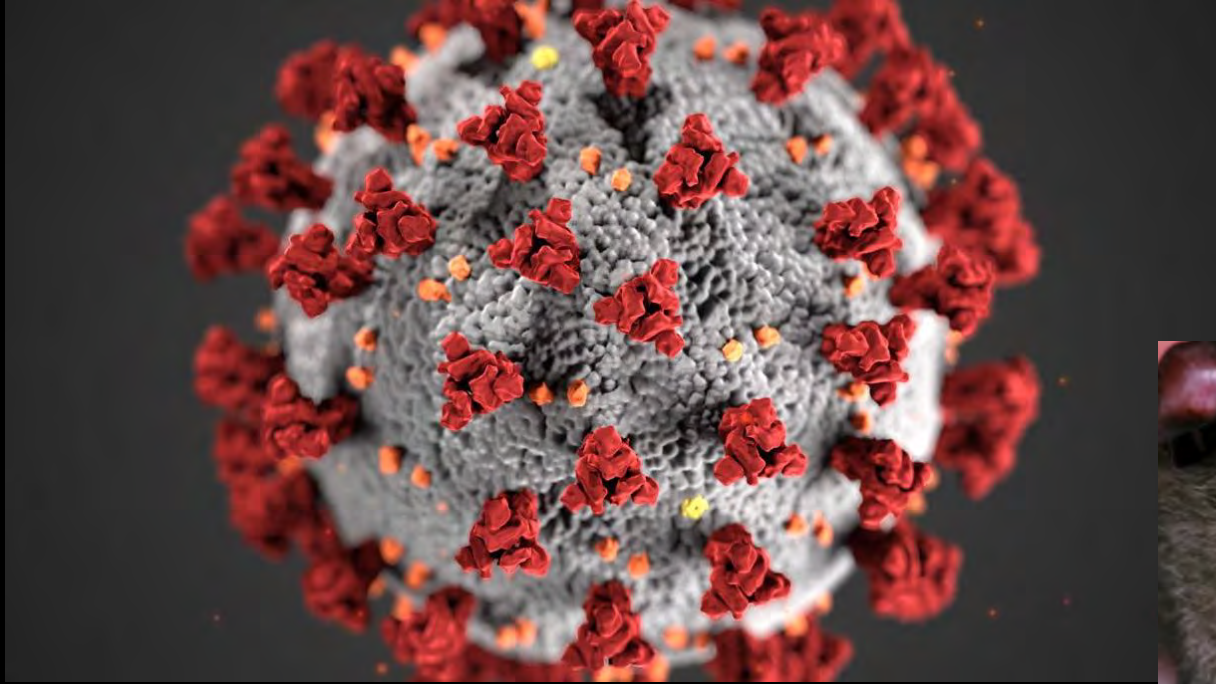


Global  
Health  
Security:  
Utilizing the  
One Health  
Approach to  
Control  
COVID-19 &  
*Disease X*





# Global Health Security Agenda



3

## Risks

- Emerging organisms
- Drug resistance
- Intentional creation



3

## Opportunities

- Public health framework
- New lab and surveillance tools
- Successful outbreak control



3

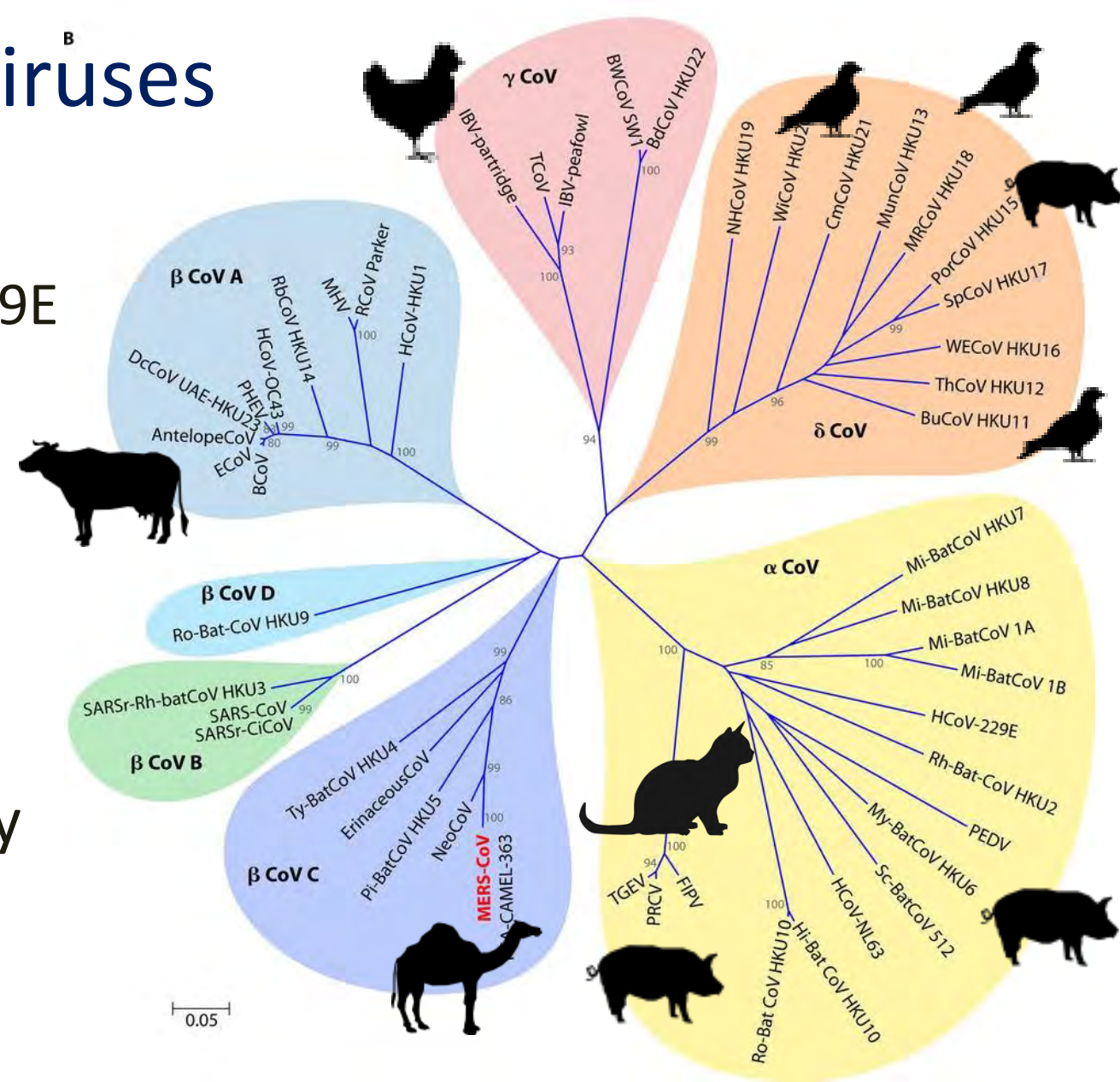
## Priorities

- Prevent wherever possible
- Detect rapidly
- Respond effectively

*Vision: A world safe and secure from global health threats posed by infectious diseases, whether natural, deliberate, or accidental.*

# Zoonotic Origin of Coronaviruses

- 7 known Human Coronaviruses
  - Mild disease: HKU1, OC43, NL63, 229E
  - Severe outbreaks: SARS-CoV, MERS-CoV, SARS-CoV2 (COVID-19)
  - Almost all have zoonotic origins or circulate in animals:
- (bats, camels, cattle, civets?)
- Non-human CoVs such as porcine epidemic diarrhea virus (PEDV) may have emerged by host switching
- One of the most impactful viral families in veterinary medicine

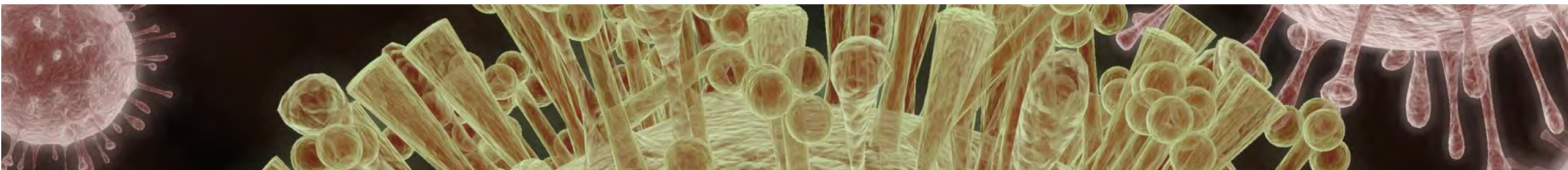






## Why should we protect bats?

- Protect biodiversity & ecosystems
  - Insectivorous – control pests
  - Pollinators – promote agricultural
  - Seed dispersers – connect fragmented landscapes
- Attempts to reduce populations:
  - Generally unsuccessful
  - Encourage recruitment of susceptibles, increasing transmission potential
  - Allow immigration from other areas
  - Stress populations, increasing virus shedding



# PREDICT



**USAID**  
FROM THE AMERICAN PEOPLE



**DEVELOPED** the One Health Workforce by training more than 6,800 people in over 30 countries.



**OPERATIONALIZED** One Health surveillance and sampled over 164K animals and people, helping minimize the spillover of zoonotic disease threats from animals into human populations.



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



**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.

**PREDICT  
PARTNERS:**



# Laboratory Capacity and COVID-19 Response

- PREDICT improved testing capacity in 67 labs in 36 countries
- Built a network of linkages between laboratories, countries and government ministries
- Laboratories have additional tools and the ability to detect newly emerging viruses when assays or sequences do not yet exist
- Importance of these skills was underscored following the emergence of SARS CoV-2 in China
- Teams around the world able to call on the PREDICT network to share experience using PREDICT assays to detect the new virus & provide technical assistance to disease control plans



# Ongoing Obstacles





# ONE HEALTH WORKFORCE CAPACITY STRENGTHENING



AFROHUN



Knight's Landing



**USAID**  
FROM THE AMERICAN PEOPLE



**UC DAVIS**  
One Health Institute  
School of Veterinary Medicine



**SEA OHUN**  
Southeast Asia One Health  
University Network



Ata Health Strategies



**ICAP**  
Columbia University  
Mailman School  
of Public Health

**Berkeley**  
UNIVERSITY OF CALIFORNIA




**UCI** University of  
California, Irvine





GLOBAL  
VIROME  
PROJECT

The Global Virome Project (GVP) is an innovative 10-year partnership to detect the majority of our planet's unknown viral threats. It will pivot our approach from responding to outbreaks to proactively preparing for them. The GVP will mark the beginning of the end of the Pandemic Era.



# Spillover and Wildlife Trade for Consumption: Rethinking our Relationship with Wildlife and Wild Places

Prof. Dr. med.vet. Chris Walzer  
Wildlife Conservation Society  
VetMed Univ. Vienna, Austria



# What **do** we know?

- Zoonoses are diseases that move between animals and humans
- Emerging Infectious Diseases [EID] are dominated by zoonoses
- 72% of all zoonotic EIDs originate in wildlife
- EID frequency is increasing
  - HIV, EBOLA, H1N1, SARS, NIPAH, HENDRA, H7N9



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



## SHORT REPORT

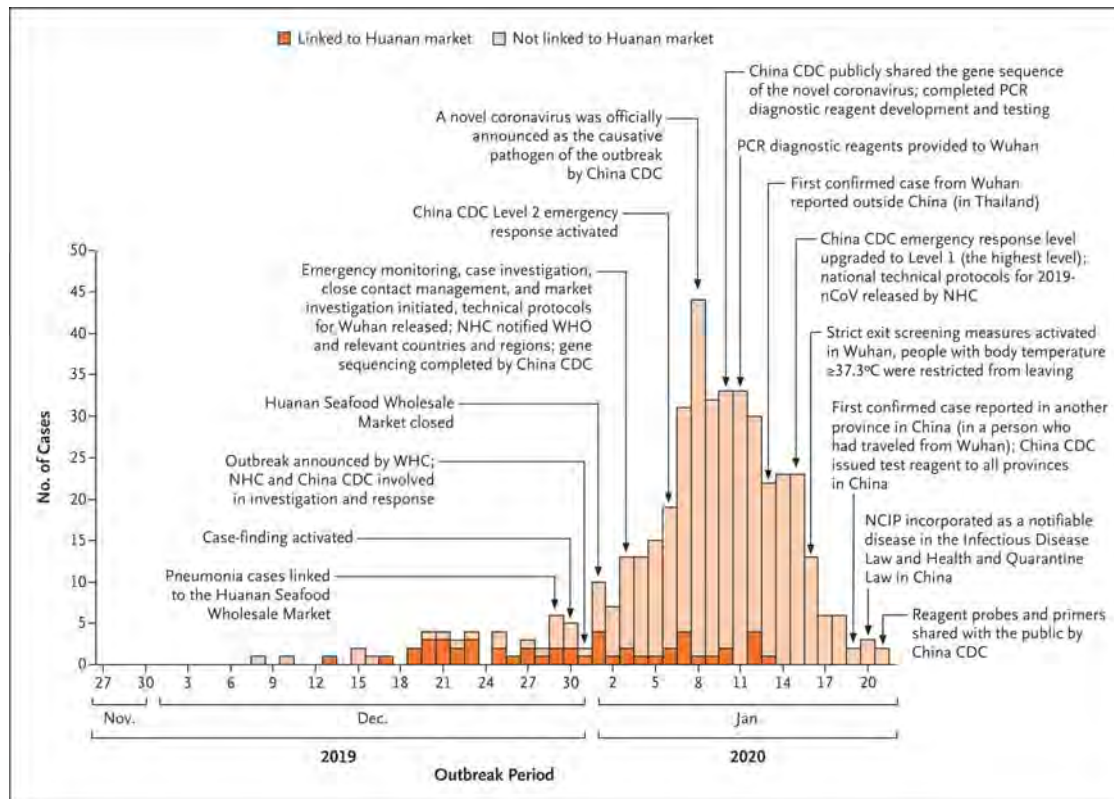
Open Access

### Origin of measles virus: divergence from rinderpest virus between the 11<sup>th</sup> and 12<sup>th</sup> centuries

Yuki Furuse, Akira Suzuki, Hitoshi Oshitani\*



# What do we know?



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

Nanshan Chen\*, Min Zhou\*, Xuesen Xing, Jiansheng Qu\*, Pengyan Gao, Yang Han, Yang Qiu, Jing Wang, Ying Li, Yuan Wei, Jia'an Xia, Ting Ye, Xuesen Xing, Li Zhang

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

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

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

THE NEW ENGLAND JOURNAL OF MEDICINE

### ORIGINAL ARTICLE

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

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

### ABSTRACT







# What do we know?



Contents lists available at ScienceDirect

Infection, Genetics and Evolution

journal homepage: [www.elsevier.com/locate/meegid](http://www.elsevier.com/locate/meegid)



Research paper

## Genetic diversity of coronaviruses in bats in Lao PDR and Cambodia

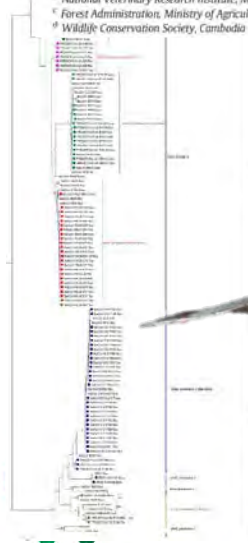
Audrey Lacroix<sup>a</sup>, Veasna Duong<sup>a</sup>, Vibol Hul<sup>a</sup>, Sorn San<sup>b</sup>, Hull Davun<sup>b</sup>, Keo Omaliss<sup>c</sup>, Sokha Chea<sup>d</sup>, Alexandre Hassanin<sup>e</sup>, Watthana Theppangna<sup>f</sup>, Soubanh Silithammavong<sup>g,h</sup>, Kongsy Khammavong<sup>g</sup>,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

<sup>a</sup> Institut Pasteur du Cambodge, Virology Unit, Phnom Penh, Cambodia

<sup>b</sup> National Veterinary Research Institute, Ministry of Agriculture Forestry and Fisheries, Cambodia

<sup>c</sup> Forest Administration, Ministry of Agriculture Forestry and Fisheries, Cambodia

<sup>d</sup> Wildlife Conservation Society, Cambodia



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

### Phylogeny

Admin division

Hubei  
Zhejiang  
Guangdong  
Taiwan  
Nonthaburi  
Ile De France

Washington  
California  
Arizona  
Illinois

WHU02  
WHU01  
Guangdong/20SF014/2020  
WIV06/2019  
Nonthaburi/61/2020  
IPBCAMS-WH-02/2019  
WIV04/2019  
IVDC-HB-01/2019  
IPBCAMS-WH-04/2019  
Guangdong/20SF028/2020  
Guangdong/20SF040/2020  
Guangdong/20SF174/2020  
Zhejiang/WZ-01/2020  
Guangdong/20SF201/2020  
Zhejiang/WZ-02/2020  
Foshan/20SF211/2020  
Foshan/20SF210/2020  
Nonthaburi/74/2020  
Guangdong/20SF025/2020  
Guangdong/20SF013/2020  
Guangdong/20SF012/2020  
USA/AZ1/2020  
Shenzhen/SZTH-002/2020

### Article

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

\*<sup>1</sup> Ben Hu<sup>1</sup>, Lei Zhang<sup>1</sup>, Wei Zhang<sup>1</sup>,  
Hu-Dong Chen<sup>1</sup>, Jing Chen<sup>1</sup>, Yun-Li  
Xiao<sup>1</sup>, Xu-Rui Shen<sup>1</sup>, Xi Wang<sup>1</sup>,  
et al., Fu-Dong Lin<sup>1</sup>, Lin-Lin Liu<sup>1</sup>, Bing Yan,  
Song Li-Si\*

A number of severe acute respiratory  
infections have been discovered in their natural  
reservoirs, including the novel bat SARS-CoV-2.  
We report the identification and  
characterization of a novel coronavirus  
of probable bat origin, which caused an epidemic of  
pneumonia in China. The epidemic, which started  
with laboratory-confirmed infections with 56  
patients, was almost identical to each other and  
furthermore, it was found that  
some level to a bat coronavirus. The  
conserved non-structural proteins show  
in CoV. The 2019-nCoV virus was then  
aid of a critically ill patient, which can be  
spontaneously, we have confirmed that this  
AC12 as SARS-CoV.





# What do we know?

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



Carroll et al. (2018) Science



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

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

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

## INFECTIOUS DISEASES

### *The Global Virome Project*

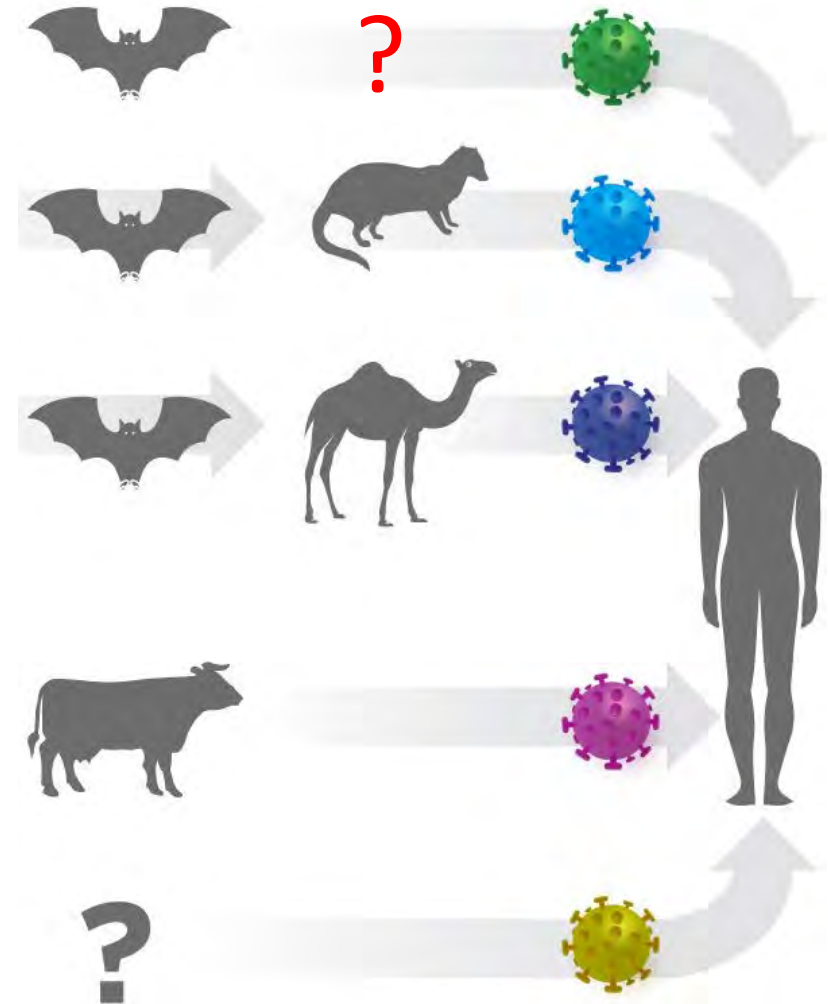
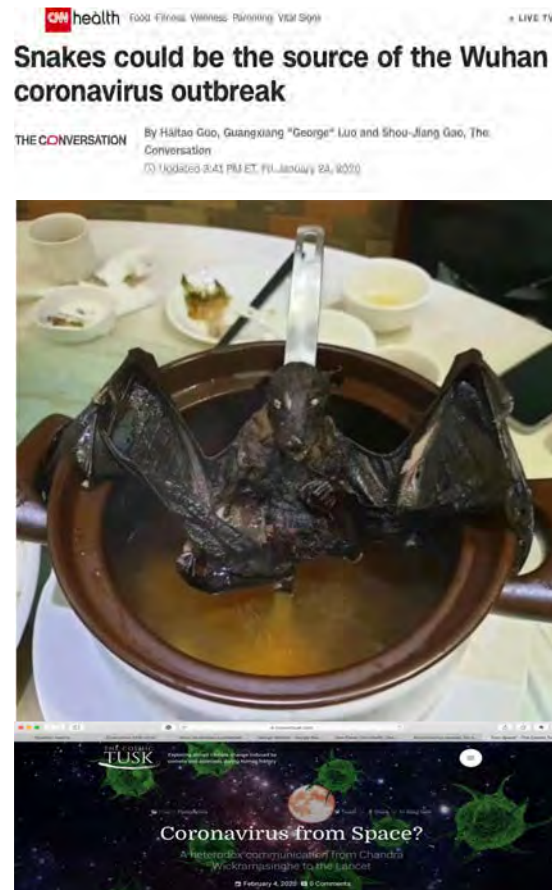
Expanded viral discovery can improve mitigation

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

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



# What do we not know?





It is not about bat-soup,  
civets or pangolins





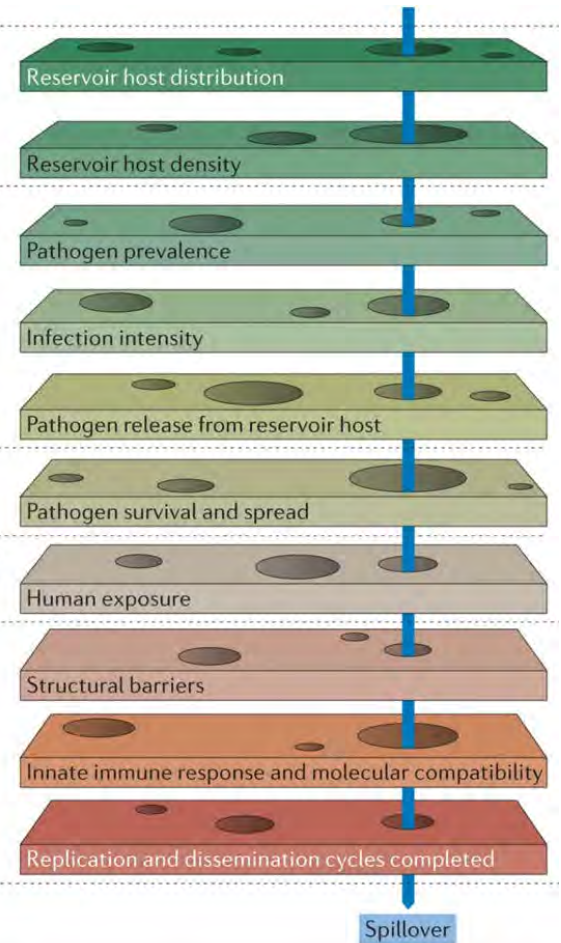
Animal ecology, population biology,  
biogeography, behavioural ecology,  
landscape ecology, agricultural sciences

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

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

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

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



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



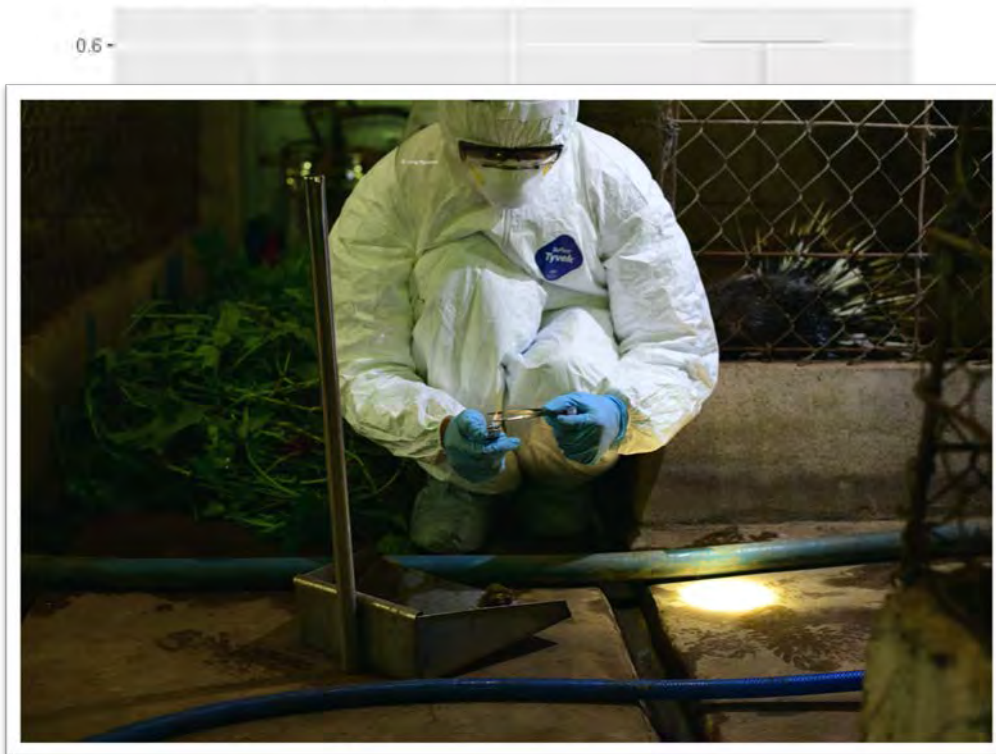




# What do we know?

Detection rates of coronaviruses

0.6 -



trade

large market

restaurant

Field rat value chain interface

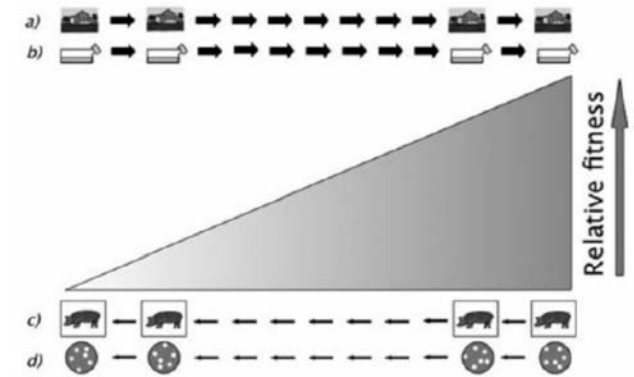


VAN ROEUN





- What do we not know?



**Fig. 1**  
A simplified schematic of fitness variation of a virus following replication in a constant environment

Drew et al 2011. Rev Scien Tech OIE



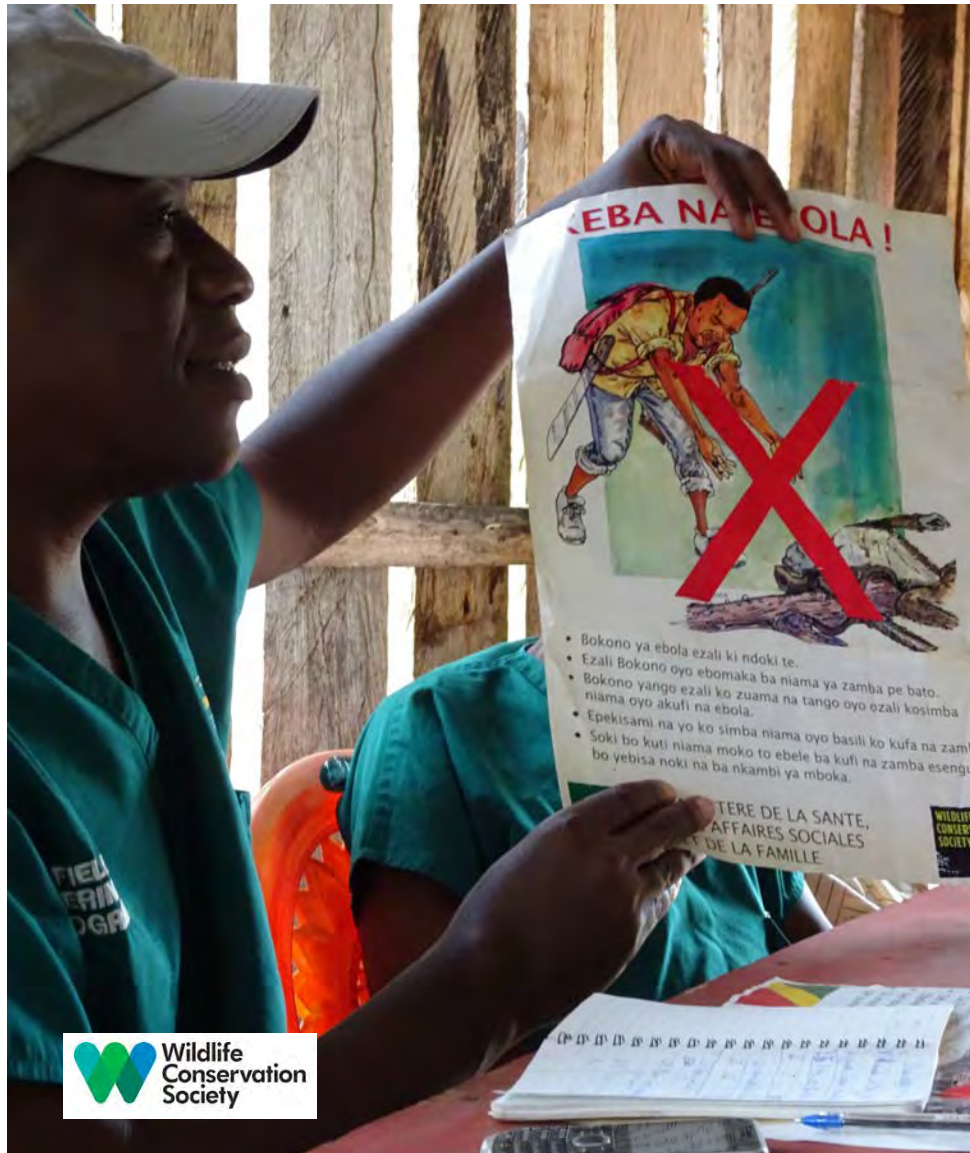
Photo/Xinhua

## IPLC - Congo Basin

- Long-standing program
  - Carcass monitoring [Ebola virus community engagement targeted 6,600 people living in northern RoC]
- Community outreach IPLC needs and rights













# One Health History

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

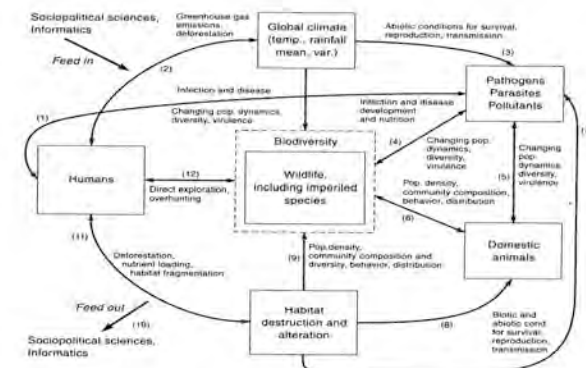


# 2019 Berlin Principles on One Health

- Recognize and take action to: retain the essential health links between humans, wildlife, domesticated animals and plants, and all nature; and ensure the conservation and protection of biodiversity which, interwoven with intact and functional ecosystems, provides the critical foundational infrastructure of life, health, and well-being on our planet



## WCS OAH ONE PLANET, ONE HEALTH, ONE FUTURE



Ostfeld et al. 2002 Mazet et al. JVME 33 2006

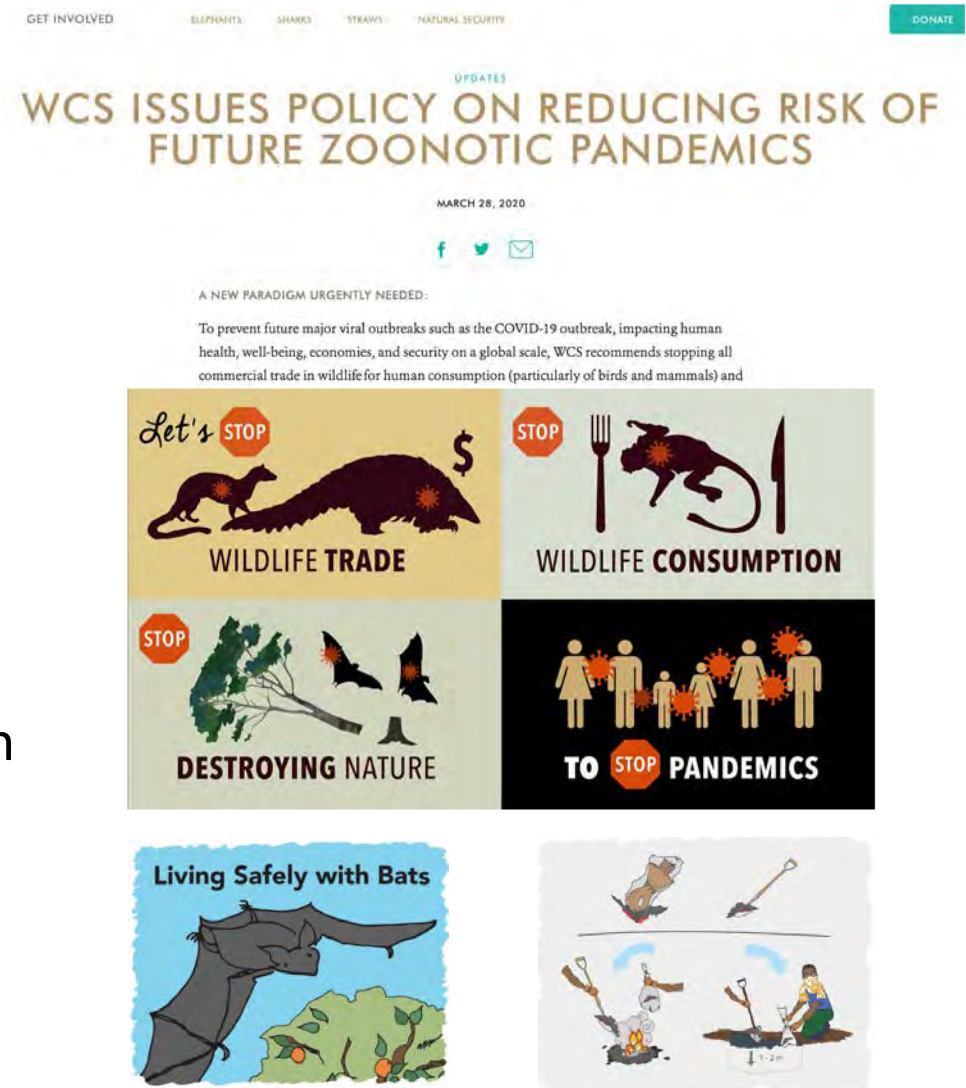
[www.wcs.org/one-planet-one-health-one-future](http://www.wcs.org/one-planet-one-health-one-future)





# What do we need to do?

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



**We Stand for Wildlife™**





# Reducing the Demand for and Trade in Wildlife Products – The View from South-East Asia



K. Yoganand

Regional Lead for Wildlife and Wildlife Crime

WWF Greater Mekong



# Outline

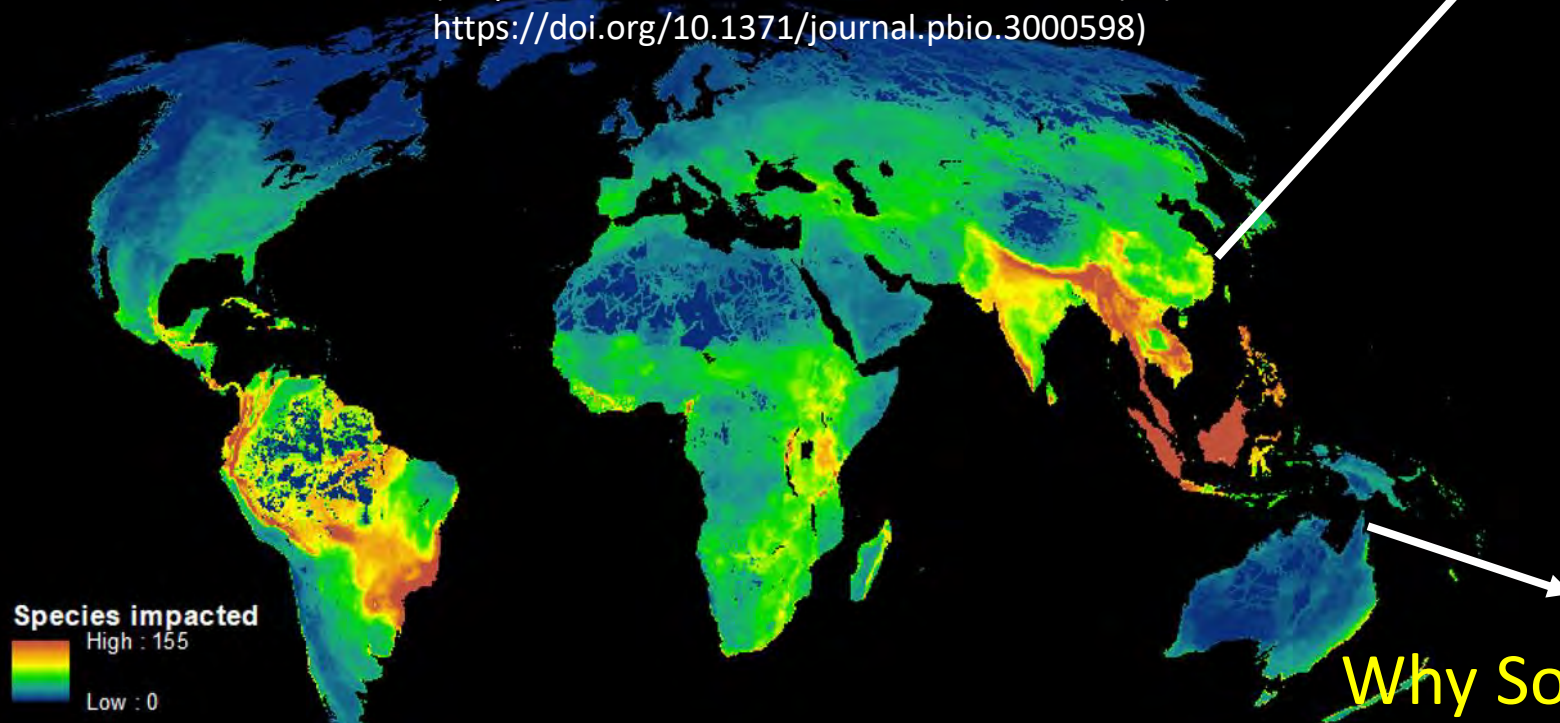
- Key ideas
- Wildlife trade →
  - Declines/extinctions
  - Infectious disease (spillover) risks
- Consumer demand





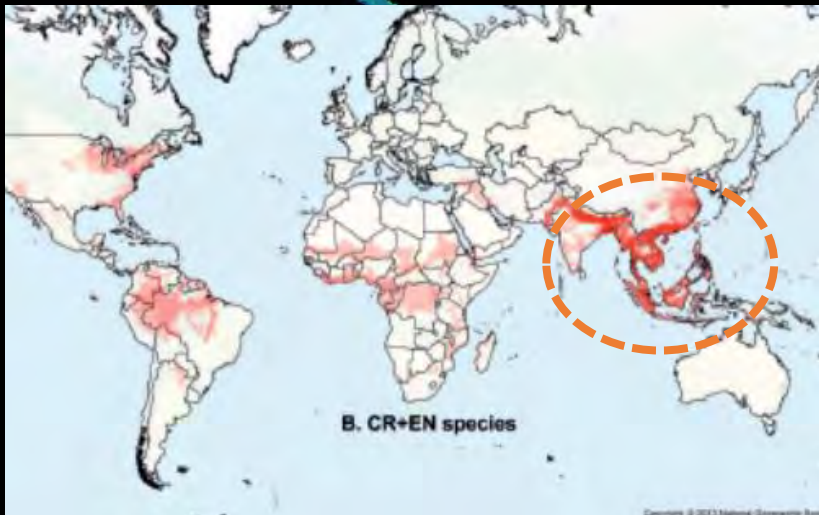
## Hotspots of human impact on threatened vertebrates

(Map credit: Allan, Watson et al. Plos Biol, 17(12): e3000598  
<https://doi.org/10.1371/journal.pbio.3000598>)



### Why South-East Asia?

- Historical species diversity – high
- Population extinctions – >90% ?
- Defaunated landscapes - widespread
- Empty forests - common
- Indiscriminate snaring – crisis



# Why South-East Asia?

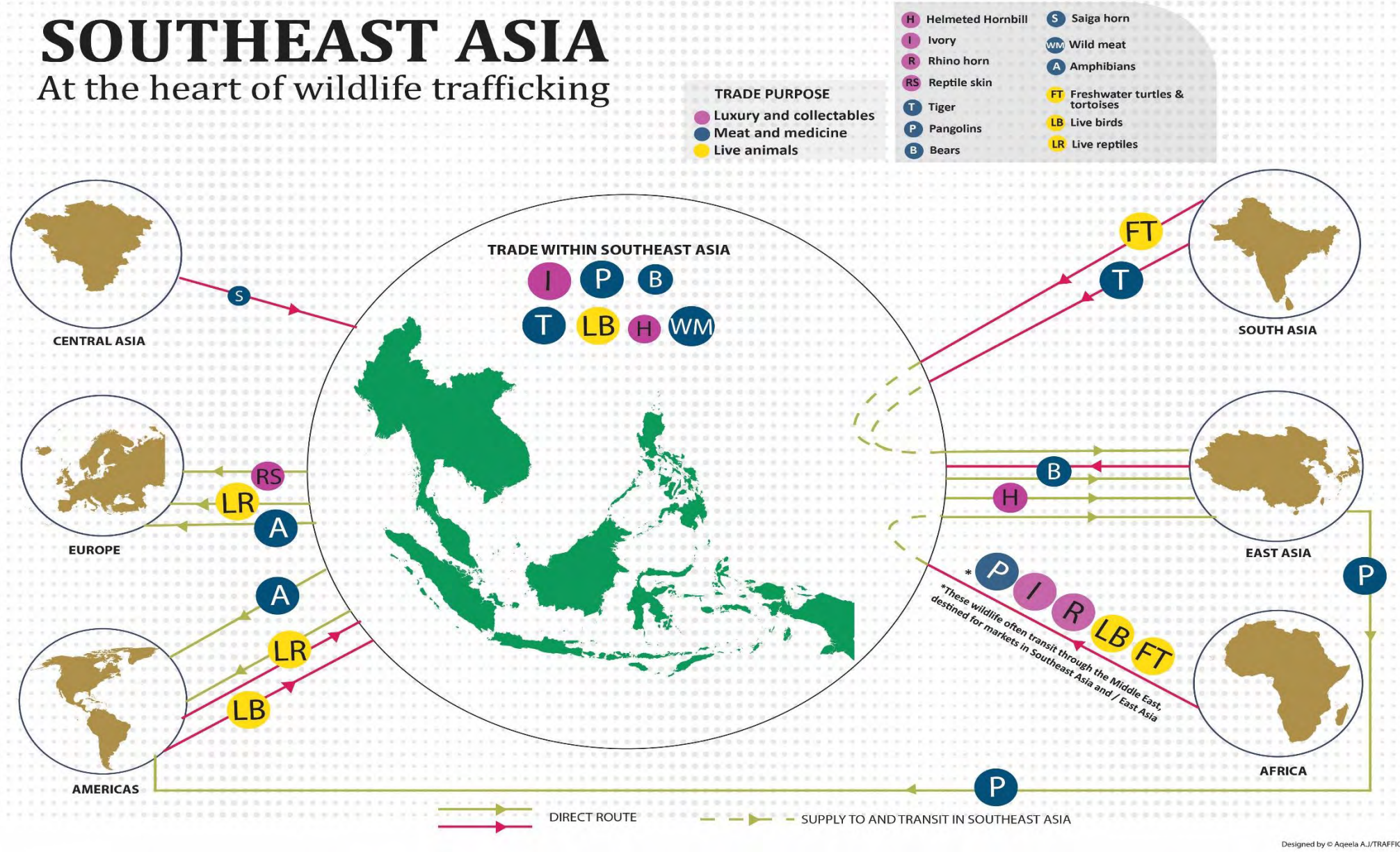
- Trade hotspot, trafficking route
- Largest wildlife market, together with East Asia
- ↑ human population
- ↑ disposal income





# SOUTHEAST ASIA

## At the heart of wildlife trafficking



(Map: Krishnasamy, K. and Zavagli, M. (2020). *Southeast Asia: At the heart of wildlife trade*. TRAFFIC Southeast Asia, Petaling Jaya, Selangor, Malaysia)



# How large is the wildlife trade / market?

(not including timber and fisheries)

Speculative estimates – reliable data is limited

Region	Illegal trade (in billion USD)	Legal trade (in billion USD)
Southeast Asia	1 – 2 /year	3 – 10 /year
East Asia	5 – 10 /year	50 – 100 /year
Global total (including domestic legal trade)	7 – 23 /year (2007 estimate)	150 – 200 /year (15 bn in international trade the early 1990s)

This involves 100s of millions of wild animals, 1000s of species every year (million+ live primates)



J. Bouhuys/TRAFFIC



# What drives the trade?

- Consumer demand
  - Live wildlife – for caged/captive display (“pets”)
  - Wildlife meat – local communities and urban consumers
  - Parts and products for traditional medicine
  - For biomedical research – often international
  - Clothing and fashion (fur, ornaments) – global supply
- Profiteering
- Corruption
- Up to 10 % of the population in SE Asia may be consumers (tbc)





# Laws on wildlife trade and consumption

- Mostly based on species status, population trends
  - often based on outdated or unreliable data
- No international or national protection for many species
- Regulate import, possession, trade, and hunting, but not eating
- Laws regulate wildlife farming, but often weak on enforcement
- **Laws rarely consider infectious disease risks of species/taxa**





# Law enforcement on illegal wildlife trade

- Weak law enforcement
- Legal trade weakly regulated
- Legal trade confuses and strains law enforcement
- Uncontrolled wild sourcing
- Laundering through farms
- Corruption and fraud
- Illegal trade thrives

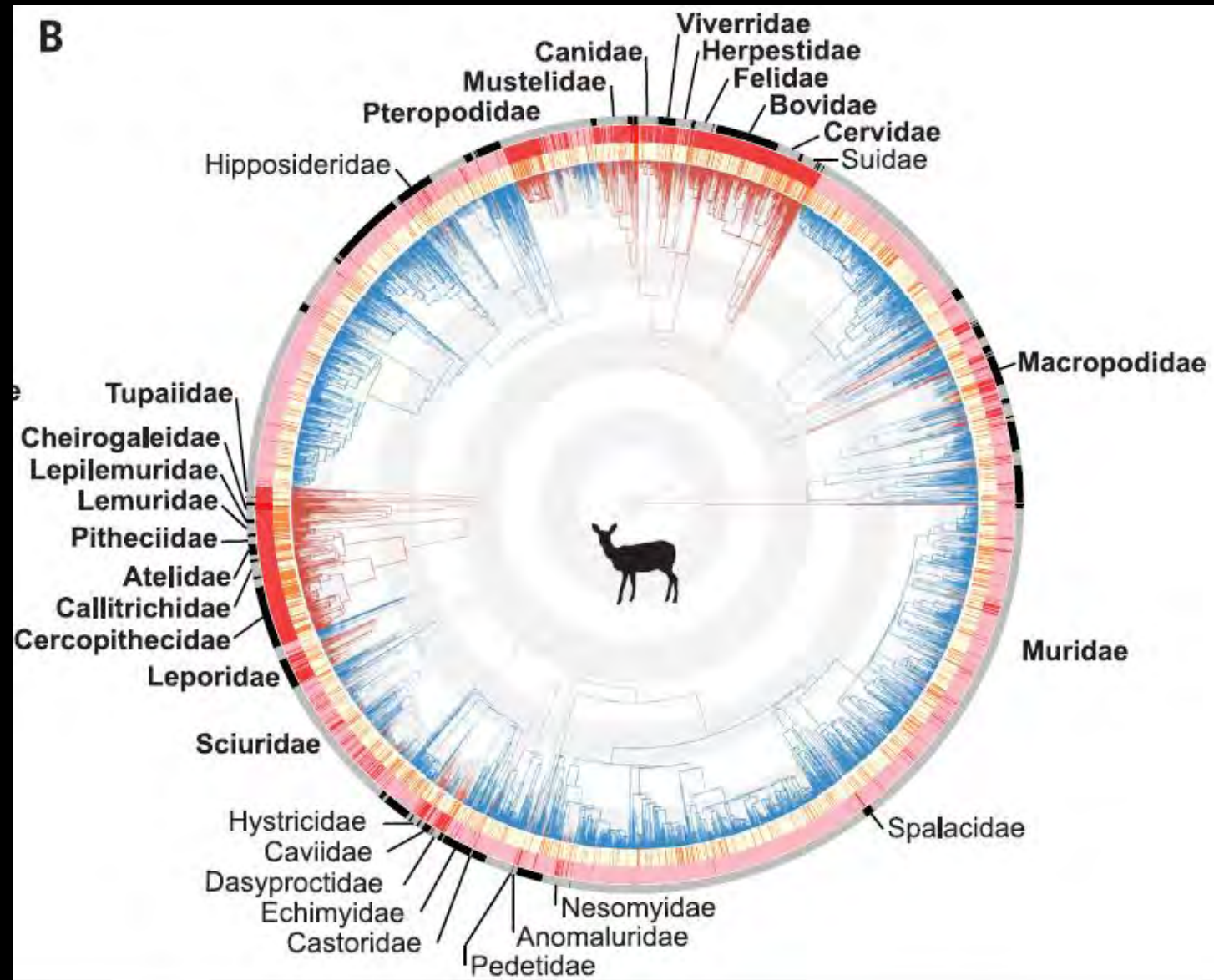




# High-risk taxa

- Prohibit trade and consumption of high-risk taxa
  - for food and traditional medicine
- High-risk taxa
  - viral pathogen transmission risk to humans
  - Provisionally include all mammals and birds
  - Assess all mammal and bird species for risks
  - Particularly high-risk are bats, primates, rodents, carnivores

Mammalian taxa globally traded, often legally  
(sourced from CITES database)



(From: Scheffers et al (2019), Science, 366, 71-76)



# High-risk wildlife trade, farms & markets

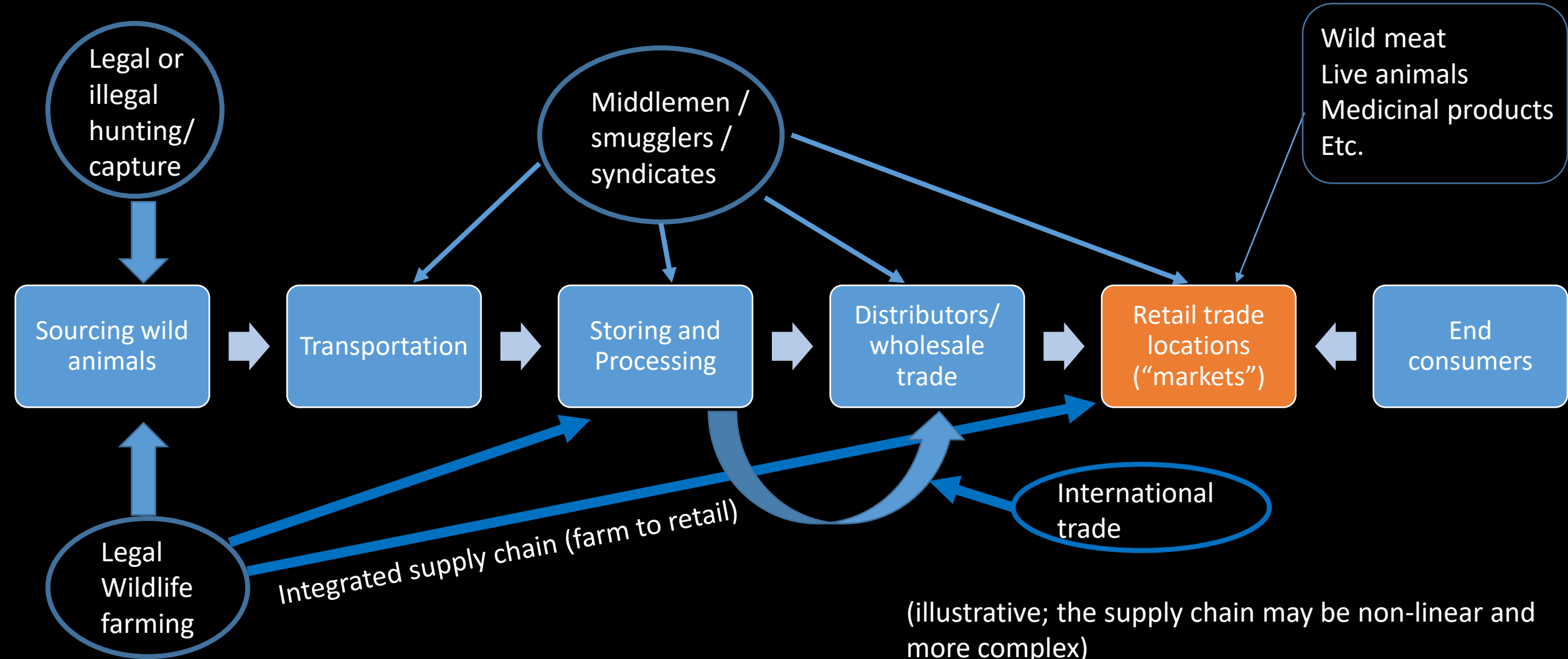
## High-risk market:

- Large volumes of trade
- High human visitation rates
- Live animal, wild meat trade
- Wet markets, highway stalls, tourist centres, wild meat restaurants and farms
- Legal vs illegal – viral disease risk same
  - Legal trade is far larger than illegal trade



# Wildlife trade supply chain –

Risks of spillover at every stage (irrespective of legality)





# Reducing consumer demand

- Identify consumers and motivations for demand
- Target urban consumers for wild meat
- Other consumer segments for medicinal products
- Conduct public outreach on disease risks of wildlife consumption
- Legal bans and ban awareness very effective in reducing demand



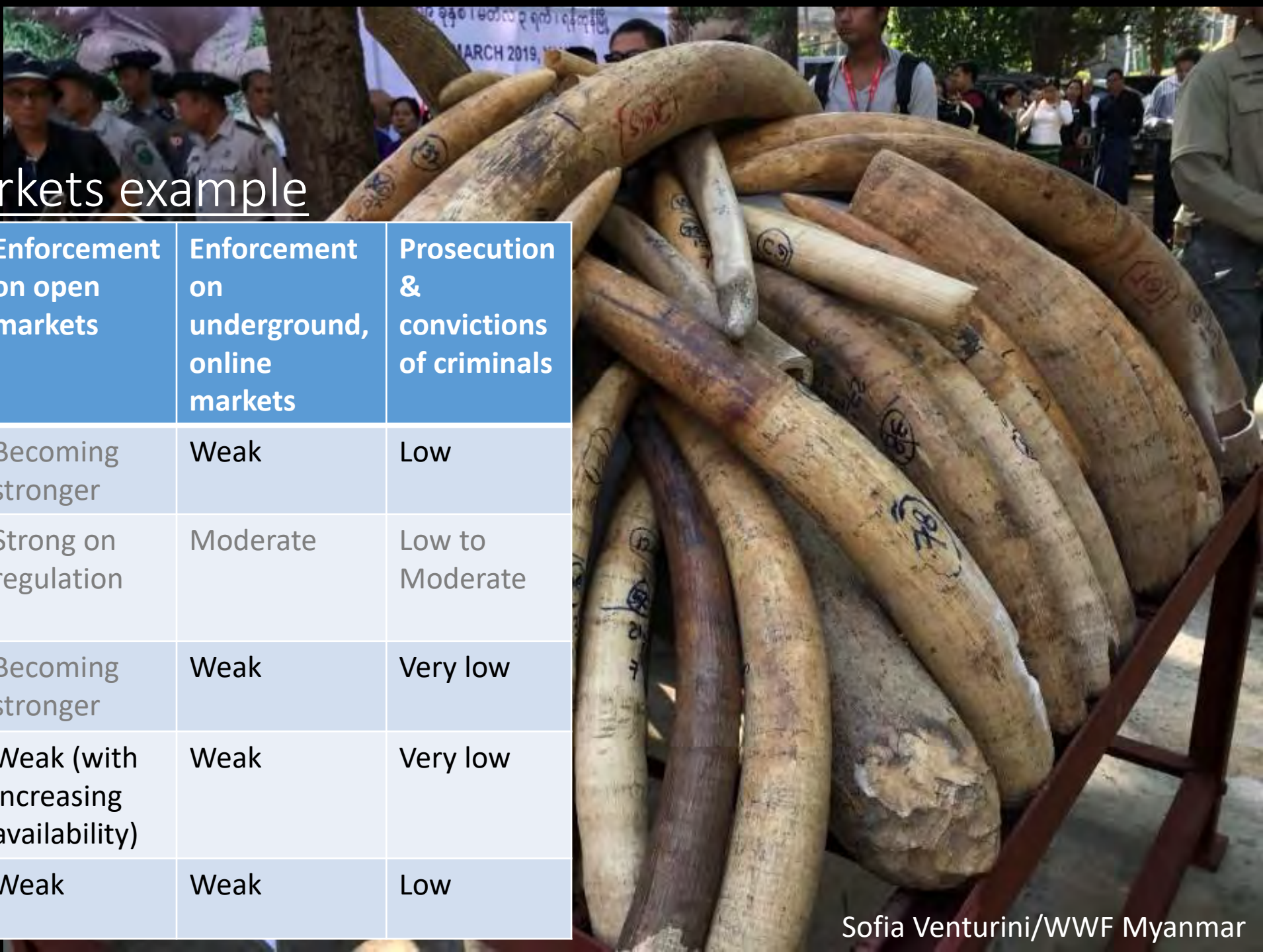
未经允许携带象牙及其制品出入境  
最高将获无期徒刑并没收财产  
Bringing ivory in or out of the country without proper  
permits can result in confiscation and imprisonment

# Policy and enforcement opportunities

- China example of prohibiting trade and consumption of certain taxa for food
- Vietnam made a start but now unknown?
- Immediate prohibition through Prime Minister Orders, followed by changes to law
- Fix policy gaps and weaknesses on other aspects of wildlife trade
- Post-COVID-19 recovery should include increased resources for law enforcement
  - On illegal trade
  - For protection in natural habitats



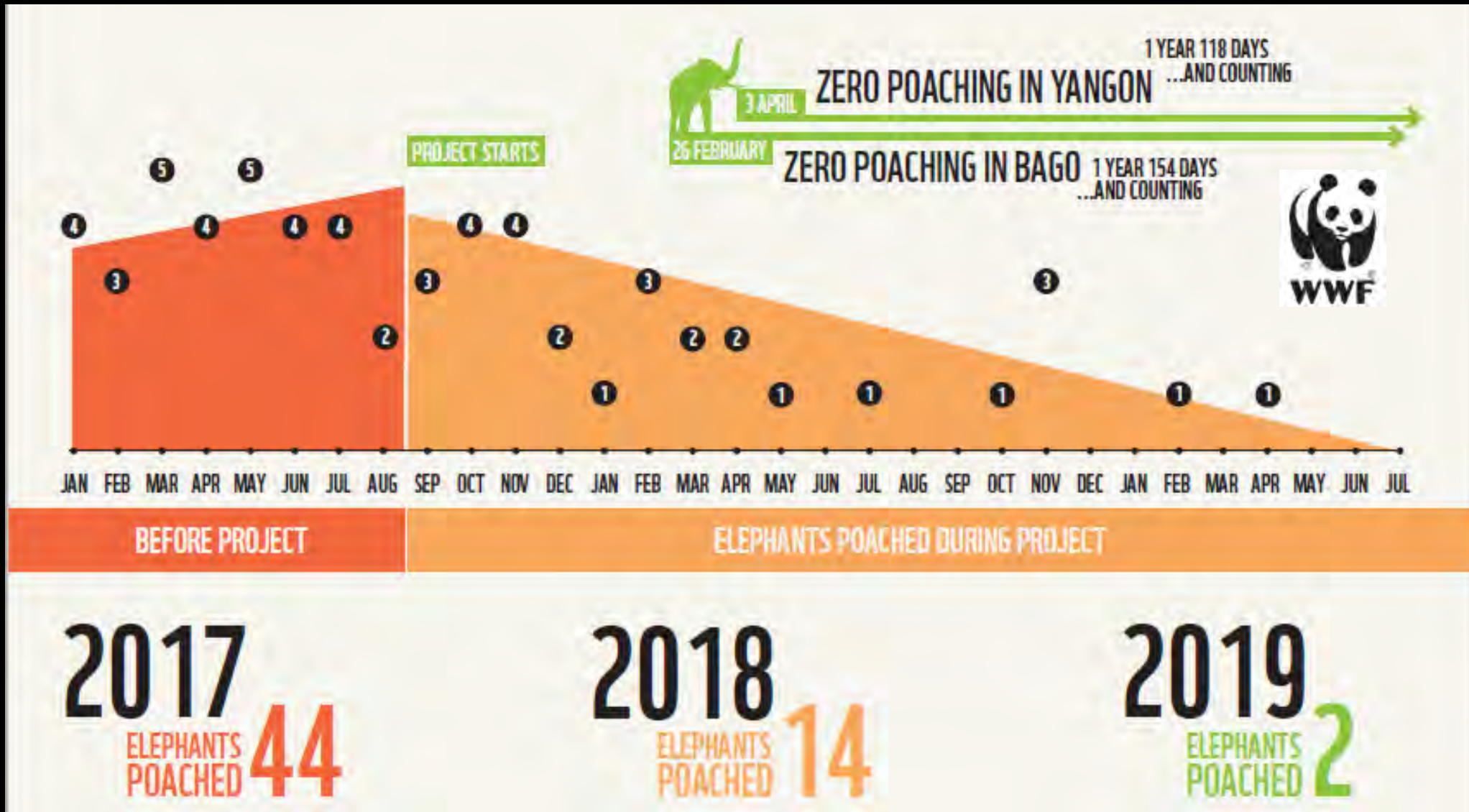




# Elephant ivory markets example

Countries	Legal status of ivory markets	Enforcement on open markets	Enforcement on underground, online markets	Prosecution & convictions of criminals
Myanmar	Closed	Becoming stronger	Weak	Low
Thailand	Partially open, regulated	Strong on regulation	Moderate	Low to Moderate
Laos	Closed	Becoming stronger	Weak	Very low
Cambodia	Closed	Weak (with increasing availability)	Weak	Very low
Vietnam	Closed	Weak	Weak	Low

# Stop the supply – WWF's Zero-poaching work in Myanmar







WWF Laos

Thank you!