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PREDICT CHINA

One Health in action (2009-2020)

A photograph of a man in a purple uniform and black boots walking past a traditional Chinese building with a tiled roof. A tree is in the foreground, and a wooden cart is visible near the building. The scene is set in a rural area with a dirt and gravel ground.

Ten-year joint effort of multi-sectoral partners to strengthen the emerging infectious disease surveillance system and disease response and preparedness capacity in China

CHINA



In the highly biodiverse southern region of China, interactions among humans, wildlife, and livestock are increasing as a result of agricultural intensification, population movements, and urbanization. These changes provide a favorable context for the emergence of zoonotic disease, posing a public health threat particularly to the rural communities where frequent contact with animals occurs, but disease prevention measures are inadequate.

PREDICT China has worked with scientists, communities, and policy makers to discover zoonotic viruses among animal populations before emerging and causing potential pandemics. The project has allowed for an improved understanding of the pathogenesis of zoonotic viruses and the risk of emergence among human communities with the goal of developing targeted approaches to preventing and responding to zoonotic diseases.

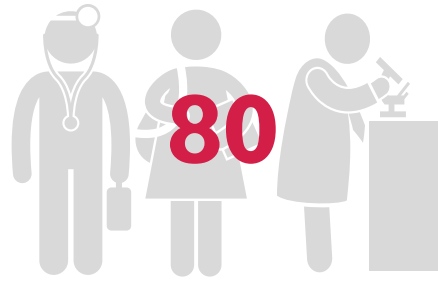
During the past 10 years, the PREDICT project increased capacity of a One Health approach for emerging infectious disease prevention and response. The PREDICT team conducted concurrent virus surveillance among wild animals and human populations in high-risk regions in China, focusing on southern China, which is considered a “hotspot” for emerging zoonotic diseases in areas undergoing

continuous land use change and overexploitation of natural resources. The PREDICT China team also collected human behavioral data to understand the risk factors for zoonotic disease emergence and identify appropriate social and behavioral interventions to reduce risk.

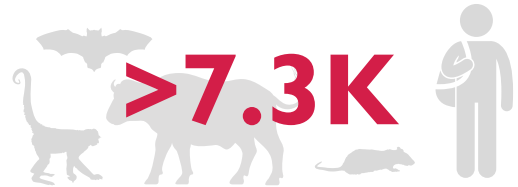
The PREDICT team worked with local laboratory partners to carry out virus characterization and pathogenesis studies to assess the zoonotic potential of detected viruses from surveillance, and developed serological assays for select bat coronaviruses. With support from the PREDICT modeling team, PREDICT China was able to use data collected over the past 10 years to better understand the virus evolution, host-pathogen dynamics, and general ecology of disease emergence.

LOCAL PARTNERS

- Chinese Center for Disease Control and Prevention
- Guangdong Provincial Center for Disease Control and Prevention
- Guangdong Provincial Institute of Public Health
- Institute of Microbiology, Chinese Academy of Sciences
- School of Health Sciences, Wuhan University
- Wuhan Institute of Virology, Chinese Academy of Sciences
- Yunnan Provincial Institute of Endemic Disease Control



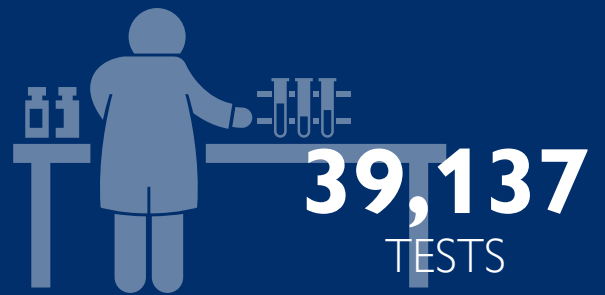
DEVELOPED the One Health Workforce by training 80 people in China.



OPERATIONALIZED One Health surveillance and sampled over 7.3K animals and people, helping minimize the spillover of zoonotic disease threats from animals into human populations.

LABORATORY STRENGTHENING

- Wuhan Institute of Virology of Chinese Academy of Sciences
- Institute of Microbiology of Chinese Academy of Sciences



DETECTED 108 unique viruses in both animal and human populations.

GUANGJIAN ZHU

Country Coordinator, EcoHealth Alliance

“During the past decade I worked for PREDICT, I have seen many scientists join the field for emerging infectious disease research. I hope my work through PREDICT can help set a gold standard for wildlife emerging infectious diseases field research practices in China.”

ACHIEVEMENTS

PREDICT China supported other findings that bats are hosts to diverse coronaviruses (CoVs). The team also detected SARS-related CoVs, and adjacent studies showed some of them can infect human cells and cause disease in the lab mouse model for SARS. Adjacent studies also showed that some of the virus sequences we identified were used to demonstrate Remdesivir's broad efficacy against SARS-CoV and 'pre-pandemic' bat-CoVs. We also found serological evidence of SARS-related viruses in rural populations, suggesting that communities in rural China could be exposed to bat coronaviruses.

We detected a new CoV that may have bat origins, which caused a new disease and killed over 25,000 pigs in south China. This virus,

SARS-CoV, is also able to infect human cells in the laboratory. Finally, adjacent work with collaborators identified the closest known relative to date to the virus causing COVID-19 (SARS-CoV-2).

Throughout our work we have shared results and raised awareness with our Chinese Government partners and other partners including the US Embassy, USG agencies, the WHO, and the public on the knowledge gained of viruses in bats and the potential for spillover of viruses such as SARS-CoV-2. As the COVID pandemic unfolded, we continued to communicate widely on the value of the PREDICT project in understanding coronaviruses in bats, other animals and people.



ONE HEALTH SURVEILLANCE

To promote One Health collaboration in emerging zoonotic disease surveillance, PREDICT China worked with the China Centers for Disease Control and Prevention and its provincial departments, National Forestry and Grassland Administration, FAO China, agricultural universities, and hospitals/clinics to conduct virus surveillance in animal and human populations. Two sites were selected as the sampling sites for concurrent animal and human surveillance (Table 1).

PREDICT China organized joint training on animal surveillance, conducted concurrent field sampling in animals and people, and established a communication and coordination network among multisectoral partners for timely results-sharing. PREDICT China's work has helped developed a culture of One Health collaboration in China that receives strong support from the government.

TABLE 1. Animals and humans sampled at concurrent community surveillance sites.

	NO. OF SAMPLING EVENTS	NO. OF ANIMALS SAMPLED	NO. OF HUMANS SAMPLED
CONCURRENT SITE 1	7	578	200
CONCURRENT SITE 2	8	473	300

VIRUS DETECTION

The PREDICT project's strategy for virus detection included screening samples using broadly reactive consensus PCR (cPCR) for priority virus families, including coronaviruses, filoviruses, flaviviruses, paramyxoviruses, and influenza virus. Viruses detected via these assays were sequenced to investigate their relationship to known pathogens, and samples were prioritized for further characterization based on these results. This approach allows for detection of both known and novel viruses and improves our understanding of the potential for the virus to cause disease in humans and/or animals.

This approach led to the discovery of a remarkable diversity of viruses in bats, particularly coronaviruses, including close relatives of SARS-CoV and SARS-CoV-2. Our work provides further evidence that both of these human pathogens originated in bats, and that there is substantial potential for further spillover. Working in collaboration with NIAID-funded partners, we demonstrated that some of the newly discovered bat-CoVs were able to bind to human cells, infect them in vitro, and cause SARS-like disease in a lab animal model. Our findings led to the discovery that Remdesivir – the only drug currently known to have efficacy against COVID – could also disrupt replication of bat-CoVs that are on the cusp of emergence.

PREDICT China also discovered a range of paramyxoviruses in bats and both paramyxoviruses and CoVs in rodents. The team sampled wild and captive bred bamboo rats (a widely farmed and consumed species) to assess whether wildlife farming amplified virus prevalence and therefore risk of spillover. We found no evidence that it did, but the sample size was small for wild rodents given their widespread hunting.

Of the 29 CoVs detected during PREDICT-2, 26 were found in bat hosts while two species of commensal rodent, the Norway rat and Oriental house rat, were found to host three known CoVs: Murine CoV, Rodent CoV, and Longquan Aa mouse CoV. Insectivorous bats, primarily members of the genera *Hipposideros*, *Rhinolophus*, *Miniopterus*, and *Myotis*, were host to 23 of the 26 (88.5%) bat-CoVs, seven of which are novel viruses detected as a result of PREDICT project surveillance. Members of the fruit bat family, Pteropodidae, hosted five CoVs, two of which are novel viruses. Furthermore, two CoVs were found in both insectivorous and fruit bat

species, demonstrating the ability of these viruses to infect a diversity of bat hosts.

Paramyxovirus (PMV) diversity was also high – a total of 20 unique viruses (three known and 17 novel) were detected in bats and rodents throughout PREDICT-2. Similar to CoV findings, insectivorous bats were the dominant hosts (18 of 20 viruses). However, bat-PMV abundance was relatively low, as each virus was only detected 1-2 times in contrast to bat-CoVs, where we detected each virus an average of 16 times (range: 1 – 69). In addition to the insectivorous bat-PMV findings, one novel virus, PREDICT-PMV-123, was found in a single fruit bat (Dawn bat; *Eonycteris spelaea*), and multiple Norway rats tested positive for the known Beilong virus.

The only virus to be detected in humans was Influenza A, a well-known pathogen of humans and animals, found in an adult male. This single detection was a result of syndromic surveillance efforts in Guangdong Province.

TABLE 2. Virus heatmap for bats and rodents/shrews and by disease transmission interface

	Viral Test Type				
	Coronaviruses	Filoviruses	Flaviviruses	Influenzas	Paramyxoviruses
Aselliscus (bats)	0.9% (1236)	0% (618)	0% (216)	0% (834)	0.3% (618)
Chaerephon (bats)	0% (128)	0% (64)	0% (50)	0% (114)	0% (64)
Eonycteris (bats)	15% (520)	0% (260)	0% (260)	0% (520)	0.4% (260)
Hipposideros (bats)	1.6% (812)	0% (406)	0% (388)	0% (794)	0.5% (406)
la (bats)	0% (72)	0% (36)	0% (32)	0% (68)	8.3% (36)
Megaderma (bats)	0% (60)	0% (30)	0% (30)	0% (60)	0% (30)
Miniopterus (bats)	16.8% (956)	0% (478)	0% (294)	0% (760)	1% (478)
Myotis (bats)	10.8% (1356)	0% (678)	0% (300)	0% (978)	0.4% (678)
Rhinolophus (bats)	10.2% (1916)	0% (958)	0% (756)	0% (1714)	0.4% (958)
Rousettus (bats)	6.5% (260)	0% (130)	0% (98)	0% (228)	0% (130)
Tadarida (bats)	0% (136)	0% (68)	0% (62)	0% (130)	0% (68)
Taphozous (bats)	0% (580)	0% (290)	0% (290)	0% (580)	1% (290)
Tylonycteris (bats)	0% (288)	0% (144)	0% (144)	0% (288)	0% (144)
Apodemus (rodents/shrews)	0% (8)	0% (4)		0% (4)	0% (4)
Crocidura (rodents/shrews)	0% (48)	0% (24)		0% (24)	0% (24)
Eothenomys (rodents/shrews)	0% (24)	0% (12)		0% (12)	0% (12)
Mus (rodents/shrews)	0% (160)	0% (80)		0% (80)	0% (80)
Niviventer (rodents/shrews)	0% (76)	0% (38)		0% (38)	0% (38)
Rattus (rodents/shrews)	4.2% (1392)	0% (696)		0% (696)	2.7% (696)
Rhizomys (rodents/shrews)	0% (516)	0% (258)		0% (258)	0% (258)
Tupaia (rodents/shrews)	0% (44)	0% (22)		0% (22)	0% (22)
Unknown (rodents/shrews)	0% (12)	0% (6)		0% (6)	0% (6)
	Coronaviruses	Filoviruses	Flaviviruses	Influenzas	Paramyxoviruses
animal production	0% (560)	0% (280)		0% (280)	0% (280)
crop production	0% (80)	0% (40)		0% (40)	0% (40)
crop production; dwellings	0% (56)	0% (28)	0% (28)	0% (56)	0% (28)
crop production; dwellings; natural areas	3.7% (3528)	0% (1764)	0% (398)	0% (2162)	0.2% (1764)
crop production; natural areas	9.9% (4316)	0% (2158)	0% (1758)	0% (3916)	0.8% (2158)
dwellings	9.2% (1060)	0% (530)	0% (236)	0% (754)	3.6% (530)
dwellings; natural areas	4.5% (516)	0% (258)	0% (258)	0% (516)	0.8% (258)
natural areas	0% (484)	0% (242)	0% (242)	0% (484)	0% (242)

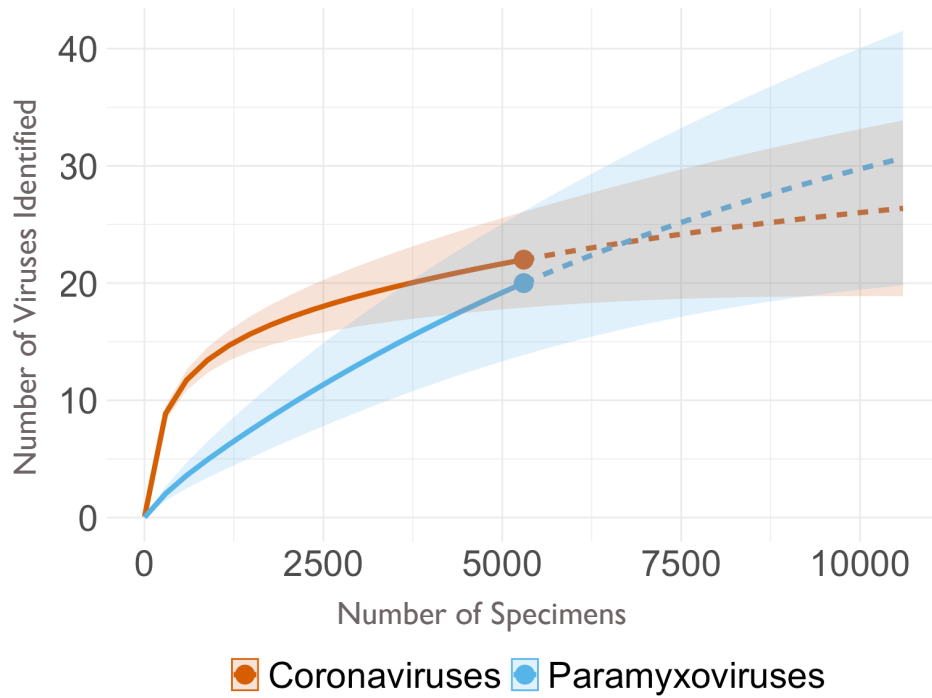


FIGURE 1. Virus discovery in China. The extensive sampling of bats in China led to evidence of the beginning of saturation of the discovery curve for coronaviruses. This suggests that it would be possible to identify the majority of currently unknown CoVs in China, given relatively unsubstantial further sampling and testing.

VIRUS TABLE

VIRUS FAMILY	VIRUS	SPECIES	SAMPLING LOCATION	# OF POSITIVE INDIVIDUALS
Coronavirus	PREDICT_CoV-22	Dawn Bat, Leschenault's Rousette	Xishuangbanna	43
	PREDICT_CoV-23	Dawn Bat	Xishuangbanna	1
	PREDICT_CoV-53	Intermediate Roundleaf Bat	Guilin	2
	PREDICT_CoV-60	Chinese Water Myotis	Chuxiong	17
	PREDICT_CoV-79	Least Horseshoe Bat	Guilin	37
	PREDICT_CoV-95	Intermediate Roundleaf Bat	Guilin	2
	PREDICT_CoV-107	Rickett's Big-Footed Bat	Chuxiong	3
	PREDICT_CoV-108	Himalayan Whiskered Myotis, Least Horseshoe Bat	Guilin	7
	PREDICT_CoV-111	Chinese Water Myotis	Chuxiong	1
	Bat coronavirus 1	Schreiber's Long-Fingered Bat, Small Long-Fingered Bat	Guangzhou, Jinning	69
	Bat coronavirus 512/2005	Rickett's Big-Footed Bat	Chuxiong	1
	Bat coronavirus Anlong 57/43	Himalayan Whiskered Myotis	Guilin	1

	Bat coronavirus HKU2	Chinese Horseshoe Bat, Himalayan Whiskered Myotis, Intermediate Horseshoe Bat, Least Horseshoe Bat, Stoliczka's Trident Bat, Thomas's Horseshoe Bat	Chuxiong, Guandong, Guilin, Jinning, Xishuangbanna	77	
	Bat coronavirus HKU6	Chinese Water Myotis, Daubenton's Myotis, Himalayan Whiskered Myotis, Rickett's Big-Footed Bat, Small Long-Fingered Bat	Chuxiong, Guandong, Guilin, Jinning	62	
	Bat coronavirus HKU8	Schreiber's Long-Fingered Bat	Guangzhou, Jinning	7	
	Bat coronavirus HKU9	Dawn Bat, Intermediate Roundleaf Bat, Leschenault's Rousette	Chuxiong, Guilin, Xishuangbanna	11	
	Bat coronavirus HKU10	Large-Eared Roundleaf Bat, Stoliczka's Trident Bat	Guilin, Xishuangbanna	6	
	Bat coronavirus RS3376	Chinese Horseshoe Bat	Jinning	1	
	Bat coronavirus RS4125/4259	Thomas's Horseshoe Bat	Xishuangbanna	1	
	Hipposideros bat alphacoronavirus MJ/67C	Intermediate Horseshoe Bat, Stoliczka's Trident Bat	Xishuangbanna	6	
	Myotis alphacoronavirus	Fringed Long-Footed Myotis	Chuxiong	1	
	Rhinolophus/Hipposideros alphacoronavirus	Intermediate Horseshoe Bat	Xishuangbanna	4	
	Rousettus bat coronavirus GCCDC1/346/356	Chinese Horseshoe Bat, Dawn Bat, Leschenault's Rousette	Jinning, Xishuangbanna	36	
	Rousettus bat coronavirus/NRC-2	Leschenault's Rousette	Chuxiong	1	
	SARS-related bat coronavirus RsSHC014	Intermediate Horseshoe Bat	Chuxiong	1	
	SARS-related betacoronavirus Rp3/2004	Chinese Horseshoe Bat, Intermediate Horseshoe Bat, Thomas's Horseshoe Bat	Chuxiong, Guangzhou, Jinning, Xishuangbanna	17	
	Longquan Aa mouse coronavirus	Norway Rat	Guangzhou	3	
	Murine coronavirus	Norway Rat, Oriental House Rat	Guangzhou, Xishuangbanna	17	
	Rodent coronavirus	Norway Rat	Guangzhou	14	
Paramyxovirus	PREDICT_PMV-47	Great Evening Bat	Chuxiong	2	
	PREDICT_PMV-49	Black-Bearded Tomb Bat, Unidentified Taphozous Bat	Guilin	2	
	PREDICT_PMV-88	Intermediate Horseshoe Bat	Xishuangbanna	1	
	PREDICT_PMV-89	Chinese Horseshoe Bat	Jinning	1	
	PREDICT_PMV-90	Black-Bearded Tomb Bat	Guilin	1	
	PREDICT_PMV-123	Dawn Bat	Xishuangbanna	1	
	PREDICT_PMV-129	Chinese Horseshoe Bat	Guangzhou	1	
	PREDICT_PMV-130	Fringed Long-Footed Myotis	Chuxiong	1	
	PREDICT_PMV-134	Chinese Horseshoe Bat	Guilin	1	
	PREDICT_PMV-135	Stoliczka's Trident Bat	Xishuangbanna	1	
	PREDICT_PMV-136	Unidentified Taphozous Bat	Guilin	1	
	PREDICT_PMV-157	Schreiber's Long-Fingered Bat	Jinning	2	
	PREDICT_PMV-158	Schreiber's Long-Fingered Bat	Jinning	2	
	PREDICT_PMV-162	Schreiber's Long-Fingered Bat	Jinning	1	
	PREDICT_PMV-164	Stoliczka's Trident Bat	Xishuangbanna	1	
	PREDICT_PMV-165	Chinese Water Myotis	Chuxiong	1	
	PREDICT_PMV-166	Chinese Water Myotis	Jinning	1	
	Bat paramyxovirus BtHp-ParaV/GD2012	Intermediate Roundleaf Bat	Guilin	2	
	Bat paramyxovirus/B16-40	Schreiber's Long-Fingered Bat	Jinning	1	
	Beilong virus	Norway Rat	Guangzhou	19	
	Influenza virus	Influenza A	Human	The 1st Affiliated Hospital of Shantou University	1

Total

493

EPIDEMIOLOGIC & BEHAVIORAL RISK

For PREDICT-2, our team in China conducted surveillance in both community and clinical settings by employing an integrated biological-behavioral surveillance approach. Through this approach, PREDICT China aimed to assess spillover potential of emerging

zoonotic viruses at high-risk, human-animal interfaces and to use an evidence-based approach to identify behavioral risk factors associated with those interfaces. Ultimately this surveillance resulted in development of risk-mitigation strategies tailored to local contexts, including community education around our *Living Safely with Bats* risk reduction and behavior change communication resource.

DEMOGRAPHIC CHARACTERISTICS OF STUDY PARTICIPANTS

Variable		Community (n=500)		Hospital (n=218)	
		n	%	n	%
Gender	Female	280	56	103	47
	Male	220	44	115	53
Age	Under 18 years	1	0	116	53
	18-44 years	108	22	30	14
	45-64 years	280	56	42	19
	65 or older	111	22	30	14
Residence time	< 1 month	0	0	2	1
	> 1 month - 1 year	0	0	7	3
	> 1 - 5 years	4	1	96	44
	> 5 -10 years	22	4	16	7
	> 10 years	474	95	97	44
Education	None	92	18	103	47
	Primary	255	51	32	15
	Secondary	141	28	53	24
	College/University	10	2	30	14
Livelihood	Crop production	440	88	0	0
	Labor work	25	5	8	4
	Homemaker	7	1	7	3
	Animal production	9	2	3	1
	Non-animal business	8	2	44	20
	Children/Student	0	0	117	54
	Medical worker	1	0	2	1
	Unemployed	8	2	37	17
Self-report unusual symptoms in the past 12 months	Fever with headache and severe fatigue or weakness (encephalitis)	73	15	11	5
	Fever with cough and shortness of breath or difficulty breathing (SARI)	54	11	48	22
	Fever with muscle aches, cough, or sore throat (ILI)	69	14	68	31
	Fever with bleeding or bruising not related to injury (hemorrhagic fever)	2	0	1	0
	Fever with diarrhea or vomiting	10	2	15	7
	Others	23	5	7	3
	None	378	76	85	39

PREDICT China conducted biological-behavioral surveillance among rural residents in Yunnan, Guangxi, and Guangdong districts of Southern China, where the team had previously identified SARS-related CoVs in bats. In addition to the samples collected for virus detection, the PREDICT team

collected serum samples from people that were evaluated for antibodies against four bat-borne coronaviruses (using a new ELISA assay based on selected nucleocapsid proteins). Surveys were administered to collect data on human-animal contact and zoonotic disease spillover risk. In this

research, almost 20% of participants reported severe acute respiratory infections (SARI) and/or influenza-like illness (ILI) symptoms in the past year. Risk factors associated with these self-reported symptoms included poultry, carnivore, rodent/shrew, or bat contact along with socioeconomic factors, such as income and district of residence. Nine participants (0.6%) tested positive for antibodies against bat coronaviruses, suggesting bat coronavirus spillover in individuals in these communities. These results highlight the utility of an hypothesized early-warning system under non-outbreak conditions to detect the spillover event of emerging zoonotic diseases by extending the traditional clinical-based surveillance to at-risk communities.

The decade-long PREDICT project allowed the team to establish a biobank and database which will enable cost-effective future surveillance programs and in-depth studies for zoonotic disease prevention and control.

BEHAVIORAL RISK INVESTIGATIONS

PREDICT China also conducted ethnographic interviews and field studies in the rural communities of Yunnan, Guangxi, and Guangdong provinces. Data were analyzed to identify both risk and protective factors for zoonotic disease emergence at the individual, community, and policy levels (Figure 2). A total of 88 ethnographic interviews and 55 field observations were conducted at nine sites. The study provides evidence of frequent human-animal interactions in these communities and identifies key behavioral risk factors that can be targeted for mitigation strategies to reduce the risk of disease emergence. Existing local programs and policies around human and animal health, community development, and conservation are considered effective resources for developing cost-effective strategies to mitigate zoonotic disease risks.

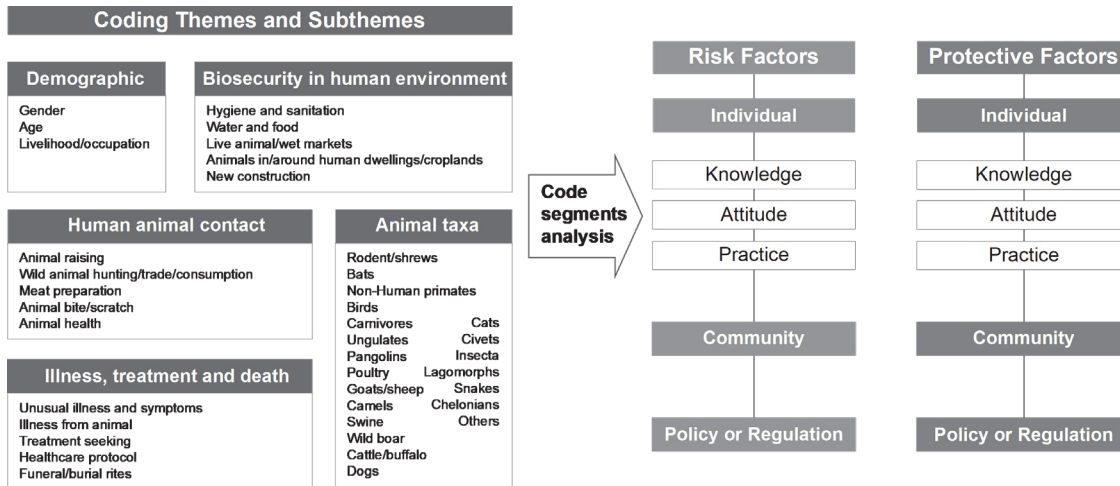


FIGURE 2. Qualitative method to identify the risk factors of zoonotic disease emergence.



Given the likely large number of undiscovered zoonotic pathogens currently in circulation in China, measures to reduce human-wildlife contact due to specific behaviors are urgently needed. This is particularly important for rural communities where close contact with bats and rodents was reported and zoonotic pathogens have been detected in animal populations. Enforcement of current wildlife protection policies coupled with capacity building in local clinics would likely significantly reduce high-risk contact between humans, wildlife, and livestock and risk for disease emergence and spread.



COMMUNITY ENGAGEMENT & RISK COMMUNICATION

PREDICT China presented the results of surveillance activities to agency leads from the China CDC, Provincial and city CDCs in Yunnan, Guangdong, Beijing, and Shanghai. Behavioral risk surveys at all sites included presentation of results to communities where sampling and analysis took place.

CAPACITY STRENGTHENING

Although a national emerging infectious disease surveillance and reporting system was established in China following the SARS outbreak in 2002, the clinical-based effort is reaction-driven versus a proactive approach. PREDICT China worked with Chinese researchers and the government to expand surveillance to animals for early detection and proactive prevention. By working with both humans and animals, PREDICT China built communication and collaboration platforms which brought multisectoral stakeholders together for more effective and efficient surveillance.

In addition, the PREDICT China field team has significantly contributed to increased capacity for in-country field practices by providing training to different ecology, zoology, and virology research groups on field biosafety and humane animal sampling. Through the in-country partners, training was conducted for broad external partners from African and Asian countries.

OUTBREAK PREPAREDNESS & RESPONSE

A novel bat-origin coronavirus, swine acute diarrhea syndrome coronavirus (SADS-CoV), caused fatal swine disease outbreaks in Guangdong Province, during 2016-2018, leading to the death of more than 25,000 pigs. PREDICT China worked closely with agricultural researchers to identify the pathogen and investigate the ecology of transmission to provide recommendations for prevention measures. In the two years following the outbreak, PREDICT China has conducted regular surveillance among bat populations around farms in Guangdong Province, and worked with the global modeling team to assess the potential for future spillover from bats to pigs across China.

PRACTICAL IMPLICATIONS

- Identification of hundreds of bat-origin CoV sequences
- Discovery of a large diversity of CoVs closely related to SARS-CoV and SARS-CoV-2
- Identification of bat-CoVs with clear potential to emerge directly in people
- Identification of a novel bat-origin virus, SADS-CoV, causing widespread outbreak in pigs in Southern China

FURTHER READING

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SPECIAL FEATURES



ONE HEALTH ACTION RESPONDING TO THE FATAL SWINE ACUTE DIARRHEA (SADS) SYNDROME OUTBREAKS

From October 2016, a fatal swine disease outbreak was observed in a pig farm in Guangdong province, China, causing severe acute diarrhea and vomiting, leading to death in newborn piglets (younger than five days) with a mortality of 90%. By May 2017, the disease had caused 24,693 piglet deaths at four farms. The clinical signs and preliminary lab testing suggested it was a novel disease caused by coronaviruses.

Learn more at p2.predict.global/strengthening-health-security



UNDERSTANDING THE CROSS-SPECIES TRANSMISSION OF BAT CORONAVIRUSES IN CHINA

Over the past decade, PREDICT China's surveillance efforts have generated a rich database with over 500 bat coronavirus (CoV) sequences. This includes alphacoronavirus sequences from 41 bat species and betacoronavirus sequences (the group that includes SARS-related CoVs) from 31 bat species. Our team has used these data to analyze the evolutionary origins and potential for cross-species transmission of bat CoVs in China.

Learn more at p2.predict.global/insights



ENHANCING THE CHINA-US COLLABORATION ON THE ECOLOGY & EVOLUTION OF EMERGING INFECTIOUS DISEASES (EEID) RESEARCH

To counter the significant global health threat that emerging infectious diseases (EIDs) represent, China and the US have been leading efforts in preparedness with unparalleled resources, widespread engagement, and national and geopolitical imperatives to contribute to global health security. This commitment has been essential to the advancement of our understanding of pandemic threats. Even though the US and China have both invested in EID research, integrated scientific studies with strong ecological and evolutionary components are yet well-supported.

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