COVID-19 through a One Health Lens: The Wonders of Wildlife and Wilderness

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We are a globally-connected society...
We start, and end, in communities...
What is risk?

EXPOSURES → OUTCOMES
What kind of wildlife do we live with?
One Health Approach
ENDANGERED POLLINATORS
AND THEIR HABITATS
Bats and Mosquito Control
One Health

Holistic

Collaborative and transdisciplinary

Focused on integrated solutions

ANIMAL

HUMAN

ECOSYSTEM
One Health

The collaborative efforts of multiple disciplines working locally, nationally and globally to attain optimal health for people, animal and our environment

(FAO, OIE, WHO, WB...)

From theoretical to operational definition:

“One Health” can be defined as the **added value** in terms of **lives** of animals and humans **saved, financial savings and improved ecosystem services** from a **closer cooperation of human and animal health** as compared to single sector approaches (Zinsstag et al., 2012)

http://www.cdc.gov/onehealth
One Health Framework
Transdisciplinary Problems

Drivers:
- Land use
- Climate change
- Economic development
- Globalization
- Energy extraction
- Migration

Influences:
- Culture
- Economics
- Policy
- Behavior
- Education

Problems:
- Zoonotic disease emergence
- Pathogen distribution
- Health disparities
- Food and water safety & security
- Endangered species & habitat conservation
- Poverty alleviation
- Loss of biodiversity
- Environmental contamination
- Diagnostic limitations

Animals
Humans
Environment
Coronaviruses are Global

Global distribution evidence of multi-species infection and host-jumping

**MAJOR ANIMAL PATHOGENS**

- Pigs – Transmissible gastroenteritis virus, Porcine epidemic diarrheal virus
- Cats – Feline Infectious Peritonitis virus (antiviral GS-441524)
- Chickens – Infectious bronchitis virus
- Cattle – Bovine coronavirus complex
- Many other species…
Coronaviruses are Global

Global distribution evidence of multi-species infection and host-jumping

**HUMANS**

- α/β1 Several mild respiratory viruses
- β2b 2003 SARS-CoV-1 (bats, civet cats, ?)
- β2b 2012 MERS-CoV (bats, camels)
- β2b 2019 SARS-CoV-2/COVID19 (bats?, ??)

Unknown if SARS-CoV2 can infect and cause disease other domesticated species

Recommended that persons sick should avoid contact with pets and other domesticated animals
Coronaviruses are Global

**Bats** have the largest number of known coronaviruses

— SARS-CoV-2 may be bat-borne but that is **not yet known**

Spillover of many emerging viruses from wildlife to people is driven by bat and human contact (bushmeat, guano harvesting, land use change)
Coronavirus Evolution and Spillover

SARS-CoV-2

Coronavirus ancestor

Genus  Alphacoronavirus  Group A, B, C, D  Betacoronavirus  Gammaporonavirus  Deltacoronavirus

Land use change & population density drive viral spillover events...

**Climate**

- Increased: Middle atmosphere temperature
- Increased: Water vapour
- Increased: Air temperature over ocean
- Increased: Sea surface temperature
- Increased: Ocean heat content

- Decreased: Net decrease in glacier volumes
- Decreased: Net decrease in global sea-ice extent
- Decreased: Polar ice sheets
- Increased: Air temperature over land
- Increased: Sea level

**Population Growth**
Drivers in Emerging Infectious Diseases

- Globalization
- Changing Ecosystems
- Human Demographics & Behavior
- Markets & Trade
- Migration & Conflict
- Poverty & Social Inequality
- Microbial Adaptation

and more…

Source: Author San Jose, 27 November 2006, based on the [http://gmt.soest.hawaii.edu/ Generic Mapping Tools]
Global travel & trade can turn local epidemics into pandemics
The threat from emerging viruses is increasing

Each year, approx. **3 new Viral Diseases** emerge

**Driven by**
- Population expansion (1.6 billion in 1900 to 11.5 billion people in 2100)
- Increased encroachment into wildlife habitat which accelerates the “spillover” from wildlife to humans

Source: Jones et al. (2008) Nature
The Ministries of Health, Agriculture & Environment and Implementing University and NGO Partners in 35 Countries
One Health Interface

- Majority of emerging infectious diseases (EIDs) in people are of animal origin (zoonotic)
- 75% of emerging zoonoses have wildlife origins
- Human activities at the interface linked to EIDs (Nipah virus, SARS, Ebola)
- Annual population growth among highest in buffers to protected areas near wildlife
Targeted, Risk-based Surveillance

- Primates
- Bats
- Rodents
- Birds
- Suids
- Carnivores
- Ungulates
PREDICT Surveillance Strategy

Target = zoonotic viruses that causes disease in animals & people
High Risk Interfaces
Bat Guano Farms

Vietnam, Cambodia & Thailand
Developed & Operationalized Diagnostic Platform
PREDICT OVERVIEW

**DEVELOPED** the One Health Workforce by training more than 6,000 people in over 30 countries.

**STRENGTHENED** laboratory systems and zoonotic disease detection capabilities in over 60 labs around the world.

**OPERATIONALIZED** One Health surveillance and sampled over 163K animals and people, helping minimize the spillover of zoonotic disease threats from animals into human populations.

**DETECTED** over 1,100 unique viruses, including zoonotic diseases of public health concern such as Bombali ebolavirus, Zaire ebolavirus, Marburg virus, and MERS- and SARS-like coronaviruses.
Novel MERS-like Corona Virus from Uganda

Bat sampled in Kisoro District, Southwest Uganda

Distribution of Pipistrellus hesperidus
Bats Are Natural Reservoirs of SARS-Like Coronaviruses

Wendong Li,1,2 Zhengli Shi,2,4 Meng Yu,3 Wuze Ren,3 Craig Smith,4 Jonathan H. Epstein,5 Hanzhong Wang,7 Gary Crameri,6 Zhihong Hu,2 Huajun Zhang,2 Jianhong Zhang,2 Jennifer McEachern,3 Hume Field,4 Peter Daszak,5 Bryan T. Eaton,5 Shuyi Zhang,1,6* Lin-Fa Wang1,6*

Severe acute respiratory syndrome (SARS) emerged in 2002 to 2003 in southern China. The origin of its etiological agent, the SARS coronavirus (SARS-CoV), remains elusive. Here we report that species of bats are a natural host of coronaviruses closely related to those responsible for the SARS outbreak. These viruses, termed SARS-like coronaviruses (SL-CoV), display greater genetic variation than SARS-CoV isolated from humans or from civets. The human and civet isolates of SARS-CoV nestle phylogenetically within the spectrum of SL-CoVs, indicating that the virus responsible for the SARS outbreak was a member of this coronavirus group.

In this study, conducted from March to December of 2004, we sampled 408 bats representing nine species, six genera, and three families, from four locations in China (Guangdong, Guangxi, Hubei, and Tianjin) after trapping them in their native habitat (Table 1). Blood, fecal, and throat swabs were collected; serum samples and cDNA from fecal or throat samples were independently analyzed, double-blind, with different methods in Wuhan and Geelong (14).

Among six genera of bat species surveyed (Rousettus, Cynopterus, Myotis, Rhinolophus, Vespertilio, and Miniopterus), three commensal, cave-dwelling species from the genus Rhinolophus (horse-shoe bats) in the family Rhinolophidae demonstrated a high SARS-CoV antibody prevalence: 13 out of 46 bats (28%) in R. pumilus from Guangxi, 2 out of 6 bats (33%) in R. pumilus from Guangxi, and 5 out
COVID-19

COVID-19 Dashboard

Total Confirmed
12,169,400

Confirmed Cases by Country/Region/Sovereignty

3,105,315 US
1,713,160 Brazil
767,296 India
706,240 Russia
316,448 Peru
306,216 Chile
289,154 United Kingdom
275,003 Mexico
253,056 Spain

https://coronavirus.jhu.edu/map.html
COVID-19 Case Map – July 9, 2020

https://coronavirus.jhu.edu/map.html
COVID-19 What now?

Masks, Good Hygiene & Social Distancing
Questions & Discussion

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