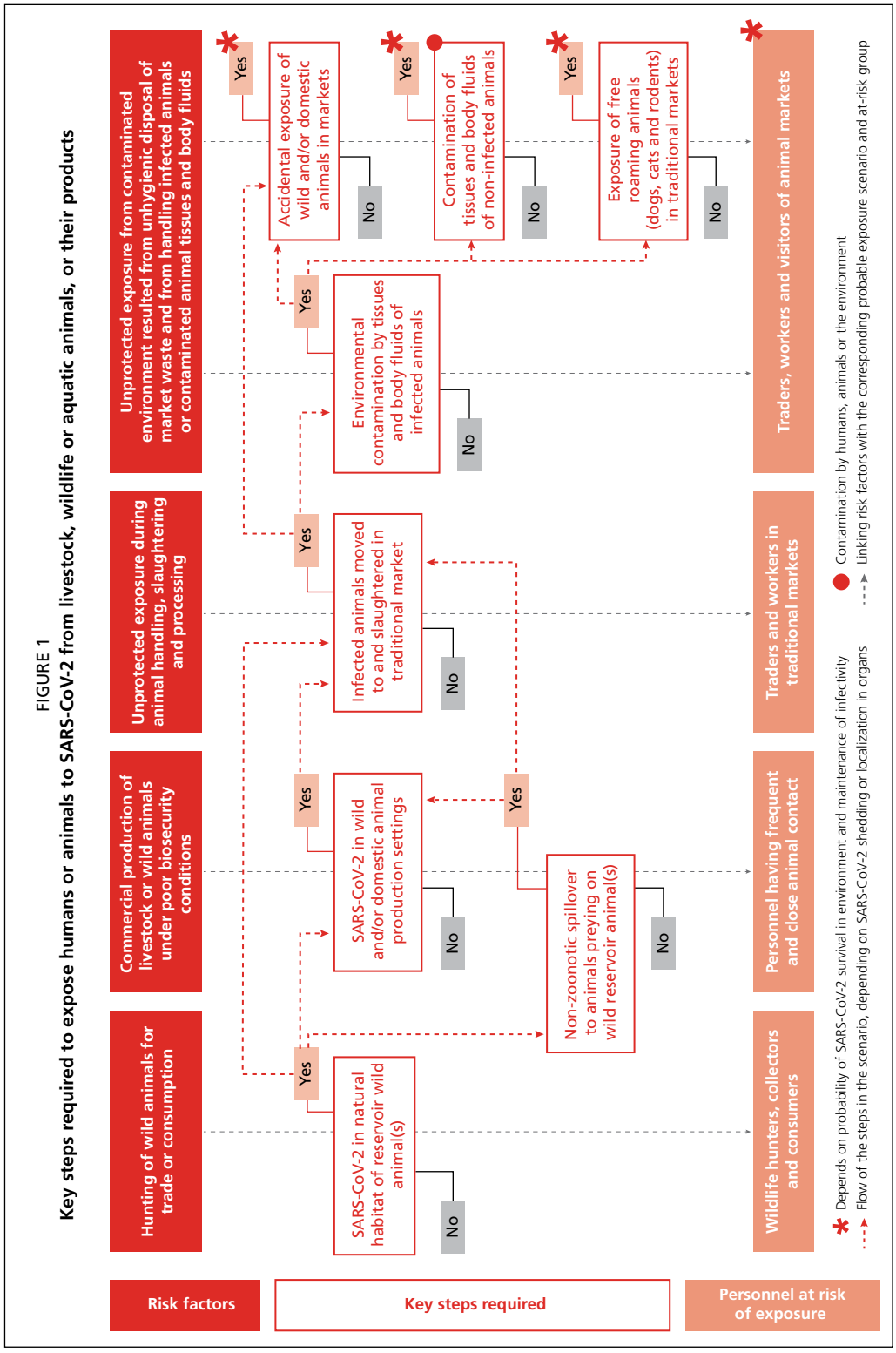
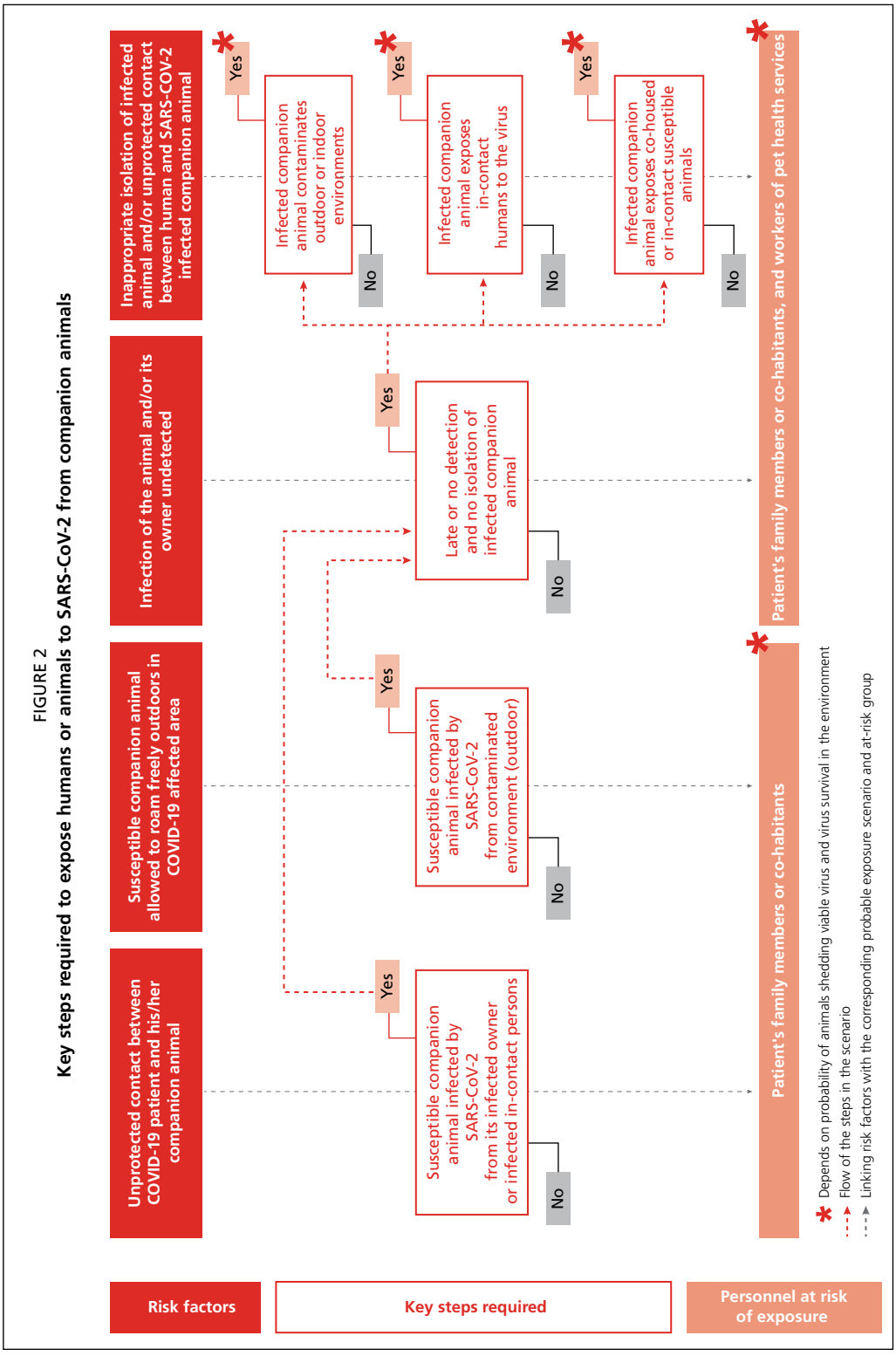


FIGURE 2

Key steps required to expose humans or animals to SARS-CoV-2 from companion animals



ANNEX 2

Information and evidence considered for assessing likelihood levels for each risk question

RISK QUESTION 1:
What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of wild animals or their products?

Assessment of likelihoods for exposure considered the following information and evidence (quotes or summaries of papers or publications are given below):

1. Drivers and barriers of emerging zoonoses

- Wild animal trade presents particular risks in the context of zoonotic spillover, because it involves movement of animals away from their natural range, where historical human exposure might have led to some build-up of immunity. Such trade, by definition, brings live animals and animal products into close proximity with people engaged in commerce and consumption/use, whether as food, pets, medicinal ingredients or for other purposes. It also typically leads to species of different origin, wild and domesticated, captive or free-living being in proximity along transport routes and in markets. Animal-to-animal, species-to-species and wildlife-to-human transmission is therefore greatly facilitated by such trade (TRAFFIC, 2020).
- Hunters, marketers, consumers and other actors in the food chain have either direct or indirect contact with animals as they are traded. Other wild and domestic animals can be temporarily exposed in parts of the market/value chain, and wild scavengers, rodents or dogs in market areas consume waste from slaughtered animals. Combined data from publications suggest that billions of direct and indirect contacts annually among wildlife, humans, and domestic animals result from legal and illegal wildlife hunting and trade and other activities such as eco-tourism (Karesh *et al.*, 2005).
- Emerging infectious diseases (EIDs) of wildlife origin can be classified into the following three groups: EIDs associated with mixing of wild and domestic populations living in proximity of one another; EIDs directly related to human intervention, resulting in translocation of either host or pathogen; and EIDs without evident involvement of domestic animals or humans (Cupertino *et al.*, 2020).

- Emerging diseases usually originate from reservoirs of infection in other host species (Haydon *et al.*, 2002). Reservoirs of infection can be ecologically complicated structures comprising one or more interacting populations or species (Viana *et al.*, 2014).
- Spillover, including successful human infection, may result from a complex interplay of factors that allow pathogens to overcome a series of barriers; these factors include reservoir host distribution and density, pathogen prevalence, release from reservoir host, survival in environment, human exposure, molecular compatibility, and replication and dissemination cycle completed (Plowright *et al.*, 2017).
- Reservoir hosts must be infected and, in most cases, shed virus in order for spillover to occur. However, direct consumption or handling of raw tissues may exclude the need for shedding (Plowright *et al.*, 2015).
- Shrinking wildlife habitat and reduced access to their food sources following expanding urban and suburban land use have brought wildlife and humans into conflict. Human encroachment into wildlife habitat and increased demand for of wildlife meat have led to: more legal and illegal translocation of wild animals and their products; more contact between humans and domestic animals, and wildlife (as domestic animals follow humans into these new environments); the development of wildlife-associated and captive wildlife industries; and more intensive management of selected wild species. All these factors increase the potential for dramatically altering the frequency, duration, and intensity of many interfaces, including those among wildlife species and other free-living or captive wildlife, domestic animals and humans (Rhyan and Sparker, 2010).

2. Coronavirus host range, with emphasis on *betacoronaviruses*

- Molecular analysis has shown that bats contribute to the evolution and dissemination of *alphacoronaviruses* and *betacoronaviruses* while birds do so for gammacoronaviruses and deltacoronaviruses (Woo *et al.*, 2012).
- Within the *Betacoronavirus* genus, five subgenera (*Embecovirus, Hibecovirus, Merbecovirus, Nobecovirus,* and *Sarbecovirus*) are recognized. However, only *betacoronaviruses* of subgenera *Sarbecovirus, Merbecovirus, Nobecovirus* and *Hibecovirus* have been detected in bats so far. Given that several *betacoronaviruses* from the subgenus *Embecovirus* have been discovered in rodents, it was speculated that rodent CoVs may be the ancestors of currently circulating viruses belonging to this subgenus. *Embecovirus* consists of different viral species which include HCoV-OC43 and HKU1, mouse hepatitis virus, porcine hemagglutinating encephalomyelitis virus, in addition to equine, rabbit, camel, bovine, antelope-derived animal CoVs. *Sarbecovirus* includes SARS-CoV, SARSr-CoV of bats (*Rhinolophus*) and palm civet. *Merbecovirus* includes MERS-CoV and some bat-derived viruses. *Hibecovirus* and *Nobecovirus* include CoVs detected in bats (Decaro and Lorusso, 2020).
- Ribonucleic acid (RNA) of *betacoronaviruses* has been detected in some wild birds in Brazil, namely owls (*Megascops choliba* and *Asio clamator*), hawk (*Rupornis magnirostris*), vulture (*Coragyps atratus*), great kiskadees (*Pitangus sulphuratus*) and the family *Cotingidae*, including *Pyroderus scutatus* (Durães-Carvalho *et al.*, 2015). It is noteworthy that these species reportedly prey on bats (*see evidence in '8. Animals*

preying on potential SARS-CoV-2 reservoir or intermediate hosts' below), and some of them prey on rodents.

- Some *alpha-* and *betacoronaviruses* showed a wide host range within the same family of a given order of mammals. For instance, within the family *Camelidae*, dromedaries are confirmed as the natural reservoir host, while Bactrian camels, llamas and alpacas are also susceptible to MERS-CoV infection (David *et al.*, 2018; Reusken *et al.*, 2016; Lau *et al.*, 2020); within the family *Felidae*, domestic cats as well as medium size and big wild cats are all susceptible to feline coronavirus (Kennedy *et al.*, 2002) and SARS-CoV-2 has been detected in both domestic cats and big cats (tiger and lion) in captivity exposed to humans with and without COVID-19 symptoms (OIE, 2020b); within the family *Mustelidae*, mink (Rijksoverheid, 2020b) and ferrets (Shi *et al.*, 2020) were susceptible to SARS-CoV-2 infection in natural and experimental settings; different species of old world monkeys were susceptible to SARS-CoV-2 infection in experimental settings (Lu *et al.*, 2020), lastly, domestic dogs and wild *Canidae* are all susceptible to canine coronavirus (Wang *et al.*, 2006),

3. Environmental stability of SARS-CoV-2

- SARS-COV-2, like other SARSr-CoV, appears to be relatively stable. This has implications for contamination of and persistence in the environment and on fomites (OIE, 2020c).
- In the presence of protein substance, SARS-CoV-2 viability was shown to be preserved during the whole duration of the experiment (96 hours) on polystyrene plastic, aluminium and glass at 45-55 percent relative humidity and temperature 19-21 °C (Pastorino *et al.*, 2020).
- Air samples collected from the isolation rooms of three COVID-19 patients tested negative for SARS-CoV-2 RNA (Ong *et al.*, 2020).
- Air samples from intensive care units (ICU) and general wards (GW) with COVID-19 patients were 35.0 percent and 12.5 percent positive for SARS-CoV-2, respectively. Furthermore, SARS-CoV-2 was widely distributed on computer mice (ICU 6/8, 75 percent; GW 1/5, 20 percent), followed by trash cans (ICU 3/5, 60 percent; GW 0/8), sickbed handrails (ICU 6/14, 42.9 percent; GW 0/12), and doorknobs (GW 1/12, 8.3 percent), and in 100 percent of samples collected from the floor of a pharmacy that no COVID-19 patients had accessed (Guo *et al.*, 2020). These findings suggest similar heavy environmental contamination in places where SARS-CoV-2 infected humans or animals are present.
- SARS-CoV-2 remained viable in aerosols throughout the duration of an experiment (3 hours), plastic (72 hours), stainless steel (72 hours), copper (4 hours) and cardboard (24 hours), and the estimated median half-life of the virus is approximately 5.6 hours on stainless steel and 6.8 hours on plastic (van Doremalen *et al.*, 2020).
- SARS-CoV-2 RNA has been detected in four out of nine inhalable dust samples taken at different locations in two infected mink farms in the Netherlands; the samples were collected once a week, over three weeks (i.e. with one week intervals). RNA was only detected in samples collected in the first rounds, i.e. 10 and 13 days after onset of clinical signs in minks in the first and second farm, respectively (Oreshkova *et al.*, 2020).

- SARS-CoV-2 RNA was detected in one of five secondary-treated wastewater samples (before chlorination) in Yamanashi Prefecture, Japan with a concentration of 2.4 × 103 copies/L (Haramoto *et al.*, 2020).
- Out of 78 wastewater samples collected from 38 districts across Pakistan including three from drains of COVID-19 infected areas and one from a COVID 19 quarantine centre drainage, 21 samples (27 percent) from 13 districts resulted COVID-19 positive on RT-qPCR (Sharif *et al.*, 2020).
- SARS-CoV-2 is extremely stable in a wide range of pH values (pH 3–10) at room temperature. At 4 °C there was only around a 0.7 log-unit reduction of SARS-CoV-2 infectious titre. However, on day 14 of incubated tissue culture, virus inactivation was reduced to 5 minutes at 70 °C. At room temperature (22 °C) and with a relative humidity of around 65 percent, infectious virus could be recovered: from printing and tissue paper for up to 3 hours; treated wood and cloth for up to 2 days; treated smooth surfaces like glass and banknotes for up to 4 days; and stainless steel, plastic and outer layers of a surgical masks for up to 7 days (Chin *et al.*, 2020).

4. Natural and experimental infection of wildlife with SARS-CoV-2 and closely clustered SARS-CoV-related viruses

- Full-length genome sequences were obtained from five patients early in the COVID-19 outbreak. The five SARS-CoV-2 sequences are almost identical but share only 79.6 percent sequence identity to SARS-CoV. However, SARS-CoV-2 is 96 percent identical at the whole-genome level to a *Betacoronavirus* (RaTG13) of intermediate horseshoe bat (*Rhinolophus affinis*) (Zhou *et al.*,2020a), suggesting a probable zoonotic origin of COVID-19 (Del Rio and Malani, 2020).
- Although SARS-CoV-2 uses the ACE2 receptor, five out six critical amino acid residues in RBD were different between SARS-CoV-2 and SARS-CoV; the same five amino acid residues were instead identical to those of pangolin SARSr-CoVs and, in turn, only one of these residues was identical to those of BatCoV RaTG13 although the latter shows the highest nucleotide sequence identity with SARS-CoV-2 along the whole genome. Thus, it is tempting to speculate that the SARS-CoV-2 RBD region might have originated from a recent recombination event in pangolins or that SARS-CoV-2 and SARSr-CoVs of pangolins represent the result of coincidental evolution (Andersen *et al.*, 2020).
- A novel pangolin coronavirus, a SARS-CoV-related CoV, has been identified in specimens from lung, intestine, blood and scales of Malayan pangolins (*Manis javanica*) seized during anti-smuggling operations in southern China. SARS-CoV-2 has 85.5–92.4 percent sequence similarity with the novel pangolin coronavirus genomes obtained from six specimens, representing two sub-lineages of SARS-CoV-related viruses in the phylogenetic tree, one of which is very closely related to SARS-CoV-2 (Lam *et al.*, 2020a).
- SARS-CoV-2 exhibits 97.4 percent amino acid similarity to the novel pangolin coronavirus in the RBD. Both viruses possess identical amino acids at the five critical residues of the RBD, whereas the *betacoronavirus* (RaTG13) isolated from the intermediate horseshoe bat (*Rhinolophus affinis*) only shares 89.2 percent amino acid similarity with SARS-CoV-2 in the RBD (Lam *et al.*, 2020a).

- Egyptian fruit bats (*Rousettus aegyptiacus*), of the family *Pteropodidae*, showed susceptibility to SARS-CoV-2 after experimental infection and viral RNA could be detected from oral and faecal swabs. The inoculated bats were able to transmit the virus to co-housed naïve bats of the same species. Furthermore, the virus could be isolated from trachea and nasal epithelium of necropsied bats, whereas RNA (but no viable virus) was detected in lungs, lung associated lymphatic tissue, heart, skin, duodenum and adrenal gland (Schlottau *et al.*, 2020).
- Intestinal organoid cultures derived from horseshoe bats (*Rhinolophus sinicus*) that can recapitulate bat intestinal epithelium showed high susceptibility to SARS-CoV-2 infection and sustained robust viral replication (Zhou *et al.*, 2020b), however another study concluded that SARS-CoV-2 cannot replicate in kidney cells of the same bat species (Chu *et al.*, 2020).
- Ferrets, of the family *Mustelidae*, showed susceptibility to SARS-CoV-2 after experimental infection and viral RNA could be detected, mainly from the upper respiratory tract and poorly from rectal swabs (Shi *et al.*, 2020; Richard *et al.*, 2020; Ryan *et al.*, 2020). Other experimental infection studies on ferrets reported similar findings as well as transmission of infection to co-housed naïve ferrets and detection of the RNA in muscle, lungs, cerebrum, cerebellum, trachea, lymph node, skin and adrenal gland in some inoculated ferrets (Schlottau *et al.*, 2020), as well as nasal wash, saliva, urine, faeces, nasal turbinate, trachea, lungs, and intestine (Kim *et al.*, 2020). Re-challenged ferrets were shown to be fully protected from acute lung pathology (Ryan *et al.*, 2020).
- Syrian hamsters (*Mesocricetus auratus*), of the family *Cricetidae*, showed susceptibility to SARS-CoV-2 after experimental infection, and viral RNA could be detected from both the upper and lower respiratory tract and the intestinal tract. Experimentally infected animals transmitted the virus to co-housed naïve animals of the same species in experimental conditions (Chan *et al.*, 2020; Sia *et al.*, 2020).
- Tree shrews (*Tupaia belangeri chinensis*), of the family *Tupaiidae*, showed susceptibility to SARS-CoV-2 after experimental infection, and viral RNA could be detected in blood as well as nasal, throat and rectal swabs. Furthermore, viral RNA was detected post-mortem in lung, oesophagus, liver, spleen, pancreas, uterus, kidney, small intestine, hilar lymph node and brain of some experimentally infected animals (Zhao *et al.*, 2020a).
- Of the non-human primates of family *Cercopithecidae*, Rhesus macaques (Macaca mulatta) (Deng *et al.*, 2020a; Bao *et al.*, 2020; Singh *et al.*, 2020) and Baboons (*Papio hamadryas*) (Singh *et al.*, 2020) showed susceptibility to SARS-CoV-2 after experimental infection, whereas of the family *Callitrichidae*, common marmosets (*Callithrix jacchus*) were susceptible to infection as well but with mild pathology (Singh *et al.*, 2020).
- Experimentally infected cynomolgus macaques (*Macaca fascicularis*), of the family *Cercopithecidae*, excreted SARS-CoV-2 from their nose and throat in the absence of clinical signs; viral RNA could be isolated post mortem from nasal cavity, trachea, bronchi and lung lobes, and to a lesser extent from ileum and tracheo-bronchial lymph nodes, but not from blood, urinary, and cardiovascular tracts, endocrine and central nervous systems (Rockx *et al.*, 2020).

- SARS-CoV-2 RNA was detected in nasal swabs, throat swabs, anal swabs and blood from all experimentally infected old world monkeys of the family *Cercopithecidae* (*Macaca mulatta, Macaca fascicularis*) and new world monkeys of the family *Callitrichidae* (*Callithrix jacchus*). In addition, lung, oesophagus, bronchi and spleen tissues from *M. mulatta* and *M. fascicularis* tested positive for virus RNA while no viral genome was detected in any of the tissues taken from *C. jacchus* (Lu *et al.*, 2020).
- SARS-CoV-2 RNA was detected in bronco-alveolar lavage, in addition to nasal, oral and rectal swabs of experimentally infected African green monkeys (*Chlorocebus aethiops*) (Woolsey *et al.*, 2020), another study isolated replicating SARS-CoV-2 from oral, nasal, ocular and rectal swabs (Hartman *et al.*, 2020).
- Seven of eight lions and tigers at Bronx Zoo in New York, United States of America, showed signs of respiratory illness after having been in contact with a zoo employee who was asymptomatically infected with the virus or before that person developed symptoms; laboratory investigation revealed SARS-CoV-2 RNA from specimens of one tiger (USDA, 2020) and a lion (OIE, 2020d). Follow up laboratory testing of faecal specimens from the additional seven large cats, three sick tigers, three sick lions and one asymptomatic tiger identified SARS-CoV-2 RNA (WCS, 2020).
- Infection with SARS-CoV-2 has been confirmed in nine mink farms in the Netherlands; the infected minks showed disease signs, including respiratory symptoms (Rijksoverheid, 2020c). Asymptomatic infection in mink in a farm in Denmark has been detected as part of the investigation following confirmed SARS-CoV-2 infection in one of the farm workers (OIE, 2020b).
- Serum samples collected from wild species in China between November 2019 and March 2020 including camel (31), fox (89), mink (91), alpaca (10), ferret (2), bamboo rat (8), peacock (4), eagle (1), tiger (8), rhinoceros (4), pangolin (17), leopard cat (3), jackal (1), giant panda (14), masked civet (10), porcupine (2), bear (9), yellow-throated marten (4), weasel (1), red panda (3) and wild boar (1) were used for detection of SARS-CoV-2-specific antibodies using double-antigen sandwich ELISA after validating its specificity and sensitivity. No SARS-CoV2-specific antibodies were detected (Deng *et al.*, 2020b).
- SARS-CoV-2 RNA was detected in conchae, lung, throat and rectal swabs of all seven minks sampled from SARS-CoV-2 infected farms. In addition, viral RNA was detected in the liver of one, and the intestines of three animals. Spleens of all seven animals were negative for viral RNA. The viral loads were higher in the throat compared to rectal swabs (Oreshkova *et al.*, 2020).

5. Spillover of SARS-CoV and SARS-related CoVs

- Serological evidence of human exposure to bat SARS-CoVs or related viruses was reported in 2.7 percent of people pertaining to a high risk group of residents living in close proximity to bat caves in China (Wang *et al.*, 2018).
- Viruses with 99.8 percent similarity to SARS-CoV were isolated from nasal and faecal swab samples collected from Himalayan palm civets (*Paguma larvata*) and Raccoon dogs (*Nyctereutes procyonoides*) respectively, in a traditional market in China. Neutralizing antibodies were detected in 11 wildlife traders and workers in the same market (Guan *et al.*, 2003).

- An investigation conducted by public health authorities in Guangdong Province, China, compared seroprevalence of SARS-CoV IgG antibody in animal traders, working in live animal markets, with that of people in control groups. The results indicated that 13 percent of animal traders had IgG antibodies against SARS-CoV even though none of them had been diagnosed with SARS, compared to 1–3 percent of people in three control groups (CDC, 2003).
- RNA of SARS-CoV-related virus was detected in four cats (*Felis catus*), three red foxes (*Vulpes vulpes*) and one Lesser rice field rat (*Rattus losea*) sampled at a live animal market in Guangzhou, China (Wang *et al.*, 2005) and from palm civets (*Paguma larvata*) and raccoon dogs (*Nyctereutes procyonoides*) of another market in Guangzhou, China (Kan *et al.*, 2005). However, it is unknown whether these animals were reservoirs of the virus in their natural habitat or accidently acquired infection in animal markets.
- Spillover of SARS-CoV-2 from infected farmed mink to humans has been evidenced in the Netherlands (Rijksoverheid, 2020a).

6. Epidemiological animal-related data on SARS-CoV-2 available to date

- Current evidence suggests it is likely that the virus responsible for COVID-19 had an animal source. Yet, to date, there is not enough scientific evidence to identify that source or to explain the route of transmission from any animal source to humans (OIE, 2020b).
- While the specific mechanism of SARS-CoV-2 emergence has not been definitively identified, at some point or over time interactions occurred that allowed for cross – and perhaps multiple – species pathogen transmission (OIE, 2020e).
- As the ancestral animal origin of the COVID-19 virus is unknown at present, the risk of reintroduction into previously affected areas and maintenance in animal populations must be constantly considered (WHO, 2020c).
- Available evidence on SARS-CoV-2 and previous experience with other coronaviruses (MERS-CoV and SARS-CoV) and other respiratory viruses (e.g. avian influenza) suggest that there may be zoonotic transmission associated with SARS-CoV-2 (WHO, 2020d).
- Out of 41 early COVID-19 human cases, 27 reported exposure to the Huanan Seafood Wholesale Market in Wuhan City (Huang *et al.*, 2020a), where various livestock and wildlife species and their products were on display (Li *et al.*, 2020a) including fish, carcasses, meat and live wild animals from a variety of species including hedgehogs, badgers, snakes and birds (turtledoves; *Streptopelia turtur*) (Wu *et al.*, 2020a). However, some of the early human cases had no epidemiological link with this market and it is not certain whether this market can be confirmed as the site of initial zoonotic spillover. The precise location/s where these patients might have been exposed to SARS-CoV-2 in such a huge market (around 50 000 square meters with around 1 000 shops) is unknown. This history of exposure does not necessarily imply these patients were exposed to the virus from infected animals. Such markets or the animals or animal products within them cannot be directly incriminated as the source of infection since human-to-human infection may have occurred where the market could have simply acted as a congregation point.

- A molecular study of SARS-CoV-2 S glycoprotein features, polybasic furin cleavage and prefusion conformation and recombination analysis led to the hypothesis that a recombination event between ancestors of human SARS-CoV-2, or a closely related bat-SARSr-CoV, and ancestors of pangolin-CoV lineage b strains, is the likely origin of the currently circulating pandemic strain (Tagliamonte *et al.*, 2020).
- Analysis of the expression of ACE2 and furin in human oral mucosa led to speculation that SARS-CoV-2 could effectively invade human oral mucosal cells though two possible routes: binding to the ACE2 receptor and fusion with cell membrane activated by furin protease (Zhong *et al.*, 2020).
- Experimental infection of three mosquito species, *Aedes aegypti, Aedes. albopictus* and *Culex quinquefasciatus*, through intrathoracic inoculation with SARS-CoV-2 revealed that infectious viruses could only be recovered from mosquitoes collected within two hours of inoculation. Waning of infectious titres was rapid, suggesting that mosquitoes of the genera Aedes and Culex are refractory to SARS-CoV-2 (Huang *et al.*, 2020b).
- The assessment of risk of exposure to SARS-CoV-2 from animals, does not only address the likelihood of animals being infected and shedding virus or harbouring virus in raw tissues, but also considers that carcasses and raw meat (including offal) of non-infected or non-susceptible animals in unhygienic conditions in areas likely to be contaminated with SARS-CoV-2 by animals or handlers, may be a source for hand contamination, same as for other products and fomites, with the potential for subsequent hand to the nose/mouth/eye infection of humans.

7. Affinity of ACE2 receptors found in wild animal species to bind SARS-CoV-2 RBD

Note: Studies investigating ACE2 receptors found in different animal species and their potential to bind SARS-CoV-2 RBD require confirmation by ex-vivo cell or experimental animal infection studies and evidence from comprehensive epidemiological and animal pathology studies. In addition to ACE2, SARS-CoV-2 is suggested to invade host cells via binding of the spike protein to CD147, another receptor found on host cells, thereby mediating the viral invasion (Wang *et al.*, 2020).

- In silico analysis of the receptor binding domains may give a first indication of potential susceptibility. However, discrepancies have been observed in which animals with predicted high binding ACE2 sequences have had poor susceptibility and limited infection. It has also been suggested that host binding involved different receptors in some animals and these animals have become infected despite predicted low binding ACE2 sequences (Koopmans, personal communication, April 2020).
- The expression of ACE2 varies across animal ages, cell types, tissues and species which may lead to discrepancies between SARS-CoV-2 susceptibility gleaned from experimental infections or laboratory experiments and predictions made on the basis of the ACE2-based binding score (Damas *et al.* 2020).
- In brief, there is consensus among different analyses that ACE2 of several studied species of wild felines, apes, old world monkeys, hamsters, wild species of the family *Bovidae* are able to effectively bind SARS-CoV-2 RBD, whereas ACE2 of rodents of

the family *Muridae* and most of the studied wild birds were consistently reported as having poor binding affinity. It is worth mentioning that contradictory conclusions among several studies for the same species have been observed, for example bat, pangolin, ferret and some wild bird species.

The data published to date for more than 500 domestic and wild animal species is summarized in the supplementary tables.

- Infection of HeLa cells expressing different ACE2 orthologs of lynx (*Lynx canadensis*), monkey (*Macaca nemestrina*), pangolin (*Manis javanica*), mustela (*Mustela ermine*), black flying fox (*Pteropus alecto*), crocodile (*Crocodylus porosus*), viper snake (*Protobothrops mucrosquamatus*), mouse (*Mus musculus*) and civet (*Paguma larvata*) with SARS-CoV-2 pseudovirus demonstrated efficient pseudovirus entry in the cells expressing ACE2 for these species, with the exception of crocodile, viper snake, mouse and civet (Qiu *et al.*, 2020a).
- Infection of HEK293T cells expressing full-length cDNA fragments of ACE2 from Chinese horseshoe bat (*Rhinolophus sinicus*) and Malayan pangolin (*Manis javanica*) by SARS-CoV-2 demonstrated efficient virus entry, whereas none of the ACE2 proteins of greater horseshoe bat (*Rhinolophus ferrumequinum*), mainland tiger snake (*Notechis scutatus)*, Rhesus monkey (*Macaca mulatta*) and house mouse (*Mus musculus*) rendered SARS-CoV-2 entry (Tang *et al.*, 2020).

8. Animals preying on potential SARS-CoV-2 reservoir or intermediate hosts (i.e. predators of bats and pangolins)

- Predators often acquire multi-host pathogens from their prey (Johnson *et al.*, 2006).
- Big and medium-size wild cats are reportedly the most common mammals to prey on pangolins (Coggins, 2020; Pietersen *et al.*, 2014; Jakl, 2019).
- Monkeys of the species *Saimiri oerstedii* (Boinski and Timm, 1985), *Saimiri sciureu* (Souza *et al.*, 1997), *Scimmia cappuccina* (Milano and Monteiro-Filho, 2009) and *Cercopithecus* (Tapanes *et al.*, 2016) are reported to prey on bats.
- Raccoons (McAlpine *et al.*, 2011; Sparks *et al.*, 2003), weasels (Quick, 1951; Zhigalin, 2019), otters (Forman *et al.*, 2004) and mink (Goodpaster and Hoffmeister, 1950) are the non-primate mammals reported to prey on bats.
- Owls, of nocturnal birds (Ibanez *et al.*, 1992), diurnal wild birds belonging to *Accipitriformes* and *Falconiformes* (Mikula *et al.*, 2016), and other wild birds such as American crows (*Corvus brachyrhynchos*) (Lefevre, 2005), blue-crowned motmots (*Momotus momota*) momota) (Chacón-Madrigal and Barrantes, 2004), Great Kiskadees (*Pitangus sulphuratus*) (Fischer *et al.*, 2010) and those belonging to the family *Cotingidae*, including *Pyroderus scutatus* (Pizo *et al.*, 2002) have been reported to prey on bats.
- Giant centipedes are reported to prey on bats (Srbek-Araujo *et al.*, 2012; de Noronha *et al.*, 2015). They can perform two actions that most other bat predators cannot: they climb cave ceilings to catch and eat flying or perching bats and they are able to subdue bats substantially heavier than themselves (Molinari *et al.*, 2005).
- Spiders preying on bats have been reported mainly in web-building spiders and, to a lesser extent, in hunting spiders. Spiders were observed to actively attack, kill and eat captured bats (Nyffeler and Knörnschild, 2013).

- A total of 20 species of snakes have been recorded as predators of bats in the neotropical region (Esbérard and Vrcibradic, 2007), furthermore many studies reported snakes as one of the common predators of bats.

9. Wildlife movement, captive breeding/ranching and wild meat consumption

- In sub-Saharan Africa, wild meat of over 500 different species is consumed. In southern and Southeast Asia, more than 400 wild terrestrial animal species are hunted for food. In South America almost 200 species of wild meat are consumed. Globally, the majority of wild meat harvest in terms of numbers and biomass are from mammalian species (Cawthorn and Hoffman, 2015).
- Primates, pangolins, antelopes, rodents and reptiles, among many other taxa, are commonly involved in the wild meat trade and consumed worldwide, particularly across Latin America, Asia and Africa (Chaber *et al.*, 2020).
- A significant proportion of trade in some wildlife species is not directly sourced from free-living wild populations, but instead derived from breeding and keeping in captivity in controlled conditions. In terms of disease transmission, wildlife "farms" have potential to provide controlled sanitary conditions that reduce certain risks. Such farms are key locations where people and wild animals are often in close proximity over significant periods of time. Sanitary control measures in wildlife farms are not always ideal, supplementary stocking of additional wild-sourced individuals may be part of the production system and exposure (animal-to-animal or animal-to-person) along trade routes and at market level remains a significant risk irrespective of whether the original point of origin is wild-sourcing or farming (TRAFFIC, 2020).
- Legal wildlife farming (captive wildlife) in Southeast Asia facilitates the 'laundering' of illegally wild caught animals and exacerbates the challenges associated with enforcement of wildlife trade bans, in addition to helping legalize the consumption of wildlife products (Gray *et al.*, 2018).
- Southern China harbours abundant wildlife while also undergoing land use change and overexploitation of natural resources. This leads to intensified human–animal interactions that facilitate the emergence of zoonotic diseases (Li *et al.*, 2020b).
- Rearing domestic animals in free-range settings is reported from southern China, providing opportunity for interactions between domestic and wild animals (Li *et al.*, 2020b).
- There are nearly 8 000 tigers kept in captivity in four major 'tiger farming' countries namely China, Viet Nam, Thailand and Lao People's Democratic Republic (EIA, 2017). In China, rhesus monkeys are raised in farms (He *et al.*, 2017), while farms holding both tigers and bears are reported in Lao People's Democratic Republic (Livingstone *et al.*, 2018).
- Approximately 12.32 percent (n=1 574) kinds of traditional medicine resources are derived from animals, consequently many wild animals commonly used in traditional medicines have declined and market demand exceeds their availability (Liu *et al.*, 2016).
- Increased urbanization and a growing middle class in Asia have increased demand for wild meat. Wild meat may be seen as a luxury and a status item (Lee *et al.*, 2014).
- Bat guano is sold as fertilizer in several countries, including Thailand, Indonesia, Mexico, Cuba, and Jamaica. The practice of collecting and harvesting bat guano may pose

a considerable health risk because guano miners are exposed to bat-borne pathogens (Wacharapluesadee *et al.*, 2013).

- Bats have the ability to migrate, with some species covering 2 000 km (Hutterer *et al.*, 2005). In southern China, bats may be served in some restaurants, sold in local markets (Zhang *et al.*, 2009), and, occasionally hunted and consumed in rural areas (Li *et al.*, 2020b).
- Census of the wildlife farms in 12 pilot provinces in Viet Nam in 2014, documented 4 099 operating wildlife farms. The most common types of farms were for rearing of porcupines (1 535 farms/25 385 animals), oriental rat-snakes (675 farms/112 023 animals) and deer (524 farms/3 452 animals) while the highest in overall numbers of individuals were those farming crocodiles, softshell turtles, and oriental snakes, accounting for 618 540 individuals (62.1 percent) of all animals. Most wildlife farms (95 percent) kept 1-2 wild animal species. There were only 17 farms that kept more than 10 species. Seventy percent of the wildlife farms also had domestic animals, with dogs (53.7 percent), chickens (37.1 percent), cats (9 percent) and pigs (9 percent) being the most common. Of those farms, 54 percent kept 1-2 livestock or domestic species while 14.3 percent kept 3-4 livestock or domestic species (FAO, 2015).
- Approximately 85 percent of fur animals are not hunted or trapped, but farmed. Of these, mink accounts for 80 percent of international trade in fur skins. Other animals include fox, chinchilla, nutria, Finn raccoon, and sable (Fur Europe, 2015).
- Pangolins are the world's most trafficked mammal, and China is identified as the most common destination for international trafficking of live pangolin and scales (Heinrich *et al.*, 2017).
- International trade in pangolins reported to the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) has primarily involved the Asian species and trade in skins and scales. In the year 2000, zero export quotas were established for Asian pangolins, and there has been comparatively little trade reported since. The Democratic Republic of the Congo, Nigeria, Togo and Uganda have exported around 1 000 live pangolins[3] including *M. gigantea, M. tricuspis* and *M. tetradactyla* to China, Lao People's Democratic Republic and Viet Nam for the purpose of captive breeding. Most of this trade involved *M. tricuspis* (Challender and Waterman, 2017).
- Most international trafficking of pangolins (including their by-products) occurs within Asia, both in terms of number of incidents and quantity. Of the ten countries and territories involved in the most trafficking incidents, seven were in Asia; namely China, Hong Kong SAR, Indonesia, Lao People's Democratic Republic, Malaysia, Thailand and Viet Nam. The remaining three were Germany, Nigeria, and the United States of America (Heinrich *et al.*, 2017).
- Pangolins are used as food and for traditional medicinal purposes (Zhang and Yin, 2014) as it is believed that their meat, blood and bile (Li *et al.*, 2020a) as well as scales (Challender, 2011) are remedies for some diseases. Between 2007 and 2016, Indonesia, Malaysia and Viet Nam were the major source countries for whole pangolins, while major source countries for smuggled pangolin scales were Cameroon, Myanmar and Nigeria (Xu *et al.* 2016).

[3] The report does not specify the timeframe related to this statement.

- Some traditional markets have been reported to sell domestic cats, snakes, raccoons and other wildlife (Hui, 2006).

RISK QUESTION 2: What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of livestock or their products?

Assessment of likelihoods for exposure considered the following information and evidence (quotes or summaries of papers or publications are given below):

- Considerations 1., 2. and 3. in risk question 1.
- There is consensus among different analyses that ACE2 of several studied species of domestic cattle, buffalo, sheep, goat and rabbit are likely to bind SARS-CoV-2 RBD, whereas those of chicken, duck, geese and ostrich cannot. The results related to other livestock such as camel species, horse and donkey are contradictory.
  The data published to date for more than 500 domestic and wild animal species is summarized in the supplementary tables.
- Infection of HeLa cells expressing ACE2 orthologs of cattle (*Bos taurus*), goat (*Capra hircus*), horse (*Equus caballus*), rabbit (*Oryctolagus cuniculus*), swine (*Sus scrofa*) and chicken (*Gallus gallus*) with SARS-CoV-2 pseudovirus demonstrated efficient pseudovirus entry in the cells expressing ACE2 of these species, except for chicken (Qiu *et al.*, 2020a).
- Infection of HEK293T cells expressing full-length cDNA fragments of ACE2 from pig (*Sus scrofa*) and goat (*Capra hircus*) with SARS-CoV-2 demonstrated efficient virus entry, whereas ACE2 protein of chicken (*Gallus gallus*) did not render SARS-CoV-2 entry (Tang *et al.*, 2020).
- Intranasal experimental infection of pigs and chickens (Shi *et al.*, 2020; Schlottau *et al.*, 2020), and ducks (Shi *et al.*, 2020) with SARS-CoV-2 failed to cause clinical signs, RNA oropharyngeal and rectal shedding, seroconversion or virus transmission to co-housed naïve animals of the same species, indicating that these animals are not susceptible to SARS-CoV-2.
- Experimentally infected chickens, turkeys, ducks, quail and geese demonstrated no susceptibility to SARS-CoV-2 as no antibodies were detected 14 days post challenge, and no virus RNA was detected in any cloacal or oropharyngeal swab collected 2, 4 and 7 days post challenge (Suarez *et al.*, 2020).
- Early COVID-19 patients may have had contact with wild animals in the market, but none recalled exposure to live poultry (Wu *et al.*, 2020a).
- Serum samples collected from domestic livestock in China between November 2019 and March 2020 including pig (187), cow (107), sheep (133), horse (18), chicken (153), duck (153), and goose (25) were used for detection of SARS-CoV-2-specific antibodies using double-antigen sandwich ELISA after validating its specificity and sensitivity. No SARS-CoV2-specific antibodies were detected (Deng *et al.*, 2020b).

RISK QUESTION 3:
What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with or handling of companion animal species or handling or consumption of dog and cat products?

Assessment of likelihoods for exposure considered the following information and evidence (quotes or summaries of papers or publications are given below):

- Considerations mentioned risk question 1 and risk question 2.
- Two out of fifteen dogs from households with confirmed human cases of COVID-19 in Hong Kong SAR were found to be infected using quantitative real-time PCR, serology, sequencing the viral genome, and, in one dog, virus isolation. SARS-CoV-2 RNA was detected in a 17-year-old neutered male Pomeranian from five nasal swabs collected over a 13-day period. A 2.5 year-old male German Shepherd dog was found to have SARS-CoV-2 RNA on two occasions and virus was isolated from nasal and oral swabs. Both dogs mounted antibody responses, detected using plaque reduction neutralization assay. Genetic sequences of the viruses from the two dogs were identical to the virus detected in the human cases. The animals remained asymptomatic during quarantine (Sit *et al.*, 2020).
- A pet German Shepherd dog from a household with known COVID-19 affected inhabitants was sampled for respiratory illness. Clinical signs included severe lethargy. The dog tested positive for SARS-CoV-2 based upon molecular testing (PCR and sequencing). Virus neutralizing antibodies were detected in follow-up samples from the affected dog as well as a second pet German Shepherd dog in the same household who showed no clinical signs and tested negative by PCR (OIE, 2020b).
- A companion cat of a COVID-19 patient in Hong Kong SAR tested positive for SARS-CoV-2 RNA on 30 March 2020 in all nasal, oral and rectal swab samples. The cat did not exhibit any specific clinical signs. Follow-up oral and nasal swab samples taken on 1 April 2020 continued to test positive (OIE, 2020f).
- Infection of domestic cats with SARS-CoV-2 has been reported in Germany (1), Spain (1), Belgium (1) Russia (1) and France (2) (OIE, 2020b).
- The United States Centers for Disease Control and Prevention (US CDC) and the United States Department of Agriculture's (USDA) National Veterinary Services Laboratories (NVSL) announced the first confirmed cases of SARS-CoV-2 infection in two pet cats in the United States of America. Both cats had mild respiratory illness and were expected to make a full recovery. A veterinarian tested the first cat after it showed mild respiratory signs. No individuals in the household were confirmed to be ill with COVID-19. The virus may have been transmitted to this cat by mildly ill or asymptomatic household members or through contact with an infected person outside its home. Samples from the second cat were taken after it showed signs of respiratory illness. The owner of the cat tested positive for COVID-19 prior to the cat showing signs. Another cat in the household has shown no signs of illness (CDC & USDA, 2020).

- Experimental infection of cats with SARS-CoV-2 resulted in efficient replication and shedding of infectious virus with spread to co-housed naïve cats in some groups (Shi *et al.*, 2020; Halfmann *et al.*, 2020; Bosco-Lauth *et al.*, 2020), whereas SARS-CoV-2 replicated poorly in experimentally infected dogs and the virus did not spread to co-housed naïve dogs (Shi *et al.*, 2020; Bosco-Lauth *et al.*, 2020).
- SARS-CoV-2 has been isolated from nasal turbinate, trachea and oesophagus of experimentally infected cats, but not from mediastinal lymph nodes, lungs, liver, spleen, kidney, small intestine, uterus and olfactory bulb (Bosco-Lauth *et al.*, 2020). Another experimental infection study isolated the virus from nasal turbinate, soft palates, tonsils, trachea and lungs, but not from small intestine (Shi *et al.*, 2020).
- SARS-CoV-2 experimentally infected cats developed a robust neutralizing antibody response that prevented re-infection to a second viral challenge (Bosco-Lauth *et al.*, 2020).
- Out of 102 cat sera collected in Wuhan City, China after the COVID-19 outbreak, 15 (14.7 percent) were found positive for the RBD of SARS-CoV-2 by indirect ELISA. Among the positive samples, 11 sera collected from stray cats, companion cats in contact with COVID-19 patients, and cats in pet hospitals had SARS-CoV-2 neutralizing antibodies with a titre ranging from 1/20 to 1/1080 (Zhang *et al.*, 2020).
- There is consensus among different analyses that ACE2 of domestic cat are likely to bind SARS-CoV-2 RBD, whereas those related to dogs are contradictory.

  The data published to date for more than 500 domestic and wild animal species is summarized in the supplementary tables.
- Infection of HeLa cells expressing different ACE2 orthologs of domestic cats (*Felis catus*) and dogs (*Canis lupus familiaris*) with SARS-CoV-2 pseudovirus, demonstrated efficient pseudovirus entry (Qiu *et al.*, 2020a). Infection of HEK293T cells expressing full-length cDNA fragments of ACE2 from domestic cat (*Felis catus*) and dog (*Canis lupus familiaris*) with SARS-CoV-2, demonstrated efficient virus entry (Tang *et al.*, 2020).
- Free roaming cat species (*Felis catus*) are reported to prey on bats (Delpietro *et al.*, 1994; Scrimgeour *et al.*, 2012; Roch, 2015), in particular in sparse urban and rural areas, where free-ranging cats occur more frequently (Ancillottoa *et al.*, 2013).
- Hamsters (Eberli *et al.*, 2011) and ferrets (Castanheira de Matos and Morrisey, 2006), as pets, and hedgehogs, chinchillas and prairie dogs, as exotic mammalian pets, were all responsible for zoonotic disease transmission (Chomel *et al.*, 2007).
- In most industrialized countries, pets are an integral part of households, sharing human lifestyles, bedrooms and beds. The estimated percentage of pet owners who allow dogs and cats on their beds is 14–62 percent, while other close contact such as licking, kissing and sniffing is also observed (Chomel and Sun, 2011).
- Dogs in Southeast Asia (Sorenson and Matsuoka, 2019; Li *et al.*, 2017; ACPA, 2013) and Africa (Ukamaka *et al.*, 2020), and cats in Southeast Asia (ACPA, 2013) are slaughtered for the purpose of meat consumption. Furthermore, it has been reported that thousands of dog farms exist mostly in rural areas in South Korea for the purpose of dog meat consumption (Czajkowski, 2014).
- There is no current evidence of dogs or cats playing a role in the spread of COVID-19 (OIE, 2020b).

RISK QUESTION 4:
What is the likelihood of exposure of humans or animals to SARS-CoV-2 in COVID-19 affected areas through contact with, handling or consumption of aquatic animals or their products?

Assessment of likelihoods for exposure considered the following information and evidence (quotes or summaries of papers or publications are given below):

- Considerations 1, 2 and 3 under risk question 1.
- There is consensus among different analyses that ACE2 of several studied species of cetaceans are likely to bind SARS-CoV-2 RBD, whereas the results related to most other aquatic mammals are contradictory. Analysis of key amino acid residues of 82 fish and four amphibian species supported the hypothesis of very low affinity to bind SARS-CoV-2 RBD, only one study supported the hypothesis of a binding energy favourable for SARS-CoV-2 infection for ten fish species, contradicting, however, results of another study.
  The data published to date for more than 500 domestic and wild animal species is summarized in the supplementary tables.
- Infection of HeLa cells expressing ACE2 orthologs of golden crucian (*Carassius auratus*) with SARS-CoV-2 pseudovirus demonstrated inefficient pseudovirus entry (Qiu *et al.*, 2020a).
- Incidences of marine mammals for sale, both cooked and uncooked, in fish markets in China have been reported by media, and opportunistic hunting of marine mammals is practiced in Asia either for trade or consumption (Porter and Lai, 2017).
- *Alphacoronaviruses* have been isolated from harbour seals (*Phoca vitulina*) that died in 1987 (Bossart and Schwartz, 1990).
- *Gammacoronavirus* has been identified in liver specimens of beluga whale (*Delphinapterus leucas*) that died from pulmonary disease and acute liver failure (Mihindukulasuriya *et al.*, 2008).
- Surveillance for coronaviruses in respiratory and faecal swabs of marine mammals, namely; California sea lion (*Zalophus californianus*), Harbour seal (*Phoca vitulina*) and indo-pacific bottlenose dolphin (*Tursiops aduncus)* has detected *gammacoronavirus* in faecal swabs of indo-pacific bottlenose dolphin (Woo *et al.*, 2014).
- None of the *betacoronaviruses* have been detected in fish. However, unclassified coronaviruses were detected in freshwater cyprinid species such as white bream (*Blicca bjoerkna*) and fathead minnow (*Pimephales promelas*). However, not all of these viruses are officially classified as coronaviruses by the International Committee of Taxonomy of Viruses (Schütze, 2016).

- Few cases of human disease from contact with marine mammals have been reported, among them occupationally acquired severe illnesses included tuberculosis, leptospirosis and brucellosis (Hunt *et al.*, 2008).
- Aquatic food animals and their products, like any other surface, may potentially become contaminated with SARS-CoV-2, especially when handled by people who are infected with the virus. Nevertheless, with proper food handling and sanitation, the likelihood of contamination of aquatic animals or their products with SARS-CoV-2 should be negligible (Bondad-Reantaso, *et al.*, 2020).
- 14 fish and 14 frog species were observed to prey on bats. However, this is thought to be a very rare and opportunistic behaviour (Mikula, 2015).

ANNEX 3

Progressive approach to investigate SARS-CoV-2 wildlife reservoir(s) or intermediate host(s)

	Objective	Targeted animal species	Sites
Phase 1	Screening to detect SARS-CoV-2 RNA and anti-SARS-CoV-2 antibodies.	Animals classified as high priority (see Annex 4).	Sites of highest animal-animal or human-animal interface intensity (traditional markets and live animal congregation sites/collection points prior to reaching a market) in COVID-19 affected areas, with priority given to Southeast Asia and sub-Saharan Africa for identification of reservoir hosts.
Phase 2		Wildlife species of same family of animals testing positive in phase 1.	
Phase 3		Predators of the wildlife species testing positive in phases 1 and 2 (if applicable), priority to mammalian predators.	
Phase 4	Narrow down investigation to exclude hypothesis of accidental infection.	Species tested positive in phases 1, 2 and 3.	High risk areas (highest density of target species - natural habitat and captive farming).

ANNEX 4

Prioritization of animal species[4] to be investigated further through field surveillance

	Natural infection confirmed*	Experimental infection**		Infectious virus produced in tissue explant	ACE2 affinity to bind RBD	Same family of a susceptible animal	Mammalian predator of susceptible animal	Score	Priority
		High susceptibility	Poor or no susceptibility						
Malayan tiger	☑	☐	☐	☐	☑	☑	☑	13	High
Caracal	☐	☐	☐	☐	☐	☑	☑	4	Medium
Rhesus macaque	☐	☑	☐	☐	☑	☑	☐	11	High
Ferret	☐	☑	☐	☐	☑	☐	☐	9	High
Mink	☑	☐	☐	☐	☐	☑	☑	10	High
Pangolin	☑	☐	☐	☐	☑	☐	☐	9	High
Cat	☑	☑	☐	☐	☑	☑	☑	19	High
Dog	☑	☐	☑	☐	☑	☐	☑	5	Medium
Cattle	☐	☐	☐	☐	☑	☐	☐	3	Low
Pig	☐	☐	☑	☐	☑	☐	☐	-3	Negligible
	☐	☐	☐	☐	☐	☐	☐	0	
	☐	☐	☐	☐	☐	☐	☐	0	

* Natural infection refers to SARS-CoV-2 and other closely related viruses.

** Susceptibility after experimental infection refers to evidenced replication and shedding of infectious virus rather than positive PCR test results alone.

Scoring method used to prioritize animal species for sampling in SARS-CoV-2 field investigation and research studies:

Six criteria are ranked from highest to lowest priority with the following scoring:

- Natural infection: score 6.
- Susceptibility to infection (experimental): high susceptibility (score 6), poor or no susceptibility (score -6).
- Infectious virus produced in tissue explants: score 4.

[4] The filled cells serve as example; relevant check boxes have been ticked according to the information available at the time of publication.

- ACE2 affinity to bind SARS-CoV RBD: score 3. The relevant checkbox is selected if at least one study predicted a likely binding affinity of ACE2 of the given species (regardless if other studies predicted contradictory results).
- Animal belongs to same family of susceptible species: score 2.
- Animal being a mammalian predator of susceptible species: score 2.

Prioritization:

- High: sum of scores ≥6
- Medium: sum of scores = 4 or 5
- Low: sum of scores = 2 or 3
- Negligible: sum of scores <2

FAO TECHNICAL PAPERS
FAO ANIMAL PRODUCTION AND HEALTH PAPERS

1 Animal breeding: selected articles from the *World Animal Review*, 1977 (En, Fr, Es, Zh)
2 Eradication of hog cholera and African swine fever, 1976 (En, Fr, Es)
3 Insecticides and application equipment for tsetse control, 1977 (En, Fr)
4 New feed resources, 1977 (En/Fr/Es)
5 Bibliography of the criollo cattle of the Americas, 1977 (En/Es)
6 Mediterranean cattle and sheep in crossbreeding, 1977 (En, Fr)
7 The environmental impact of tsetse control operations, 1977 (En, Fr)
7 Rev.1 The environmental impact of tsetse control operations, 1980 (En, Fr)
8 Declining breeds of Mediterranean sheep, 1978 (En, Fr)
9 Slaughterhouse and slaughterslab design and construction, 1978 (En, Fr, Es)
10 Treating straw for animal feeding, 1978 (En, Fr, Es, Zh)
11 Packaging, storage and distribution of processed milk, 1978 (En)
12 Ruminant nutrition: selected articles from the *World Animal Review*, 1978 (En, Fr, Es, Zh)
13 Buffalo reproduction and artificial insemination, 1979 (En*)
14 The African trypanosomiases, 1979 (En, Fr)
15 Establishment of dairy training centres, 1979 (En)
16 Open yard housing for young cattle, 1981 (Ar, En, Fr, Es)
17 Prolific tropical sheep, 1980 (En, Fr, Es)
18 Feed from animal wastes: state of knowledge, 1980 (En, Zh)
19 East Coast fever and related tick-borne diseases, 1980 (En)
20/1 Trypanotolerant livestock in West and Central Africa – Vol. 1. General study, 1980 (En, Fr)
20/2 Trypanotolerant livestock in West and Central Africa – Vol. 2. Country studies, 1980 (En, Fr)
20/3 Le bétail trypanotolérant en Afrique occidentale et centrale – Vol. 3. Bilan d'une décennie, 1988 (Fr)
21 Guideline for dairy accounting, 1980 (En)
22 Recursos genéticos animales en América Latina, 1981 (Es)
23 Disease control in semen and embryos, 1981 (En, Fr, Es, Zh)
24 Animal genetic resources – conservation and management, 1981 (En, Zh)
25 Reproductive efficiency in cattle, 1982 (En, Fr, Es, Zh)
26 Camels and camel milk, 1982 (En)
27 Deer farming, 1982 (En)
28 Feed from animal wastes: feeding manual, 1982 (En, Zh)
29 Echinococcosis/hydatidosis surveillance, prevention and control: FAO/UNEP/WHO guidelines, 1982 (En)
30 Sheep and goat breeds of India, 1982 (En)
31 Hormones in animal production, 1982 (En)
32 Crop residues and agro-industrial by-products in animal feeding, 1982 (En/Fr)
33 Haemorrhagic septicaemia, 1982 (En, Fr)
34 Breeding plans for ruminant livestock in the tropics, 1982 (En, Fr, Es)
35 Off-tastes in raw and reconstituted milk, 1983 (Ar, En, Fr, Es)
36 Ticks and tick-borne diseases: selected articles from the *World Animal Review*, 1983 (En, Fr, Es)
37 African animal trypanosomiasis: selected articles from the *World Animal Review*, 1983 (En, Fr)
38 Diagnosis and vaccination for the control of brucellosis in the Near East, 1982 (Ar, En)
39 Solar energy in small-scale milk collection and processing, 1983 (En, Fr)
40 Intensive sheep production in the Near East, 1983 (Ar, En)

41 Integrating crops and livestock in West Africa, 1983 (En, Fr)
42 Animal energy in agriculture in Africa and Asia, 1984 (En/Fr, Es)
43 Olive by-products for animal feed, 1985 (Ar, En, Fr, Es)
44/1 Animal genetic resources conservation by management, data banks and training, 1984 (En)
44/2 Animal genetic resources: cryogenic storage of germplasm and molecular engineering, 1984 (En)
45 Maintenance systems for the dairy plant, 1984 (En)
46 Livestock breeds of China, 1984 (En, Fr, Es)
47 Réfrigération du lait à la ferme et organisation des transports, 1985 (Fr)
48 La fromagerie et les variétés de fromages du bassin méditerranéen, 1985 (Fr)
49 Manual for the slaughter of small ruminants in developing countries, 1985 (En)
50 Better utilization of crop residues and by-products in animal feeding: research guidelines – 1. State of knowledge, 1985 (En)
50/2 Better utilization of crop residues and by-products in animal feeding: research guidelines – 2. A practical manual for research workers, 1986 (En)
51 Dried salted meats: charque and carne-de-sol, 1985 (En)
52 Small-scale sausage production, 1985 (En)
53 Slaughterhouse cleaning and sanitation, 1985 (En)
54 Small ruminants in the Near East – Vol. I. Selected papers presented for the Expert Consultation on Small Ruminant Research and Development in the Near East (Tunis, 1985), 1987 (En)
55 Small ruminants in the Near East – Vol. II. Selected articles from *World Animal Review* 1972-1986, 1987 (Ar, En)
56 Sheep and goats in Pakistan, 1985 (En)
57 The Awassi sheep with special reference to the improved dairy type, 1985 (En)
58 Small ruminant production in the developing countries, 1986 (En)
59/1 Animal genetic resources data banks – 1. Computer systems study for regional data banks, 1986 (En)
59/2 Animal genetic resources data banks – 2. Descriptor lists for cattle, buffalo, pigs, sheep and goats, 1986 (En, Fr, Es)
59/3 Animal genetic resources data banks – 3. Descriptor lists for poultry, 1986 (En, Fr, Es)
60 Sheep and goats in Turkey, 1986 (En)
61 The Przewalski horse and restoration to its natural habitat in Mongolia, 1986 (En)
62 Milk and dairy products: production and processing costs, 1988 (En, Fr, Es)
63 Proceedings of the FAO expert consultation on the substitution of imported concentrate feeds in animal production systems in developing countries, 1987 (En, Zh)
64 Poultry management and diseases in the Near East, 1987 (Ar)
65 Animal genetic resources of the USSR, 1989 (En)
66 Animal genetic resources – strategies for improved use and conservation, 1987 (En)
67/1 Trypanotolerant cattle and livestock development in West and Central Africa – Vol. I, 1987 (En)
67/2 Trypanotolerant cattle and livestock development in West and Central Africa – Vol. II, 1987 (En)
68 Crossbreeding *Bos indicus* and *Bos taurus* for milk production in the tropics, 1987 (En)
69 Village milk processing, 1988 (En, Fr, Es)
70 Sheep and goat meat production in the humid tropics of West Africa, 1989 (En/Fr)
71 The development of village-based sheep production in West Africa, 1988 (Ar, En, Fr, Es) (Published as Training manual for extension workers, M/S5840E)
72 Sugarcane as feed, 1988 (En/Es)
73 Standard design for small-scale modular slaughterhouses, 1988 (En)

74 Small ruminants in the Near East – Vol. III. North Africa, 1989 (En)
75 The eradication of ticks, 1989 (En/Es)
76 Ex situ cryoconservation of genomes and genes of endangered cattle breeds by means of modern biotechnological methods, 1989 (En)
77 Training manual for embryo transfer in cattle, 1991 (En)
78 Milking, milk production hygiene and udder health, 1989 (En)
79 Manual of simple methods of meat preservation, 1990 (En)
80 Animal genetic resources – a global programme for sustainable development, 1990 (En)
81 Veterinary diagnostic bacteriology – a manual of laboratory procedures of selected diseases of livestock, 1990 (En, Fr)
82 Reproduction in camels – a review, 1990 (En)
83 Training manual on artificial insemination in sheep and goats, 1991 (En, Fr)
84 Training manual for embryo transfer in water buffaloes, 1991 (En)
85 The technology of traditional milk products in developing countries, 1990 (En)
86 Feeding dairy cows in the tropics, 1991 (En)
87 Manual for the production of anthrax and blackleg vaccines, 1991 (En, Fr)
88 Small ruminant production and the small ruminant genetic resource in tropical Africa, 1991 (En)
89 Manual for the production of Marek's disease, Gumboro disease and inactivated Newcastle disease vaccines, 1991 (En, Fr)
90 Application of biotechnology to nutrition of animals in developing countries, 1991 (En, Fr)
91 Guidelines for slaughtering, meat cutting and further processing, 1991 (En, Fr)
92 Manual on meat cold store operation and management, 1991 (En, Es)
93 Utilization of renewable energy sources and energy-saving technologies by small-scale milk plants and collection centres, 1992 (En)
94 Proceedings of the FAO expert consultation on the genetic aspects of trypanotolerance, 1992 (En)
95 Roots, tubers, plantains and bananas in animal feeding, 1992 (En)
96 Distribution and impact of helminth diseases of livestock in developing countries, 1992 (En)
97 Construction and operation of medium-sized abattoirs in developing countries, 1992 (En)
98 Small-scale poultry processing, 1992 (Ar, En)
99 In situ conservation of livestock and poultry, 1992 (En)
100 Programme for the control of African animal trypanosomiasis and related development, 1992 (En)
101 Genetic improvement of hair sheep in the tropics, 1992 (En)
102 Legume trees and other fodder trees as protein sources for livestock, 1992 (En)
103 Improving sheep reproduction in the Near East, 1992 (Ar)
104 The management of global animal genetic resources, 1992 (En)
105 Sustainable livestock production in the mountain agro-ecosystem of Nepal, 1992 (En)
106 Sustainable animal production from small farm systems in South-East Asia, 1993 (En)
107 Strategies for sustainable animal agriculture in developing countries, 1993 (En, Fr)
108 Evaluation of breeds and crosses of domestic animals, 1993 (En)
109 Bovine spongiform encephalopathy, 1993 (Ar, En)
110 L'amélioration génétique des bovins en Afrique de l'Ouest, 1993 (Fr)
111 L'utilización sostenible de hembras F1 en la producción del ganado lechero tropical, 1993 (Es)
112 Physiologie de la reproduction des bovins trypanotolérants, 1993 (Fr)
113 The technology of making cheese from camel milk (*Camelus dromedarius*), 2001 (En, Fr)
114 Food losses due to non-infectious and production diseases in developing countries, 1993 (En)
115 Manuel de formation pratique pour la transplantation embryonnaire chez la brebis et la chèvre, 1993 (Fr, Es)

116 Quality control of veterinary vaccines in developing countries, 1993 (En)
117 L'hygiène dans l'industrie alimentaire, 1993 – Les produits et l'aplication de l'hygiène, 1993 (Fr)
118 Quality control testing of rinderpest cell culture vaccine, 1994 (En)
119 Manual on meat inspection for developing countries, 1994 (En)
120 Manual para la instalación del pequeño matadero modular de la FAO, 1994 (Es)
121 A systematic approach to tsetse and trypanosomiasis control, 1994 (En/Fr)
122 El capibara (*Hydrochoerus hydrochaeris*) – Estado actual de su producción, 1994 (Es)
123 Edible by-products of slaughter animals, 1995 (En, Es)
124 L'approvisionnement des villes africaines en lait et produits laitiers, 1995 (Fr)
125 Veterinary education, 1995 (En)
126 Tropical animal feeding – A manual for research workers, 1995 (En)
127 World livestock production systems – Current status, issues and trends, 1996 (En)
128 Quality control testing of contagious bovine pleuropneumonia live attenuated vaccine – Standard operating procedures, 1996 (En, Fr)
129 The world without rinderpest, 1996 (En)
130 Manual de prácticas de manejo de alpacas y llamas, 1996 (Es)
131 Les perspectives de développement de la filière lait de chèvre dans le bassin méditerranéen, 1996 (Fr)
132 Feeding pigs in the tropics, 1997 (En)
133 Prevention and control of transboundary animal diseases, 1997 (En)
134 Tratamiento y utilización de residuos de origen animal, pesquero y alimenticio en la alimentación animal, 1997 (Es)
135 Roughage utilization in warm climates, 1997 (En, Fr)
136 Proceedings of the first Internet Conference on Salivarian Trypanosomes, 1997 (En)
137 Developing national emergency prevention systems for transboundary animal diseases, 1997 (En)
138 Producción de cuyes (*Cavia porcellus*), 1997 (Es)
139 Tree foliage in ruminant nutrition, 1997 (En)
140/1 Analisis de sistemas de producción animal – Tomo 1: Las bases conceptuales, 1997 (Es)
140/2 Analisis de sistemas de producción animal – Tomo 2: Las herramientas basicas, 1997 (Es)
141 Biological control of gastro-intestinal nematodes of ruminants using predacious fungi, 1998 (En)
142 Village chicken production systems in rural Africa – Household food security and gender issues, 1998 (En)
143 Agroforestería para la producción animal en América Latina, 1999 (Es)
144 Ostrich production systems, 1999 (En)
145 New technologies in the fight against transboundary animal diseases, 1999 (En)
146 El burro como animal de trabajo – Manual de capacitación, 2000 (Es)
147 Mulberry for animal production, 2001 (En)
148 Los cerdos locales en los sistemas tradicionales de producción, 2001 (Es)
149 Animal production based on crop residues – Chinese experiences, 2001 (En, Zh)
150 Pastoralism in the new millennium, 2001 (En)
151 Livestock keeping in urban areas – A review of traditional technologies based on literature and field experiences, 2001 (En)
152 Mixed crop-livestock farming – A review of traditional technologies based on literature and field experiences, 2001 (En)
153 Improved animal health for poverty reduction and sustainable livelihoods, 2002 (En)
154 Goose production, 2002 (En, Fr)
155 Agroforestería para la producción animal en América Latina – II, 2003 (Es)
156 Guidelines for coordinated human and animal brucellosis surveillance, 2003 (En)
157 Resistencia a los antiparasitarios – Estado actual con énfasis en América Latina, 2003 (Es)

158 Employment generation through small-scale dairy marketing and processing, 2003 (En)
159 Good practices in planning and management of integrated commercial poultry production in South Asia, 2003 (En)
160 Assessing quality and safety of animal feeds, 2004 (En, Zh)
161 FAO technology review: Newcastle disease, 2004 (En)
162 Uso de antimicrobianos en animales de consumo – Incidencia del desarrollo de resistencias en la salud pública, 2004 (Es)
163 HIV infections and zoonoses, 2004 (En, Fr, Es)
164 Feed supplementation blocks – Urea-molasses multinutrient blocks: simple and effective feed supplement technology for ruminant agriculture, 2007 (En)
165 Biosecurity for Highly Pathogenic Avian Influenza – Issues and options, 2008 (En, Fr, Ar, Vi)
166 International trade in wild birds, and related bird movements, in Latin America and the Caribbean, 2009 (Es[e] En[e])
167 Livestock keepers – guardians of biodiversity, 2009 (En)
168 Adding value to livestock diversity – Marketing to promote local breeds and improve livelihoods, 2010 (En, Fr, Es)
169 Good practices for biosecurity in the pig sector – Issues and options in developing and transition countries, 2010 (En, Fr, Zh, Ru** Es**)
170 La salud pública veterinaria en situaciones de desastres naturales y provocados, 2010 (Es)
171 Approaches to controlling, preventing and eliminating H5N1 HPAI in endemic countries, 2011 (En, Ar)
172 Crop residue based densified total mixed ration – A user-friendly approach to utilise food crop by-products for ruminant production, 2012 (En)
173 Balanced feeding for improving livestock productivity – Increase in milk production and nutrient use efficiency and decrease in methane emission, 2012 (En)
174 Invisible Guardians - Women manage livestock diversity, 2012 (En)
175 Enhancing animal welfare and farmer income through strategic animal feeding – Some case studies, 2013 (En)
176 Lessons from HPAI – A technical stocktaking of coutputs, outcomes, best practices and lessons learned from the fight against highly pathogenic avian influenza in Asia 2005–2011, 2013 (En)
177 Mitigation of greenhouse gas emissions in livestock production – A review of technical options for non-CO_2 emissions, 2013 (En, Es[e])
178 Африканская Чума Свиней в Российской Федерации (2007-2012), 2014 (Ru)
179 Probiotics in animal nutrition – Production, impact and regulation, 2016 (En)
180 Control of Contagious Bovine Pleuropneumonia – A policy for coordinated actions, 2018 (En)
181 Exposure of humans or animals to SARS-CoV-2 from wild, livestock,companion and aquatic animals. Qualitative exposure assessment, 2020 (En)

Availability: July 2020

Ar – Arabic
En – English
Es – Spanish
Fr – French
Pt – Portuguese
Ru – Russian
Vi – Vietnamese
Zh – Chinese

Multil – Multilingual
* Out of print
** In preparation
[e] E-publication
(En, Fr, Es) = Separate editions in English, French and Spanish
(En/Fr/Es) = Trilingual edition

The *FAO Animal production and health Papers* are available through authorized FAO Sales Agents or directly from Sales and Marketing Group, FAO, Viale delle Terme di Caracalla, 00153 Rome, Italy.

Find more publications at
http://www.fao.org/ag/againfo/resources/en/publications.html

Understanding the risk of exposure of humans or animals to SARS-CoV-2 from animals and their products is essential for containing virus spread, prioritizing research, protecting food systems, and informing national One Health investigations and mitigation measures. This Qualitative Exposure Assessment provides a comprehensive review of available scientific evidence and assessment of exposure risk from different wild or domestic animal species. Results can inform country-level risk assessment and provide the evidence base for targeted SARS-CoV-2 investigations in animals and mitigation options.

This publication provides:

I. assessment of the risk of human or animal exposure to SARS-CoV-2 through contact with, handling or consumption of wild, domestic and aquatic animal species or their products;
II. identification of current knowledge gaps regarding the zoonotic origin or animal-human spillover of SARS-CoV-2 and recommendations on priority studies;
III. summary of available evidence for SARS-CoV-2 susceptibility of different animal species;
IV. evidence-based recommendations on how to prioritize animal species for targeted field investigations or research studies;
V. recommendations for targeted One Health investigations and epidemiological, laboratory, anthropological or seasonality studies to fill critical knowledge gaps evidenced by this exposure assessment.

ISBN 978-92-5-133008-1 ISSN 0254-6019

9 789251 330081

CA9959EN/1/07.20