
CIVAS
Center for Indonesian Veterinary Analytical Studies
WEBINAR
ASLIQEWAN
Tema: COVID-19: PANGGILAN UNTUK MEMULIHKAN KESEIMBANGAN MANUSIA, BIODIVERSITAS DAN LINGKUNGAN
7 Agustus 2021

PDHI

Asosiasi Dokter Hewan Satwa Liar, Akuatik dan Hewan Eksotik Indonesia

ASLIQEWAN

Dokter Hewan Satwa Liar & Zoonosis

Yumni K G, Nur Purba P, Huda S Darusman

COVID-19: Panggilan untuk Memulihkan Keseimbangan Manusia, Biodiversitas, dan Lingkungan

7 Agustus 2021

IPB University
Bogor Indonesia

One health & Zoonosis

"roles & significances"

Huda S Darusman

Disampaikan pada Semnas "Role of one health in zoonotic disease control from wildlife", 7 Maret 2021

IPB University
Bogor Indonesia

Temu Koordinasi Pelaku Usaha dan *Stakeholder*
BKIPM, 3 Desember 2020

METODE SAMPLING DAN METODE UJI VIRUS COVID-19 PADA HASIL PERIKANAN DENGAN TEKNIK REAL TIME PCR

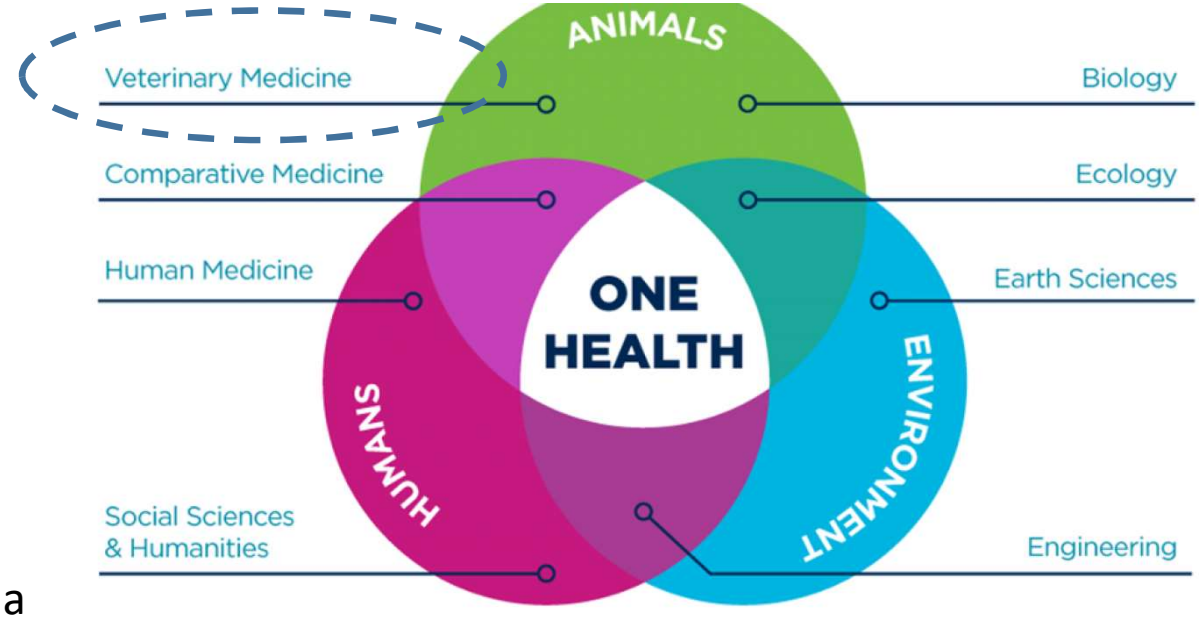
Dr Uus Saepuloh MBiomed[1], Huda S Darusman[1,2]

[1]Pusat Studi Satwa Primata, LPPM - IPB University
[2]Fakultas Kedokteran Hewan - IPB University

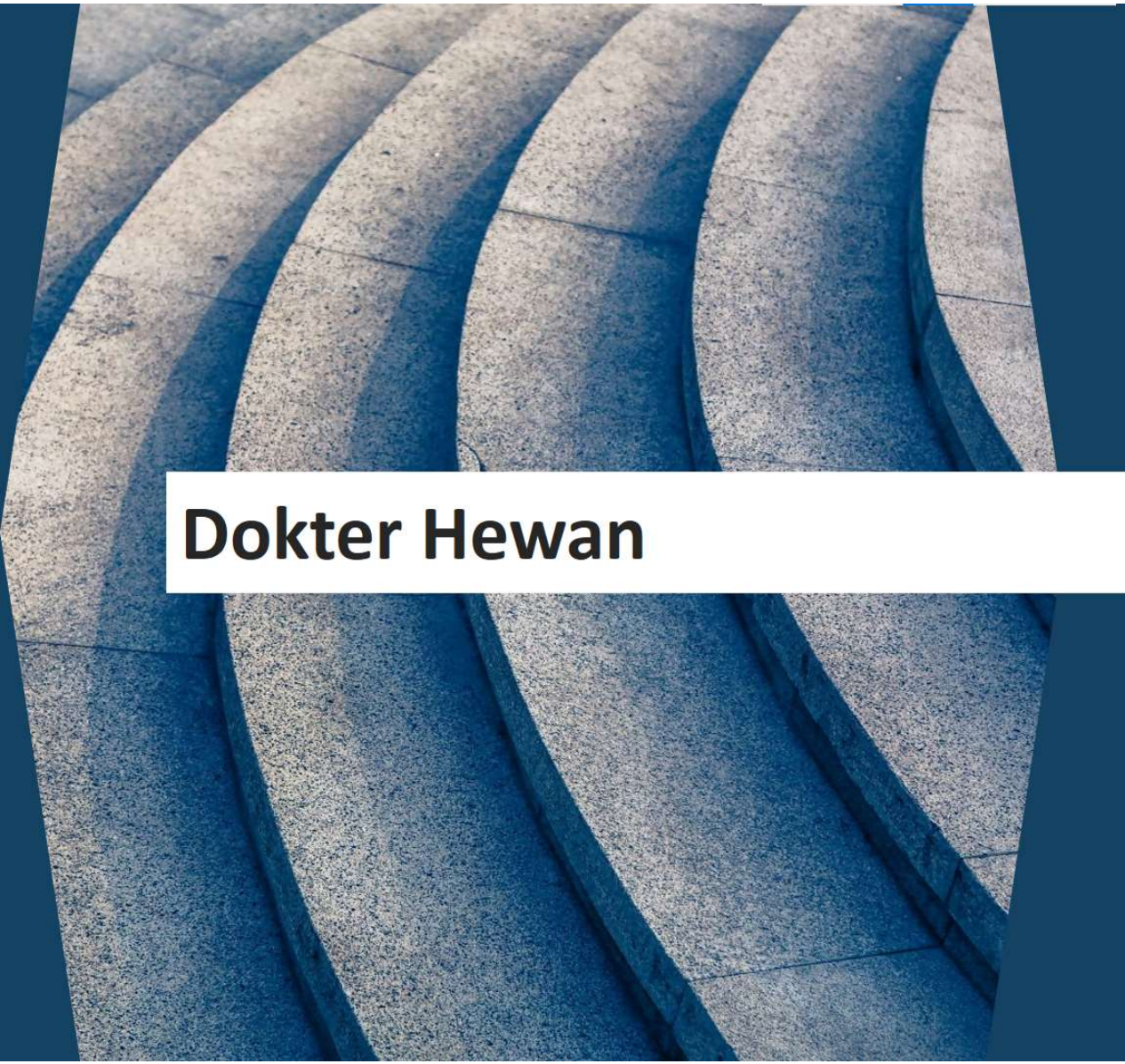
PUSAT STUDI SATWA PRIMATA
Institut Pertanian Bogor

Materi

- Prinsip utama - moto dokter hewan
- Peran global & faktual - one health frame
  - Peran kepada kesehatan hewan
  - Peran kepada kesehatan manusia
  - Peran kepada kesehatan lingkungan
- Peran terstruktur - *medic conservation*



https://ce.vetmed.ucdavis.edu/symposia-events/5th-annual-one-health-symp



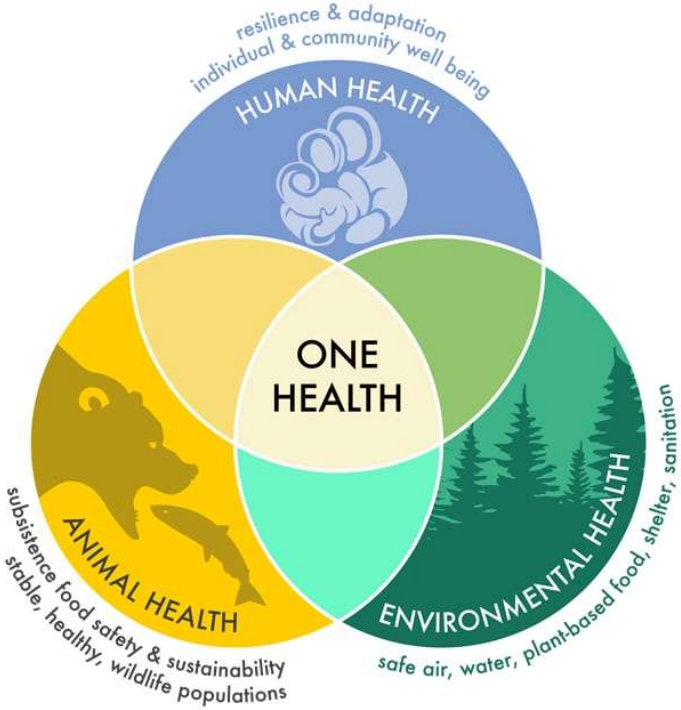
Dokter Hewan

Manusya mriga satwa sewaka

- Menyejahterakan manusia melalui hewan

Peran global & faktual

- Peran dalam kesehatan hewan
  - Satwa liar = Medik konservasi
- Peran dalam kesehatan manusia
  - Zoonosis & spillover
- Peran dalam kesehatan lingkungan
  - Toksikologi lingkungan

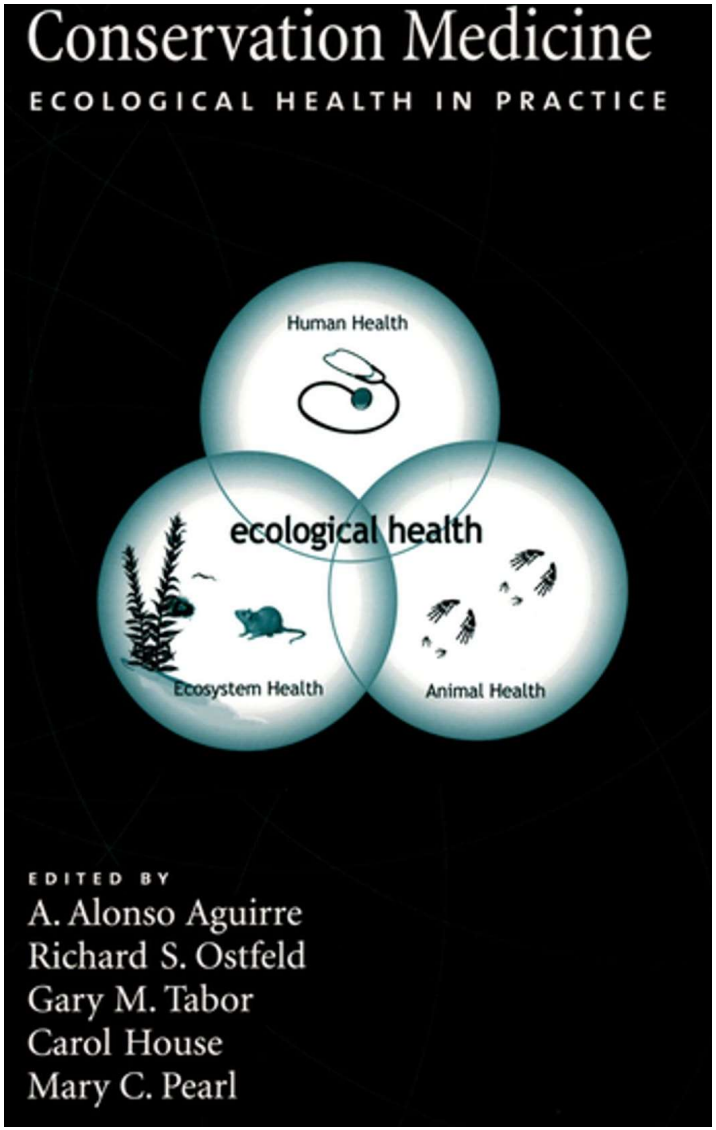


- A **collaborative, multisectoral, and transdisciplinary** approach—working at the local, regional, national, and global levels—with the goal of achieving optimal health outcomes recognizing the interconnection between people, animals, plants, and their shared environment

CDC Centers for Disease Control and Prevention
CDC 24/7: Saving Lives, Protecting People™

Conservation medicine

- An emerging, interdisciplinary field that studies the relationship between human and animal health an d environmental conditions. It is also known as **ecological medicine**, **environmental medicine**, or **medical geology (Aguire et al 2002)**



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Asosiasi Dokter Hewan Satwa Liar, Akuatik dan Hewan Eksotik Indonesia
ASLIQEWAN

UU No. 41

Tahun 2014

Medik konservasi adalah penerapan medik veteriner dalam penyelenggaraan kesehatan hewan di bidang konservasi satwa liar.

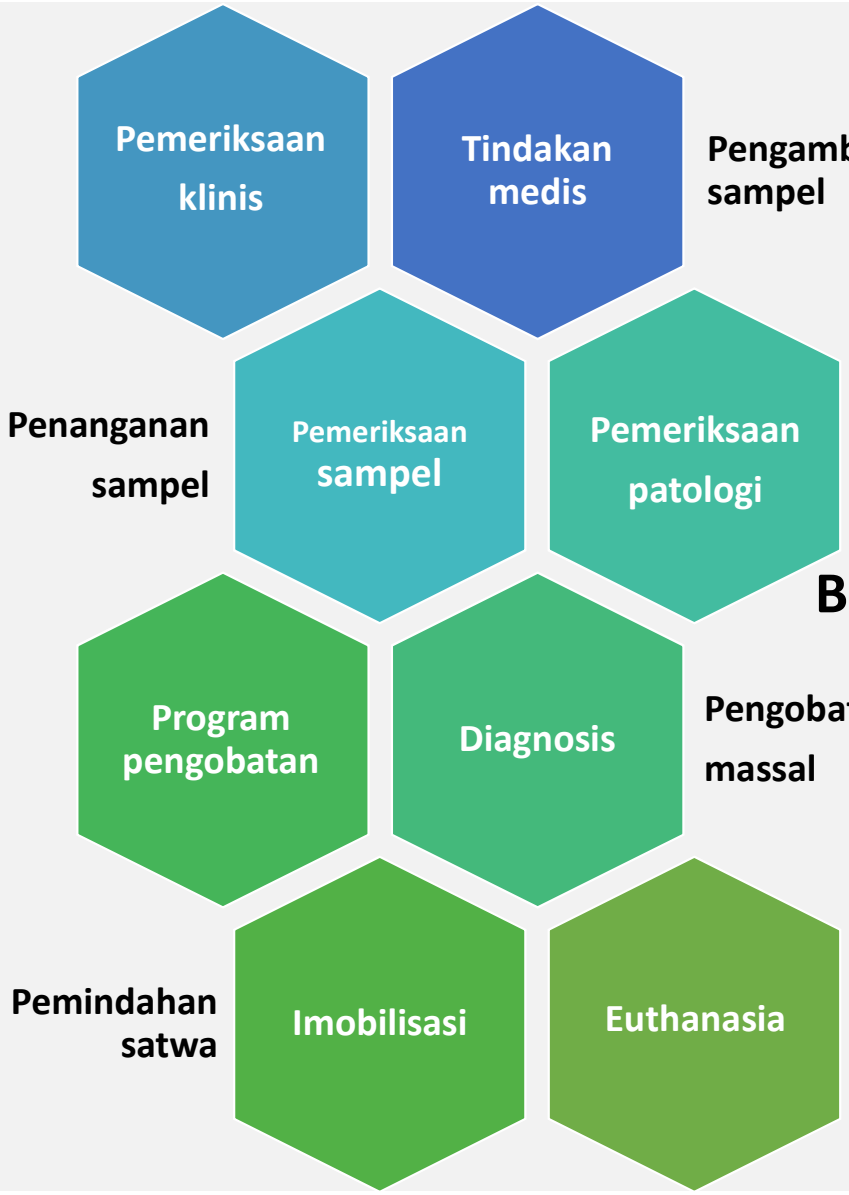
Medik Konservasi

Upaya pelestarian jenis, populasi, dan habitat satwa liar Indonesia melalui intervensi medik veteriner

Memetakan status medik konservasi dan epidemiologik satwa liar Indonesia

Mengantisipasi munculnya penyakit hewan baru yang berasal dari satwa liar Indonesia

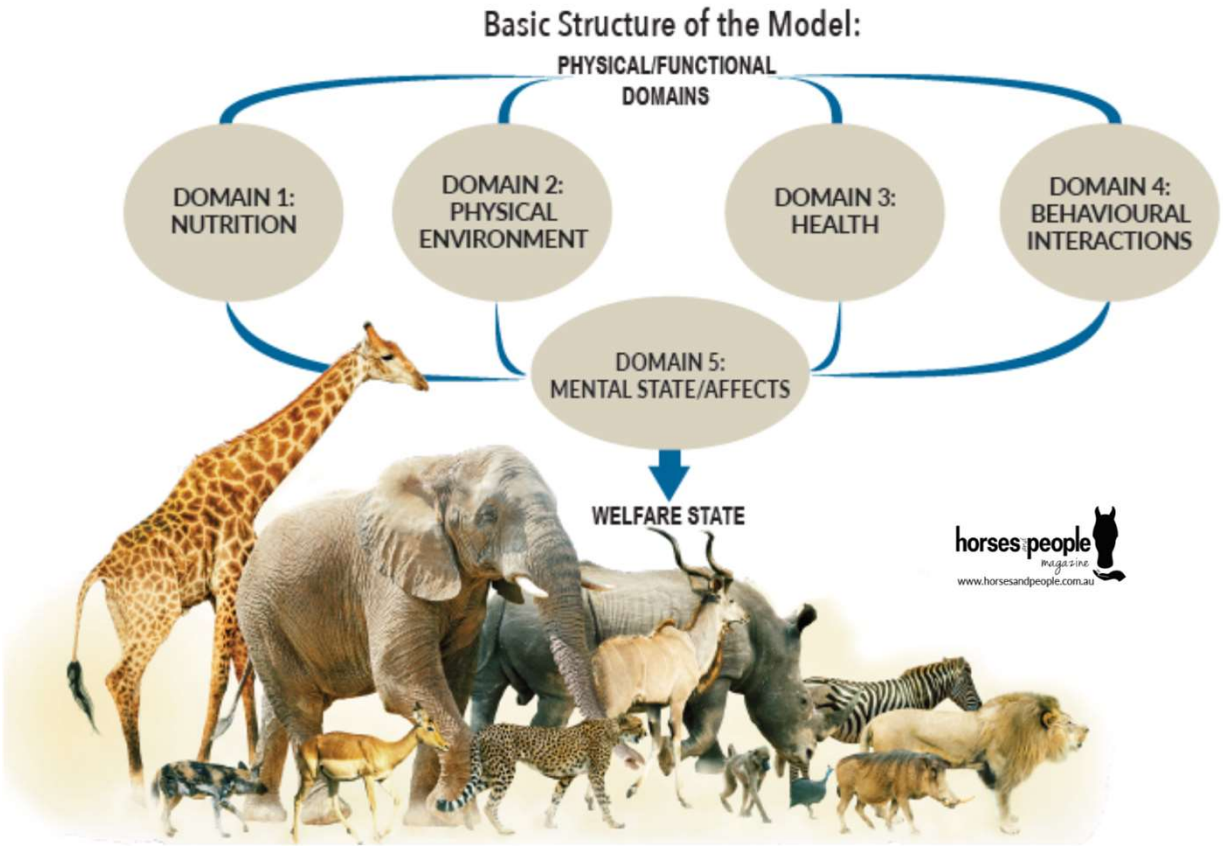
Memantapkan manajemen medik konservasi pada lembaga-lembaga konservasi



Bagaimana kerja dokter hewan satwa liar?

Bagaimana kerja dokter hewan satwa liar?

5 *Domains* (Mellor, 1994)



Peran global & faktual

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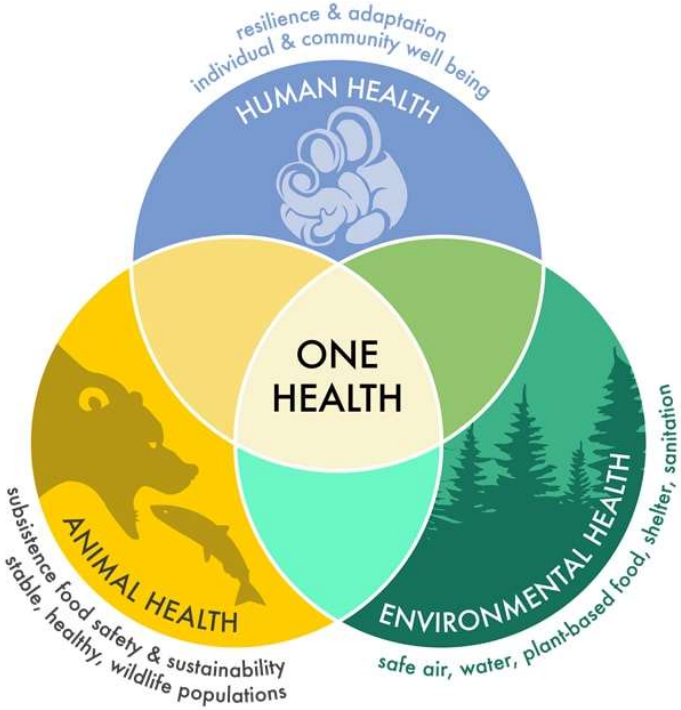

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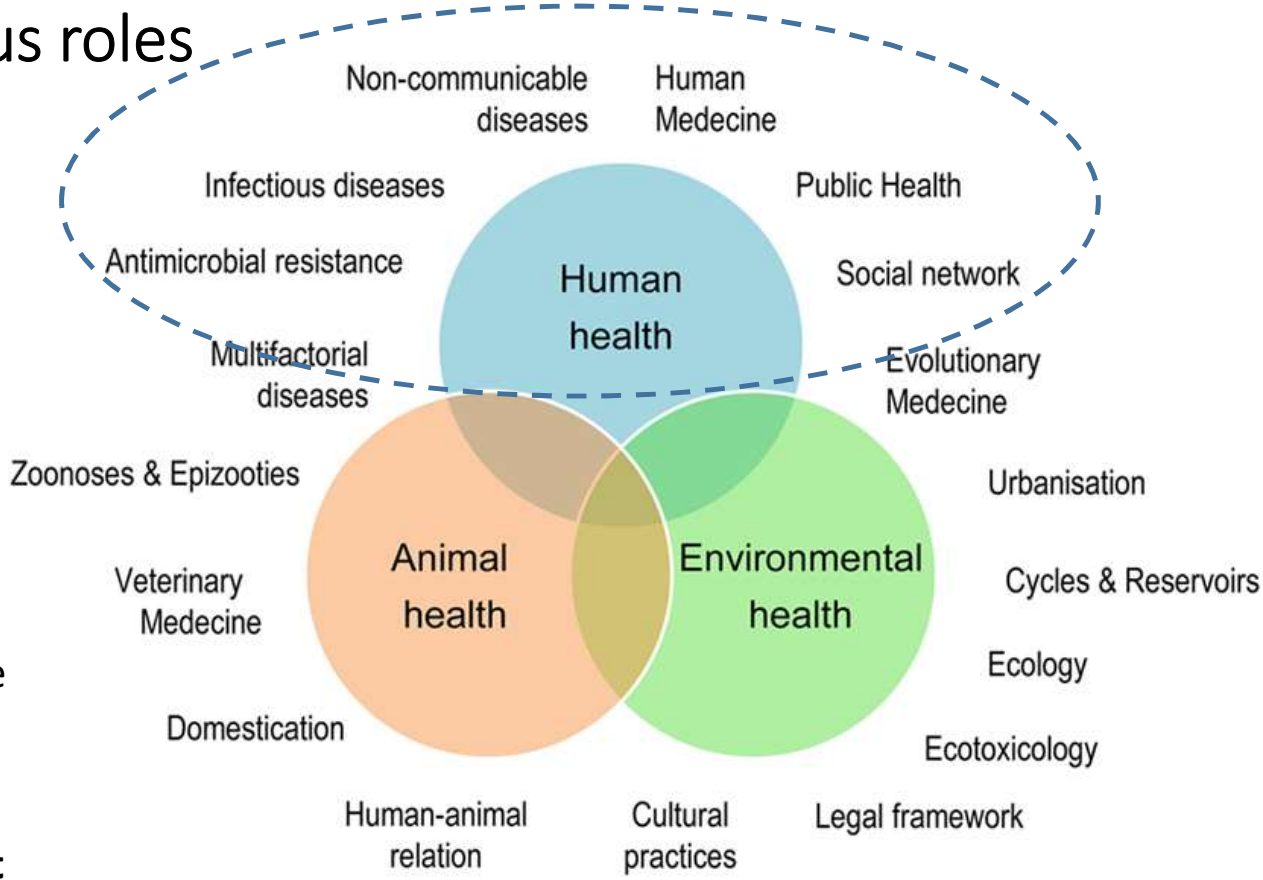
Human health & vet's plus roles

- **Public health - vet's PH**
- **Infectious disease -zoonosis**
- **AMR - residue**
- Human medicine – biomedical
- Evolutionary medicine - comparative studies
- **Social network - vet's authority & community services/empowerment**



Garzon et al 2018

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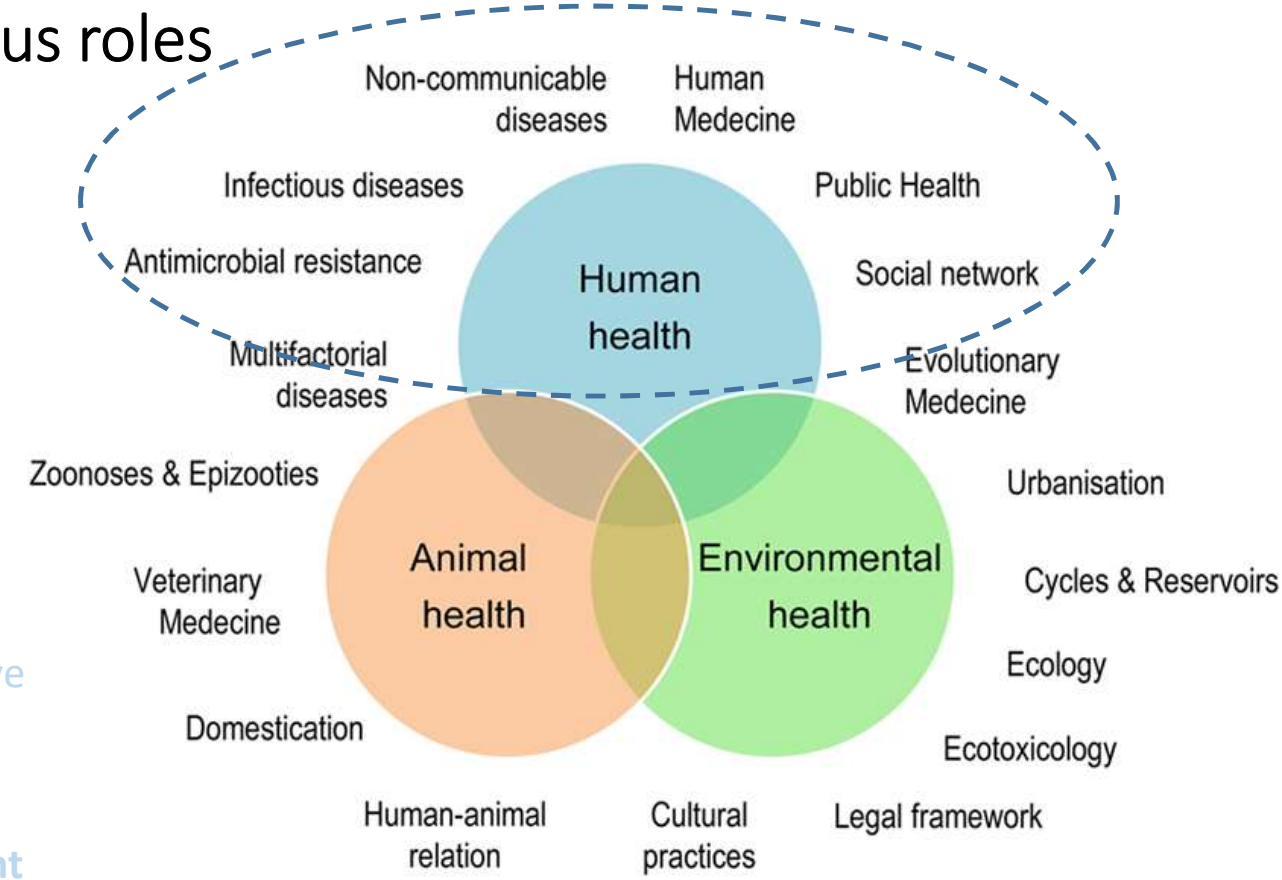
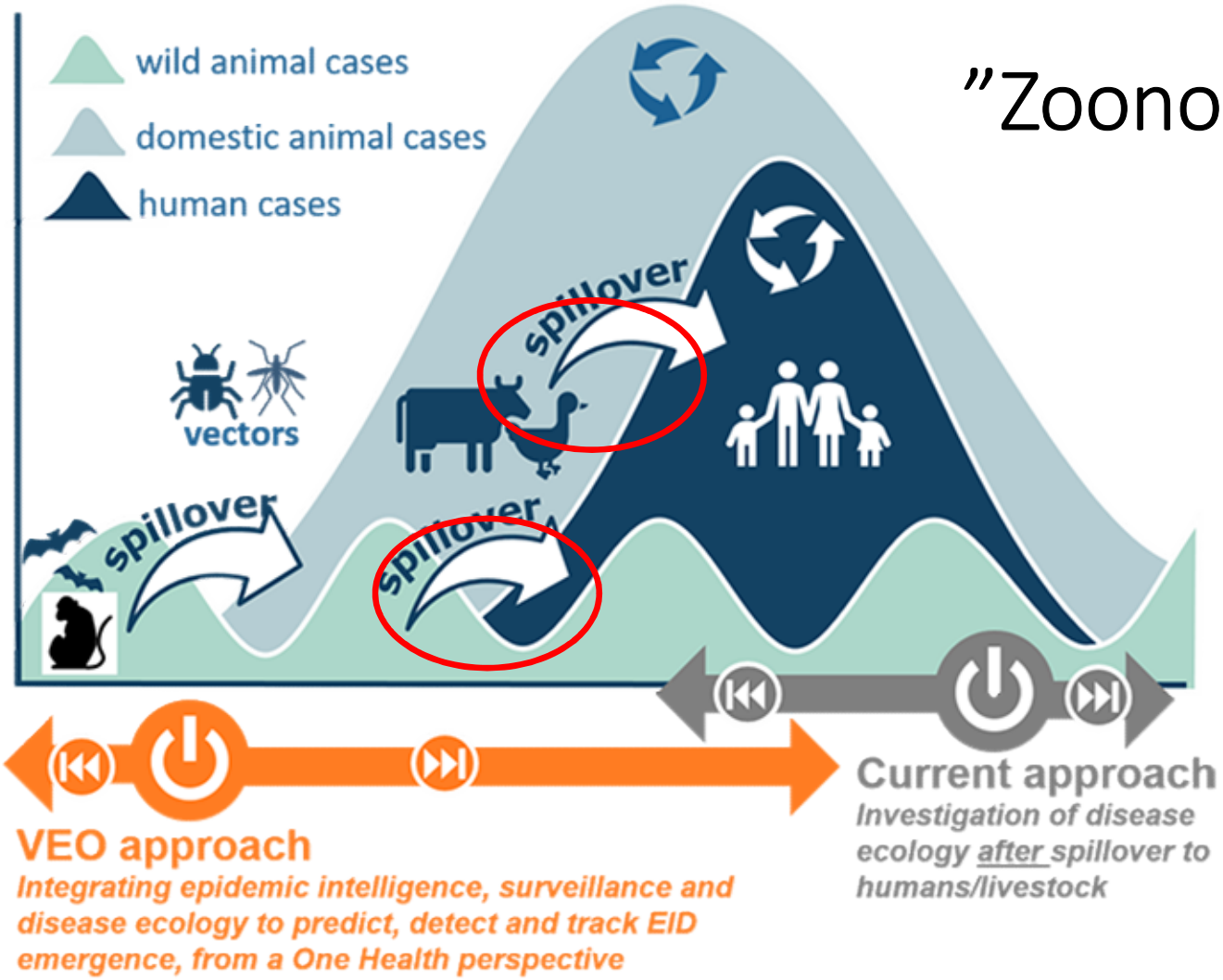


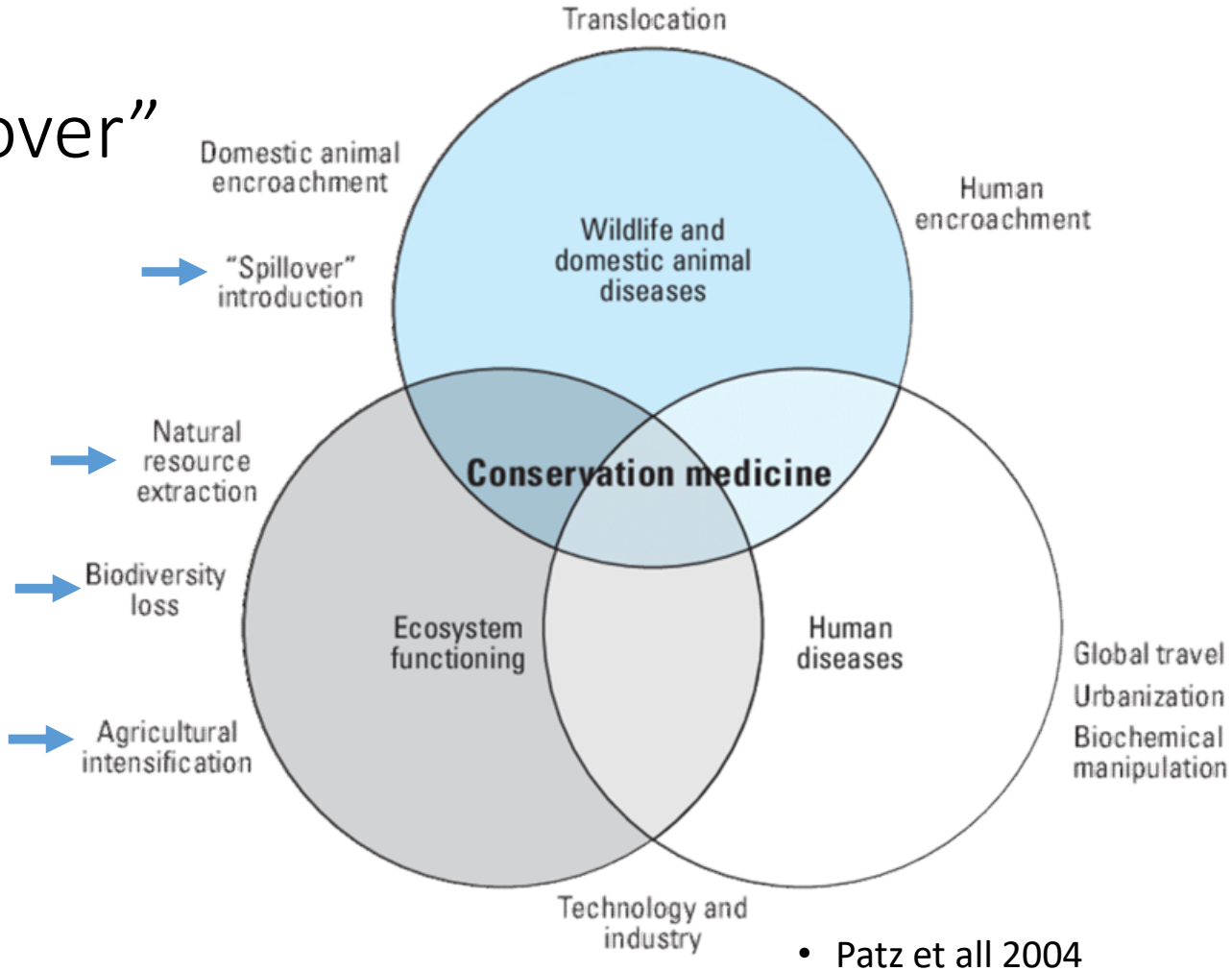
Garzon et al 2018

”Zoonosis spillover”



- veo-europe.eu

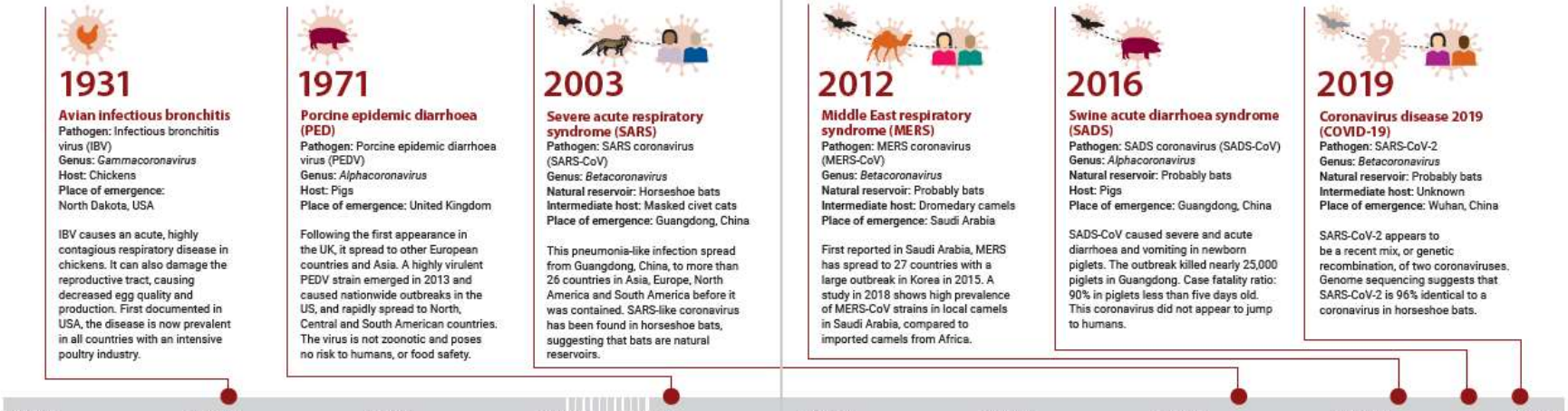
How it relates
“Cons Med & Spillover”



- Patz et all 2004

Preventing the next pandemic:
Zoonotic diseases and how to break the chain of transmission

Emergence of significant diseases caused by coronaviruses and other pathogens



1920s

Human Immunodeficiency Virus (HIV) infection

Pathogen: HIV
Genus: *Lentivirus*
Natural reservoir: Chimpanzee for HIV type 1, and Sooty Mangabey for HIV type 2
Place of emergence: Kinshasa, Democratic Republic of Congo

Based on genetic sequencing and historical records, the emergence of HIV is traced back to 1920s in Kinshasa, DRC. It is thought that simian immunodeficiency viruses (SIVs) in primates crossed over to humans at the time, presumably as a result of hunting and meat consumption. SIVs then adapted to the new human host to become HIV.

1931

Avian infectious bronchitis

Pathogen: Infectious bronchitis virus (IBV)
Genus: *Gammacoronavirus*
Host: Chickens
Place of emergence: North Dakota, USA

IBV causes an acute, highly contagious respiratory disease in chickens. It can also damage the reproductive tract, causing decreased egg quality and production. First documented in USA, the disease is now prevalent in all countries with an intensive poultry industry.

1937

West Nile fever

Pathogen: West Nile virus
Genus: *Flavivirus*
Host: Birds
Place of emergence: West Nile district, Uganda

Mosquitoes serve as disease vectors carrying the virus from infected birds to people and some mammals. Humans are usually incidental and dead-end hosts for the virus. The first recognized outbreak occurred in Israel in 1951, then Egypt. The virus re-emerged in Romania in 1996, and has established itself in the US since 1999. West Nile virus belongs to the same genus as dengue virus and yellow fever virus.

1947

Zika virus disease

Pathogen: Zika virus (ZIKV)
Genus: *Flavivirus*
Natural reservoir: Primates including humans
Place of emergence: The Zika forest, Uganda

ZIKV was first discovered in a febrile sentinel rhesus monkey from the Zika forest, and in the *Aedes africanus* mosquito from the same forest a year later. The first human cases were detected in Uganda and Tanzania in 1952. An outbreak occurred in the Yap Islands, Federated State of Micronesia in 2007, followed by a major epidemic in the Americas in 2015-16.

1971

Porcine epidemic diarrhoea (PED)

Pathogen: Porcine epidemic diarrhoea virus (PEDV)
Genus: *Alphacoronavirus*
Host: Pigs
Place of emergence: United Kingdom

Following the first appearance in the UK, it spread to other European countries and Asia. A highly virulent PEDV strain emerged in 2013 and caused nationwide outbreaks in the US, and rapidly spread to North, Central and South American countries. The virus is not zoonotic and poses no risk to humans, or food safety.

1976

Ebola virus disease

Pathogen: Ebola virus
Genus: *Ebolavirus*
Natural reservoir: Unconfirmed but likely to be African fruit bats of the *Pteropodidae* family
Intermediate host: Apes and monkeys
Place of emergence: Two simultaneous outbreaks in Democratic Republic of Congo (DRC) and South Sudan

The largest outbreak in history occurred primarily in Guinea, Liberia and Sierra Leone from 2014 to 2016, killing 11,323 people. The virus also recently re-emerged in eastern DRC from 2018 to 2019. Case fatality ratio of Ebola varied from 25% to 90%.

2003

Severe acute respiratory syndrome (SARS)

Pathogen: SARS coronavirus (SARS-CoV)
Genus: *Betacoronavirus*
Natural reservoir: Horseshoe bats
Intermediate host: Masked civet cats
Place of emergence: Guangdong, China

This pneumonia-like infection spread from Guangdong, China, to more than 26 countries in Asia, Europe, North America and South America before it was contained. SARS-like coronavirus has been found in horseshoe bats, suggesting that bats are natural reservoirs.

1986

Bovine spongiform encephalopathy or mad cow disease

Agent: Pathogenic prions
Host: Cattle
Place of emergence: United Kingdom

Mad cow disease is a progressive, fatal neurological disorder in cattle. The human form of the mad cow disease known as variant Creutzfeldt-Jakob disease is linked to consumption of beef from cattle infected with the disease.

1994

Hendra virus infection

Pathogen: Hendra virus
Genus: *Henipavirus*
Natural reservoir: Large fruit bats (*Pteropus* spp.) or flying fox
Host: Horses
Place of emergence: Hendra, Australia

Sporadic outbreaks have occurred in Australia over the years since its initial appearance in 1994. So far, no cases have been reported outside Australia. Case fatality ratio is 75% in horses, and 50% in humans. Hendra virus belongs to the same genus as Nipah virus.

1996

Highly pathogenic avian influenza (HPAI) or bird flu

Pathogen: HPAI virus subtype H5N1
Genus: *Alphainfluenzavirus*
Natural reservoir: Wild waterfowl
Host: Poultry
Place of emergence: Guangdong, China

First human cases found in Hong Kong in 1997 were traced back to wild and domestic waterfowl in Guangdong in 1996. Re-emerging in Hong Kong in 2002, the virus spread rapidly to South East Asian countries. Over 100 million domesticated chickens and ducks either died of the disease or were culled to stop the outbreak in Asia.

1998

Nipah virus infection

Pathogen: Paramyxovirus
Genus: *Henipavirus*
Natural reservoir: Large fruit bats (*Pteropus* spp.) or flying fox
Host: Pigs
Place of emergence: Guangdong, China

Nipah virus emerged as a respiratory and neurologic disease in pigs, and then spread to humans. A large outbreak in Malaysia from 1998 to 1999 was followed by five outbreaks in Bangladesh from 2001 to 2005. To control the outbreak in Malaysia, at least one million pigs were culled.

2012

Middle East respiratory syndrome (MERS)

Pathogen: MERS coronavirus (MERS-CoV)
Genus: *Betacoronavirus*
Natural reservoir: Probably bats
Intermediate host: Dromedary camels
Place of emergence: Saudi Arabia

First reported in Saudi Arabia, MERS has spread to 27 countries with a large outbreak in Korea in 2015. A study in 2018 shows high prevalence of MERS-CoV strains in local camels in Saudi Arabia, compared to imported camels from Africa.

2016

Swine acute diarrhoea syndrome (SADS)

Pathogen: SADS coronavirus (SADS-CoV)
Genus: *Alphacoronavirus*
Natural reservoir: Probably bats
Host: Pigs
Place of emergence: Guangdong, China

SADS-CoV caused severe and acute diarrhoea and vomiting in newborn piglets. The outbreak killed nearly 25,000 piglets in Guangdong. Case fatality ratio: 90% in piglets less than five days old. This coronavirus did not appear to jump to humans.

2019

Coronavirus disease 2019 (COVID-19)

Pathogen: SARS-CoV-2
Genus: *Betacoronavirus*
Natural reservoir: Probably bats
Intermediate host: Unknown
Place of emergence: Wuhan, China

SARS-CoV-2 appears to be a recent mix, or genetic recombination, of two coronaviruses. Genome sequencing suggests that SARS-CoV-2 is 96% identical to a coronavirus in horseshoe bats.

For references see page 61.

J Wildl Dis. 2020 Oct 1;56(4):922-927. doi: 10.7589/2019-10-243.

Detection of Antimicrobial Resistance Genes in Escherichia coli Isolated from Black Howler Monkeys (Alouatta pigra) and Domestic Animals in Fragmented Rain-Forest Areas in Tabasco, Mexico

Antonio Acini Vásquez-Aguilar [1], Fernanda Odett Toledo-Manuel [2], Arturo Barbachano-Guerrero [3], Dolores Hernández-Rodríguez [4]

Affiliations + expand

PMID: 32402234 DOI: 10.7589/2019-10-243

Abstract

The appearance and spread of antimicrobial resistance (AMR) in bacteria in natural environments and wildlife are related to agricultural and livestock activities and are a global health and conservation problem. We assessed the presence of AMR genes in Escherichia coli isolated from black howler monkeys (Alouatta pigra), sheep (Ovis aries), cattle (Bos taurus), and horses (Equus caballus) from a highly fragmented forest in southern Mexico. Fresh fecal samples were collected using swabs, seeded

antibiotics

MDPI

Article

Methicillin-Resistant and Methicillin-Susceptible *Staphylococcus* from Vervet Monkeys (*Chlorocebus sabaeus*) in Saint Kitts

Andreas Hoefer [1], Filip Boyen [2], Amy Beierschmitt [1,3], Arshnee Moodley [4,5], Marilyn C. Roberts [6] and Patrick Butaye [1,2,*]

1 School of Veterinary Medicine, Ross University, West Farm 000265, Saint Kitts and Nevis; andreashoefer@hotmail.com (A.H.); ABeierschmitt@rossvet.edu.kn (A.B.)
2 Department of Pathology, Bacteriology and Avian Diseases, Faculty of Veterinary Medicine, Ghent University, 9000 Merelbeke, Belgium; filip.boyen@Ugent.be
3 Behavioral Science Foundation, Basseterre KN 0101, Saint Kitts and Nevis
4 Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, 1165 Copenhagen, Denmark; asm@sund.ku.dk or a.moodley@cgiar.org
5 CGIAR AMR Hub, International Livestock Research Institute, Nairobi, Kenya
6 Department of Environmental and Occupational Health, School of Public Health, University of Washington, Seattle, WA 98195, USA; marilynr@uw.edu
* Correspondence: pbutaye@rossvet.edu.kn

frontiers in Microbiology | Antimicrobials, Resistance and Chemotherapy

SECTION ABOUT ARTICLES RESEARCH TOPICS FOR AUTHORS EDITORIAL BOARD ARTICLE ALERTS

‹ Articles

THIS ARTICLE IS PART OF THE RESEARCH TOPIC
Surveying Antimicrobial Resistance: The New Complexity of the Problem View a

ORIGINAL RESEARCH article
Front. Microbiol., 09 October 2018 | https://doi.org/10.3389/fmicb.2018.02366

Antimicrobial Resistance Profiles in *Enterococcus* spp. Isolates From Fecal Samples of Wild and Captive Black Capuchin Monkeys (*Sapajus nigritus*) in South Brazil

Tiela Trapp Grassotti[1], Dejoara de Angelis Zvoboda[1], Letícia da Fontoura Xavier Costa[1], Alberto Jorge Gomes de Araújo[2], Rebeca Inhoque Pereira[2], Renata Oliveira Soares[2], Paulo Guilherme Carniel Wagner[3], Jeverson Frazzon[4] and Ana Paula Guedes Frazzon[1*]

[1]Microbiology, Immunology, and Parasitology Department, Institute of Basic Health Sciences, Federal University of Rio Grande do Sul, Porto Alegre, Brazil
[2]Gram-Positive Cocci Laboratory, Federal University of Health Sciences of Porto Alegre, Porto Alegre, Brazil
[3]Brazilian Institute of Environment and Renewable Natural Resources, IBAMA, Brasília, Brazil
[4]Institute of Food Science and Technology, Federal University of Rio Grande do Sul, Porto Alegre, Brazil

The environment, human, and animals play an important role in the spread of antibiotic-resistant bacteria. Enterococci are members of the gastrointestinal tracts of humans and animals and represent important reservoirs of antibiotic resistance genes. Until today, few studies have examined antibiotic susceptibility in enterococci isolated from primates. Therefore, the present study investigated species distribution, antibiotic susceptibility, and resistance genes in enterococci isolated from wild and captive black capuchins monkeys (*Sapajus nigritus*) in Rio Grande do Sul, South Brazil. A total of 24 swabs/fecal samples were collected, including 19 from wild monkeys living in two forest fragments [São Sebastião do Caí (SSC) and Santa Cruz do Sul (SCS)], and five in captive [Parque Zoológico da Fundação Zoobotânica (ZOO)], between August 2016 and November 2017. Fifteen colonies were randomly selected from each sample. Enterococci were identified by MALDI-TOF, tested for susceptibility

Human health & vet's plus roles

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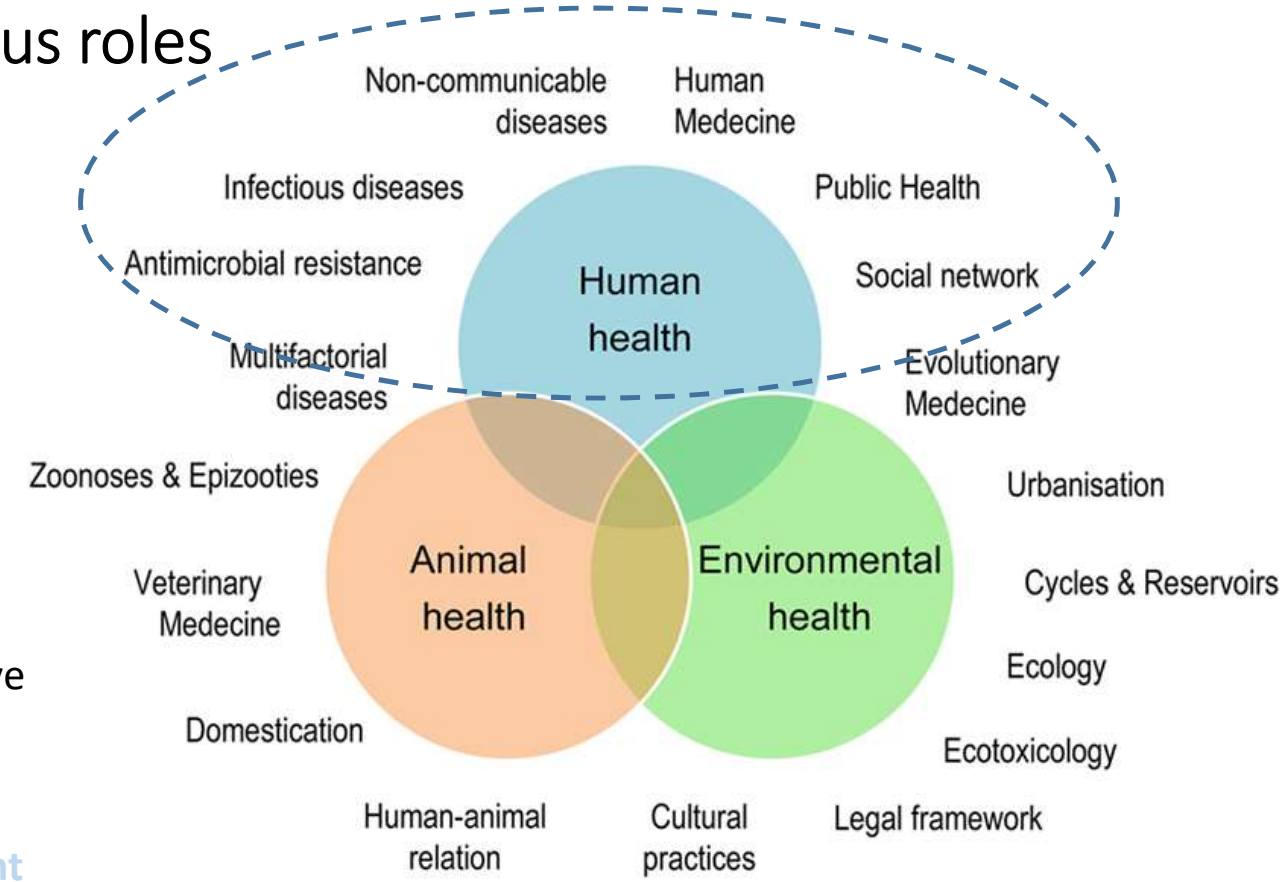
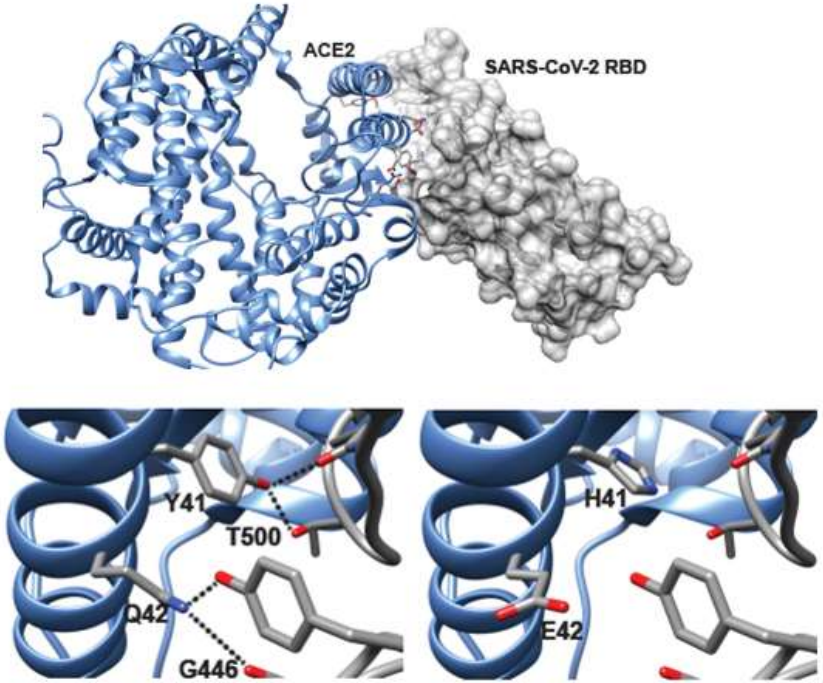
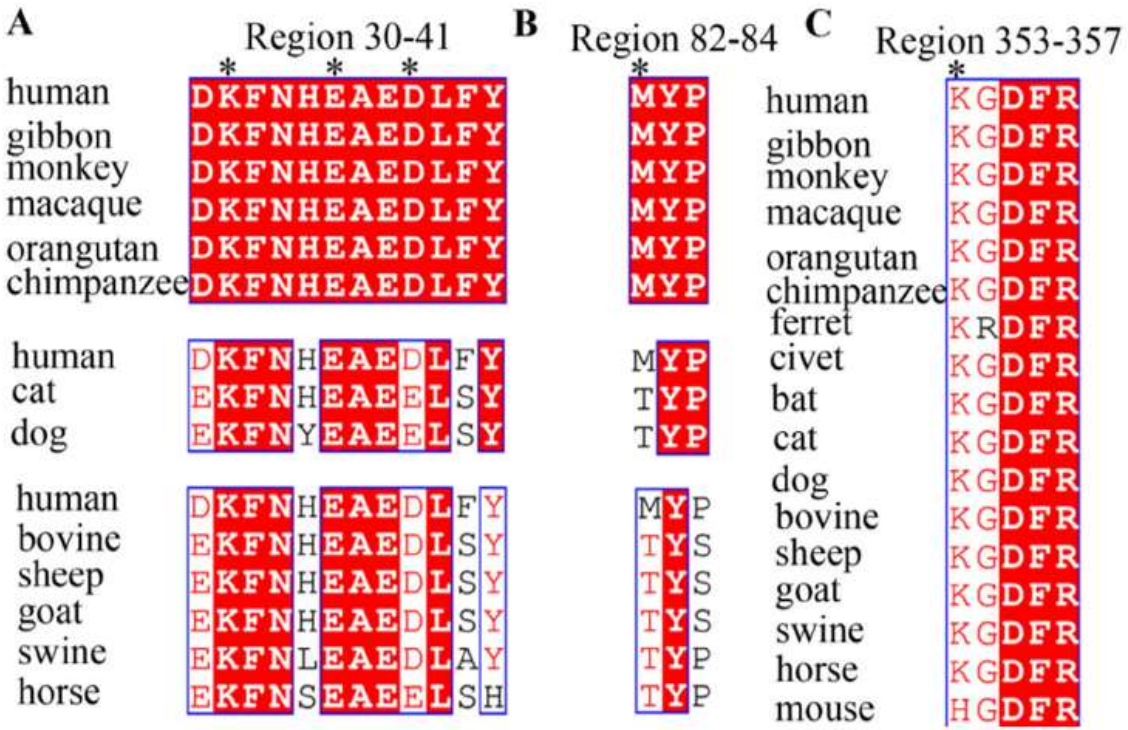


Garzon et al 2018

Penelitian Terkait COVID-19

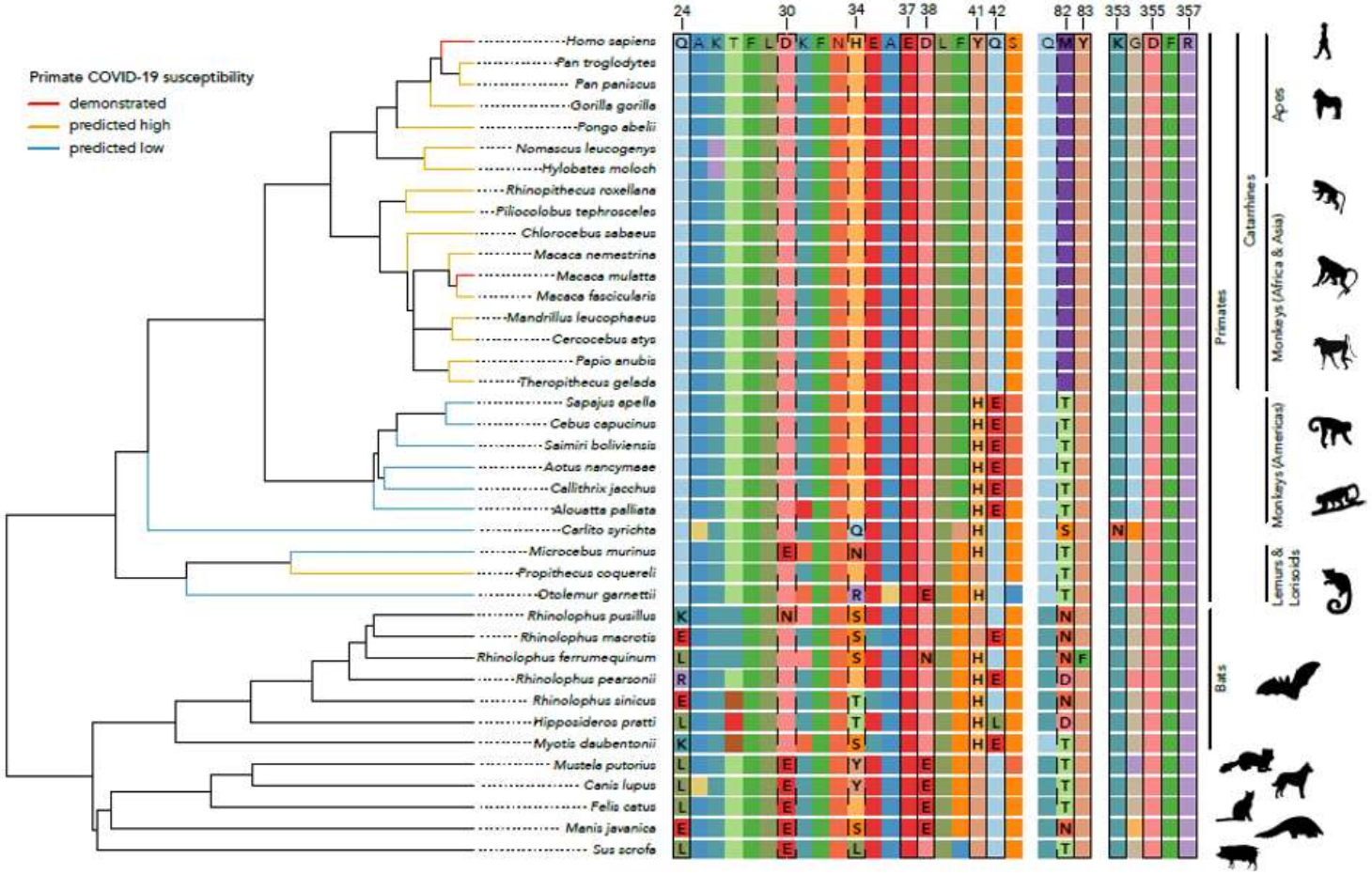


Melin et al, 2020. doi: https://doi.org/10.1101/2020.04.09.034967



Journal of Infection 80 (2020) 469–496

ACE2 Protein Sequence Alignment and Phylogeny of Study Species



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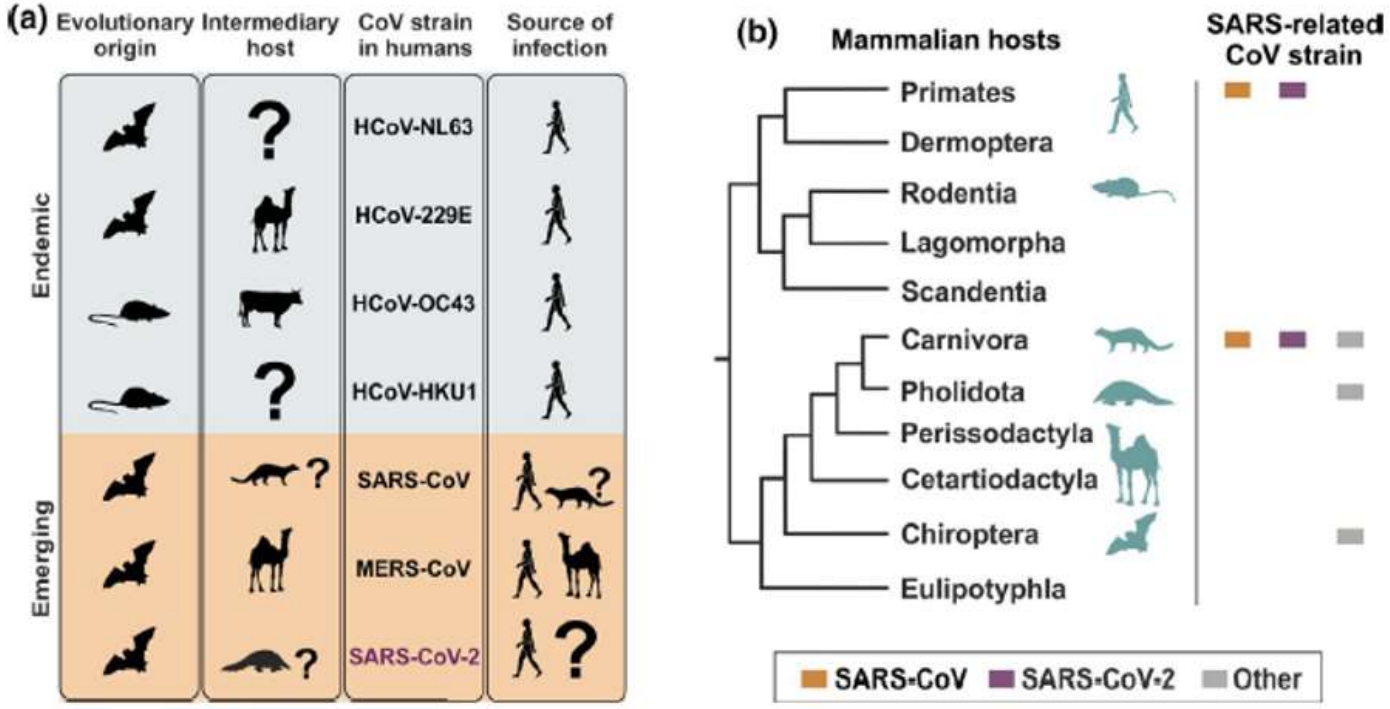
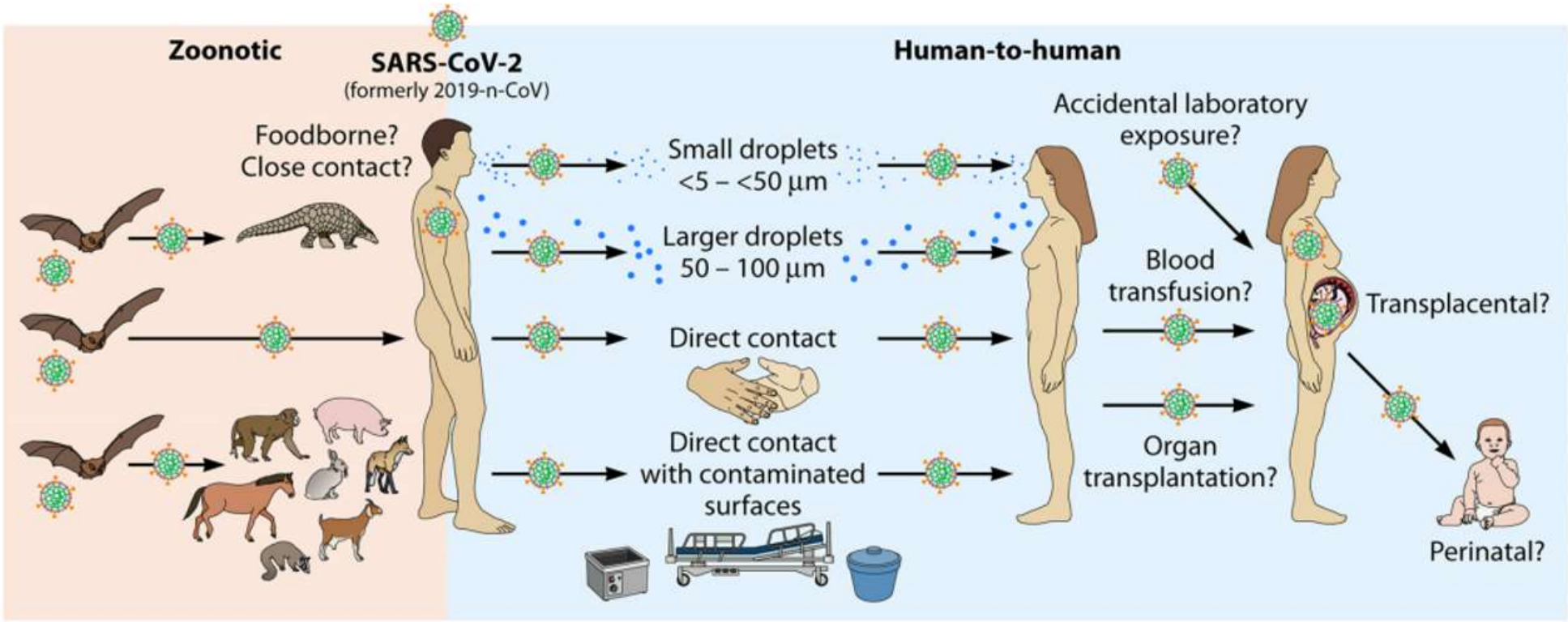
Mammals as Reservoirs and Intermediary Hosts of Endemic and Emerging Human coronaviruses



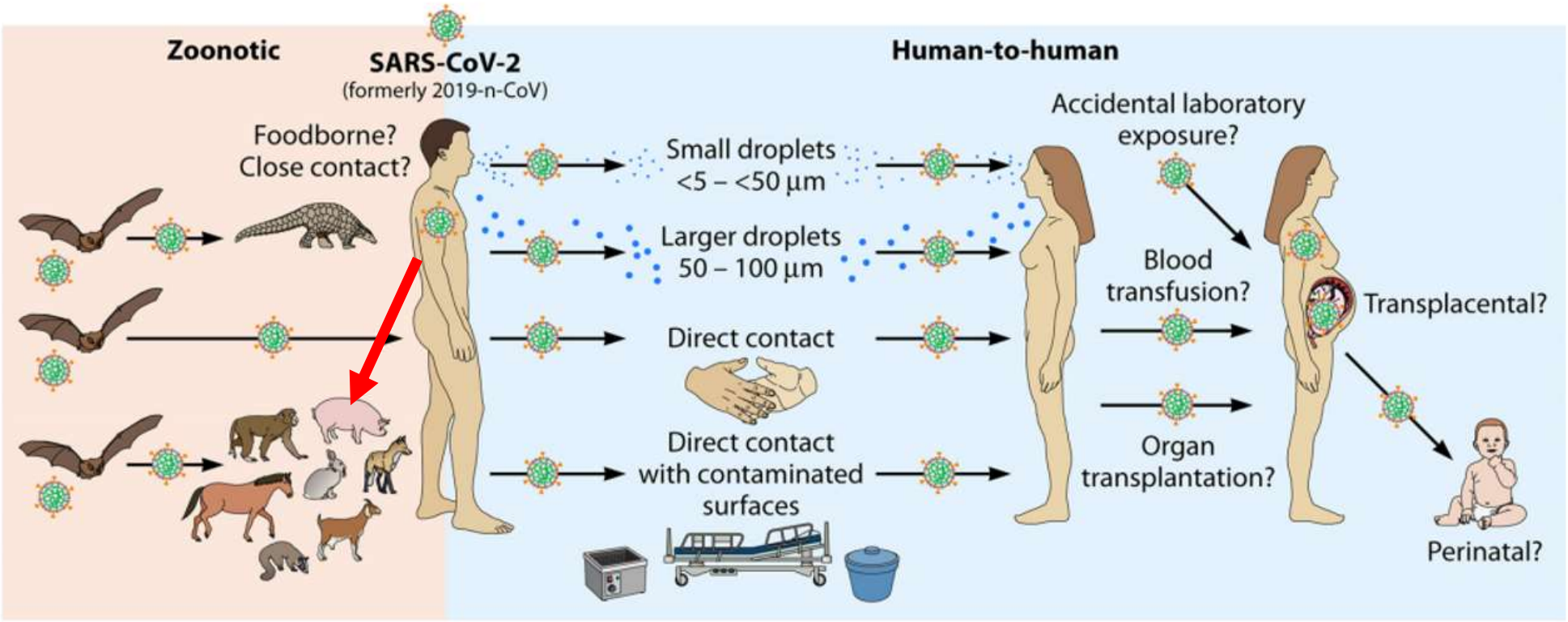
Jo et al 2020. Transbound Emerg Dis. 2020; 00:1–11.

Potential Transmission Routes for SARS-CoV-2



Dhama K, et al. 2020. Clin Microbiol Rev 33:e00028-20. https://doi.org/10.1128/CMR.00028-20

Potential Transmission Routes for SARS-CoV-2



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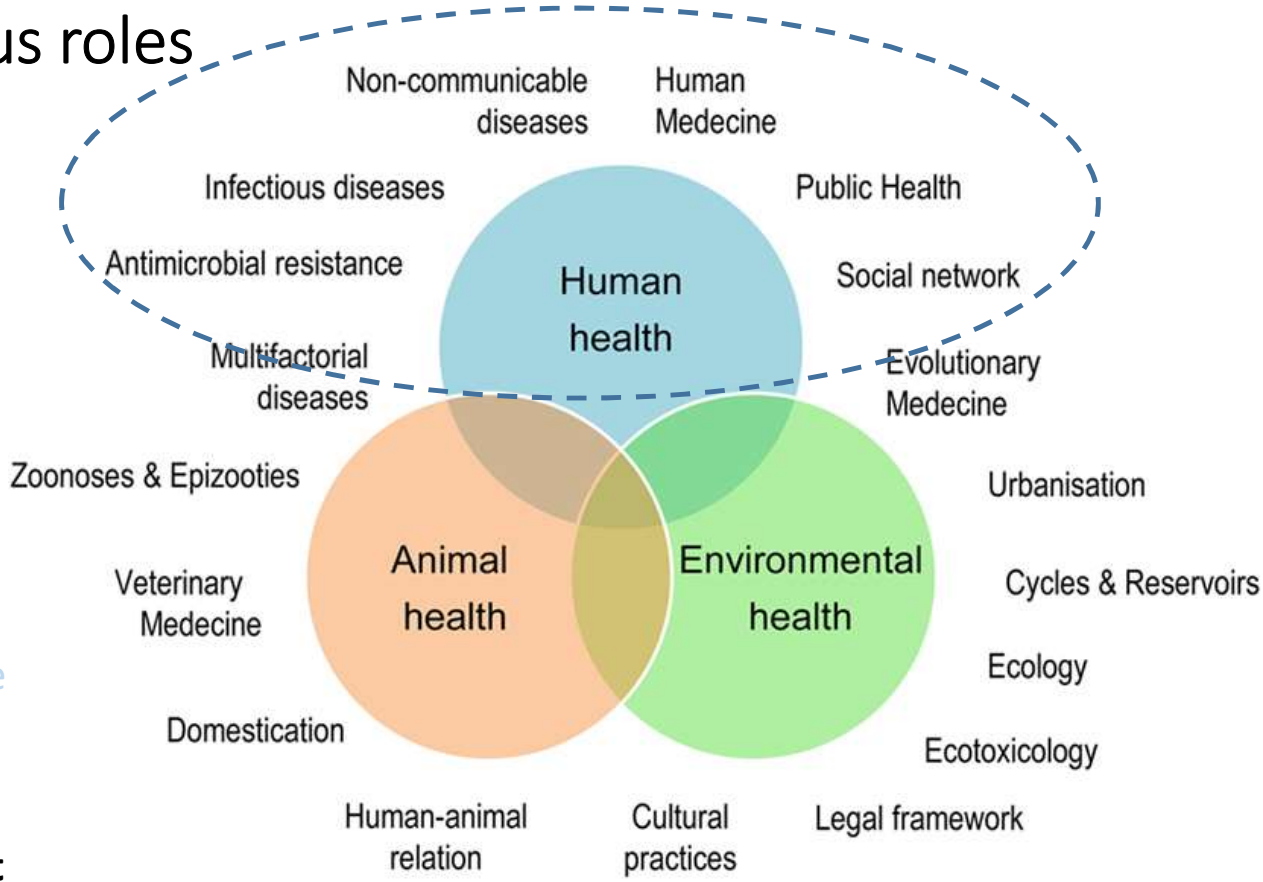
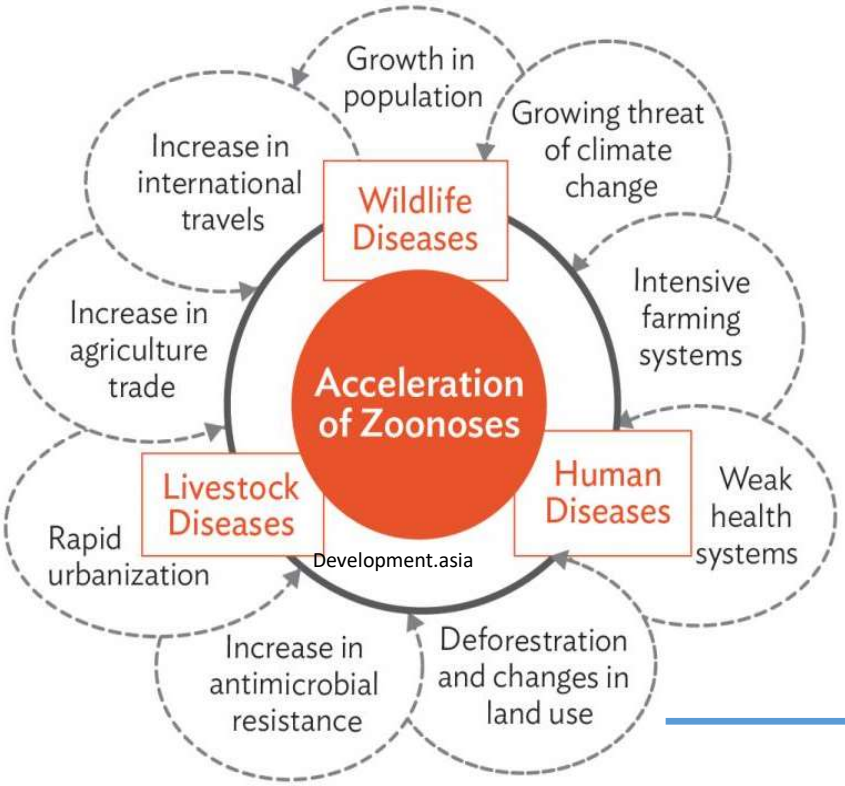


Garzon et al 2018


Growth in population
Growing threat of climate change
Increase in international travels
Wildlife Diseases
Intensive farming systems
Increase in agriculture trade
Acceleration of Zoonoses
Livestock Diseases
Human Diseases
Weak health systems
Rapid urbanization
Increase in antimicrobial resistance
Deforestration and changes in land use
Development.asia


The pathway of epidemics
4. Risk of zoonosis
3. Animal markets
2. Species collecting and trafficking
1. Deforestation
WWF

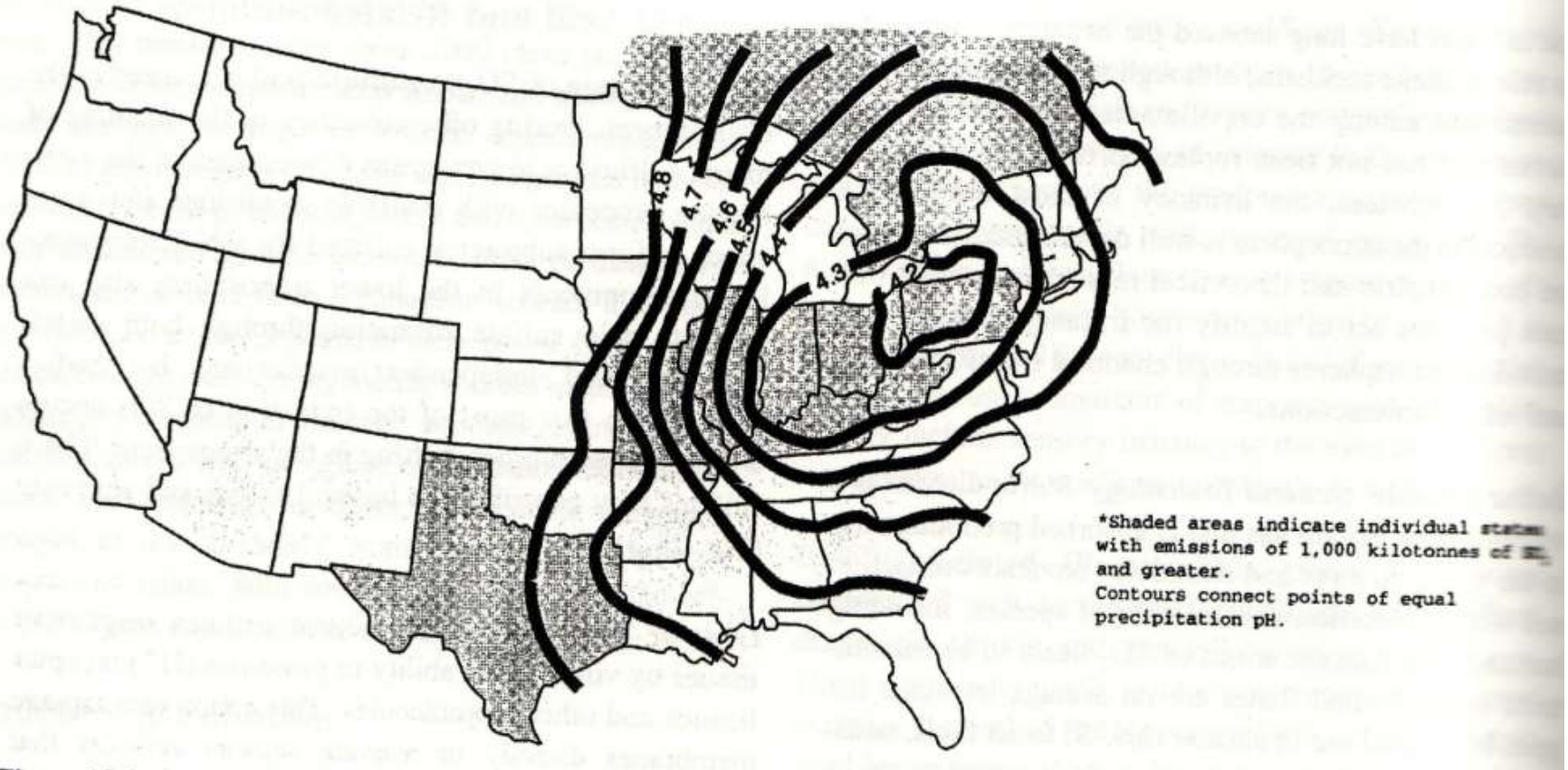
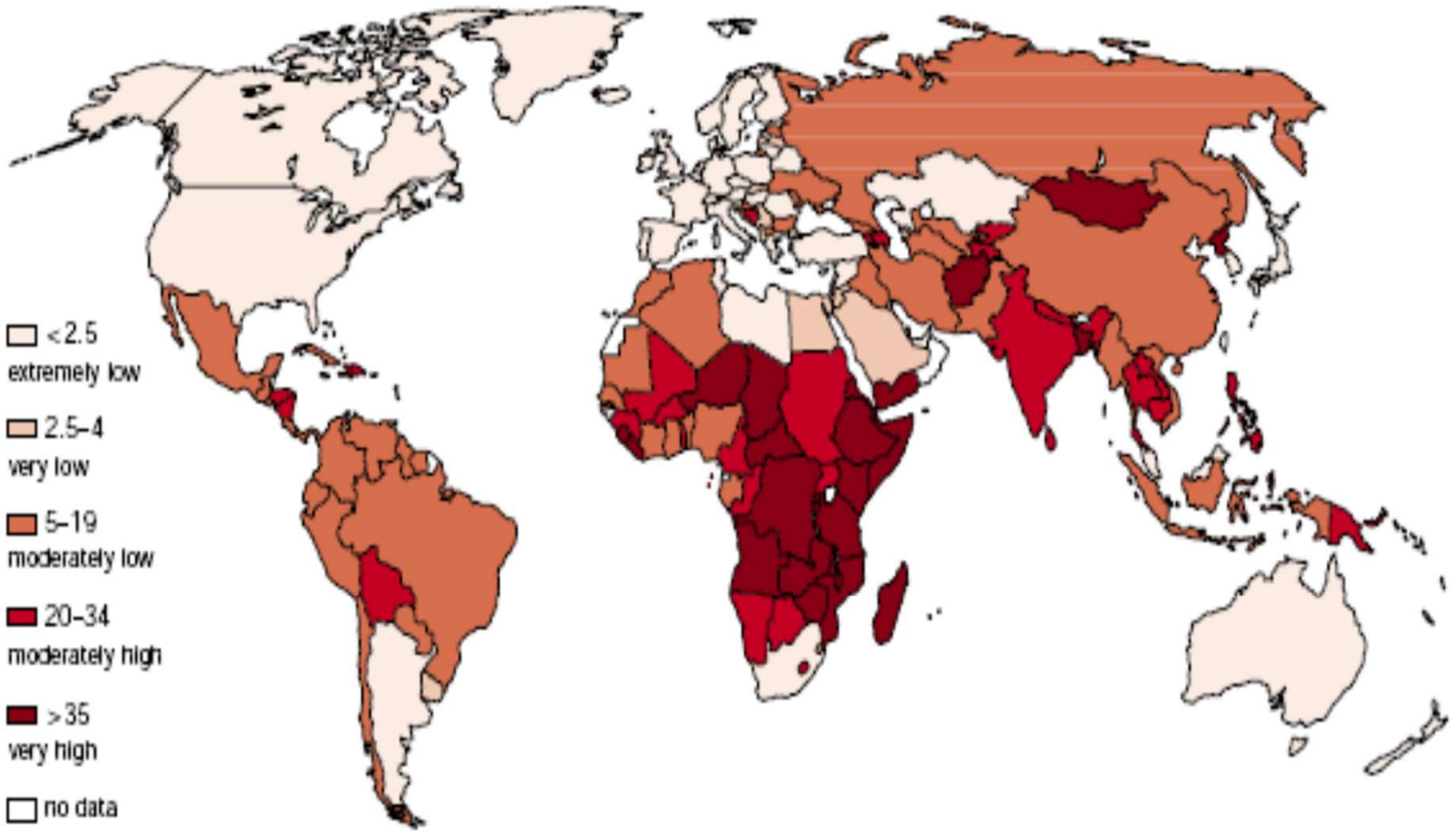


Figure 28-3. Areas in 1988 where precipitation in the east fell below pH 5: acid rain. The acidity of the air in the east is thought to result from air mass transport of fine sulfated particulate matter from the industrial centers of the midwest.



Vulnerability to hunger is reflected in this map of the global state of under-nourishment. Undernourished people are unable to obtain the food they need from production or imports, either because it is not available or because they cannot afford it

Source: FAO 2000

Community-based

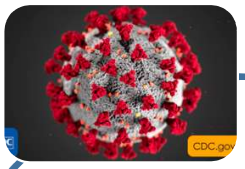
- Education & campaign
  - Cultural & religion
- Empowerment
  - Provide living opportunities

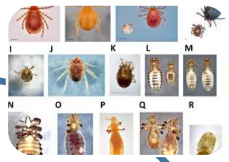
So, the verdict...

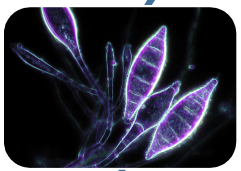
Pandemi Selanjutnya? Profesi & masyarakat interest

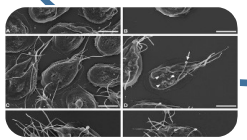
Perburuan & perdagangan

Akselerasi zoonosis









Pandemi (lama/baru)

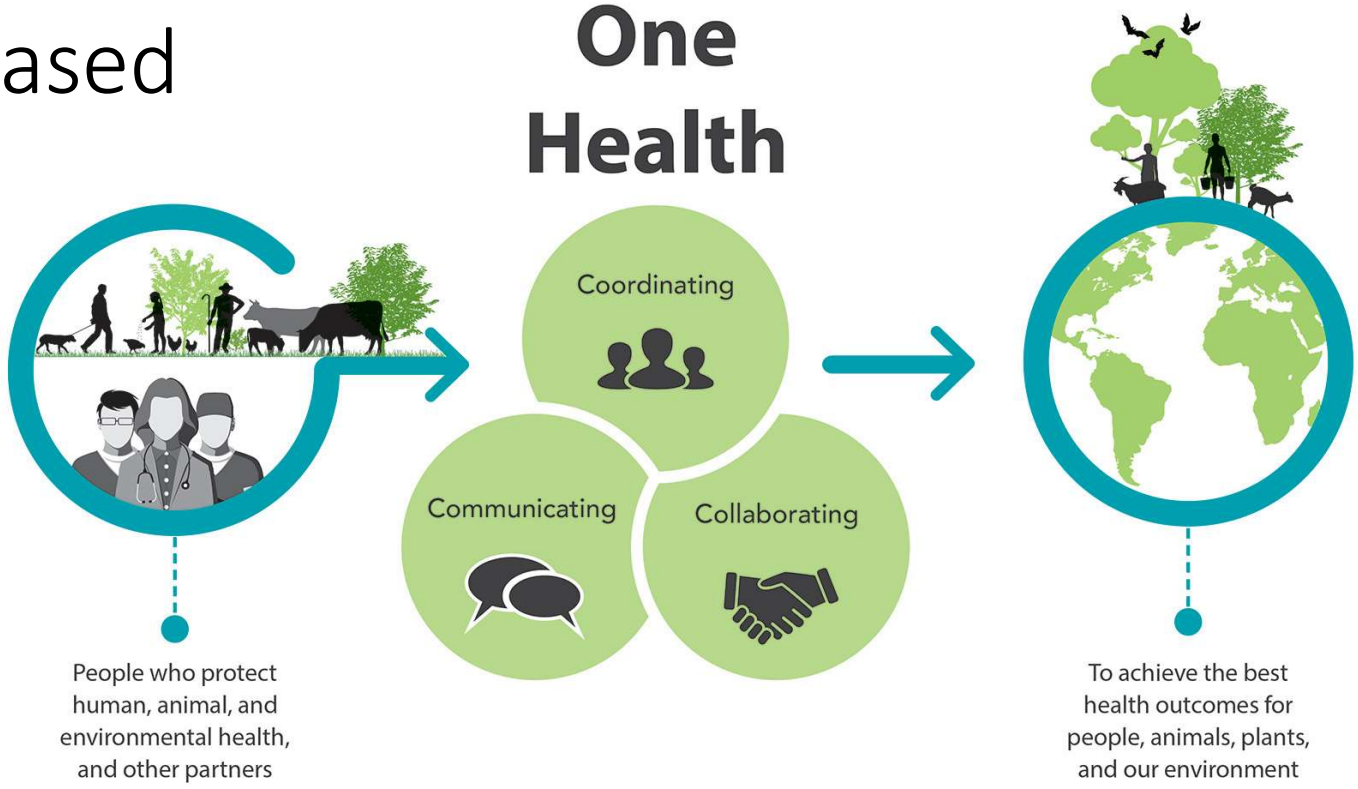
Community-based

One Health *is the idea that the health of people is connected to the health of animals and our shared environment.*

CDC

*When we protect **one**,*

*we help to protect **all**.*

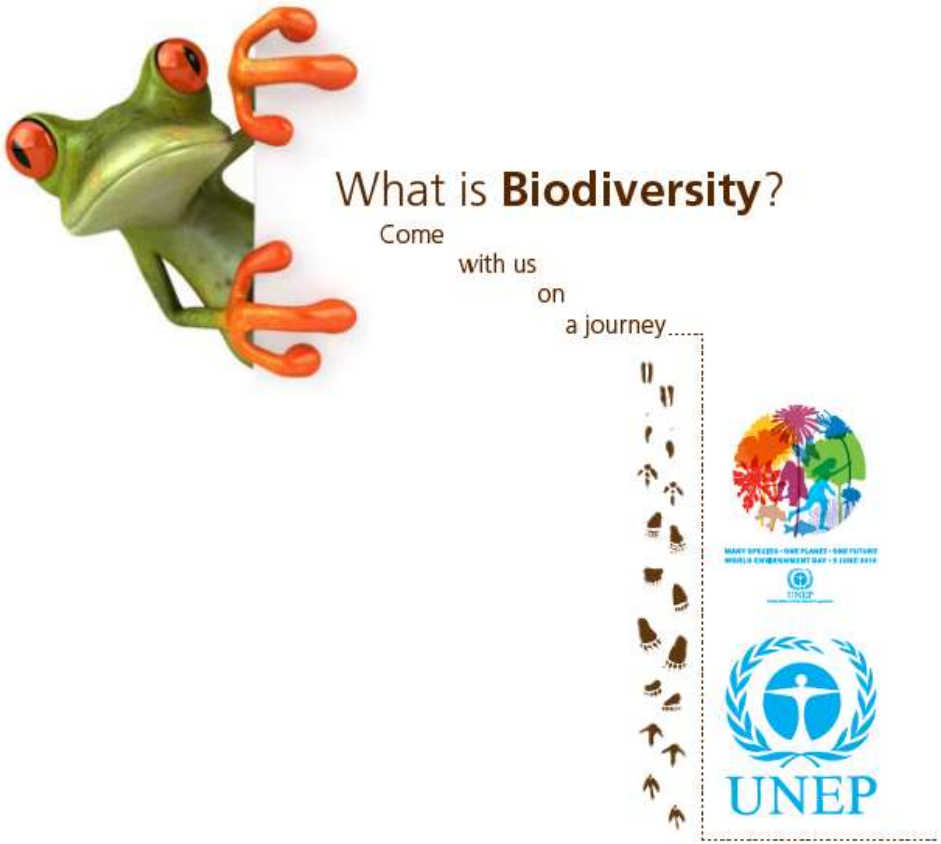


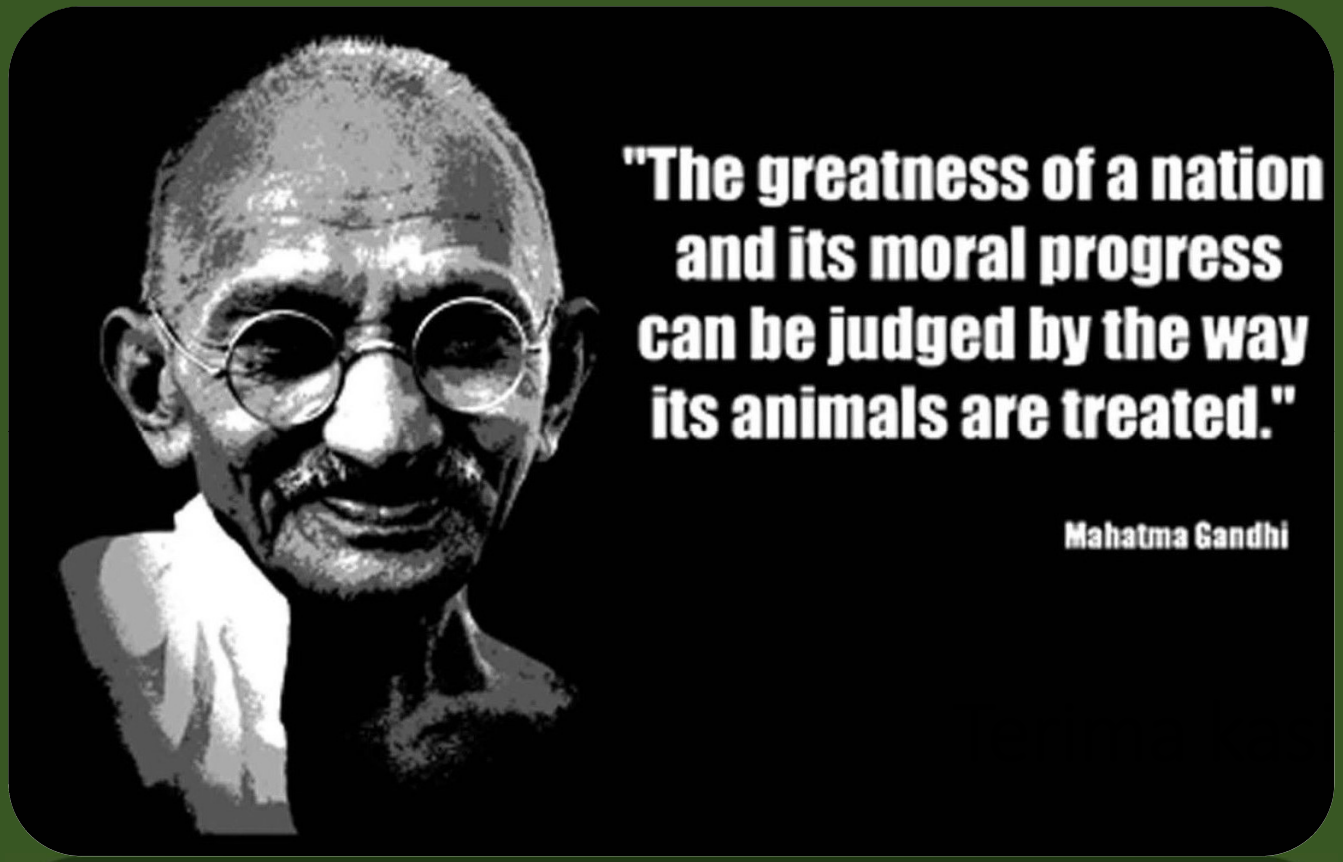
“collaborative efforts”

CS302365-A

Centers for Disease Control and Prevention
National Center for Emerging and Zoonotic Infectious Diseases

Sustainable Biodiversity




"The greatness of a nation
and its moral progress
can be judged by the way
its animals are treated."
Mahatma Gandhi

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