Obtained via FOIA by Judicial Watch, Inc.

DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

National Institutes of Health
Freedom of Information Office
Building 31, Room 5B-35
31 Center Drive, MSC 2107
Bethesda, Maryland 20892-2107
phone: (301) 496-5633
fax: (301) 402-4541

Via Email: porfanedes@judicialwatch.org

August 31, 2021

Paul Orfanedes
Judicial Watch, Inc.
425 Third Street SW, Suite 800
Washington, DC 20024

Re: NIH FOIA Case No.: 54052; Judicial Watch v. HHS, Case No. 21-cv-00696

Dear Mr. Orfanedes:

This is a partial response to the Freedom of Information Act (FOIA) request that is the subject of the complaint filed in *Judicial Watch v. HHS*, 21-cv-00696, now pending in the U.S. District Court for the District of Columbia. Your FOIA request, dated April 22, 2020, was received by the National Institutes of Allergy and Infectious Diseases (NIAID) on the same day.

You requested the following:

1. All internal NIAID communications regarding the Wuhan Institute of Virology in Wuhan, China.
2. All agreements, contracts and related documents between NIAID and the Wuhan Institute of Virology.
3. All records, including agreements, funds disbursement records and related NIAID communications regarding a reported $3.7 million in grants provided by NIH to the Wuhan Institute of Virology.

The date range for the records request is January 1, 2013 to April 22, 2020.

In accordance with the Court's order dated March 16, 2021, we have processed 221 pages of responsive records this month. The information being withheld is protected from release pursuant to Exemptions 4, 5, and 6 of the FOIA, 5 U.S.C. § 552 (b)(4), (b)(5) and (b)(6); and sections 5.31(d), (e) and (f) of the HHS FOIA Regulations, 45 CFR Part 5. Exemption 4 protects from disclosure trade secrets and commercial or financial information that is privileged and confidential. Exemption 5 permits the withholding of internal government records which are predecisional and contain staff advice, opinion, and recommendations. This exemption is intended to preserve free and candid internal dialogue leading to decision-making. Exemption 6 exempts from disclosure records the release of which would cause a clearly unwarranted invasion of personal privacy.

Please direct any questions regarding this response to Derek Hammond of the Department of Justice, who can be reached at derek.hammond@usdoj.gov, or (202) 252-2511.

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Sincerely,

for Gorka Garcia-Malene
Freedom of Information Act Officer, NIH

Obtained via FOIA by Judicial Watch, Inc.

From: Folkers, Greg (NIH/NIAID) [E]
Sent: Wed, 4 Mar 2020 13:34:12 +0000
Subject: Daily Mail: TWO strains of the killer coronavirus are spreading around the world – and 70% of infected patients have caught the more aggressive and contagious type, study claims

Advertisement

TWO strains of the killer coronavirus are spreading around the world – and 70% of infected patients have caught the more aggressive and contagious type, study claims

- **Researchers from Beijing and Shanghai studied 103 samples of the coronavirus**
- **They found two strains of it, named them L and S and found L was most common**
- **L is also the most aggressive, but it has become less common since early January**
- **A virus which is too aggressive may burn itself out by landing patients in hospital**
- **More than 94,000 people have now caught the coronavirus and 3,200 have died**

By Sam Blanchard Senior Health Reporter For Mailonline
Published: 05:54 EST, 4 March 2020 | Updated: 08:09 EST, 4 March 2020

The **coronavirus** has mutated into at least two separate strains since the outbreak began in December, according to Chinese scientists.

Researchers say there are now two types of the same coronavirus infecting people – and most people seem to have caught the most aggressive form of it.

At least 94,000 people have been infected around the world and almost 3,200 have died, while 50,000 have recovered from the disease.

The team of experts from Beijing and Shanghai said 70 per cent of people have caught the most aggressive strain of the virus but that this causes such bad illness that it has struggled to spread since early January.

Now an older, milder strain seems to be becoming more common.

Knowing that the virus can mutate may make it harder to keep track of or to treat, and raises the prospect that recovered patients could become reinfected.

The experts cautioned that the study that discovered the mutation only used a tiny amount of data – 103 samples – so more research is needed.

Scientists in Beijing and Shanghai said 'human intervention measures' may have forced the most aggressive strain of the coronavirus into submission (Pictured: Medical workers at the Botkin Infectious Diseases Hospital in St. Petersburg, Russia)

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More than 93,000 people have caught the coronavirus worldwide and at least 3,204 have died, according to today's figures

The research was done by experts at Peking University in Beijing, Shanghai University and the Chinese Academy of Sciences.

In their study of genes in 103 samples of the coronavirus, which is named SARS-CoV-2 and causes a disease called COVID-19, they revealed they had discovered two distinct versions of it, which they named L and S.

They claimed that around 70 per cent of patients have caught the L strain, which is more aggressive and faster-spreading than S.

But L has become less common as the outbreak has gone on, with it apparently struggling to spread since early January, while S has become more common.

S is less aggressive but is thought to be the first strain of the virus which made the jump into humans and is continuing to infect new patients.

This could be because the disease it causes is less severe, meaning people carry it for longer before ending up in hospital, increasing the risk of them passing it on.

In the paper the researchers, led by Professor Jian Lu and Dr Jie Cui, said: 'Whereas the L type was more prevalent in the early stages of the outbreak

in Wuhan, the frequency of the L type decreased after early January 2020.

'Human intervention may have placed more severe selective pressure on the L type, which might be more aggressive and spread more quickly.

'On the other hand, the S type, which is evolutionarily older and less aggressive, might have increased in relative frequency due to relatively weaker selective pressure.'

The scientists' explanation suggests that, because the L strain surged at the beginning of the outbreak and made people so ill, those who caught it were quickly diagnosed and isolated, meaning it had less opportunity to spread widely.

This 'human intervention' is thought to be the hospitalisation of people with the virus and the lockdown of areas where it was spreading fast.

Human interventions like isolating and disinfecting areas where the virus was spreading fast may have largely stopped the most aggressive form of the virus (Pictured: South Korean military personnel disinfect streets in the city of Gyengan-dong)

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Coronaviruses are so named because their structure has jagged edges which look like a royal crown – corona is crown in Latin (Pictured, an illustration of the 2019-nCoV released by the US Centers for Disease Control and Prevention)

If people with a certain strain of the virus are taken into hospital faster than those with another strain, this limits the number of other people that strain can infect.

A virus must make people ill enough that they spread it through coughing or sneezing, for example, but not so ill that they quickly become bed-bound or die, which would keep them away from other potential victims.

If the virus is prevented from infecting a lot of people, that strain may die off and evolution – via survival of the fittest – will allow another strain which can infect more people to become the dominant one.

The S strain may be winning because it causes milder symptoms so patients take longer to realise they're sick, increasing the risk of them passing it on.

Professor Jian and Dr Jie added: 'These findings strongly support an urgent need for further immediate, comprehensive studies that combine genomic data, epidemiological data, and chart records of the clinical symptoms of patients with coronavirus disease 2019 (COVID-19).'

The study was published in the scientific journal National Science Review, which is managed by the Chinese Academy of Sciences.

WHAT DO WE KNOW ABOUT THE CORONAVIRUS?

Someone who is infected with the coronavirus can spread it with just a simple cough or a sneeze, scientists say.

More than 3,200 people with the virus are now confirmed to have died and over 94,000 have been infected. Here's what we know so far:

What is the coronavirus?

A coronavirus is a type of virus which can cause illness in animals and people. Viruses break into cells inside their host and use them to reproduce itself and disrupt the body's normal functions.

Coronaviruses are named after the Latin word 'corona', which means crown, because they are encased by a spiked shell which resembles a royal crown.

The coronavirus from Wuhan is one which has never been seen before this outbreak. It has been named SARS-CoV-2 by the International Committee on Taxonomy of Viruses. The name stands for Severe Acute Respiratory Syndrome coronavirus 2.

Experts say the bug, which has killed around one in 50 patients since the outbreak began in December, is a 'sister' of the SARS illness which hit China in 2002, so has been named after it.

The disease that the virus causes has been named COVID-19, which stands for coronavirus disease 2019.

Dr Helena Maier, from the Pirbright Institute, said: 'Coronaviruses are a family of viruses that infect a wide range of different species including humans, cattle, pigs, chickens, dogs, cats and wild animals.

'Until this new coronavirus was identified, there were only six different coronaviruses known to infect humans. Four of these cause a mild common cold-type illness, but since 2002 there has been the emergence of two new coronaviruses that can infect humans and result in more severe disease (Severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) coronaviruses).

'Coronaviruses are known to be able to occasionally jump from one species to another and that is what happened in the case of SARS, MERS and the new coronavirus. The animal origin of the new coronavirus is not yet known.'

The first human cases were publicly reported from the Chinese city of Wuhan, where approximately 11million people live, after medics first started publicly reporting infections on December 31.

By January 8, 59 suspected cases had been reported and seven people were in critical condition. Tests were developed for the new virus and recorded cases started to surge.

Obtained via FOIA by Judicial Watch, Inc.

The first person died that week and, by January 16, two were dead and 41 cases were confirmed. The next day, scientists predicted that 1,700 people had become infected, possibly up to 7,000.
Just a week after that, there had been more than 800 confirmed cases and those same scientists estimated that some 4,000 – possibly 9,700 – were infected in Wuhan alone. By that point, 26 people had died.
By January 27, more than 2,800 people were confirmed to have been infected, 81 had died, and estimates of the total number of cases ranged from 100,000 to 350,000 in Wuhan alone.
By January 29, the number of deaths had risen to 132 and cases were in excess of 6,000.
By February 5, there were more than 24,000 cases and 492 deaths.
By February 11, this had risen to more than 43,000 cases and 1,000 deaths.
A change in the way cases are confirmed on February 13 – doctors decided to start using lung scans as a formal diagnosis, as well as laboratory tests – caused a spike in the number of cases, to more than 60,000 and to 1,369 deaths.
By February 25, around 80,000 people had been infected and some 2,700 had died. February 25 was the first day in the outbreak when fewer cases were diagnosed within China than in the rest of the world.
Where does the virus come from?
According to scientists, the virus almost certainly came from bats. Coronaviruses in general tend to originate in animals – the similar SARS and MERS viruses are believed to have originated in civet cats and camels, respectively.
The first cases of COVID-19 came from people visiting or working in a live animal market in Wuhan, which has since been closed down for investigation.
Although the market is officially a seafood market, other dead and living animals were being sold there, including wolf cubs, salamanders, snakes, peacocks, porcupines and camel meat.
A study by the Wuhan Institute of Virology, published in February 2020 in the scientific journal Nature, found that the genetic make-up virus samples found in patients in China is 96 per cent identical to a coronavirus they found in bats.
However, there were not many bats at the market so scientists say it was likely there was an animal which acted as a middle-man, contracting it from a bat before then transmitting it to a human. It has not yet been confirmed what type of animal this was.
Dr Michael Skinner, a virologist at Imperial College London, was not involved with the research but said: 'The discovery definitely places the origin of nCoV in bats in China.
'We still do not know whether another species served as an intermediate host to amplify the virus, and possibly even to bring it to the market, nor what species that host might have been.'
So far the fatalities are quite low. Why are health experts so worried about it?
Experts say the international community is concerned about the virus because so little is known about it and it appears to be spreading quickly.
It is similar to SARS, which infected 8,000 people and killed nearly 800 in an outbreak in Asia in 2003, in that it is a type of coronavirus which infects humans' lungs. It is less deadly than SARS, however, which killed around one in 10 people, compared to approximately one in 50 for COVID-19.
Another reason for concern is that nobody has any immunity to the virus because they've never encountered it before. This means it may be able to cause more damage than viruses we come across often, like the flu or common cold.
Speaking at a briefing in January, Oxford University professor, Dr Peter Horby, said: 'Novel viruses can spread much faster through the population than viruses which circulate all the time because we have no immunity to them.
'Most seasonal flu viruses have a case fatality rate of less than one in 1,000 people. Here we're talking about a virus where we don't understand fully the severity spectrum but it's possible the case fatality rate could be as high as two per cent.'

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If the death rate is truly two per cent, that means two out of every 100 patients who get it will die.
'My feeling is it's lower,' Dr Horby added. 'We're probably missing this iceberg of milder cases. But that's the current circumstance we're in.
'Two per cent case fatality rate is comparable to the Spanish Flu pandemic in 1918 so it is a significant concern globally.'
How does the virus spread?
The illness can spread between people just through coughs and sneezes, making it an extremely contagious infection. And it may also spread even before someone has symptoms.
It is believed to travel in the saliva and even through water in the eyes, therefore close contact, kissing, and sharing cutlery or utensils are all risky.
Originally, people were thought to be catching it from a live animal market in Wuhan city. But cases soon began to emerge in people who had never been there, which forced medics to realise it was spreading from person to person.
There is now evidence that it can spread third hand – to someone from a person who caught it from another person.
What does the virus do to you? What are the symptoms?
Once someone has caught the COVID-19 virus it may take between two and 14 days, or even longer, for them to show any symptoms – but they may still be contagious during this time.
If and when they do become ill, typical signs include a runny nose, a cough, sore throat and a fever (high temperature). The vast majority of patients will recover from these without any issues, and many will need no medical help at all.
In a small group of patients, who seem mainly to be the elderly or those with long-term illnesses, it can lead to pneumonia. Pneumonia is an infection in which the insides of the lungs swell up and fill with fluid. It makes it increasingly difficult to breathe and, if left untreated, can be fatal and suffocate people.
Figures are showing that young children do not seem to be particularly badly affected by the virus, which they say is peculiar considering their susceptibility to flu, but it is not clear why.
What have genetic tests revealed about the virus?
Scientists in China have recorded the genetic sequences of around 19 strains of the virus and released them to experts working around the world.
This allows others to study them, develop tests and potentially look into treating the illness they cause.
Examinations have revealed the coronavirus did not change much – changing is known as mutating – much during the early stages of its spread.
However, the director-general of China's Center for Disease Control and Prevention, Gao Fu, said the virus was mutating and adapting as it spread through people.
This means efforts to study the virus and to potentially control it may be made extra difficult because the virus might look different every time scientists analyse it.
More study may be able to reveal whether the virus first infected a small number of people then change and spread from them, or whether there were various versions of the virus coming from animals which have developed separately.
How dangerous is the virus?
The virus has a death rate of around two per cent. This is a similar death rate to the Spanish Flu outbreak which, in 1918, went on to kill around 50million people.
Experts have been conflicted since the beginning of the outbreak about whether the true number of people who are infected is significantly higher than the official numbers of recorded cases. Some people are expected to have such mild symptoms that they never even realise they are ill unless they're tested, so only the more serious cases get discovered, making the death toll seem higher than it really is.
However, an investigation into government surveillance in China said it had found no reason to believe this was true.

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Dr Bruce Aylward, a World Health Organization official who went on a mission to China, said there was no evidence that figures were only showing the tip of the iceberg, and said recording appeared to be accurate, **Stat News** reported.

Can the virus be cured?

The COVID-19 virus cannot be cured and it is proving difficult to contain.

Antibiotics do not work against viruses, so they are out of the question. Antiviral drugs can work, but the process of understanding a virus then developing and producing drugs to treat it would take years and huge amounts of money.

No vaccine exists for the coronavirus yet and it's not likely one will be developed in time to be of any use in this outbreak, for similar reasons to the above.

The National Institutes of Health in the US, and Baylor University in Waco, Texas, say they are working on a vaccine based on what they know about coronaviruses in general, using information from the SARS outbreak. But this may take a year or more to develop, according to **Pharmaceutical Technology**.

Currently, governments and health authorities are working to contain the virus and to care for patients who are sick and stop them infecting other people.

People who catch the illness are being quarantined in hospitals, where their symptoms can be treated and they will be away from the uninfected public.

And airports around the world are putting in place screening measures such as having doctors on-site, taking people's temperatures to check for fevers and using thermal screening to spot those who might be ill (infection causes a raised temperature).

However, it can take weeks for symptoms to appear, so there is only a small likelihood that patients will be spotted up in an airport.

Is this outbreak an epidemic or a pandemic?

The outbreak is an epidemic, which is when a disease takes hold of one community such as a country or region.

Although it has spread to dozens of countries, the outbreak is not yet classed as a pandemic, which is defined by the World Health Organization as the 'worldwide spread of a new disease'.

The head of WHO's global infectious hazard preparedness, Dr Sylvie Briand, said: 'Currently we are not in a pandemic. We are at the phase where it is an epidemic with multiple foci, and we try to extinguish the transmission in each of these foci,' the Guardian reported.

She said that most cases outside of Hubei had been 'spillover' from the epicentre, so the disease wasn't actually spreading actively around the world.

Advertisement

Read more:

- On the origin and continuing evolution of SARS-CoV-2 | National Science Review | Oxford Academic

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From: Folkers, Greg (NIH/NIAID) [E]
Sent: Mon, 27 Jan 2020 23:08:38 +0000
To: Fauci, Anthony (NIH/NIAID) [E]
Cc: Morens, David (NIH/NIAID) [E];Doepel, Laurie (NIH/NIAID) [E];Eisinger, Robert (NIH/NIAID) [E];Folkers, Greg (NIH/NIAID) [E];Lerner, Andrea (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E]
Subject: some background on our support of the EcoHealth group

Thanks david

[redacted] (b) (5)

From: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, January 27, 2020 5:04 PM
To: Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6)
Subject:

Hi Greg,

some background on our support of the EcoHealth group (Peter Daszak et al), which has for years been among the biggest players in coronavirus work, also in collaboration with Ralph Baric, Ian Lipkin and others. [redacted] (b) (5)

NIAID has been funding Peter's group for coronavirus work in China for the past 5 years through R01 1R01AI110964: "Understanding the Risk of Bat Coronavirus Emergence". That's now been renewed, with a specific focus to identify cohorts of people highly exposed to bats in China, and work out if they're getting sick from CoVs. Erik Stemmy is the Program Officer. Collaborators include Wuhan Institute of Virology (currently working on the nCoV), and Ralph Baric. The results of the work to date include:

[redacted] (b) (5)

- Discovered Swine Acute Diarrheal Syndrome Virus (SADS-CoV) killing >25,000 pigs in Guangdong Province (Published in *Nature*)
- Found SARS-related CoVs that can bind to human cells (Published in *Nature*), and that cause SARS-like disease in humanized mouse models.

[redacted] (b) (5)

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Also – prior to the above R01, Peter's folks worked under an R01 with Eun-Chung Park as Program Officer on viral discovery in bats, and originally identified SARS-CoV as having a likely origin in bats (published in *Science*)

(b) (5)

David

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director
Office of the Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health
Building 31, Room 7A-03
31 Center Drive, MSC 2520
Bethesda, MD 20892-2520
(b) (6) (assistants: Kimberly Barasch; Whitney Robinson)
301 496 4409
(b) (6)

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(b) (6)

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Notice of Award

RESEARCH
Department of Health and Human Services
National Institutes of Health

Federal Award Date: 07/13/2020

NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grant Number: 2R01AI110964-06 REVISED
FAIN: R01AI110964

Principal Investigator(s):
PETER DASZAK, PHD

Project Title: Understanding the Risk of Bat Coronavirus Emergence

Dr. Daszak, Peter
PD/PI
460 West 34th Street
Suite 1701
New York, NY 100012320

Award e-mailed to: (b) (6)

Period Of Performance:
Budget Period: 07/24/2019 – 06/30/2021
Project Period: 06/01/2014 – 06/30/2025

Dear Business Official:

The National Institutes of Health hereby revises this award to reflect an increase in the amount of $369,819 (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to ECOHEALTH ALLIANCE, INC. in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number R01AI110964. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

Obtained via FOIA by Judicial Watch, Inc.

Emily Linde
Grants Management Officer
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Additional information follows

SECTION I – AWARD DATA – 2R01AI110964-06 REVISED

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Award Calculation (U.S. Dollars)

Salaries and Wages	$170,325
Fringe Benefits	$53,654
Personnel Costs (Subtotal)	$223,979
Consultant Services	$49,809
Materials & Supplies	$20,170
Travel	$15,045
Subawards/Consortium/Contractual Costs	$229,923
Federal Direct Costs	$538,926
Federal F&A Costs	$123,054
Approved Budget	$661,980
Total Amount of Federal Funds Obligated (Federal Share)	$661,980
TOTAL FEDERAL AWARD AMOUNT	$661,980
AMOUNT OF THIS ACTION (FEDERAL SHARE)	$369,819

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
6	$661,980	$661,980
7	$637,980	$637,980
8	$637,980	$637,980
9	$637,980	$637,980
10	$637,980	$637,980

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Name:	Allergy and Infectious Diseases Research
CFDA Number:	93.855
EIN:	1311726494A1
Document Number:	RAI110964B
PMS Account Type:	P (Subaccount)
Fiscal Year:	2019

IC	CAN	2019	2021	2022	2023	2024
AI	8472364	$661,980	$637,980	$637,980	$637,980	$637,980

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: M51C B / **OC**: 41022 / **Released**: (b) (6) 07/13/2020
Award Processed: 07/15/2020 12:00:48 AM

SECTION II – PAYMENT/HOTLINE INFORMATION – 2R01AI110964-06 REVISED

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 2R01AI110964-06 REVISED

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.
b. Conditions on activities and expenditure of funds in other statutory requirements, such as those included in appropriations acts.

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c. 45 CFR Part 75.
d. National Policy Requirements and all other requirements described in the NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. Federal Award Performance Goals: As required by the periodic report in the RPPR or in the final progress report when applicable.
f. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

Research and Development (R&D): All awards issued by the National Institutes of Health (NIH) meet the definition of "Research and Development" at 45 CFR Part§ 75.2**.** As such, auditees should identify NIH awards as part of the R&D cluster on the Schedule of Expenditures of Federal Awards (SEFA). The auditor should test NIH awards for compliance as instructed in Part V, Clusters of Programs. NIH recognizes that some awards may have another classification for purposes of indirect costs. The auditor is not required to report the disconnect (i.e., the award is classified as R&D for Federal Audit Requirement purposes but non-research for indirect cost rate purposes), unless the auditee is charging indirect costs at a rate other than the rate(s) specified in the award document(s).

An unobligated balance may be carried over into the next budget period without Grants Management Officer prior approval.

This grant is subject to Streamlined Noncompeting Award Procedures (SNAP).

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the System for Award Management (SAM). Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) R01AI110964. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

In accordance with the regulatory requirements provided at 45 CFR 75.113 and Appendix XII to 45 CFR Part 75, recipients that have currently active Federal grants, cooperative agreements, and procurement contracts with cumulative total value greater than $10,000,000 must report and maintain information in the System for Award Management (SAM) about civil, criminal, and administrative proceedings in connection with the award or performance of a Federal award that reached final disposition within the most recent five-year period. The recipient must also make semiannual disclosures regarding such proceedings. Proceedings information will be made publicly available in the designated integrity and performance system (currently the Federal Awardee Performance and Integrity Information System (FAPIIS)). Full reporting requirements and procedures are found in Appendix XII to 45 CFR Part 75. This term does not apply to NIH fellowships.

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SECTION IV – AI Special Terms and Conditions – 2R01AI110964-06 REVISED

Clinical Trial Indicator: No
This award does not support any NIH-defined Clinical Trials. See the NIH Grants Policy Statement Section 1.2 for NIH definition of Clinical Trial.

REVISED AWARD: Pursuant to the letter to EcoHealth Alliance, Inc. dated July 8, 2020, this award has been reinstated; however, all activities are suspended until such time as these concerns in the letter have been addressed to NIH's satisfaction.

Supersedes previous Notice of Award dated 04/27/2020. All other terms and conditions still apply to this award.

REVISED AWARD: This award is revised to adjust the budget in accordance with the letter from Aleksei Chmura/ECOHealth Alliance.

Supersedes previous Notice of Award dated **07/24/2019**.

****

This Notice of Award (NoA) includes funds for activity with **The University of North Carolina at Chapel Hill** in the amount of **$77,750** (**$50,000** direct costs + **$27,750**F&A costs).

This Notice of Award (NoA) includes funds for activity with **Wuhan Institute of Virology** in the amount of **$76,301** (**$70,649** direct costs + **$5,652** F&A costs).

This Notice of Award (NoA) includes funds for activity with **Institute of Pathogen Biology** in the amount of **$75,600** (**$70,000** direct costs + **$5,600** F&A costs).

****

The Research Performance Progress Report (RPPR), Section G.9 (Foreign component), includes reporting requirements for all research performed outside of the United States. Research conducted at the following site(s) must be reported in your RPPR:

Wuhan Institute of Virology, CHINA

Institute of Pathogen Biology, CHINA

East China Normal University, CHINA

Duke-NUS Medical School, SINGAPORE

****

This award reflects current Federal policies regarding Facilities & Administrative (F&A) Costs for foreign grantees including foreign sub-awardees, and domestic awards with foreign sub-awardees. Please see: Chapter 16 Grants to Foreign Organizations, International Organizations, and Domestic Grants with Foreign Components, Section 16.6 "Allowable and Unallowable Cost" of the NIH Grants Policy.

****

This award may include collaborations with and/or between foreign organizations. Please be advised that short term travel visa expenses are an allowable expense on this grant, if justified as critical and necessary for the conduct of the project.

****

The budget period anniversary start date for future year(s) will be **July** 1.

****

Dissemination of study data will be in accord with the Recipient's accepted genomic data sharing plan as stated in the page(s) **203** of the application. Failure to adhere to the sharing plan as mutually agreed upon by the Recipient and the NIAID may result in Enforcement Actions as described in the NIH Grants Policy Statement.

Obtained via FOIA by Judicial Watch, Inc.

****

This award is subject to the Clinical Terms of Award referenced in the NIH Guide for Grants and Contracts, July 8, 2002, NOT AI-02-032. These terms and conditions are hereby incorporated by reference, and can be accessed via the following World Wide Web address: https://www.niaid.nih.gov/grants-contracts/niaid-clinical-terms-award All submissions required by the NIAID Clinical Terms of Award must be forwarded electronically or by mail to the responsible NIAID Program Official identified on this Notice of Award.

****

Awardees who conduct research involving Select Agents (see 42 CFR 73 for the Select Agent list; and 7 CFR 331 and 9 CFR 121 for the relevant animal and plant pathogens at http://www.selectagents.gov/Regulations.html) must complete registration with CDC (or APHIS, depending on the agent) before using NIH funds. No funds can be used for research involving Select Agents if the final registration certificate is denied.

Prior to conducting a restricted experiment with a Select Agent or Toxin, awardees must notify the NIAID and must request and receive approval from CDC or APHIS.

****

Select Agents:
Awardee of a project that at any time involves a restricted experiment with a select agent, is responsible for notifying and receiving prior approval from the NIAID. Please be advised that changes in the use of a Select Agent will be considered a change in scope and require NIH awarding office prior approval. The approval is necessary for new select agent experiments as well as changes in on-going experiments that would require change in the biosafety plan and/or biosafety containment level. An approval to conduct a restricted experiment granted to an individual cannot be assumed an approval to other individuals who conduct the same restricted experiment as defined in the Select Agents Regulation 42 CFR Part 73, Section 13.b (http://www.selectagents.gov/Regulations.html).

Highly Pathogenic Agent:
NIAID defines a Highly Pathogenic Agent as an infectious Agent or Toxin that may warrant a biocontainment safety level of BSL3 or higher according to the current edition of the CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL) (http://www.cdc.gov/OD/ohs/biosfty/bmbl5/bmbl5toc.htm). Research funded under this grant must adhere to the BMBL, including using the BMBL-recommended biocontainment level at a minimum. If your Institutional Biosafety Committee (or equivalent body) or designated institutional biosafety official recommend a higher biocontainment level, the highest recommended containment level must be used.
When submitting future Progress Reports indicate at the beginning of the report:

If no research with a Highly Pathogenic Agent or Select Agent has been performed or is planned to be performed under this grant.

If your IBC or equivalent body or official has determined, for example, by conducting a risk assessment, that the work being planned or performed under this grant may be conducted at a biocontainment safety level that is lower than BSL3.

If the work involves Select Agents and/or Highly Pathogenic Agents, also address the following points:

Any changes in the use of the Agent(s) or Toxin(s) including its restricted experiments that have resulted in a change in the required biocontainment level, and any resultant change in location, if applicable, as determined by your IBC or equivalent body or official.

If work with a new or additional Agent(s)/Toxin(s) is proposed in the upcoming project period, provide:

o A list of the new and/or additional Agent(s) that will be studied;
o A description of the work that will be done with the Agent(s), and whether or not the work is a restricted experiment;
o The title and location for each biocontainment resource/facility, including the name of the organization that operates the facility, and the biocontainment level at which the work will be conducted, with documentation of approval by your IBC or equivalent body or official. It is important to note if the work is being done in a new location.

Obtained via FOIA by Judicial Watch, Inc.

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Shaun W Gratton
Email: (b) (6) **Phone**: (b) (6)

Program Official: Erik J. Stemmy
Email: (b) (6) **Phone**: (b) (6)

SPREADSHEET SUMMARY
GRANT NUMBER: 2R01AI110964-06 REVISED

INSTITUTION: ECOHEALTH ALLIANCE, INC.

Budget	Year 6	Year 7	Year 8	Year 9	Year 10
Salaries and Wages	$170,325	$170,123	$170,123	$170,123	$170,123
Fringe Benefits	$53,654	$53,590	$53,590	$53,590	$53,590
Personnel Costs (Subtotal)	$223,979	$223,713	$223,713	$223,713	$223,713
Consultant Services	$49,809	$49,750	$49,750	$49,750	$49,750
Materials & Supplies	$20,170	$14,850	$14,850	$14,850	$14,850
Travel	$15,045	$15,027	$15,027	$15,027	$15,027
Subawards/Consortium/Contractual Costs	$229,923	$229,651	$229,651	$229,651	$229,651
Publication Costs		$6,000	$6,000	$6,000	$6,000
TOTAL FEDERAL DC	$538,926	$538,991	$538,991	$538,991	$538,991
TOTAL FEDERAL F&A	$123,054	$98,989	$98,989	$98,989	$98,989
TOTAL COST	$661,980	$637,980	$637,980	$637,980	$637,980

Facilities and Administrative Costs	Year 6	Year 7	Year 8	Year 9	Year 10
F&A Cost Rate 1	32%	32%	32%	32%	32%
F&A Cost Base 1	$384,547	$309,340	$309,340	$309,340	$309,340
F&A Costs 1	$123,054	$98,989	$98,989	$98,989	$98,989

Obtained via FOIA by Judicial Watch, Inc.

PI: **DASZAK, PETER**	Title: Understanding the Risk of Bat Coronavirus Emergence	
Received: 11/05/2018	FOA: PA18-484 Clinical Trial:Not Allowed	Council: 05/2019
Competition ID: FORMS-E	FOA Title: NIH Research Project Grant (Parent R01 Clinical Trial Not Allowed)	
2 R01 AI110964-06	Dual:	Accession Number: 4237214
IPF: 4415701	Organization: ECOHEALTH ALLIANCE, INC.	
Former Number:	Department:	
IRG/SRG: CRFS	AIDS: N	Expedited: N
Subtotal Direct Costs (excludes consortium F&A) Year 6: 515,358 Year 7: 515,358 Year 8: 515,358 Year 9: 515,358 Year 10: 515,358	Animals: Y Humans: Y Clinical Trial: N Current HS Code: (b) (4) HESC: N	New Investigator: N Early Stage Investigator: N

Senior/Key Personnel:	*Organization:*	*Role Category:*
PETER DASZAK	ECOHEALTH ALLIANCE, INC.	PD/PI
Zheng Li Shi	Wuhan Institute of Virology	Co-Investigator
Kevin Olival	EcoHealth Alliance	Co-Investigator
Ralph Baric	University of North Carolina	Co-Investigator
Noam Ross	EcoHealth Alliance	Co-Investigator
Alice Latinne	EcoHealth Alliance	Other (Specify)-Research Scientist
HongYing Li	EcoHealth Alliance	Other (Specify)-Research Scientist
Leilani Francisco	EcoHealth Alliance	Co-Investigator
Amy Sims	University of North Carolina at Chapel Hill	Co-Investigator
Emily Hagan	EcoHealth Alliance	Other (Specify)-Research Scientist
Guangjian Zhu	East China Normal University	Co-Investigator
Linfa Wang	Duke-NUS Medical School	Co-Investigator
Lili Ren	Institute of Pathogen Biology	Co-Investigator
Li Guo	Institute of Pathogen Biology	Co-Investigator
Peng Zhou	Wuhan Institute of Virology	Co-Investigator
Ben Hu	Wuhan Institute of Virology	Co-Investigator
Aleksei Chmura	EcoHealth Alliance	Other (Specify)-Research Scientist

OMB Number: 4040-0001
Expiration Date: 10/31/2019

APPLICATION FOR FEDERAL ASSISTANCE
SF 424 (R&R)

Obtained via FOIA by Judicial Watch, Inc.

3. DATE RECEIVED BY STATE	State Application Identifier

1. TYPE OF SUBMISSION*

❍ Pre-application ● Application ❍ Changed/Corrected Application

4.a. Federal Identifier
AI110964

b. Agency Routing Number

2. DATE SUBMITTED	Application Identifier	c. Previous Grants.gov Tracking Number

5. APPLICANT INFORMATION **Organizational DUNS*:** 0770900660000

Legal Name*: ECOHEALTH ALLIANCE, INC.
Department:
Division:
Street1*: ECOHEALTH ALLIANCE, INC.
Street2: 460 W 34TH ST
City*: NEW YORK
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
ZIP / Postal Code*: 100012320

Person to be contacted on matters involving this application
Prefix: Dr. First Name*: Peter Middle Name: Last Name*: Daszak Suffix:
Position/Title: PD/PI
Street1*: 460 West 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
ZIP / Postal Code*: 100012320
Phone Number*: 2123804474 Fax Number: 2123804465 Email: daszak@ecohealthalliance.org

6. EMPLOYER IDENTIFICATION NUMBER *(EIN) or (TIN)** 311726494

7. TYPE OF APPLICANT* M: Nonprofit with 501C3 IRS Status (Other than Institution of Higher Education)

Other (Specify):
Small Business Organization Type ❍ Women Owned ❍ Socially and Economically Disadvantaged

8. TYPE OF APPLICATION*
❍ New ❍ Resubmission
● Renewal ❍ Continuation ❍ Revision

If Revision, mark appropriate box(es).
❍ A. Increase Award ❍ B. Decrease Award ❍ C. Increase Duration
❍ D. Decrease Duration ❍ E. Other *(specify)* :

Is this application being submitted to other agencies?* ❍Yes ●No What other Agencies?

9. NAME OF FEDERAL AGENCY*
National Institutes of Health

10. CATALOG OF FEDERAL DOMESTIC ASSISTANCE NUMBER
TITLE:

11. DESCRIPTIVE TITLE OF APPLICANT'S PROJECT*
Understanding the Risk of Bat Coronavirus Emergence

12. PROPOSED PROJECT		13. CONGRESSIONAL DISTRICTS OF APPLICANT
Start Date*	Ending Date*	NY-010
06/01/2019	05/31/2024	

Obtained via FOIA by Judicial Watch, Inc.

SF 424 (R&R) APPLICATION FOR FEDERAL ASSISTANCE

14. PROJECT DIRECTOR/PRINCIPAL INVESTIGATOR CONTACT INFORMATION

Prefix: Dr. First Name*: PETER Middle Name: Last Name*: DASZAK Suffix:
Position/Title: President
Organization Name*: ECOHEALTH ALLIANCE, INC.
Department:
Division:
Street1*: 460 West 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
ZIP / Postal Code*: 100012317
Phone Number*: (b) (6) Fax Number: +12123804465 Email*: (b) (6)

15. ESTIMATED PROJECT FUNDING

a. Total Federal Funds Requested*	$3,586,760.00
b. Total Non-Federal Funds*	$0.00
c. Total Federal & Non-Federal Funds*	$3,586,760.00
d. Estimated Program Income*	$0.00

16.IS APPLICATION SUBJECT TO REVIEW BY STATE EXECUTIVE ORDER 12372 PROCESS?*

a. YES ○ THIS PREAPPLICATION/APPLICATION WAS MADE AVAILABLE TO THE STATE EXECUTIVE ORDER 12372 PROCESS FOR REVIEW ON:
DATE:

b. NO ● PROGRAM IS NOT COVERED BY E.O. 12372; OR
○ PROGRAM HAS NOT BEEN SELECTED BY STATE FOR REVIEW

17. By signing this application, I certify (1) to the statements contained in the list of certifications* and (2) that the statements herein are true, complete and accurate to the best of my knowledge. I also provide the required assurances * and agree to comply with any resulting terms if I accept an award. I am aware that any false, fictitious, or fraudulent statements or claims may subject me to criminal, civil, or administrative penalties. (U.S. Code, Title 18, Section 1001)

● I agree*

** The list of certifications and assurances, or an Internet site where you may obtain this list, is contained in the announcement or agency specific instructions.*

18. SFLLL or OTHER EXPLANATORY DOCUMENTATION File Name:

19. AUTHORIZED REPRESENTATIVE

Prefix: Dr. First Name*: Aleksei Middle Name: Last Name*: Chmura Suffix:
Position/Title*: Authorized Organizational Representative
Organization Name*: EcoHealth Alliance, Inc.
Department:
Division:
Street1*: 460 West 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
ZIP / Postal Code*: 100012320
Phone Number*: (b) (6) Fax Number: 2123804465 Email*: (b) (6)

Signature of Authorized Representative*
Aleksei Chmura

Date Signed*
11/05/2018

20. PRE-APPLICATION File Name:

21. COVER LETTER ATTACHMENT File Name:NIAID_COV_2018_Cover_Letter_Final.pdf

Obtained via FOIA by Judicial Watch, Inc.

424 R&R and PHS-398 Specific
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OMB Number: 4040-0010
Expiration Date: 10/31/2019

Obtained via FOIA by Judicial Watch, Inc.

Project/Performance Site Location(s)

Project/Performance Site Primary Location

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name:	ECOHEALTH ALLIANCE, INC.
Duns Number:	0770900660000
Street1*:	ECOHEALTH ALLIANCE, INC.
Street2:	460 W 34TH ST
City*:	NEW YORK
County:	
State*:	NY: New York
Province:	
Country*:	USA: UNITED STATES
Zip / Postal Code*:	100012320
Project/Performance Site Congressional District*:	NY-010

Project/Performance Site Location 1

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name:	University of North Carolina at Chapel Hill
DUNS Number:	6081952770000
Street1*:	McGavran-Greenberg Hall
Street2:	Campus Box 7435
City*:	Chapel Hill
County:	
State*:	NC: North Carolina
Province:	
Country*:	USA: UNITED STATES
Zip / Postal Code*:	275997435
Project/Performance Site Congressional District*:	NC-004

Obtained via FOIA by Judicial Watch, Inc.

Project/Performance Site Location 2

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name: Wuhan Institute of Virology
DUNS Number: 5290274740000
Street1*: Xiao Hong SHan, No. 44
Street2: Wuchang District
City*: Wuhan
County:
State*:
Province:
Country*: CHN: CHINA
Zip / Postal Code*: 430071
Project/Performance Site Congressional District*: 00-000

Project/Performance Site Location 3

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name: Institute of Pathogen Biology
DUNS Number: 5281563570000
Street1*: Dong Dan San Tiao, No. 9
Street2: Dongcheng District
City*: Beijing
County:
State*:
Province:
Country*: CHN: CHINA
Zip / Postal Code*: 100730
Project/Performance Site Congressional District*: 00-000

Additional Location(s) File Name:

Obtained via FOIA by Judicial Watch, Inc.

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED Other Project Information

1. Are Human Subjects Involved?* ● **Yes** ○ **No**

1.a. If YES to Human Subjects

Is the Project Exempt from Federal regulations? ○ Yes ● No

If YES, check appropriate exemption number: _ 1 _ 2 _ 3 _ 4 _ 5 _ 6 _ 7 _ 8

If NO, is the IRB review Pending? ● **Yes** ○ **No**

IRB Approval Date: 03-15-2019

Human Subject Assurance Number None

2. Are Vertebrate Animals Used?* ● **Yes** ○ **No**

2.a. If YES to Vertebrate Animals

Is the IACUC review Pending? ● Yes ○ No

IACUC Approval Date: 03-15-2019

Animal Welfare Assurance Number None

3. Is proprietary/privileged information included in the application?* ○ **Yes** ● **No**

4.a. Does this project have an actual or potential impact - positive or negative - on the environment?* ○ **Yes** ● **No**

4.b. If yes, please explain:

4.c. If this project has an actual or potential impact on the environment, has an exemption been authorized or an environmental assessment (EA) or environmental impact statement (EIS) been performed? ○ Yes ○ No

4.d. If yes, please explain:

5. Is the research performance site designated, or eligible to be designated, as a historic place?* ○ **Yes** ● **No**

5.a. If yes, please explain:

6. Does this project involve activities outside the United States or partnership with international collaborators?* ● **Yes** ○ **No**

6.a. If yes, identify countries: China

6.b. Optional Explanation:

	Filename
7. Project Summary/Abstract*	NIAID_COV_2019_PROJECT_SUMMARY_final.pdf
8. Project Narrative*	NIAID_COV_2019_NARRATIVE_Final.pdf
9. Bibliography & References Cited	NIAID_COV_2019_REFERENCES.pdf
10.Facilities & Other Resources	NIAID_COV_2019_FACILITIES_v01_PD.pdf
11.Equipment	NIAID_COV_2019_EQUIPMENT_v01.pdf

Funding Opportunity Number: PA-18-484. Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

Project Summary: Understanding the Risk of Bat Coronavirus Emergence

Novel zoonotic, bat-origin CoVs are a significant threat to global health and food security, as the cause of SARS in China in 2002, the ongoing outbreak of MERS, and of a newly emerged Swine Acute Diarrhea Syndrome in China. In a previous R01 we found that bats in southern China harbor an extraordinary diversity of SARSr-CoVs, some of which can use human ACE2 to enter cells, infect humanized mouse models causing SARS-like illness, and evade available therapies or vaccines. We found that people living close to bat habitats are the primary risk groups for spillover, that at one site diverse SARSr-CoVs exist that contain every genetic element of the SARS-CoV genome, and identified serological evidence of human exposure among people living nearby. These findings have led to **18 published peer-reviewed papers, including two papers in *Nature*, and a review in *Cell*.** Yet salient questions remain on the origin, diversity, capacity to cause illness, and risk of spillover of these viruses. In this R01 renewal we will address these issues through 3 specific aims:

Aim 1. Characterize the diversity and distribution of high spillover-risk SARSr-CoVs in bats in southern China. We will use phylogeographic and viral discovery curve analyses to target additional bat sample collection and molecular CoV screening to fill in gaps in our previous sampling and fully characterize natural SARSr-CoV diversity in southern China. We will sequence receptor binding domains (spike proteins) to identify viruses with the highest potential for spillover which we will include in our experimental investigations (Aim 3).

Aim 2. Community, and clinic-based syndromic, surveillance to capture SARSr-CoV spillover, routes of exposure and potential public health consequences. We will conduct biological-behavioral surveillance in high-risk populations, with known bat contact, in community and clinical settings to 1) identify risk factors for serological and PCR evidence of bat SARSr-CoVs; & 2) assess possible health effects of SARSr-CoVs infection in people. We will analyze bat-CoV serology against human-wildlife contact and exposure data to quantify risk factors and health impacts of SARSr-CoV spillover.

Aim 3. *In vitro* and *in vivo* characterization of SARSr-CoV spillover risk, coupled with spatial and phylogenetic analyses to identify the regions and viruses of public health concern. We will use S protein sequence data, infectious clone technology, *in vitro* and *in vivo* infection experiments and analysis of receptor binding to test the hypothesis that % divergence thresholds in S protein sequences predict spillover potential. We will combine these data with bat host distribution, viral diversity and phylogeny, human survey of risk behaviors and illness, and serology to identify SARSr-CoV spillover risk hotspots across southern China. Together these data and analyses will be critical for the future development of public health interventions and enhanced surveillance to prevent the re-emergence of SARS or the emergence of a novel SARSr-CoV.

Obtained via FOIA by Judicial Watch, Inc.

Renewal: Understanding the Risk of Bat Coronavirus Emergence

Project Narrative

Most emerging human viruses come from wildlife, and these represent a significant threat to public health and biosecurity in the US and globally, as was demonstrated by the SARS coronavirus pandemic of 2002-03. This project seeks to understand what factors allow coronaviruses, including close relatives to SARS, to evolve and jump into the human population by studying viral diversity in their animal reservoirs (bats), surveying people that live in high-risk communities in China for evidence of bat-coronavirus infection, and conducting laboratory experiments to analyze and predict which newly-discovered viruses pose the greatest threat to human health.

Obtained via FOIA by Judicial Watch, Inc.

Facilities, Equipment, and Other Resources

EcoHealth Alliance, New York, USA (Drs. Daszak, Olival, Francisco, Ross)

EcoHealth Alliance is a New York-based 501(c) 3 non-profit institution that conducts scientific research on emerging zoonoses and global health capacity building. EcoHealth Alliance New York headquarters has (b) (4) square feet of office space including a meeting room and basic laboratory – freezer storage and light microscopy. The scientific staff (34 core scientists, 100+ field staff) is supported by a core admin staff of 18 who are available for work on this project and funded through private donor and federal support. EcoHealth Alliance does not support diagnostic facilities at its core headquarters and works in partnership with a network of leading diagnostic labs both in the USA and around the world.

EcoHealth Alliance is equipped with fiber optic Internet access and video conferencing facilities to facilitate easy communication between collaborators. EcoHealth Alliance employees have around-the-clock access to servers, VPNs, encryption software, IT support, and all necessary software including Git and Github (Hosted software revision/audit service), Sublime and Vim text editors, Vagrant and Oracle Virtualbox virtual machines, Google Apps (Hosted email and collaboration web based software), Ansible (Server provisioning software framework), Python, NodeJS, and R programming languages, Meteor (Javascript framework), Bash shell scripts, Jenkins (Continuous Integration server), Microsoft Office and Adobe CS6 running on both Apple Mac OS X, Ubuntu linux, and Windows Operating Systems. EcoHealth Alliance has a dedicated quad-core Linux server and another dedicated dual quad-core Mac Pro Server - each with 4TB hard drives. Either server individually or in combination may be used for intensive computational modeling and/or database processing by all the grantees. Access to the cloud and supercomputing services (Amazon) is provided by core funding to EcoHealth Alliance.

EcoHealth Alliance is the headquarters of a global network of over 70 partners that provides exceptional leverage for the core scientists. This network includes staff from: academic institutions at leading national universities; intergovernmental agencies (WHO, OIE, FAO, DIVERSITAS, IUCN); infectious disease surveillance laboratories including BSL-3 and -4 laboratories; national government agency offices and labs; locally-based wildlife conservation organizations in Asia, Africa and Latin America. EcoHealth Alliance is the headquarters of: The Consortium for Conservation Medicine (CCM); the journal *EcoHealth*; an NSF Research Coordination Network (EcoHealthNET); the IUCN Wildlife Health Specialist Group; and the OIE Wildlife Health Network. EcoHealth Alliance is a voting member of the IUCN and a partner in Columbia University's Earth Institute Center for Environmental Sustainability (EICES) and all senior scientific staff members are Adjunct Faculty at Columbia University's Department of Ecology, Evolution, and Environmental Biology or at the Mailman School of Public Health.

Institute of Pathogen Biology, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China (Drs. Ren, Guo)

The Institute of Pathogen Biology (IPB) is a key (flagship) institute within the Chinese Academy of Medical Sciences & Peking Union Medical College. IPB's mission is to conduct high quality research in basic and applied biology of critically important human pathogens. The ultimate goal is to conduct research and develop technology for better diagnosis, treatment, and prevention of infectious diseases. IPB specializes in multi-disciplinary approaches to pathogen research and technological development focused on improving China's capability to diagnose, treat and prevent infectious diseases.

Human Resources. The department involved in this project consists of 30 staff members: 10 with a clinical medicine background, 12 biological research scientists, 3 bioinformaticists, 3 animal technicians, and 2 biochemists working on protein expression and purification.

Lab Facilities. The IPB includes the Ministry of Health Key Laboratory of Systems Biology of Pathogens, Christophe Merieux Laboratory, the AIDS Research Center, laboratories focused on Bacteriology, Virology, Mycology, Parasitology, and the Epidemiological Information Analysis Department. The institute has established platforms in metagenomics, transcriptome, morphology, molecular biology, and immunology. All of these are funded centrally and available to conduct the research proposed in the current R01.

Obtained via FOIA by Judicial Watch, Inc.

BSL2 Facility. The institute has three laboratories of (b) (4) equipped as BSL2 space for virology, immunology and clinical sample preparation. Equipment includes an Illumina Hiseq 2500, Miseq and BGI 500, gel electrophoresis, power supplies, thermal cyclers, a programmable heat block, heat blocks, water baths, CO_2 incubators (2), several -70°C freezers, one -140°C freezer, refrigerators, DNA documentation system, DNA sequencing and computer assisted sequence analysis programs, several microfuges, Nikon and Zeiss microscopes with photographic and fluorescent capabilities, several class 2 environmental hoods, refrigerated water baths, real time thermocyclers, and spectrophotometers. The laboratory has an ELISA plate reader, an illuminometer, ELISA plate washer, spectrophotometers, and other equipment that is routinely used in characterizing antibody-protein interactions.

BSL 3 Facility. The institute shares an additional (b) (4) of BSL3 facilities equipped with sterile hoods (BSCIIA), CO_2 incubators, -70C freezer, an inverted Nikon fluorescent microscope, and equipment for virus isolation and culture, and molecular genetics research.

University of North Carolina at Chapel Hill, USA (Baric and Sims)

The Department of Epidemiology is an internationally recognized leader in epidemiologic research and training. The department offers research training in most specialized areas including cancer, cardiovascular diseases, environmental and occupational health, health services/clinical epidemiology, reproductive health and infectious diseases. The department's current faculty consists of 51 regular full-time faculty and 151 adjunct faculty members. The department has 218 graduate students enrolled, including 20 in the MPH program, 5 in the MSPH program, 20 in the MSCR program and 173 in the Ph.D. program. The Department of Epidemiology is headquartered in the four-story McGavran-Greenberg Building. The epidemiology administrative and office space occupies (b) (4) square feet and provides additional classroom space. Most of the department's research staff occupies a research annex consisting of approximately (b) (4) square feet of contiguous rental space in a commercial office building.

Dr. Baric has three laboratories of (b) (4) square feet each equipped as BL2 space for molecular biology, virology, immunology and recombinant DNA techniques, as laid out in the current R01 proposal. Equipment is available for gel electrophoresis, PCR, and BSL2 sample storage and handling facilities. It includes a DNA documentation system, DNA sequencing and computer assisted sequence analysis programs, several microfuges, a microscopy suite, 10+ IBM and Apple Pentium II/III computers with accompanying software, three thermocyclers, a fume hood, Nuclisens reader, hybridization oven, real time thermocyclers, three fluorescent inverted scopes with computer software (Olympus IX51), and a spectrophotometer. A Roche Light Cycler 480II is available for real time measurements. The laboratory has an ELISA plate reader, an illuminometer, 200 cages for animal maintenance and breeding in Seal-Safe housing, Bio Rad low pressure chromatography system, ELISA plate washer, spectrophotometers, and other equipment that is routinely used in characterizing antibody-protein interactions.

The Baric laboratory contains an additional (b) (4) square feet of newly renovated BSL3 facilities with enhanced features including shower in/shower out facility; dual anteroom access; Hepa filtered exhaust; redundant exhaust fans; card key access; an alarm system to Public Health/Campus Police; laboratory controlled combination lock; and Techniplast Sealsafe™ Hepa filtered animal housing for 300+ rodents. PAPR and tyvek suits are worn at all times in the BSL3 facility. The BL3 facilities are in an adjacent and attached building (b) (4) or in (b) (4), the latter space is directly adjacent to Dr. Baric's BSL2 laboratory resources. Each facility is equipped with sterile hoods (BSCIIA), four CO_2 incubators, gel electrophoresis equipment, thermal cyclers and power supplies, and related equipment necessary for virus cultivation and molecular genetic research. The facilities each house a -70°C freezer, an inverted Nikon fluorescent microscope with a digital camera, an ELISA plate reader and illuminometer. Both facilities contain rodent-sized Seal-Safe systems (~192 cages) for maintaining animals in a Hepa-filtered Air in/out environment, exhausted into the BSL3 Hepa-filtered exhaust system. An 8 chamber Buxco plethysmography system that allows for repetitive, noninvasive measures of the number of breaths, tidal volume, airway responsiveness, enhanced pause, and respiratory gases from live control and infected mice in a contained system is housed in the main BSL3 laboratory in (b) (4).

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The Department of Epidemiology provides cold-room, autoclave, centralized dishwashing and a darkroom with an automated developer. The campus has central facilities for DNA oligonucleotide synthesis, histopathology, DNA sequencing, EM, light and confocal microscopy, automated PCR genotyping and Taqman facilities, and Fluorescent activated cell sorter facilities (FAC). As a member of the Department of Microbiology and Immunology and UNC Cancer center, Dr. Baric and his team have access to these facilities at a discounted cost. The University provides a variety of core services including: sequencing and deep sequencing cores, genomics cores, oligonucleotide synthesis cores, hybridoma cores, transgenic cores, structural biology cores, etc. typical of any world class research institution. Campus wide core facilities are available for oligonucleotide synthesis, Sanger and 454 sequencing, RNAseq, pathology and histology services, and Flow Cytometry. Approximately, 40,000 cages are available for CC RIX production in the (b) (4) on UNC Campus.

Wuhan Institute of Virology, Chinese Academy of Sciences, Hubei, China (Shi, Zhou, and Hu)

The Wuhan Institute of Virology (WIV), Chinese Academy of Sciences (CAS) is the only institute specializing in virology, viral pathology and virus technology among 19 other biological and biomedical research institutes in CAS. WIV is China's premier institute for virologic research. It consists of three research departments and one center: the Departments of Molecular Virology, of Bio-control, of Analytical Biochemistry and Biotechnology, and the Virus Resource and Bioinformation Center. It contains the Key Laboratory of Molecular Virology of CAS, the Joint-laboratory of Invertebrate Virology, an HIV Pre-screening Lab and the Hubei Engineering and Technology Research Center for Viral Diseases. The institute is further divided into 14 research groups, one of which (the Emerging Virus Laboratory) is headed by Dr. Zhengli Shi. The supporting system of the institute consists of an analytical equipment center, an experimental animal center, the editorial office of *Virologica Sinica* and a computer network center. The virus resource and bio-information center of China contains the largest virus bank in Asia, curating around 800 viral strains.

The Wuhan Institute of Virology is a World Health Organization collaborating center. It also has partnerships, research collaborations and contracts with universities and research institutes in more than 30 counties and regions including a long-time (>15 years) partnership with EcoHealth Alliance. There are 14 professors, 36 associated professors, and 47 assistant professors conducting research on virology and five of these have been awarded honors in the “Hundred Talents Project”. In 2013, the first BSL-4 lab in China was opened at this Institute in a bespoke facility which was designed with the assistance of the US CDC and L’Institut Pasteur of France.

The WIV Emerging Virus Laboratory, headed by Dr. Shi, was set up to carry out exactly the sort of experimental activities on emerging viruses listed in the current R01 proposal. This lab possesses all necessary facilities for molecular biology and virology including a bank of -80˚C freezers, PCR machines, gel electrophoresis and imaging systems, biosafety cabinets, super-clean benches, and cell culture rooms. A Core Facility Center was established at WIV to provide technological services to faculty, students, and visiting researchers. Core Facility Center equipment includes: a transmission electron microscope, ultracentrifugation machines, small animal *in vivo* imaging systems, confocal laser scanning microscopes, flow cytometry, a real-time qPCR system, and a high-throughput sequencing and analyzing system. In addition, WIV owns a complete biosafety research platform, which consists of the first national BSL-4 laboratory in China, and a cluster of BSL-3 and BSL-2 labs.

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Equipment

EcoHealth Alliance (Daszak, Francisco, Olival, Ross)
EcoHealth Alliance is equipped with fiber optic Internet access and video conferencing facilities to facilitate easy communication between collaborators. EcoHealth Alliance employees have around the clock access to servers, VPNs, encryption software, IT support, and all necessary software including Git and Github (Hosted software revision/audit service), Sublime and Vim text editors, Vagrant and Oracle Virtualbox virtual machines, Google Apps (Hosted email and collaboration web based software), Ansible (Server provisioning software framework), Python, NodeJS, and R programming languages, Meteor (Javascript framework), Bash shell scripts, Jenkins (Continuous Integration server), Microsoft Office and Adobe CS6 running on both Apple Mac OS X, Ubuntu linux, and Windows Operating Systems. Additionally, EcoHealth Alliance has a dedicated quad-core Linux server and another dedicated dual quad-core Mac Pro Server - each with 4TB hard drives. Either server individually or in combination may be used for intensive computational modeling and/or database processing by all the grantees. Access to the cloud and supercomputing services (Amazon) is provided by core funding to EcoHealth Alliance.

Institute of Pathogen Biology (Ren, Guo)
The Institute of Pathogen Biology laboratories have equipment required for general microbiological, molecular, and biochemical work including microcentrifuges, agarose and polyacrylamide electrophoresis equipment, spectrophotometer, rocking and shaking platforms, bead-beater cell disruptor, and incubators (shaking and static). Major equipment relevant to this proposal which are available include:

BSL2 Facility. The institute has three laboratories of (b) (4) equipped as BSL2 space for the virology, immunology and clinical samples pretreatment. Equipment includes Illumina Hiseq 2500, Miseq and BGI 500, gel electrophoresis equipment, power supplies, thermal cyclers, a programmable heat block, heat blocks, water baths, CO_2 incubators (2), several -70°C freezers, one -140°C freezer, refrigerators, DNA documentation system, DNA sequencing and computer assisted sequence analysis programs, several microfuges, Nikon and Zeiss microscopes with photographic and fluorescent capabilities, several class 2 environmental hoods, refrigerated water baths, real time thermocyclers, and spectrophotometer. The laboratory has an ELISA plate reader, an illuminometer, ELISA plate washer, spectrophotometers, and other equipment that is routinely used in characterizing antibody-protein interactions.

BSL 3 Facility. The institute shares an additional (b) (4) of BSL3 facilities equipped with sterile hoods (BSCIIA), CO_2 incubators, -70°C freezer, an inverted Nikon fluorescent microscope with an assortment of filters, magnifications and digital camera, and related equipment necessary for virus cultivation and molecular genetic research.

Wuhan Institute of Virology (Shi, Zhou, Hu)
Institute of Virology's Emerging Virus Laboratory has equipment required for general microbiological, molecular, and biochemical work including microcentrifuges, agarose and polyacrylamide electrophoresis equipment, spectrophotometer, rocking and shaking platforms, bead-beater cell disruptor, and incubators (shaking and static). Major equipment relevant to this proposal which are available include: -80°C freezers, PCR machines, gel electrophoresis and imaging system, biosafety cabinets, super-clean benches, and cell culture rooms.

A Core Facility Center was established at Wuhan Institute of Virology to provide technological services to faculty, students, and visiting researchers. The equipment installed in the Core Facility Center include: transmission electron microscope, ultracentrifugation machines, small animal *in vivo* imaging systems, confocal laser scanning microscopes, flow cytometry, a real-time qPCR system, and a high-throughput sequencing and analyzing system.

In addition, the Wuhan Institute of Virology owns a complete biosafety research platform, which consists of the first national BSL-4 laboratory in China, and a cluster of BSL-3 and BSL-2 labs. These labs contain gel electrophoresis equipment, power supplies, thermal cyclers, programmable heat blocks, heat blocks, water

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baths, CO_2 incubators, -70°C freezers, -140°C freezers, refrigerators, DNA documentation system, DNA sequencing and computer assisted sequence analysis programs, microfuges, Nikon and Zeiss microscopes with photographic and fluorescent capabilities, several class 2 environmental hoods, refrigerated water baths, real time thermocyclers, and spectrophotometers. The laboratory also has an ELISA plate reader, an illuminometer, ELISA plate washer, spectrophotometers, and other equipment that is routinely used in characterizing antibody-protein interactions.

University of North Carolina at Chapel Hill Baric Laboratory (Baric, Sims)
The three laboratories of the Baric Lab in the Department of Epidemiology have equipment required for general microbiological, molecular, and biochemical work including microcentrifuges, agarose and polyacrylamide electrophoresis equipment, spectrophotometer, rocking and shaking platforms, bead-beater cell disruptor, and incubators (shaking and static). Major equipment relevant to this proposal which are available include: gel electrophoresis equipment, power supplies, thermal cyclers, a programmable heat block, heat blocks, water baths, CO_2 incubators (2), several -70°C freezers, one -140°C freezer, refrigerators, DNA documentation system, DNA sequencing and computer assisted sequence analysis programs, several microfuges, two Nikon microscopes with photographic and fluorescent capabilities, several class 2 environmental hoods, refrigerated water baths, 10+ IBM and Apple Pentium II/III computers with accompanying software, three thermocyclers, a fume hood, Nuclisens reader, hybridization oven, real time thermocyclers, three fluorescent inverted scopes with computer software (Olympus IX51), and a spectrophotometer. A Roche Light Cycler 480II is available for real time measurements. The laboratory has an ELISA plate reader, an illuminometer, 200 cages for animal maintenance and breeding in Seal-Safe housing, Bio Rad low pressure chromatography system, ELISA plate washer, spectrophotometers, and other equipment that is routinely used in characterizing antibody-protein interactions.

BSL3 Facility features include: shower in/shower out facility; dual anteroom access; Hepa filtered exhaust; redundant exhaust fans; card key access; an alarm system to Public Health/Campus Police; laboratory controlled combination lock; and Techniplast Sealsafe™ Hepa filtered animal housing for 300+ rodents. PAPR and tyvek suits are worn at all times in the BSL3 facility. The BL3 facilities are in an adjacent and attached building (b) (4) or in (b) (4), the latter space is directly adjacent to Dr. Baric's BSL2 laboratory resources. Each facility is equipped with sterile hoods (BSCIIA), four CO_2 incubators, gel electrophoresis equipment, thermal cyclers and power supplies, and related equipment necessary for virus cultivation and molecular genetic research. The facilities each house a -70°C freezer, an inverted Nikon fluorescent microscope with an assortment of filters, magnifications and digital camera, an ELISA plate reader and illuminometer. Both facilities contain rodent-sized Seal-Safe systems (~192 cages) for maintaining animals in a Hepa-filtered Air in/out environment, exhausted into the BSL3 Hepa-filtered exhaust system. An 8 chamber Buxco plethysmography system that allows for repetitive, noninvasive measures of the number of breaths, tidal volume, airway responsiveness, enhanced pause, and respiratory gases from live control and infected mice in a contained system is housed in the main BSL3 laboratory in (b) (4)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

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RESEARCH & RELATED Senior/Key Person Profile (Expanded)

PROFILE - Project Director/Principal Investigator			
Prefix: Dr.	First Name*: PETER	Middle Name	Last Name*: DASZAK	Suffix:

Position/Title*:	President
Organization Name*:	ECOHEALTH ALLIANCE, INC.
Department:	
Division:	
Street1*:	460 West 34th Street
Street2:	Suite 1701
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County:	
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Phone Number*: (b) (6) Fax Number: +12123804465

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: PD/PI Other Project Role Category:

Degree Type: PHD Degree Year: 1993

Attach Biographical Sketch*: File Name: DASZAK_Peter_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

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PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Zheng Li Middle Name Last Name*: Shi Suffix:

Position/Title*: Senior Scientist
Organization Name*: Wuhan Institute of Virology
Department:
Division:
Street1*: Xiao Hong Shan, no. 44
Street2:
City*: Wuhan
County:
State*:
Province:
Country*: CHN: CHINA
Zip / Postal Code*: 430071

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2000

Attach Biographical Sketch*: File Name: SHI_Zhengli_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Kevin Middle Name J. Last Name*: Olival Suffix:

Position/Title*: Senior Research Scientist
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 West 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 100012317

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2008

Attach Biographical Sketch*: File Name: OLIVAL_Kevin_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

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PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Ralph Middle Name S Last Name*: Baric Suffix:

Position/Title*: Professor
Organization Name*: University of North Carolina
Department:
Division:
Street1*: UNIVERSITY OF NORTH CAROLINA
Street2: DEPT EPIDEMIOLOGY
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State*: NC: North Carolina
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Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 1977

Attach Biographical Sketch*: File Name: BARIC_Ralph_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Noam Middle Name Last Name*: Ross Suffix:

Position/Title*: Disease Ecologist
Organization Name*: EcoHealth Alliance
Department:
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Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2015

Attach Biographical Sketch*: File Name: ROSS_Noam_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

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PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Alice Middle Name Last Name*: Latinne Suffix:

Position/Title*: Research Scientist
Organization Name*: EcoHealth Alliance
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Credential, e.g., agency login: (b) (6)

Project Role*: Other (Specify) Other Project Role Category: Research Scientist

Degree Type: PHD Degree Year: 2012

Attach Biographical Sketch*: File Name: LATINNE_Alice_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Ms. First Name*: HongYing Middle Name Last Name*: Li Suffix:

Position/Title*: Research Scientist & China Programs Coord.
Organization Name*: EcoHealth Alliance
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Country*: USA: UNITED STATES
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E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Other (Specify) Other Project Role Category: Research Scientist

Degree Type: MPH Degree Year: 2015

Attach Biographical Sketch*: File Name: LI_Hongying_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

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PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Leilani Middle Name Last Name*: Francisco Suffix:

Position/Title*: Senior Behavioral Risk Surveillance Coord.
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E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2010

Attach Biographical Sketch*: File Name: FRANCESCO_Leilani_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Amy Middle Name C Last Name*: Sims Suffix:

Position/Title*: Associate Professor
Organization Name*: University of North Carolina at Chapel Hill
Department:
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State*: NC: North Carolina
Province:
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Zip / Postal Code*: 275997290

Phone Number*: (b) (6) Fax Number: (919) 966-0584

E-Mail*: S (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2001

Attach Biographical Sketch*: File Name: SIMS_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

Obtained via FOIA by Judicial Watch, Inc.

PROFILE - Senior/Key Person

Prefix: Ms. First Name*: Emily Middle Name E Last Name*: Hagan Suffix:

Position/Title*: Behavioral Research Scientist
Organization Name*: EcoHealth Alliance
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Division:
Street1*: 460 West 34th Street
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Phone Number*: (b) (6) Fax Number: +12123804465

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Other (Specify) Other Project Role Category: Research Scientist

Degree Type: MPH Degree Year: 2013

Attach Biographical Sketch*: File Name: HAGAN_Emily_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Guangjian Middle Name Last Name*: Zhu Suffix:

Position/Title*: Research Scientist & China Field Coordinator
Organization Name*: East China Normal University
Department:
Division:
Street1*: School of Life Science, B327
Street2: Science building, 3663 Zhongshan Beilu
City*: Shanghai
County:
State*:
Province:
Country*: CHN: CHINA
Zip / Postal Code*: 200062

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2012

Attach Biographical Sketch*: File Name: ZHU_GuangJian_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

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PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Linfa Middle Name Last Name*: Wang Suffix:

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State*:
Province:
Country*: SGP: SINGAPORE
Zip / Postal Code*: 169857

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 1986

Attach Biographical Sketch*: File Name: WANG_Linfa_Final.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Lili Middle Name Last Name*: Ren Suffix:

Position/Title*: Research Scientist
Organization Name*: Institute of Pathogen Biology
Department:
Division:
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Street2: Dongcheng District
City*: Beijing
County:
State*:
Province:
Country*: CHN: CHINA
Zip / Postal Code*: 100730

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2005

Attach Biographical Sketch*: File Name: REN_Lili_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

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PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Li Middle Name Last Name*: Guo Suffix:

Position/Title*: Professor
Organization Name*: Institute of Pathogen Biology
Department:
Division:
Street1*: No. 9 Dong Dan San Tiao
Street2: Dongcheng District
City*: Beijing
County:
State*:
Province:
Country*: CHN: CHINA
Zip / Postal Code*: 100730

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: MD Degree Year: 2006

Attach Biographical Sketch*: File Name: GUO_Li_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Peng Middle Name Last Name*: Zhou Suffix:

Position/Title*: Principal Investigator
Organization Name*: Wuhan Institute of Virology
Department:
Division:
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Street2:
City*: Wuhan
County:
State*:
Province:
Country*: CHN: CHINA
Zip / Postal Code*: 430071

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2011

Attach Biographical Sketch*: File Name: ZHOU_Peng_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

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PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Ben Middle Name Last Name*: Hu Suffix:

Position/Title*: Research Scientist
Organization Name*: Wuhan Institute of Virology
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Division:
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City*: Wuhan
County:
State*:
Province:
Country*: CHN: CHINA
Zip / Postal Code*: 430071

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2015

Attach Biographical Sketch*: File Name: HU_Ben_Biosketch_final.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Aleksei Middle Name Last Name*: Chmura Suffix:

Position/Title*: Research Scientist
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 West 34th Street
Street2: Suite 1701
City*: New York
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State*: NY: New York
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 100012317

Phone Number*: (b) (6) Fax Number: +12123804465

E-Mail*: (b) (6)

Credential, e.g., agency login: (b) (6)

Project Role*: Other (Specify) Other Project Role Category: Research Scientist

Degree Type: PHD Degree Year: 2018

Attach Biographical Sketch*: File Name: CHMURA_Aleksei_Biosketch_Final.pdf

Attach Current & Pending Support: File Name:

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BIOGRAPHICAL SKETCH
DO NOT EXCEED FIVE PAGES.

NAME: Peter Daszak

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: President & Chief Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Bangor University, UK	B.S (hons)	07/1986	Zoology
University of East London, UK	Ph.D.	03/1993	Infectious Diseases

A. Personal Statement

I have the broad expertise in emerging viral zoonoses, and scientific management experience to support this proposed work that involves an international interdisciplinary team working on field collection of wildlife and human samples, human behavioral risk surveys, modeling and analytics, and viral characterization *in vitro* and *in vivo*. I am President and Chief Scientist of EcoHealth Alliance, a US-based 501 (c) 3 institution that conducts research on emerging zoonoses and global health capacity building. My 20+ years of NIH-funded research focuses on understanding the links among disease emergence in wildlife, livestock and people, particularly viral zoonoses. This includes identifying the bat origin of SARS-CoV and SADS-CoV, analyzing the ecology of West Nile, Nipah and Hendra virus emergence, publishing the first unbiased analysis of global emerging disease hotspots, and developing the scientific rationale for the Global Virome Project (GVP). Over the past 18 years I have been the PI on 4 multidisciplinary R01s that use modeling, epidemiology, laboratory and field science to test hypotheses on the emergence of wildlife-origin viral zoonoses, including SARS-CoV, Nipah and Hendra virus, Avian influenza and novel viruses from bats. I have successfully managed teams of virologists, field biologists, mathematical modelers, veterinarians, epidemiologists, laboratorians and anthropologists. Much of the groundwork for the current proposal has developed from my previous collaborative research with each member of the team assembled in the current R01 renewal proposal.

1. Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, McEachern J, Field H, **Daszak P**, Eaton BT, Zhang S & Wang L-F (2005). Bats are natural reservoirs of SARS-like coronaviruses. **Science** 310: 676-679.
2. Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, and **Daszak P*** (2008). Global trends in emerging infectious diseases. **Nature** 451:990-993
3. Olival KJ*, Hosseini PR, Zambrana-Torrelio C, Ross N, Bogich TL, **Daszak P*** (2017). Host and viral traits predict zoonotic spillover from mammals. **Nature** 546, 646–650.
4. Carroll D, **Daszak P***, Wolfe ND, Gao GF, Morel C, Morzaria S, Pablos-Méndez A, Tomori O, Mazet JAK (2018). The global virome project. **Science** 359: 872-874.

Obtained via FOIA by Judicial Watch, Inc.

B. Positions and Honors

Positions and Employment

1993 -98 Senior Faculty Research Scientist, Kingston University UK
1998 Guest Researcher, Centers for Disease Control and Prevention (CDC)
1999 -01 Faculty Research Scientist, University of Georgia
2001 - Sr. Adjunct Faculty, Columbia University
2001 - 09 Executive Director, Consortium for Conservation Medicine, EcoHealth Alliance, New York
2009 - President & Chief Scientist, EcoHealth Alliance New York

Other Experience and Professional Membership

2003 - 7 NIH: ad hoc member, ZRG1 IDM-G 90 (2003-5) ZRG1 IRAP-Q (2005-7)
2004 - Editorial Board, *Conserv. Biol.*
2005 NIAID: Steering Committee, workshop on virus-host shifts & emergence of new pathogens
2010 - Editor-in-Chief, *EcoHealth*; Member of IOM Forum on Microbial Threats; External Advisory Board, DHS and Kansas State Univ. Ctr. of Excellence for Emerg. & Zoonotic Animal Diseases (CEEZAD)
2011 Steering Committeee, NIAID Workshop on Arboviruses
2014 - Member NRC Advisory Committee to advise the US Global Change Research Program (USGCRP)
2015 - Member of Supervisory Board, One Health Platform; Editorial Board *One Health*
2016 - Member, WHO Expert group on Public Health Emergency Disease Prioritization
2016 - Member, Core Steering Committee & Co-Chair, Science & Technol WG, Global Virome Project
2017 External Review Committee, CSIRO Health & Biosecurity Business Unit
2017 - Chair, Forum on Microbial Threats, National Academies of Science, Engineering & Medicine

Honors

1999 Meritorious service award, CDC
2000 CSIRO silver medal for collaborative research
2002 Honored by the naming of a new species of centipede, *Cryptops daszaki* (*J Nat Hist* 36: 76-106)
2003 6th Annual Lecturer, Medicine & Humanities, Texas A&M
2007 Finalist, Director's Pioneer Award
2008 Presidential Lecturer, University of Montana
2012 Elected member of the Cosmos Club, Washington DC
2013 Honored by the naming of a new parasite species, *Isospora daszaki* (*Parasit. Res*. 111:1463-1466)
2013 Hsu-Li Distinguished Lectureship in International Epidemiology, Univ. Iowa
2015 Robert Leader Endowed Lecture in Food Safety, Michigan State Univ.
2018 - Member, National Institute of Medicine (NAM), USA.

C. Contribution to Science

1. Research on the bat origins of emerging viruses. A range high impact emerging viruses appear to have bat reservoirs (e.g. SARS-CoV, EBOV, NiV, HeV, MERS-CoV, SADS-CoV). As PI on four prior R01s, my work has helped demonstrate the bat-origin for some of these (SARS-CoV, SADS-CoV), analyze the drivers of emergence and risk factors for spillover. Collaborating with virologists in China, we have isolated and characterized SARS-like CoVs from bats that use the same human host cell receptor (ACE-2) as SARS-CoV. This work provides critical reagents and resources that have helped advance understanding of virus-host binding and may contribute to vaccine development. My other work identified factors underlying the emergence of NiV from *Pteropus* bats in Malaysia and Bangladesh; that MERS-CoV likely originated in bats; that SADS-CoV originates in bats; and that bats harbor a significantly higher proportion of zoonoses than all other mammalian groups after correcting for reporting biases.

Obtained via FOIA by Judicial Watch, Inc.

a. Pulliam JRC, Epstein JH, Dushoff J, Rahman SA, Bunning M, HERG, Jamaluddin AA, Hyatt AD, Field HE, Dobson AP & **Daszak P*** and the Henipavirus Ecology Research Group (HERG). (2012). Agricultural intensification, priming for persistence, and the emergence of Nipah virus: a lethal bat-borne zoonosis. **J Roy Soc Interface** 9:89-101

b. Ge X-Y, Li J-L, Yang X-L, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang Y-J, Luo C-M, Tan B, Wang N, Zhu Y, Crameri G, Zhang S-Y, Wang L-F, **Daszak P***, Shi Z-L* (2013). Isolation and characterization of a bat SARS-like Coronavirus that uses the ACE2 receptor. **Nature** 503: 535-538.

c. Memish ZA, Mishra N, Olival KJ, Fagbo SF, Kapoor V, Epstein JH, Al Hakeem R, Durosinloun A, Al Asmari M, Islam A, Kapoor A, Briese T, **Daszak P**, Al Rabeeah A, Lipkin WI. (2013). Middle East respiratory syndrome coronavirus in bats, Saudi Arabia. **EID** 19(11): 1819-1823.

d. Zhou P, Fan H, Lan T, Yang X-L, Shi W-F, Zhang W, Zhu Y, Zhang Y-W, Xie Q-M, Mani S, Zheng X-S, Li B, Li J-M, Guo H, Pei G-Q, An X-P, Chen J-W, Zhou L, Mai K-J, Wu Z-X, Li D, Anderson DE, Zhang L-B, Li S-Y, Mi Z-Q, He T-T, Cong F, Fuo P-J, Huang R, Luo Y, Liu X-L, Chen J, Huang Y, Sun Q, Zhang X-L-L, Wang Y-Y, Xing S-Z, Chen Y-S, Sun Y, Li J, **Daszak P***, Wang L-F*, Shi Z-L*, Tong Y-G*, Ma J-Y* (2018). Fatal Swine Acute Diarrhea Syndrome caused by an HKU2-related Coronavirus of Bat Origin. **Nature** 556: 255-258.

2. **Analyzing the process of disease emergence.** Emerging infectious diseases are a significant threat to global health. However, their emergence is sporadic, complex, and seemingly unpredictable. In the early 2000s I started to use analytical approaches to see if there are patterns in disease emergence, and if these are predictable. By collating a database of all known prior EID events, identifying their point origins, and correcting for reporting biases, I published the first ever predictive 'hotspots' maps of where disease emergence is most likely. Under various grants that I have led, or been a co-investigator on, I have published spatial analyses of the drivers of disease spread, and strategies to predict pandemic emergence.

a. Kilpatrick AM, Chmura AA, Gibbons DW, Fleischer RC, Marra PP & **Daszak P** (2006). Predicting the global spread of H5N1 avian influenza. **PNAS** 103: 19368-19373.

b. Morse SS, Mazet JAK, Woolhouse M, Parrish CR, Carroll D, Karesh WB, Zambrana-Torrelio C, Lipkin WI, **Daszak P*** (2012). Prediction and prevention of the next pandemic zoonosis. **Lancet** 380:1956-1965.

c. **Daszak P***, Zambrana-Torellio C, Bogich TL, Fernandez M, Epstein JH, Murray KA, Hamilton H (2013). Interdisciplinary approaches to understanding disease emergence: The past, present and future drivers of Nipah virus emergence. **PNAS** 110: 3681-3688

d. Allen T, Murray KA, Zambrana-Torrelio C, Morse SS, Rondinini C, Di Marco M, Breit N, Olival KJ, **Daszak P*** (2017). Global hotspots and correlates of emerging zoonotic diseases. **Nature Comm** 8: 1124

3. **Studies of wildlife disease ecology to understand emerging zoonoses.** The majority of EIDs are zoonotic, with the majority of these originating in wildlife. In the 1990s, new collaborations among ecologists and medical researchers began to show that understanding disease dynamics in wildlife can allow better forecasting of disease risk in people. I reviewed this field in a paper in *Science* in 2000 and in a more recent paper in *Nature* on the links among biodiversity and health. During the last two decades, I have led collaborative research programs on how the ecology of specific wildlife-origin zoonoses can help explain patterns of risk to people. This includes my work in 4 R01s and as EHA institutional lead for USAID-EPT-PREDICT, and Chief of Party for USAID-IDEEAL. This work has led to strategies to estimate the diversity of yet-to-be discovered viruses, and a program to identify them (the Global Virome Project).

Obtained via FOIA by Judicial Watch, Inc.

a. **Daszak P***, Cunningham AA, Hyatt AD (2000). Emerging infectious diseases of wildlife - threats to biodiversity and human health. **Science** 287: 443-449

b. Keesing F, Belden LK, **Daszak P**, Dobson A, Harvell CD, Holt RD, Hudson P, Jolles A, Jones KE, Mitchell CE, Myers SS, Bogich T & Ostfeld RS. (2010). Impacts of biodiversity on the emergence and transmission of infectious diseases. **Nature** 468:647-652.

c. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, Zambrana-Torrelio CM, Solovyov A, Ojeda-Flores R, Arrigo NC, Islam A, Ali Khan S, Hosseini P, Bogich TL, Olival KJ, Sanchez-Leon MD, Karesh W, Goldstein T, Luby SP, Morse SS, Mazet JAK, **Daszak P**, Lipkin WI. (2013). A strategy to estimate unknown viral diversity in mammals. **MBio** 4(5): e00598-13.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 – 09/30/19
PREDICT-2
The goal of this work is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries
Role: PI on Subcontract

1R01 AI110964 Daszak (PI) 06/01/14 – 05/31/19
Understanding the Risk of Bat Coronavirus Emergence
The goal of this work is to conduct ecological and virological studies on bats in China that harbor SARS-like coronaviruses, and conduct behavioral risk surveys and testing in people, with a goal of identifying risk factors for further spillover of SARS-like CoVs, and help identify the likely drivers of the SARS-CoV outbreak in 2003.
Role: PI

USAID 1414374 (RDMA, Thailand) Daszak (CoP) 10/01/13 - 03/30/19
Infectious Disease Emergence and Economics of Altered Landscapes (IDEEAL)
The goal of this cooperative agreement is to analyze how land use change affects disease risk in SE Asia, and how economic costs of disease can be used to develop novel intervention policies.
Role: Chief of Party

Completed Research Support

NSF DEB 1414374 Perrings (PI) 10/15/14 - 04/14/18
US-UK Collab: Risks of Animal and Plant Infectious Diseases through Trade (RAPID Trade)
The goal of this NSF-NIH-USDA EEID award, joint with a UK BBSRC grant is to analyze and model how policy changes to trade affect emerging disease risk globally
Role: Co-Investigator

HDTRA1 Allen (PI) 04/15/15 - 04/14/17
Global Rapid Identification of undiagnosed EID Events
The goal of this project was to design software that can be used in the DoD biosurveillance ecosystem (BSVE) to rapidly diagnose novel EID events.
Role: Co-Investigator

1R01GM100471 (NIGMS) Perrings (PI) 09/15/11-06/30/15
MASpread: Modeling Anthropogenic Effects in the Spread of Infectious Disease
The goal of this project was to develop novel approaches to modeling and analyzing disease spread and the social decisions involved in control
Role: Co-Investigator

NSF Daszak (PI) 07/01/10-06/30/15

Obtained via FOIA by Judicial Watch, Inc.

EcoHealthNet - a Research Coordination Network
Funding for student exchange and workshops to fuse veterinary science, ecology and human medical sciences
Role: PI

USAID Emerging Pandemic Threats Mazet (PI) 10/01/09 – 09/30/14
PREDICT-1
The goal of this work was to conduct surveillance for novel pathogens in wildlife, livestock and people in developing countries
Role: PI on Subcontract

2 R01TW005869 Daszak (PI) 09/01/08 – 08/31/13
The Ecology, Emergence and Pandemic Potential of Nipah virus in Bangladesh
This project involved mathematical modeling and fieldwork on the dynamics of Nipah virus in Bangladesh
Role: PI

NSF DEB-1257513 Daszak (PI) 08/15/12-07/31/13
US-China Ecology and Evolution of Infectious Diseases Collaborative Workshop; Kunming, China
The goal of this work was to organize a workshop among NIH, NSF, leading US and Chinese scientists to discuss potential for a jointly funded NIH-NSF-China funding mechanism
Role: PI

1 R01AI079231 (NIAID) Daszak (PI) 09/18/08 – 08/31/13
Risk of viral emergence from bats.
The goal was to model hotspots for bat viral diversity, identify & characterize new bat viruses & understand their pathology
Role: PI

NSF BCS 0826779 Daszak (PI) 10/01/08 – 03/31/12
AOC - HSD – Collaborative Research: Human-related factors affecting emerging infectious diseases
The goal of this work was to analyze how socio-economic and environmental drivers predict risk of EIDs
Role: PI on lead proposal

R01TW005869 - supplemental Daszak (PI) 09/01/08 – 08/31/11
Supplemental funding: Predicting the risk of global H5N1 spread
This project involved mathematical modeling and fieldwork in Bangladesh and China to understand risk of H5N1 spread.
Role: PI

NSF EF-062239 Kilpatrick (PI) 09/01/06 - 08/30/11
Predicting spatial variation in West Nile virus transmission
The goal was to study interaction among WNV vector, reservoir host populations across an urban-to-rural gradient.
Role: Co-PI

R01 TW05869 (Fogarty Intl. Ctr.) Daszak (PI) 08/01/02 - 05/31/07
Anthropogenic change & emerging zoonotic paramyxoviruses
The goal was to identify the cause of emergence of Nipah and Hendra viruses in Malaysia and Australia.
Role: PI

NSF HSD 0525216 Daszak (PI) 10/15/05 - 10/14/06
Collaborative Research: Socio-Economic and Environmental Drivers of Emerging Diseases
The goal of this work was to analyze patterns of disease emergence globally leading to development of a global hotspots map of disease emergence.
Role: PI

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Zhengli Shi	Co-Investigator
eRA COMMONS USER NAME (credential, e.g., agency login) (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
Department of Biology, Wuhan University, China	BS	1987	Genetics
Wuhan Inst. Virol., Chinese Acad. Sci., China	MS	1990	Virology
University Montpellier II, Montpellier, France	Ph.D.	2000	Virology

A. Personal Statement

I have been working on the discovery and characterization of novel viruses from bats and other wildlife since 2004. This included the discovery that Chinese horseshoe bats are the natural reservoir of SARSr-CoVs and the likely origin of SARS-CoV. My group then isolated SARSr-CoVs from bats sharing high homology with human SARS-CoV and demonstrated their interspecies transmission risk, largely confirming bats as the source of SARs. My lab has carried out systematic studies on the epidemiology, genetic evolution, interspecies infection mechanism and pathogenesis of a series of bat-borne emerging viruses including SARSr-CoV, MERS-CoV, EBOV and others. This work has involved collaboration on all other scientists on this R01 renewal proposal, in particular Drs. Daszak and Linfa Wang, who I have collaborated with since 2003, publishing 2 papers in *Nature* and one in *Science* together on our bat-virus work, as well as dozens of others. Recently, this collaborative team discovered that an outbreak of fatal Swine Acute Diarrhea Syndrome in southern China that killed more than 24,000 piglets was caused by spillover of bat HKU2-related coronaviruses. In this proposed work, my group will be responsible for CoV testing in bat samples, serological testing in human samples, and virus characterization work such as cell entry analysis and receptor identification.

B. Positions and Honors.

Positions and Employment

1990 - 93 Research assistant, Wuhan Institute of Virology, Chinese Academy of Sciences, China
1993 - 95 Research scientist, Wuhan Institute of Virology, Chinese Academy of Sciences, China
2000 - Senior Scientist, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China

Other Experience and Professional Memberships

2011 - Director, Center for Emerging Infectious Diseases, Wuhan Inst. Virology, Chinese Acad. Sci.
2013 - Director, BSL-3 laboratory at Wuhan Institute of Virology, Chinese Acad. Sci.
2014 - Director, Committee of Biosafety, Wuhan Institute of Virology, Chinese Acad. Sci.
2014 - Director, CAS Key Laboratory of Special Pathogens and Biosafety
2015 - Vice Director, BSL-4 laboratory, Wuhan Institute of Virology, Chinese Acad. Sci.
2016 - 18 Associate Editor of *Virology Journal*
2017 - 19 Editorial Board of *Virology*
2017-2019 Editor in Chief, *Virologica Sinica*

Honors

Obtained via FOIA by Judicial Watch, Inc.

2003 Natural Science Award (the Second Prize) of Hubei Province, China.
2004 Outstanding supervisor of graduate student of Hubei Province, China.
2006 Outstanding scientist of the Chinese Academy of Sciences.
2006 Outstanding Research Article on Natural Science (the First Prize), Hubei Province, China
2014 Young and Middle-aged Scholar with Distinguished Contribution in Hubei Province, China
2014 Outstanding Research Article on Natural Science (the Grand Prize), Hubei Province, China
2016 Palm Knight Medal for Education, Government of the Republic of France
2017 Natural Science Award (the First Prize) of Hubei Province, China.

C. Selected peer-reviewed publications most relevant to the current application

* = Co-corresponding or first author

Li W*, Shi Z*, Yu M, Ren W, Smith C, Epstein HJ, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, Mceachern J, Field H, Daszak P, Eaton TB, Zhang S, Wang LF (2005). Bats are natural reservoirs of SARS-like coronaviruses. **Science**, 310: 676-679.

Ren W, Qu X, Li W, Han Z, Yu M, Zhang S, Wang LF, Deng H, Shi Z (2008) Difference in receptor usage between SARS coronavirus and SARS-like coronavirus of bat origin. **Journal of Virology** 82(4): 1899–1907.

Yuan J, Hon CC, Li Y, Wang D, Xu G, Zhang H, Zhou P, Poon LM, Lam TT, Leung FC. Shi Z (2010). Intra-species Diversity of SARS-Like Coronaviruses (CoVs) in *Rhinolophus sinicus* and Its Implications on the Origin of SARS-CoVs in human. **Journal of General Virology**, 91(4):1058-1062.

Ge XY, Li JL, Yang X-L, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang YJ, Luo CM, Tan B, Wang N, Zhu Y, Crameri G, Zhang SY, Wang LF, Daszak P*, Shi Z* (2013). Isolation and characterization of a bat SARS-like Coronavirus that uses the ACE2 receptor. **Nature** 503: 535-538.

Menachery VD, Yount BL, Debbink K, Agnihothram S, Gralinski LE, Plante JA, Graham RL, Scobey T, Ge XY, Donaldson EF, Randell SH, Lanzavecchia A, Marasco WA, Shi Z*, Baric RS* (2015). A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. **Nature Medicine**, 21:1508-1513.

Yang XL, Hu B, Wang B, Wang MN, Zhang Q, Zhang W, Wu LJ, Ge XY, Zhang YZ, Daszak P, Wang LF*, Shi Z* (2016). Isolation and Characterization of a Novel Bat Coronavirus Closely Related to the Direct Progenitor of Severe Acute Respiratory Syndrome Coronavirus. **Journal of Virology**, 90: 3253-3256.

Zeng L, Ge X, Peng C, Yang X, Tan B, Gao Y, Chen J, Chmura AA, Daszak P*, Shi Z* (2016) Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response. **Journal of Virology**, 90(14): 6573–6582.

Hu B, Zeng LP, Yang XL, Ge XY, Zhang W, Li B, Xie JZ, Shen XR, Zhang YZ, Wang N, Luo DS, Zheng XS, Wang MN, Daszak P, Wang LF, Cui J*, Shi Z* (2017). Discovery of A Rich Gene Pool of Bat SARS-related Coronaviruses Provides New Insights into the Origin of SARS Coronavirus. **PLOS Pathogens**, 13(11): e1006698.

Zhou P, Fan H, Lan T, Yang XL, Shi WF, Zhang W, Zhu Y, Zhang YW, Xie QM, Mani S, Zheng XS, Li B, Li JM, Guo H, Pei GQ, An XP, Chen JW, Zhou L, Mai KJ, Wu ZX, Li D, Anderson D, Zhang LB, Li SY, Mi ZQ, He TT, Cong F, Guo PJ, Huang R, Luo Y, Liu XL, Chen J, Huang Y, Sun Q, Zhang XLL, Wang YY, Xing SZ, Chen YS, Sun Y, Li J, Daszak P, Wang LF, Shi Z, Tong YG, Ma JY (2018) Fatal swine acute diarrhea syndrome caused by an HKU-2 related coronavirus of bat origin. **Nature**, 556: 255-258.

Luo CM, Wang N, Yang XL, Liu HZ, Zhang W, Li B, Hu B, Peng C, Geng QB, Zhu G, Li F*, Shi Z* (2018). Discovery of Novel Bat Coronaviruses in South China That Use the Same Receptor as Middle East Respiratory Syndrome Coronavirus. **Journal of Virology**, 92 (13): e00116-18.

Additional recent publications of importance to the field (in chronological order)

Obtained via FOIA by Judicial Watch, Inc.

Ge X, Li Y, Yang X, Zhang H, Zhou P, Zhang Y, Shi Z (2012). Metagenomic analysis of viruses from bat fecal samples reveals many novel viruses in insectivorous bats in china. **Journal of Virology**, 86, 4620-4630.

Yuan J, Zhang Y, Li J, Zhang Y, Wang LF*, Shi Z* (2012). Serological evidence of ebolavirus infection in bats, China. **Virology Journal**, 9: 236.

Yang XL, Zhang YZ, Jiang RD, Guo H, Zhang W, Li B, Wang N, Wang L, Waruhiu C, Zhou JH, Li SY, Daszak P, Wang LF*, Shi Z* (2017). Genetically Diverse Filoviruses in *Rousettus* and *Eonycteris* spp. Bats, China, 2009 and 2015. **Emerging Infectious Diseases**, 23(3):482-486.

Zeng LP, Ge XY, Peng C, Tai WB, Jiang SB, Du LY*, Shi Z* (2017). Cross-neutralization of SARS coronavirus-specific antibodies against bat SARS-like coronaviruses. **Science China Life Sciences**, 60(12):1399-1402.

Wang N, Li SY, Yang XL, Huang, HM, Zhang YJ, Guo H, Luo CM, Miller M, Zhu G, Chmura AA, Hagan E, Zhou JH, Zhang YZ, Wang LF, Daszak P*, Shi Z* (2018). Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. **Virologica Sinica**, 33(1):104-107.

D. Research Support

Ongoing Research Support

(b) (4)

Geographical distribution and genetic variation of pathogens in Africa
Role: PI

31770175 National Natural Science Foundation of China 01/01/2018-12/31/2021
Evolution mechanism of the adation of bat SARS-related coronaviruses to host receptor molecules and the risk of interspecies infection
Role: PI

(b) (4)

Genetic evolution and transmission mechanism of important bat-borne viruses
Role: PI

R01 AI110964 Daszak (PI) 06/01/14-05/31/19
Understanding Risk of Bat Coronaviruses
The goal of this study is to analyze the risk of coronavirus spillover from bats to humans in Southern China
Role: Co-Investigator

Emerging Pandemic Threat Program, USAID Mazet (PI) 10/01/14-09/30/19
PREDICT 2
The goal of this project is to create and implement a global virus surveillance system in animals and humans and analyze spillover risk.
Role: China Country Coordinator

Completed Research Support

(b) (4)

Metagenomic analysis of bat intestinal viruses
Role: PI

(b) (4)

Mechanism of interspecies transmission of zoonotic viruses

Obtained via FOIA by Judicial Watch, Inc.

Role: Co-PI

(b) (4)

Genetic diversity, identification and pathogenesis of bat viruses (b) (4)

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Kevin J. Olival	Co-Investigator
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
Colorado State University, Fort Collins, CO	BS	05/1997	Biology
Columbia University, New York, NY	MA	10/2003	Conservation Biology
Columbia University, New York, NY	PhD	05/2008	Ecology & Evolution
American Museum of Natural History, New York	Post Doc	08/2009	Molecular Parasitology
NIH Fogarty US Global Health Fellow, New York	Post Doc	08/2011	EIDs

A. Personal Statement

The goal of this proposal is to understand the current and future threat of bat-borne coronavirus spillover in Southern China, by identifying which viruses, host species, and human behaviors are associated with the highest risk of CoV exposure. Specifically, we will use a combination of targeted bat sampling, human behavioral risk analyses, mathematical modeling, and phylogenetic and molecular methods to test several hypotheses related to zoonotic spillover risk of β-CoVs, with specific attention paid towards SARSr-CoVs. My research experience over the last 16 years on bat-borne disease evolution, ecology, dynamics, population genetics, and viral discovery is strongly complementary to these aims. Our current proposal builds upon the findings of an ongoing NIAID R01 grant (ending 5/31/19), for which I was a co-investigator. Prior to this I coordinated research efforts under a NIAID award (2011-2016), investigating the risk of viral emergence from bats. This included sample collection and testing of thousands of bats from 8 countries globally. As an NIH Fogarty Global Health Post-Doc Fellow, I gained invaluable experience working internationally with a project focused on the ecology and evolution of Nipah virus in Bangladesh. My work over the last decade includes leading field investigations and bat viral surveillance in a wide range of countries, including: Bangladesh, Cambodia, India, Indonesia, Malaysia, Thailand, Philippines, Saudi Arabia, Georgia, Jordan, and Turkey. Discoveries include the first viral isolation of Nipah virus from the large flying fox in Malaysia; evidence of MERS-CoV in bats in Saudi Arabia; and the first serological evidence of Ebola Zaire virus in bats in Asia. I currently serve as the Modeling & Analytics coordinator under the USAID PREDICT-2 project, working with a team of analyst to develop new approaches to predict and prevent zoonoses. As part of this effort, I developed a new approach that combines phylogenetic, ecological, and life-history traits to predict viral diversity, host range, and spillover potential, leading to a recent first author paper in *Nature*.

1. (b) (4)
2. Memish ZA, Mishra N, Olival KJ, Fagbo SF, Kapoor V, Epstein JH, AlHakeem R, Al Asmari M, Islam A, Kapoor A, Briese T, Daszak P, Al Rabeeah AA, Lipkin WI. (2013). Middle East Respiratory Syndrome Coronavirus in Bats, Saudi Arabia. **Emerging Infectious Diseases**. 19(11): 1819-1823.
3. Olival KJ*, Hosseini P, Zambra-Torrellio C, Ross N, Bogich T, Daszak P*. (2017). Host and viral traits predict zoonotic spillover from mammals. **Nature** 546(7660): 646-650.

*corresponding author

B. Positions and Honors

Obtained via FOIA by Judicial Watch, Inc.

Positions and Employment

1999 - 02 Research Associate, Kewalo Marine Laboratory, University of Hawaii
2003 - 07 US Environmental Protection Agency STAR Fellow
2006 - 13 Instructor, Columbia University Secondary School Summer Program
2010 - 15 Senior Research Scientist, EcoHealth Alliance
2015 - 17 Associate Vice President for Research, EcoHealth Alliance
2009 - Visiting Scientist, American Museum of Natural History
2009 - Adjunct Faculty, Earth Institute Center for Environmental Sustainability, Columbia University
2017 - Vice President for Research, EcoHealth Alliance

Other Experience and Professional Memberships

1998 - 00 Member, AAAS
2000 - 02 Mentor, NSF Undergraduate Mentoring in Environmental Biology (UMEB), University of Hawaii
2003 - 05 Member, American Society of Mammalogists
2005 - 06 Member, New York Academy of Sciences
2011 - Scientific Steering Committee Member, Southeast Asian Bat Conservation Research Unit
2011 - Scientific Advisory Board Member, Lubee Bat Conservancy, FL
2011 - Scientific Advisor, Bat Conservation International
2011 - Review Editor, EcoHealth
2015 - US White-Nose Syndrome Stakeholder Committee and Communications Committee Member
2015 - Island and Seas, Board Member
2017 - DoD DTRA: Steering Committee Member, Bat One Health Research Network

Honors

1993-97 Colorado State University Distinguished Scholar Award
2003 NSF Graduate Student Fellowship, Honorable Mention
2005-07 Bat Conservation International Student Award and Scholarship
2004-07 US EPA STAR Fellowship Award
2008 PhD *with Distinction*, Columbia University
2013 Plenary talk on bat virus modeling at 11th Annual ASM Biodefense and EID Research Meeting
2013-14 Institute of Medicine, Forum on Microbial Threats. Invited speaker, briefings on MERS-CoV and Emerging Viral Diseases
2016 Plenary Speaker, NYC Medtech conference – Global Virome Project
2017-18 Three papers awarded the InCites Highly Cited Paper™ designation (top 1% in field) for Immunology and Microbiology

C. Contribution to Science

1. **Viral Discovery and Characterization in Bats**

A large body of my research has focused on understanding the distribution and diversity of viruses in wildlife populations to better understand the ecological risk of viral emergence. This includes the first use of species accumulation curves to estimate viral diversity using data from longitudinal surveillance of fruit bats in Bangladesh, and a large meta-analysis of viral prevalence in bats to optimize discovery strategies. Two field studies highlighted below include a broad geographic survey of bat coronaviruses in Thailand, and the first isolation and full genome characterization of Nipah virus from the large flying fox in Malaysia.

a. Rahman SA, Hassan SS, Olival KJ, Mohamed M, Chang L-Y, Hassan L, Saad NM, Shohaimi SA, Mamat ZC, Naim MS, Epstein JH, Suri AS, Field HE, Daszak P and HERG. (2010). Characterization of Nipah virus from Naturally Infected *Pteropus vampyrus* Bats, Malaysia. **Emerging Infectious Disease** 16(12): 1990-1993.

Obtained via FOIA by Judicial Watch, Inc.

b. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, Zambrana-Torrelio CM, Solovyov A, Ojeda-Flores R, Arrigo NC, Islam A, Khan SA, Hosseini P, Bogich TL, Olival KJ, Sanchez-Leon MD, Karesh WB, Goldstein T, Luby SP, Morse SS, Mazet JAK, Daszak P, Lipkin WI. (2013). A Strategy To Estimate Unknown Viral Diversity in Mammals. **Mbio.** 4(5): e00598-13.

c. Wacharapluesadee S, Duengkae P, Rodparn A, Kaewpom T, Maneeorn P, Kanchanasaka B, Yinsakmongkon S, Sittidetboripat N, Chareesaen C, Khlangsap N, Pidthong A, Leadprathom K, Ghai S, Epstein JH, Daszak P, Olival KJ, Blair PJ, Callahan MV, Hemachudha T. (2015). Diversity of Coronavirus in Bats from Eastern Thailand. **Virology Journal** 12:57.

d. Young CC and Olival KJ*. (2016). Optimizing Viral Discovery in Bats. **PLOS ONE** 11(2): e0149237.

2. Serological Surveillance

Bats are believed to harbor a unique and large diversity of viruses, including a number of pathogens that pose a risk to human health (e.g. Ebola, Nipah, SARS-CoV). I have been involved with field and laboratory investigations of several bat-borne pathogens that pose the greatest risk to humans over the years, including Filoviruses, Henipaviruses, and SARS and MERS-related Coronaviruses. Collection and analysis of serological data was critical to each of these studies. Using serological and PCR data we discovered that bats are reservoirs of Ebola Reston virus in the Philippines. Extensive, proactive surveillance of wild bat and primate populations in Thailand for Ebola viruses importantly showed that several suspected species are likely *not* important reservoirs. The work in Thailand was predicated by my own investigations in Bangladesh where we discovered the first evidence for Ebola Zaire virus infection in a wildlife species outside of Africa – changing our paradigm as to where these viruses can be found globally. Lastly, I have been involved with extensive work to identify the natural reservoir host of Reston virus in Philippines that included both molecular and serological findings.

a. Olival KJ*, Islam A, Yu M, Anthony SJ, Epstein JH, Khan SA, Khan SU, Crameri G, Wang LF, Lipkin WI, Luby SP, and Daszak P. (2013). Ebolavirus Antibodies in Fruit Bats, Bangladesh. **Emerging Infectious Diseases** 19(2): 270-273.

b. Wacharapluesadee S, Olival KJ, Kanchanasaka B, Duengkae P, Kaewchot S, Srongmongkol P, Ieamsaard G, Maneeorn P, Sittidetboripat N, Kaewpom T, Petcharat S, Yingsakmongkon S, Rollin PE, Towner JS , Hemachudha T. (2015). Surveillance for Ebola Virus in Wildlife, Thailand. **Emerging Infectious Diseases** 21(12): 2271-2273.

c. Jayme S, Yu M, Jong Cd, Olival KJ, Tagtag A, Hughes T, Foord A, Marsh G, Crameri G, Epstein JH, Santos I, Catbagan D, Lim M, Benigno C, Wang L, Daszak P, Field H, Newman S. (2015). Molecular evidence of Ebola Reston virus infection in Philippine bats. **Virology Journal**. 12(1): 107.

d. [redacted] (b) (4)

3. Modeling Disease Emergence and Spillover Risk

I have used my applied ecology background working with analyses of wildlife and their pathogens to develop new models to improve our global understanding of zoonotic spillover and disease circulation. In addition to my previously mentioned *Nature* paper, this includes studies that examined the environmental drivers of bat virus spillover to humans, cross-species transmission among bat species, spatial analysis of emerging zoonotic disease hotspots, and host-specific determinants of fungal infection in bats. These modeling approaches explicitly use data from PCR- and serology-based field studies, combined with an understanding of wildlife biology and ecology, to assess the environmental and demographic drivers of disease transmission -- bridging the gap between field investigations and modeling transmission risk.

Obtained via FOIA by Judicial Watch, Inc.

a. Brierley L, Vonhof MJ, Olival KJ, Daszak P, Jones KE. (2016). Quantifying global drivers of zoonotic bat viruses: a process-based perspective. **American Naturalist** 187: E53-64

b. Willoughby AR, Phelps K, PREDICT Consortium, Olival KJ*. (2017). "A Comparative Analysis of Viral Richness and Viral Sharing in Cave-Roosting Bats". **Diversity** 9 (35).

c. Allen T, Murray KA, Zambrana-Torrelio C, Morse SS, Rondinini C, Di Marco M, Breit N, Olival KJ, Daszak P. (2017). Global hotspots and correlates of emerging zoonotic diseases. **Nature Communications**. 8(1124): 1-10

d. Verant ML, Bohuski EA, Richgels KLD, Olival KJ, Epstein JH, and Blehert DS. (2018). Determinants of *Psudogymnoascus destructans* within bat hibernacula: implications for surveillance and management of white-nose syndrome. **Journal of Applied Ecology** 55: 820-829.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

HDTRA11710064 Olival (PI) 10/02/17-10/01/22
Understanding the Risk of Bat-Borne Zoonotic Disease Emergence in Western Asia
The goal of this project is to characterize pathogen diversity, strengthen zoonotic disease surveillance capacity, and test key hypotheses about the risk of bat-borne zoonotic disease emergence in Western Asia.
Role: PI

R01 AI110964 Daszak (PI) 06/01/14-05/31/19
Understanding Risk of Bat Coronaviruses
The goal of this study is to analyze the risk of coronavirus spillover from bats to humans in Southern China
Role: co-PI

Emerging Pandemic Threat Program, USAID Mazet (PI) 10/01/14-09/30/19
PREDICT 2
The goal of this project is to create and implement a global virus surveillance system in animals and humans and analyze spillover risk.
Role: Modeling and Analytics Coordinator; Country lead for Indonesia, South Sudan, and Thailand.

Completed Research Support

Emerging Pandemic Threat Program, USAID Mazet (PI) 10/01/09-09/30/14
PREDICT
The goal of this project was to conduct zoonotic virus surveillance in wildlife in 20 countries, and modeling hotspots and drivers for disease emergence.
Role: Key Personnel: Modeling Team; Country lead for Thailand and Indonesia

Service Award, US Fish and Wildlife Epstein (PI) 09/01/12-09/30/14
Characterization of Climatic Parameters within Bat Hibernacula, their Influence on Environmental Loads of *Geomyces destructans*, and Implications for the Migration of White-Nose Syndrome in Bats.
The goal of this project was to identify environmental and other factors that influence the progression and severity of White Nose Syndrome in bats.
Role: co-PI

R01 AI079231 Daszak (PI) 09/18/08-08/31/13

Obtained via FOIA by Judicial Watch, Inc.

Risk of viral emergence from bats
Modeled hotspots for viral diversity and emergence in bats, discovery of new viruses, and in vitro test of infectiousness for novel pathogens.
Role: Key Personnel: led project implementation, study design, and phylogenetic modeling

Endangered Species grant, USGS Russell, Vonhof, and Olival (PI) 06/18/12-06/17/13
Genetic Approaches to Defining Taxonomic and conservation Units for the Hawaiian Hoary Bat
The goal of this project was to determine the phylogenetic position and conservation genetic units for endangered hoary bats.
Role: co-PI

3R01 TW005869-06S1 Daszak (PI) 09/01/09 – 8/31/11
NIH Fogarty Ecology of Infectious Diseases ARRA award
The goal of this project was to conduct Nipah virus surveillance in wild bat populations and use genetic methods to understand viral circulation in Bangladesh.
Role: Fogarty US Global Health Fellow

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Ralph Steven Baric	Co-Investigator
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
North Carolina State University, Raleigh, NC	BS	1977	Zoology
North Carolina State University, Raleigh, NC	Ph.D.	1982	Microbiology
University of Southern CA, School of Med, (Los Angeles, CA)	Post-Doc	1986	Microbiology

A. Personal Statement: The Baric laboratory uses genetic, biochemical, molecular and immunologic approaches to study the molecular mechanisms regulating viral evolution, virus immunity, virus-host interactions and vaccine mediated protective immunity using coronaviruses (CoV), noroviruses and flaviviruses (Dengue) as models. SARS-CoV and MERS-CoV are used as models to address fundamental questions in genetics, structure-function analyses, entry and cross species transmission, fidelity regulation, host susceptibility allele mapping, pathogenesis as well as therapeutic design and testing. Synthetic genomics and reverse genetics are used to create a panel of CoV molecular cDNA clones for SARS-CoV, SARS-like bat coronaviruses (SL-CoV), MERS-CoV, several human coronavirus, Dengue 1-4 and Zika virus. The Baric laboratory has developed key animal models of human disease, including SARS-CoV and SL-CoV pathogenesis in young and aged mice, and CRISPR gene edited mice encoding permissive mutations in the murine dipeptidyl peptidase receptor, making the animals permissive for MERS-CoV infection and disease.

The Baric laboratory has longstanding expertise in CoV evolution and emergence, replication, virus-receptor interactions, genetics, animal model development and pathogenesis. Not only has the Baric laboratory made fundamental breakthroughs in all aspects of CoV genetics, biology and immunology, but it has designed, developed and tested small molecule inhibitors and vaccines against emerging CoVs. Our group has collaborated with Drs. Daszak, Shi and Wang on SARSr-CoVs for the past 3 years, and this R01 is a natural development of this collaboration.

***Qualifications by Publication*: : >314 total publications, >120 since 2013, H-index: 84.**
http://www.ncbi.nlm.nih.gov/sites/myncbi/ralph.baric.1/bibliography/40583903/public/?sort=date&direction=ascending.

Key Manuscripts

1. Sheahan TP, Sims AC, Graham RL, Menachery VD, Gralinski LE, Case JB, Leist SR, Pyrc K, Feng JY, Trantcheva I, Bannister R, Park Y, Babusis D, Clarke MO, Mackman RL, Spahn JE, Palmiotti CA, Siegel D, Ray AS, Cihlar T, Jordan R, Denison MR, Baric RS (2017). Broad-spectrum antiviral GS-5734 inhibits both epidemic and zoonotic coronaviruses. **Science Translational Medicine**, 9(396). eaal3653. PMC5567817.
2. Scobey T, Yount BL, Sims AC, Donaldson EF, Agnihothram SS, Menachery VD, Graham RL, Swanstrom J, Bove PF, Kim JD, Grego S, Randell SH, Baric RS (2013). Reverse genetics with a full-length infectious cDNA of the Middle East respiratory syndrome coronavirus. **Proceedings of the National Academy of the Sciences**, 110(40):16157-62. PMC3791741.
3. Menachery, VD, Yount, BL, Debbink, K, Agnihothram, S., Gralinski, LE, Plante, JA, Graham, RL, Scobey T, Ge SY, Donaldson EF, Randell SH, Lanzavecchia A, Marasco WA, Shi Z, Baric RS (2015). A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. **Nature Medicine**, Nov 9. doi: 10.1038/nm.3985. [Epub ahead of print]. PMID:26552008.

Obtained via FOIA by Judicial Watch, Inc.

4. Cockrell AS, Yount BL, Scobey T, Jensen K, Douglas M, Beall A, Tang XC, Marasco WA, Heise MT, Baric RS (2016). A Mouse Model for MERS Coronavirus Induced Severe Respiratory Distress Syndrome. **Nature Microbiology**, 2:16226. PMC5578707.

B. Positions and Honors.

Employment Experience:

1986-92 Assistant Professor, Department of Parasitology and Laboratory Practice and Department of Epidemiology, University of North Carolina (UNC), Chapel Hill, NC

1992-2001 Associate Professor, Departments of Epidemiology and Microbiology & Immunology, UNC Chapel Hill

2001- Professor, Departments of Epidemiology and Microbiology and Immunology, UNC Chapel Hill

Selected Awards/Honors:

2018 US Natl. Acad. Sci. "China-US Workshop on Challenges of Emerging Infections, Laboratory Safety and Global Health Security, Jan 2018, Galveston, Tx.

2015 US Natl. Acad. Sci./UK Royal Society Workshop: Sackler Scientific Forum on the Trends in Synthetic Biology and Gain of Function and Regulatory Implications, U.K.

2015 US Natl. Acad. Sci. "China-U.S. Workshop on the Challenges of Emerging Infections, Laboratory Safety, and Global Health Security" September 28-30 in Beijing, China

2015 MERS-CoV Stakeholders Workshop, invited panelist, NIH

2014 National Academy of Sciences: Working Group on Risks and Benefits of Gain of Function Research

2005-15 Review Board, *J. Virology*

2008-15 Senior Editor, *Plos Pathogens*

2008 US Natl. Acad. Sci. Working Group: Gene Sequence Methods for Classification of Select Agents

2007-08 Associate Editor, *Plos Pathogens*

2005-09 Permanent Member, NIH VirB Study Section

2003 Finalist/Runner-up, World Technology Award

1989-94 Established Investigator: American Heart Association

1984-86 Harvey Weaver Scholar, National Multiple Sclerosis Society

C. Contributions to Virology: The Baric laboratory has made significant contributions to our understanding of all aspects of CoV biology, including: i) CoV genetics and reverse genetics for SARS-CoV, MHV, MERS-CoV, HCoV NL63, PEDV, TGEV, bat SARS-like CoV (SL-CoV), BtCoV HKU-5 and others, ii) demonstration of proof-reading activities in the CoV genome, iii) identification and characterization of bat SL-CoV with prepandemic potential, iii) coronavirus transcription mechanisms, iv) mechanisms of interferon antagonism and interferon stimulated gene expression control, v) virus host susceptibility allele mapping, vi) epitope mapping of human monoclonal antibodies, vii) identification of broad spectrum human monoclonal antibodies against SARS-CoV and MERS-CoV, viii) mouse models of human disease (MERS-CoV and SARS-CoV), ix) aging and emerging coronavirus vaccine efficacy, and x) live and attenuated vaccine design in young and aged animal models of human disease. The Baric laboratory has also made major contributions to norovirus immunology and flavvirus reverse genetics and the human immune responses after infection.

Some representative major contributions outside and within the CoV field include:

1. (b) (4)

2. Gralinski LE, Ferris MT, Aylor DL, Whitmore AC, Green R, Frieman MB, Deming D, Menachery VD, Miller DR, Buus RJ, Bell TA, Churchill GA, Threadgill DW, Katze MG, McMillan L, Valdar W, Heise MT, Pardo-Manuel de Villena F, Baric RS (2015) Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. **PLOS Genetics,** 11(10): e1005504. PMID:26452100.

3. Lindesmith L, Moe C, Marionneau S, Ruvoen N, Jiang X, Lindblad L, Stewart P, LePendu J, Baric R (2003). Human susceptibility and resistance to Norwalk virus infection. **Nature Medicine**, 9(5):548-53. PMID:12692541.

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4. Lindesmith LC, Donaldson EF, Lobue AD, Cannon JL, Zheng DP, Vinje J, Baric RS (2008). Mechanisms of GII.4 norovirus persistence in human populations. **PLOS Medicine**, 5(2):e31. PMC2235898.

C.1. Coronavirus Pathogenesis and Virus Immunity. Our group has studied the role of virus-immune interactions in coronavirus and other emerging virus pathogenesis mechanisms.

1. Rasmussen AL, Okumura A, Ferris MT, Green R, Feldmann F, Kelly SM, Scott DP, Safronetz D, Haddock E, LaCasse R, Thomas MJ, Sova P, Carter VS, Weiss JM, Miller DR, Shaw GD, Korth MJ, Heise MT, Baric RS, de Villena FP, Feldmann H, Katze MG (2014). Host genetic diversity enables Ebola hemorrhagic fever pathogenesis and resistance. **Science**, 2014 346(6212):987-91. PMC4241145.
2. Gralinski LE, Sheahan TP, Morrison TE, Menachery VD, Jensen K, Leist SR, Whitmore A, Heise MT, Baric RS (2018). Complement Activation Contributes to Severe Acute Respiratory Syndrome Coronavirus Pathogenesis. **mBio**, 9(5). e01753-18. PMC6178621.
3. Menachery VD, Eisfeld AJ, Schäfer A, Josset L, Sims AC, Proll S, Fan S, Li C, Neumann G, Tilton SC, Chang J, Gralinski LE, Long C, Green R, Williams CM, Weiss J, Matzke MM, Webb-Robertson BJ, Schepmoes AA, Shukla AK, Metz TO, Smith RD, Waters KM, Katze MG, Kawaoka Y, Baric RS (2014). Pathogenic influenza viruses and coronaviruses utilize similar and contrasting approaches to control interferon-stimulated gene responses. **mBio**, 5(3): e01174-14. PMC4030454.
4. Graham RL, Becker MM, Eckerle LD, Bolles M, Denison MR, Baric RS (2012). A live, impaired-fidelity coronavirus vaccine protects in an aged, immunocompromised mouse model of lethal disease. **Nature Medicine**, 18(12):1820-6. PMCID: PMC3518599.

C.2. Coronavirus Innate Immunity/Animal Models. The Baric laboratory group has studied CoV host range expansion using experimental evolution and SARS-CoV, MERS-CoV, civet SL-CoV, bat SL-CoV, and bat CoV HKU5 as models. This includes synthetic reconstruction of civet and bat CoV from *in silico* sequence, the first reported recovery of recombinant bat viruses, and characterization of host range phenotypes *in vitro* and *in vivo*. Applications of experimental evolution have focused on molecular mechanisms associated with virus-receptor interactions in viral persistence, virus innate immune interactions, and increased virulence in mice.

1. Agnihothram S, Yount BL, Donaldson EF, Huynh J, Menachery VD, Gralinski LE, Graham RL, Becker MM, Tomar S, Scobey TD, Osswald HL, Whitmore A, Gopal R, Ghosh AK, Mesecar A, Zambon M, Heise M, Denison MR, Baric RS (2014). A mouse model for Betacoronavirus subgroup 2c using a bat coronavirus strain HKU5 variant. **mBio**, 5(2): e00047-14. PMC3977350.
2. Sheahan T, Rockx B, Donaldson E, Corti D, Baric R (2008). Pathways of cross-species transmission of synthetically reconstructed zoonotic severe acute respiratory syndrome coronavirus. **Journal of Virology,** 82(17):8721-32. PMC2519660
3. Becker MM, Graham RL, Donaldson EF, Rockx B, Sims AC, Sheahan T, Pickles RJ, Corti D, Johnston RE, Baric R*, Denison MR* (2008). Synthetic recombinant bat SARS-like coronavirus is infectious in cultured cells and in mice. **Proceedings of the National Academy of the Sciences**, 105(50):19944-9. PMC2588415. (* = co-first authors)
4. Menachery VD, Schäfer A, Burnum-Johnson KE, Mitchell HD, Eisfeld AJ, Walters KB, Nicora CD, Purvine SO, Casey CP, Monroe ME, Weitz KK, Stratton KG, Webb-Robertson BM, Gralinski LE, Metz TO, Smith RD, Waters KM, Sims AC, Kawaoka Y, Baric RS (2018). MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. **Proceedings of the National Academy of the Sciences**, 115(5): E1012-E1021. PMID: 29339515.

C.3. Virus Genetic Platforms. The Baric laboratory has pioneered reverse genetic analyses of CoVs and DENVs. Several CoV infectious cDNA clones are available in the lab, including SARS-CoV, MERS-CoV, conventional human and model CoVs, and several bat CoVs with pandemic potential. The availability of these genetic platforms allows for detailed studies into the role of viral genes in pathogenesis, innate immune antiviral immunity, vaccine performance and design, virus-receptor interactions, entry and virus evolution.

1. Yount B, Curtis, K, Fritz L, Hensley L, Jahrling P, Prentice E, Denison M, Geisbert T, Baric RS (2003). Reverse Genetics with a full length infectious cDNA for the SARS Coronavirus. **Proceedings of the National Academy of the Sciences**, 100(22): 12995-13000. PMCID: PMC240733.

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2. Rockx B, Sheahan T, Donaldson E, Harkema J, Sims A, Heise M, Pickles R, Cameron M, Kelvin D, Baric R (2007). Synthetic reconstruction of zoonotic and early human severe acute respiratory syndrome coronavirus isolates that produce fatal disease in aged mice. **Journal of Virology** 81(14):7410-23. PMC1933338.
3. Widman DG, Young E, Yount BL, Plante KS, Gallichotte EN, Carbaugh DL, Peck KM, Plante J, Swanstrom J, Heise MT, Lazear HM, Baric RS (2017). A Reverse Genetics Platform that Spans the Zika Virus Family Tree. **mBio**, 8(2): e02014-16. PMC5340872
4. Donaldson EF, Yount B, Sims AC, Burkett S, Pickles RJ, Baric RS (2008). Systematic assembly of a full-length infectious clone of human coronavirus NL63. **Journal of Virology**, 82(23):11948-57. PMC2583659.

C4. Virus Vaccine Design and Antiviral Immunotherapy. Viruses are major causes of morbidity and mortality globally. The Baric laboratory has used structure-guided immunogen design and epitope exchange to build multivalent immunogens to increase vaccine breadth and diagnostic potential.

1. Deming DJ, Sheahan T, Heise M, Yount B, Davis N, Sims A, Suthar M, Whitmore JH, Pickles R, West A, Donaldson E, Curtis K, Johnston, RE, Baric RS (2006). Vaccine efficacy in senescent mice challenged with recombinant SARS-CoV bearing epidemic and zoonotic spike variants. **PLOS Medicine**, 3(12): e525 PMCID: PMC1716185.
2. Tang XC, Agnihothram SS, Jiao Y, Stanhope J, Graham RL, Peterson EC, Avnir Y, Tallarico AS, Sheehan J, Zhu Q, Baric RS, Marasco WA (2014). Identification of human neutralizing antibodies against MERS-CoV and their role in virus adaptive evolution. **Proceedings of the National Academy of the Sciences**,111(19):E2018-26. PMC4024880
3. Lindesmith LC, Ferris MT, Mullan CW, Ferreira J, Debbink K, Swanstrom J, Richardson C, Goodwin RR, Baehner F, Mendelman PM, Bargatze RF, Baric RS (2015). Broad blockade antibody responses in human volunteers after immunization with a multivalent norovirus VLP candidate vaccine: immunological analyses from a phase I clinical trial. **PLOS Medicine**, 12(3):e1001807 PMC4371888.
4. Bolles M, Deming D, Long K, Agnihothram S, Whitmore A, Ferris M, Funkhouser W, Gralinski L, Totura A, Heise M, Baric RS (2011). A double-inactivated severe acute respiratory syndrome coronavirus vaccine provides incomplete protection in mice and induces increased eosinophilic proinflammatory pulmonary response upon challenge. **Journal of Virology**, 85(23):12201-15. PMC3209347

D.Research Support.

U19 AI 100625 Baric/Heise (MPI) 09/01/17-08/31/22
Systems Immunogenetics of Biodefense Pathogens in the Collaborative Cross
The Collaborative Cross is a mouse resource for study of complex genetic interactions in diverse populations, to identify novel polymorphic genes regulating immune responses to SARS, influenza and WNV, analyze genetic underpinning of immune phenotypes in mice and humans, and generate panels of genetically defined mice to probe polymorphic gene control of immune responses against a pathogens or other immune stimuli.

R01 AI108197 Denison/Baric (MPI) 05/01/18-04/30/23
Determinants of Coronavirus Fidelity in Replication and Pathogenesis
Experiments in this aim will test the hypothesis that nsp14 functions in maintaining high replication fidelity and viral RNA synthesis are coupled and that targeted engineered mutations across nsp14 alter: a) RNA fidelity outcomes; b) sensitivity to nucleoside mutagens and polymerase inhibitors; c) sensitivity to innate immunity.

HHSN272201000019I-HHSN27200003 Baric (PI) 09/30/17-03/31/24
MERS-CoV Mouse Model for Vaccine & Therapeutic Testing (Task Order A57)
Use generation of transgenic mice and modifications to the MERS-CoV genome to identify a mouse model for MERS-CoV that recapitulates human disease phenotypes for evaluating vaccine platforms and therapeutics.

U19 AI 109680 Whitley (PI) 03/01/14-02/28/19
Antiviral Drug Discovery and Development Center
The specific aims of the proposal will identify small molecule inhibitors of CoV fidelity and RNA capping, define their mechanism of action, and determine their efficacy against SARS-CoV and across CoV families using in vivo mouse models of acute and persistent CoV disease. Role: Co-Investigator

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U19 AI 109761 Lipkin (PI) 03/01/14-02/28/19
Diagnostic and Prognostic Biomarkers for Severe Viral Disease
The goal is to develop new platform technologies that use functional genomics as diagnostic and prognostic indicators of severe end stage lung disease, systemic and enteric diseases following virus infection, including coronaviruses, flaviviruses and noroviruses. Role: Project Leader

R01 AI110700 Baric (PI) 04/20/15-03/31/20
Mechanisms of MERS-CoV Entry, Cross-species Transmission and Pathogenesis
The overall goal is to build a comprehensive understanding of the molecular mechanisms guiding group 2c CoV receptor recognition, entry and pathogenesis.

(b) (4) Baric (PI) (b) (4)
Breadth of Blockade Antibody Responses Following Norovirus Vaccination.
(b) (4) and UNC will collaborate to evaluate the breadth of the antibody blockade response following norovirus vaccination in various human volunteer populations.

P01 AI106695 Harris (PI) 07/1/2015-6/30/20
Protective immunity following dengue virus natural infections and vaccination
Project 2: Aravinda deSilva and Ralph S. Baric (Co-PI).
The goal is to identify natural correlates of protective immunity following natural infection and or vaccination. Role: Co-Investigator

R01-AI125198 de Silva (PI) 05/01/16 – 04/30/21
Preclinical assays to predict dengue vaccine efficacy
We use samples from DENV tetravalent Sanofi Pasteur vaccine clinical trials to identify mechanisms and correlates of protective immunity or breakthrough infections in vaccinees. Role: Co-investigator.

R01 1AI132178 Baric/Sheahan(MPI) 08/15/17-8/14/22
Broad-spectrum antiviral GS-5734 to treat MERS-CoV and related emerging CoV.
The goal of this proposal is collaborate with Gilead Inc. and obtain GS-5734 preclinical data for IND development and translational studies, all designed to move the therapeutic into human trials.

(b) (4) Breuer (PI) (b) (4)
Why do Norovirus pandemics occur and how can we control them?
The program uses hospital and community cohorts of NoV infected individuals to ask fundamental questions into the molecular and evolutionary epidemiology of human NoV infections, focusing on the GII.4 strains, leading to new models of virus emergence and disease prevention. Role: Co-Investigator:

R01 AI 089728 Li (PI) 07/01/16-06/30/21
University of Minnesota/NIAID
Receptor recognition and cell entry of coronaviruses
The program studies receptor usage and cell entry mechanisms of emerging coronaviruses, focused on PEDV, MHV and SARS-like Coronaviruses. Role: Co-Investigator

R21 AI135682 Georgiou (PI) 04/01/18-03/30/20
UT Austin/NIAID
Molecular Analysis of Serum Antibody Constituents in Zika Virus Infection.
The goal of this application is to identify antibodies that make up the serologic repertoire after Zikv infection of naive and DENV preimmune individuals. Role: Co-investigator.

R21 AI137887 Moorman/Heise (MPI) 02/05/18-01/31/20
NIH/NIAID $150,000
Molecular Characterization of Functional RNA Structures in the ZikV genome
The goal of this project is to study the RNA Structure of Zika virus. Proposed studies will identify new viral virulence determinants that can be targeted to generate safer and more effective Zika virus vaccines and therapeutics. Role: Co-Investigator.

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BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Noam Ross	Co-Investigator
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
Brown University (US)	BS	05/2006	Environmental Sci.
University of California-Davis, (US)	PhD	09/2015	Ecology

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YYYY	FIELD OF STUDY
Brown University, Providence, RI	BS	05/2006	Environmental Science
University of California-Davis, Davis, CA	Ph.D	09/2015	Ecology

A. Personal Statement

The goal of our proposal is to identify and quantify the drivers of bat-borne coronavirus spillover in Southern China, by identifying which host traits, viral characteristics, and human behaviors are associated with the highest risk of CoV exposure. This will require statistical and mathematical modeling approaches that can integrate the separate ecological, evolutionary, and behavioral processes into a robust framework. My background in quantitative disease ecology makes me a natural fit to work on the statistical and mathematical aspects of this project. My research has consisted of developing both statistical and theoretical models for emerging diseases in both plants, mammals, and humans. I have developed dynamic models of diseases such as MERS and Ebola virus in wildlife populations in order to support targeting field surveillance, and applied predictive empirical and mechanistic modeling techniques to the study of Nipah virus emergence and circulation in bats. My statistical work has included analysis of survey-based evidence of new disease emergence in Uganda, global predictive models of anthrax emergence, and large-scale macroecological patterns in host-virus associations which captured previously unmodeled heterogeneity in disease burden. Importantly, this work included the creation of methods and open-source tools for simulating, fitting, and performing optimization using such models, ensuring that I will be able to support the creation of robust and reproducible statistical models this project.

a. Olival KJ, Hosseini PR, Zambrana-Torrelio C, Ross N, Bogich TL, Daszak P (2017). Host and viral traits predict zoonotic spillover from mammals. **Nature** 546: 646–650

b. Salerno J, Ross N, Ghai R, Mahero M, Travis DA, Gillespie TR, Hartter J (2017) Human-wildlife interactions predict febrile illness in park landscapes of western Uganda. **EcoHealth** 14(4):675-690.

c. Carlson CJ, Kracalik I, Ross N, Alexander K, Hugh-Jones ME, Fegan M, Elkin B, Epp T, Shury T, Bagirova M, Getz WM, Blackburn JK (2018) The global distribution of *Bacillus anthracis* and associated anthrax risk to humans, livestock, and wildlife. **Nature Microbiology** In Review.

B. Positions and Honors

Positions and Employment

2006 Contract Market Researcher: Energy Efficient Products Initiative, Wal-Mart, Providence, RI
2006 - 07 Analyst, Environmental Markets and Performance, GreenOrder, New York, NY

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2007 - 09 Senior Analyst, Environmental Markets and Performance, GreenOrder, New York, NY
2010 - 15 Graduate Researcher, University of California-Davis
2015 - 17 Disease Ecologist, EcoHealth Alliance, New York, NY
2017 - Senior Research Scientist, EcoHealth Alliance, New York, NY

Other Experience and Professional Memberships

2012 - 13 Member, NSF IGERT.org advisory board
2012 - 15 Founder and Organizer, Davis R Users' Group
2013 - Member, Ecological Society of America
2014 - Contributor and reviewer, ROpenSci
2014 - Meeting Session Organizer, Ecological Society of America
2015 - Instructor, Software Carpentry Foundation
2015 - Instructor, Data Carpentry Foundation
2015 - Associate Editor, ROpenSci
2016 - Member, R Epidemics Consortium

Reviewer: *Ecology Letters*, *Theoretical Ecology*, *EcoHealth*, *Conservation Letters, Biological Reviews, Journal of Open Source Software*

Awards and Fellowships

2010 NSF IGERT Traineeship in Rapid Environmental Change
2010 UC Davis Graduate Ecology Fellowship
2012 Don Dahlsten Memorial Grant, California Forest Pest Council
2012 NSF IGERT Bridge Fellowship

C. Contribution to Science

1. **Modeling Dynamics of Heterogeneity:** I have worked on both theoretical and applied approaches of dealing with heterogeneity when modeling ecological-epidemiological dynamics. This work focused on fungal disease epidemics using a framework traditionally used for parasites of stable populations in order to capture the role of individual variation in infection level. While the mathematical basis of these models for populations at or approximately at equilibrium is well established, their dynamic properties are less well known due to analytical intractability, and this they are little-used in emerging diseases and epidemics. My work showed how and where these models diverged from other, traditional models in their dynamical properties, and identified statistical patterns that could be used to identify where these models are appropriate. I developed numerical tools for their simulation, modeling and control, which have been used in applied disease management studies.

   a. Schreiber S, Ross N (2016) Individual-based Integral Projection Models: The role of size-structure on extinction risk and establishment success. **Methods in Ecology and Evolution.** http://dx.doi.org/10.1111/2041-210X.12537

   b. Cobb RC, Ross N, Hayden JK, Eyre CA, Dodd RS, Frankel SJ, Garbelloto M, Rizzo DM (2018) Promise and pitfalls of endemic resistance when cultural resources are threatened by exotic tree pathogens. **Phytopathology.** https://doi.org/10.1094/PHYTO-04-18-0142-R

   c. Cobb RC, Hartsough P, Ross N, Klein J, LaFever DH, Frankel SJ, Rizzo DM (2017) Resiliency or restoration: management of sudden oak death before and after outbreak. **Forest Phytophthoras**. https://doi.org/10.5399/osu/fp.7.1.4021

   d. Ross N (2015). Disease with Multiple Infections: Population Structure, Dynamics, and Control. **University of California, Davis**. Dissertation.

2. **Modeling decision-making in complex systems:** A long-standing theme of my work has been linking ecological dynamics to social systems and decision-making under uncertainty. This has included determining whether statistical signals of ecological changes are sufficient to justify management changes in fisheries, and has recently extended to optimizing investment in disease surveillance and intervention.

Obtained via FOIA by Judicial Watch, Inc.

a) Machalaba C, Smith KM, Awada L, Berry K, Berthe F, Bouley TA, Bruce M, Abrahantes JC, Turabi EL, Feferholtz Y, Flynn L, Fournié G, Andre A, Grace D, Jonas O, Kimani T, Gall FL, Jose J, Peyre MM, Pinto J, Ross N, Rüegg SR, Salerno RH, Seifman R, Zambrana-Torrelio C, Karesh WB. (2017) One Health Economics to confront disease threats. **Transactions of the Royal Society of Tropical Medicine and Hygiene** https://doi.org/10.1093/trstmh/trx039

b) Boettiger C*, Ross N*, Hastings A (2013) Early Warning Signals: The Charted And Uncharted Territories. **Theoretical Ecology** http://dx.doi.org/10.1007/s12080-013-0192-6 (*Co-equal authors)

c) Fuller K, Kling D, Kroetz K, Ross N, Sanchirico JN (2013) Economics and Ecology of Open-Access Fisheries. In: Shogren JF (ed.) **Encyclopedia of Energy, Natural Resource, and Environmental Economics, Vol. 2** p.39-49. Amsterdam: Elsevier. http://dx.doi.org/10.1016/B978-0-12-375067-9.00114-5

3. **Statistical software and reproducibility:** As associate editor of the ROpenSci project, and a member of the Software Carpentry foundation, I develop, evaluate, and set standards and develop training materials for open-source statistical software overseeing the publication of over 30 scientific software packages in the past two years. I have also worked in the development and dissemination of tools for the use of nonlinear modeling methods.

a. Ross N (2016) fasterize: high performance raster conversion for modern spatial data. https://github.com/ecohealthalliance/fasterize

b. (b) (4)

c.

d. Ross N (2018) Nonlinear Modeling in R with GAMs: An Interactive Course. **DataCamp** https://www.datacamp.com/courses/nonlinear-modeling-in-r-with-gams

D. Research Support

Ongoing

USAID EPT PREDICT-2 Mazet (PI) 10/01/14 – 09/30/19
Conducting surveillance for novel pathogens in wildlife, livestock and people; characterizing human risk behavior; modeling risk of novel disease emergence; identifying mitigation strategies
Amount: $35 Million subcontract from a $100 Million award
Role: Disease Ecologist

1R01AI110964 Daszak (PI) 06/01/14 – 05/31/19
NIAID: Understanding the Risk of Bat Coronavirus Emergence
Bat ecological, human risk behavioral and virological studies to understand the risk of bat coronavirus emergence
Role: Key Personnel

HDTRA1-14-1-0029 Karesh (PI) 5/17/16 – 5/16/18
Understanding Rift Valley Fever in Republic of South Africa
Role: Key Personnel

Completed

W911NF-13-1-0305 Hastings (PI) 9/1/13-8/31/16
Army Research Office Mathematical Sciences Core Program
Dynamics at Intermediate Time Scales and Management of Ecological Populations

Obtained via FOIA by Judicial Watch, Inc.

Role: Supported Graduate Student

EF-0622770 Rizzo (PI) 8/23/06-8/31/11
NSF Ecology of Infectious Disease Program
Collaborative Research: Sudden Oak Death: Feedback Between a Generalist Pathogen, Hosts, and Heterogeneous Environments at Multiple Spatial and Temporal Scales
Role: Supported Graduate Student

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Alice Latinne	Research Scientist
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
University of Namur, Namur, Belgium	BSC	06/2004	Biology
University of Liege, Liege, Belgium	MSC	06/2006	Animal Biology
University of Liege, Liege, Belgium	PHD	12/2012	Molecular Biology

A. Personal Statement

My research focuses on understanding the dynamics of pathogens within and among wildlife populations, livestock, and humans. I have conducted fieldwork in Asia for the past 6 years, focused on the evolutionary dynamics of host-pathogen (rodent-virus; bat-virus) interactions, the phylogenetics of co-evolution, and analysis of phylogeographic scale. My main interest is to analyze he risk of zoonotic pathogen emergence at high-risk human-wildlife interfaces. My published work analyzes patterns and likelihood of pathogen sharing among species, and to determine how the host phylogenetic and phylogeographic structure affects pathogen distribution and cross-species transmission. Prior to my current position at EcoHealth Alliance, I was a Marie Curie COFUND fellow conducting postdoctoral research at the Institut des Sciences de l'Evolution in Montpellier (ISEM, France) and at the Kasetsart University in Thailand.

B. Positions and Honors

Positions and Employment

2013-2013 Research Assistant, University of Liege, Liege, Belgium
2014- Research Associate, University of Liege, Liege, Belgium
2015- Research Scientist, EcoHealth Alliance, New York

Honors

2007 Belgian Government graduate scholarship, Belgian Fund for Research in Industry and Agriculture, Belgium
2008 Belgian Government graduate scholarship, Belgian Fund for Scientific Research, Belgium
2013 Award "VOCATIO" (Vocation grant) from the Belgian Foundation of Vocation (VOCATIO)
2013 Marie Curie COFUND fellowship from European Union

C. Contribution to Science: Selected peer-reviewed publications most relevant to the current application

1. Latinne A, Bezé F, Delhaes L, Pottier M, Gantois N, Nguyen J, Blasdell K, Dei-Cas E, Morand S, Chabé M (2017). Genetic diversity and evolution of *Pneumocystis* fungi infecting wild Southeast Asian murid rodents. **Parasitology**, 145(7): 885-900. PMID: 29117878

Obtained via FOIA by Judicial Watch, Inc.

2. Olival KJ, Latinne A, Islam A, Engstrand R, Hersch R, Amato G, Epstein JH, Daszak P (2016). Using bat population genetics to understand Nipah virus dynamics and cross-species transmission in south and southeast Asia. **International Bat Research Conference**, Durban.

3. Morand S, Bordes F, Chen H, Claude J, Cosson J, Galan M, Czirjak GA, Greenwood A D, Latinne A, Michaux J, Ribas A (2015) Global parasite and *Rattus* rodent invasions: the consequences for rodent-borne diseases. **Integrative Zoology**, 10(5), 409-423. PMID: 26037785

4. Latinne A, Meynard CN, Herbreteau V, Waengsothorn S, Morand S, Michaux J (2015). Influence of past and future climate changes on the distribution of three Southeast Asian murine rodents. **Journal of Biogeography**, 42(9), 1714-1726. doi.org/10.1111/jbi.12528

5. Blasdell K, Bordes F, Chaval Y, Claude J, Cosson J, Latinne A, Michaux J, Morand S, Pagès M, Tran A (2015). Progress on research on rodents and rodent-borne zoonoses in South-east Asia. **Wildlife Research**, 42(2), 98-107. doi.org/10.1071/WR14201

Additional recent publications

1. Mouton A, Mortelliti A, Grill A, Sara M, Kryštufek B, Juškaitis R, Latinne A, Amori G, Randi E, Büchner S, Schulz B, Ehlers S, Lang J, Adamik P, Verbeylen G, Dorenbosch M, Trout R, Elmeros M, Aloise G, Mazzoti S, Matur F, Poitevin F, Michaux JR (2017). Evolutionary history and species delimitations: a case study of the hazel dormouse, *Muscardinus avellanarius*. **Conservation Genetics**, 18(1): 181-196. doi.org/10.1007/s10592-016-0892-8

2. Smitz N, Cornélis D, Chardonnet P, Caron A, de Garine-Wichatitsky M, Jori F, Mouton A, Latinne A, Pigneur L, Melletti M, Kanapeckas KL, Marescaux J, Lopes-Pereira C, Michaux J (2014). Genetic structure of fragmented southern populations of African Cape buffalo (*Syncerus caffer caffer*). **BMC Evolutionary Biology**, 14: 203. doi.org/10.1186/s12862-014-0203-2

3. Latinne A, Galan M, Waengsothorn S, Rojanadilok P, Eiamampai K, Sribuarod K, Michaux J (2014). Diet analysis of *Leopoldamys neilli*, a cave-dwelling rodent in Southeast Asia, using Next-Generation Sequencing from feces. **Journal of Cave and Karst Studies**, 76(2): 139-145. doi.org/10.4311/2013LSC0100

4. Latinne A, Chaval Y, Waengsothorn S, Rojanadilok P, Eiamampai K, Sribuarod K, Herbreteau V, Morand S, Michaux J (2013). Is *Leopoldamys neilli* (Rodentia, Muridae) a synonym of *Leopoldamys herberti*? A reply to Balakirev *et al.* (2013). **Zootaxa**, 3731(4): 589-598. doi.org/10.11646/zootaxa.3731.4.10

5. Latinne A, Waengsothorn S, Rojanadilok P, Eiamampai K, Sribuarod K, Michaux J (2013). Diversity and endemism of Murinae rodents in Thai limestone karsts. **Systematics and Biodiversity**, 11(3): 323-344. doi.org/10.1080/14772000.2013.818587

6. Pauwels OSG, Sumontha M, Latinne A, Grismer LL (2013). *Cyrtodactylus sanook* (Squamata: Gekkonidae), a new cave-dwelling gecko from Chumphon Province, southern Thailand. **Zootaxa**, 3635(3): 275-285. PMID: 26097949

7. Latinne A, Waengsothorn S, Rojanadilok P, Eiamampai K, Sribuarod K, Michaux J (2012). Combined Mitochondrial and Nuclear Markers Revealed a Deep Vicariant History for *Leopoldamys neilli*, a Cave-Dwelling Rodent of Thailand. **PLOS One**, 7(10), e47670. PMID: 23118888

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Hongying Li	Research Scientist
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
School of Life Sciences, Sun Yat-Sen University, China	BS	06/2012	Biosciences
School of Public Health, Emory University	MPH	05/2015	Health Policy
School of Life Sciences, Kingston University, UK	Ph.D Candidate	2018-	Infectious Diseases

A. Personal Statement

I have an interdisciplinary background in ecology, public health, and human behavior, coupled with extensive on-the-ground experience working with communities, governmental and academic partners in China. For the past 3 years I have worked as China Programs Coordinator at EcoHealth Alliance, acting as the key point-of-contact among EcoHealth staff and our partners in China. I have coordinated fieldwork to conduct bat sampling, and human behavioral risk assessments across 5 provinces in southern China. I have also liaised directly with all key partners on this proposal. Additionally, I coordinate EcoHealth Alliance's wildlife trade research in China and SE Asia focusing on analyzing incentives to trade and consume wildlife. I work closely with Chinese Health and Forestry governmental departments, research institutes, and local organizations to foster collaboration and communication as part of my PhD research on *"Policy and Human Behavioral Strategies to Mitigate Zoonotic Disease Emergence in Southern China".*

B. Positions and Honors.

Positions and Employment

2011 - 12 Research Assistant of HIV Prevention Program, Yunnan Maternity and Children's Hospital, China
2013 - 14 Program Assistant of School HIV/AIDS & School Education, UNESCO Beijing, China
2015 - China Programs Coordinator & Research Scientist, EcoHealth Alliance, USA
2017 - Coordinator of the Initiative of National Virome Project in China

Other Experience and Professional Memberships

2018- Member, IUCN SSC Pangolin Specialist Group
2018- Member, Society for Applied Microbiology
2017- Member, China Health Policy and Management Society
2016- Member, International Association for Ecology & Health
2016- Columnist, *China Environment*
2016- Asian Representative, Conservation Leadership Programme

Honors

2010 National Scholarship, Ministry of Education, the People's Republic of China.
2012 Outstanding Graduate Award, Sun Yat-sen University, China
2016 Invited speaker, China Conservation Network workshop. "Impacts of wildlife trade on public health"
2017 Invited Speaker, International Association for Ecology & Health. "Understanding the wildlife trade in China"

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C. Selected peer-reviewed publications most relevant to the current application

Liang X, Zhang L, Wan Y, Yu X, Guo Y, Chen X, Li H (2012). Changes in the diurnal rhythms during a 45-day head-down bed rest. **PLOS One**, 7(10), e47984.

Wu Z, Lu L, Du J, Yang L, Ren X, Liu B, Li H, Zhu Y (2018). Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. **Microbiome**, 6(1), 178.

Additional recent publications of importance to the field (in chronological order)

Li H, Zhu G, Zhang Y, Daszak P (2018). Qualitative Approach to Developing a One Health Intervention Strategy for Zoonosis Risk Mitigation in Southern China. Poster Presentation at **One Health Congress 2018**.

Li H, Chmura AA, Ma C, Gabriel G, Daszak P (2018). Attitudes Towards Wildlife Trade and Disease Risk in China. Poster presentation at **One Health Congress 2018**.

Li H, Zhu G, Zhang Y, Daszak P (2018). Viral Pathogen Discovery in China: Understanding the Risks of Bat Coronaviruses. Poster presentation at **USAID EPT-2 PREDICT Meeting**.

D. Research Support

Ongoing Research Support

R01 AI110964 Daszak (PI) 06/01/14-05/31/19
Understanding Risk of Bat Coronaviruses
The goal of this study is to analyze the risk of coronavirus spillover from bats to humans in Southern China
Role: Project Coordinator & Human Research Lead

Emerging Pandemic Threat Program, USAID Mazet (PI) 10/01/14-09/30/19
PREDICT 2
The goal of this project is to create and implement a global virus surveillance system in animals and humans and analyze spillover risk.
Role: Country Coordinator for China

Completed Research Support

(b) (4)

Zhang (PI) 01/01/16-12/31/17
The goal of this study is to understand the current population and distribution of the critically endangered Chinese pangolin *(Manis pentadactyle)* in mainland China
Role: Community Research Lead

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Leilani V. Francisco	Co-Investigator
eRA COMMONS USER NAME (b) (4)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
University of Maryland, College Park, Maryland	BA	05/1995	Anthropology (Sociocultural)
University of South Florida, Tampa, Florida	MA	05/2002	Applied Anthropology (Medical)
Johns Hopkins University, Baltimore, Maryland	Ph.D	05/2010	Public Health (Int'l Health)
Project Management Institute, Pennsylvania	PMP	Current	Project Management

A. Personal Statement

I have a Bachelors and Masters degree in anthropology and applied anthropology, and over 20 years of professional experience managing human behavioral research projects in public health, the majority of which has been in developing countries. I have extensive experience in the private sector, managing research projects and evaluating public health interventions for infectious diseases. I have worked extensively on: quantitative, qualitative, and mixed-methods study design, data collection, and analysis; management of behavioral intervention projects, public health assessments, and behavioral research study design. My work has focused on HIV/AIDS and other zoonotic infectious diseases, and sociocultural behavior change interventions. Previously, I managed a portfolio of global health contracts valued at over $20 million in service to the U.S. Agency for International Development (USAID), (b) (4) (b) (4), and the Centers for Disease Control and Prevention (CDC). While my private sector career meant that I was not able to publish much of my work, I generated over 80 high-profile technical reports for federal and international health agencies. At EcoHealth Alliance I lead a behavioral risk team for USAID/EPT PREDICT (project ending 2019) characterizing behavioral risk in 28 countries with high-risk human-animal disease transmission interfaces. I have been (b) (4)

B. Positions and Honors

Positions and Employment

2017-Present Senior Scientist, EcoHealth Alliance, NY
2017-Present USAID PREDICT-2 Global Director for Behavioral Risk Surveillance, NY
2017-Present USAID PREDICT-2 Partner Lead for Ecological and Biological Human Surveillance, NY
2013-2017 Lead Associate / Senior Lead Scientist, Booz Allen Hamilton, Washington, DC
2010-2012 Associate / Lead Scientist, Booz Allen Hamilton, Washington, DC
2010 Research Consultant, Johns Hopkins Bloomberg School of Public Health, Center for Communication Programs, Baltimore, MD
2010 Research Consultant, Academy for Educational Development, Washington, DC
2007-2008 Research Fellow in Social Epidemiology, London School of Hygiene and Tropical Medicine, London, UK and Kampala, Uganda
2007-2008 SASA! Study Baseline Project Leader, London School of Hygiene and Tropical Medicine, London, UK and Kampala, Uganda
2005-2007 Senior Research Analyst, American Institutes for Research, Washington, DC
2004-2005 Research Analyst, American Institute for Research, Washington, DC
2003 Research Consultant, International Center for Research on Women, Washington, DC
2002-2004 Health Research Scientist, Battelle Memorial Institute, Arlington, VA

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1999-2001	Health Researcher, Battelle Memorial Institute, Arlington, VA
1998-1999	Graduate RA, Center for Urban Transportation Research, Tampa, FL
1998	Graduate RA, H. Lee Moffitt Cancer Center and Research Institute, Tampa, FL
1997-1998	Graduate RA, University of South Florida, Department of Anthropology, Tampa, FL
1996-1997	Project Manager, Cultural Systems Analysis Group, Univ Maryland, College Park, Maryland
1995-1996	RA, Cultural Systems Analysis Group, University of Maryland, College Park, Maryland

Other Experience and Professional Memberships

Member, American Public Health Association (APHA)
Member, American Evaluation Association (AEA)
Member, Global Health Council (GHC)
Member, American Anthropological Association (AAA)
Member, Society for Applied Anthropology (SfAA)

Honors

2007-2010	Johns Hopkins University Tuition Scholarship
2003	Distinguished Service Award, Latin American Youth Center
1999	Center for Urban Transportation Research Graduate Assistantship
1999	Latin American and Caribbean Studies Passport Scholarship
1998	Latin American and Caribbean Studies Research Grant
1997-1998	Department of Anthropology Graduate Assistantship

C. Contribution to Science

1. **Ethical and Robust Human Subjects Research**: My advanced training and experience in designing, carrying out, and evaluating mixed-methods research projects with vulnerable human populations, has allowed me to contribute to the body of literature and recommended practices around balancing robust study design with the ethical treatment of human subjects. With public health research and evaluation experience spanning Africa, Asia, Central America, the Caribbean, and North America, my contributions within this subject area have added to the discourse of building, implementing, and measuring scientific exploration in the name of human health improvements without compromising human privacy, dignity, and respect.

    a. Francisco LV, Abramsky T, Kiss L Michau L, Musuya T, Kerrigan D, Kaye D, Watts C (2013). Violence against Women and HIV Risk Behaviours in Kampala, Uganda: Baseline Findings from the SASA! Study. **Violence Against Women**, 19(7): 814-832.

    b. Wagman J, Francisco LV, Glass N, Sharps PW, Campbell JC (2008). Ethical challenges of research on and care for victims of intimate partner violence. **Journal of Clinical Ethics**,19(4):371-80.

    c. Campbell JC, Baty ML, Ghandour RM, Stockman JK, Francisco LV, Wagman J (2008). The intersection of intimate partner violence against women and HIV/AIDS: a review. **International Journal of Injury Control and Safety Promotion**, 15(4), 221-31.

    d. Campbell, JC, Baty ML, Ghandour RM, Stockman JK, Francisco LV, Wagman J (2008). The Intersection of Violence against Women and HIV/AIDS. In Scott KA (Rapporteur) **Violence Prevention in Low- and Middle- Income Countries: Finding a Place on the Global Agenda**, pp.149-166. Washington, DC: Institute of Medicine, National Academies Press.

2. **Scientific approaches to behavioral intervention**: Through the example of my work as a scientist with subject matter expertise in behavior change, I have built a strong case that scientific evidence can and should make its way into the hands of decision-makers and the community. This evidence-action gap is one that is often recognized, but regularly left unaddressed. My work in Kampala Uganda using a cluster randomized controlled trial to understand the impact of an intervention in preventing violence against

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women and reducing their HIV risk was recognized by Harvard University as a program that closes gender gaps in economic opportunity, politics, health, and education. It was also added to the Women and Public Policy Program's Gender Action Portal, a hub of scientific evidence providing insights on the impact of policies, strategies and practices aimed at closing gender gaps, and taking promising interventions to scale. Additionally, I led the development of a behavioral intervention resource in the form of a moderated picture book, “Living Safely with Bats,” based upon feedback from communities living in countries and in areas of regular bat-human contact in their homes. This resource became a key component in ministerial and community outreach by the USAID PREDICT consortium following the announcement of the discovery of the Bombali ebolavirus in 2018, and reflects my continued efforts to translate research to practice.

a. Abramsky T, Devries K, Kiss L, Nakuti J, Kyegombe N, Starmann E, Cundill B, Francisco LV, Kaye D, Musuya T, Michau L, Watts C (2014). Findings from the SASA! Study: a cluster randomised controlled trial to assess the impact of a community mobilisation intervention to prevent violence against women and reduce HIV risk in Kampala, Uganda. **BMC Medicine**, 12:122.

b. Francisco LV, Sullivan A, Goley J, Martinez S, Saylors K, Euren J, Epstein JH, Bird B, Goldstein T, Wolking D, Johnson C, Hagan E, Olival KJ, Karesh WB, Daszak P, Mazet JK (2018). Living Safely with Bats: a risk-reduction resource to help communities in developing countries change behavior to minimize zoonotic spillover from bats. **USAID** Washington, DC.

c. Campbell JC, Baty ML, Ghandour RM, Stockman JK, Francisco LV, Wagman J (2008). The Intersection of Violence against Women and HIV/AIDS. In Scott KA (Rapporteur). **Violence Prevention in Low- and Middle- Income Countries: Finding a Place on the Global Agenda**, pp.149-166. Washington, DC: Institute of Medicine, The National Academies Press.

3. **Applied behavioral research**: Through my advanced training and experience in quantitative, qualitative, and mixed-methods research methodology I have focused on promoting the application of behavioral research to on-the-ground problems. My authorship of over 80 technical reports and publications reinforces my track record of commitment to making robustly-generated methodologies available and accessible to those who affect policy and programming.

a. Francisco LV, *et al.* (2015). DTRA CBEP Country Assessment Manual: Guidance for Implementation of CBEP Assessments of Country Capabilities in Biosurveillance, Biosafety, and Biosecurity. **Booz Allen Hamilton**, Lorton, VA.

b. Francisco LV, *et al.* (2011). Resilience and Prevention Study: Program Evaluation Framework for the Never Leave a Marine Behind (NLMB) Program. For the Defense Centers of Excellence for Psychological Health and Traumatic Brain Injury, US Department of Defense. **Booz Allen Hamilton**, Rockville, MD.

c. Francisco LV (2010). Operational Plan for Ethnographic and Network Assessment Research Project. For Centers for Disease Control and Prevention HIV prevention project in Côte d'Ivoire and Zambia. **Academy for Educational Development**, Washington, DC.

Complete List of Published Work in MyBibliography:

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

R01 AI110964 Daszak (PI) 06/01/14-05/31/19
NIAID: Understanding the Risk of Bat Coronavirus Emergence
Bat ecological, human risk behavioral and virological studies to understand the risk of bat coronavirus emergence
Role: Research Scientist

USAID EPT PREDICT-2 Mazet (PI) 10/01/14 – 09/30/19

Obtained via FOIA by Judicial Watch, Inc.

Conducting surveillance for novel pathogens in wildlife, livestock and people; characterizing human risk behavior; modeling risk of novel disease emergence; identifying mitigation strategies
The goal of this project is to assist focal countries in monitoring viruses with pandemic potential, as well as the behaviors, practices, and conditions that are associated with viral evolution, spillover, amplification, and spread.
Role: Research Scientist

Completed Research Support

CDC CGH DGHT Zambia ART Bell (Project Director) 03/28/16 – 01/15/17
Centers for Disease Control and Prevention (CDC), Center for Global Health (CGH), Division of Global HIV/AIDS and Tuberculosis (DGHT), ART Readiness in HIV-infected Pregnant Women: From Formative Qualitative Research to Individual Randomized Trial – Zambia
Trial monitoring visits to evaluate accuracy of screening instrument and effectiveness of enhanced adherence package through early data on virologic response, mother to child transmission (MTCT) rates of HIV, and renal function.
Role: Project Manager

PFSCM Projects McLaughlin (Officer in Charge) 06/01/2014 – 01/15/17
Partnership for Supply Chain Management (PFSCM) Projects: USAID Supply Chain Management System (SCMS); Global Fund Pooled Procurement Mechanism (PPM); 3MDG Regional Supply Chain Strengthening (RSCS)
Led and oversaw all company-wide team members and activities associated with these three projects, as part of a 16-member consortium, known as the Partnership for Supply Chain Management (PFSCM). All projects focused on increasing regular and consistent HIV/AIDS treatment through health systems strengthening, performance management, country strategic planning, and technical assistance provision.
Role: Program Manager

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Amy Catherine Sims	Co-Investigator
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
University of Alabama at Birmingham	BS	05/1995	Molecular Biology
Vanderbilt University, Nashville, TN	PhD	05/2001	Microbiology & Immuno
Duke University, Durham, NC	Postdoctoral	08/2002	RNA/Protein Interaction
University of North Carolina at Chapel Hill (US)	Postdoctoral	10/2005	Virology

A. Personal Statement

The identification of highly pathogenic human coronaviruses (SARS-CoV and MERS-CoV) underscored the importance of understanding how viruses emerge from zoonotic reservoirs and how these emergent viruses replicate and cause pathogenesis in the new host. My research has focused on several key aspects of these questions by working to understand the cellular tropism of SARS-CoV and MERS-CoV in primary human lung cells, how host genetic pathways and gene networks affect virus replication and pathogenesis and how manipulating the coronavirus genome changes the host innate immune response to virus infection.Dr. Sims created the humanized transgenic mice that facilitate bat coronavirus replication in coronavirus small animal models and has significant expertise using the coronavirus reverse genetics platform established at UNC.She pioneered the use of primary human lung cell cultures for understanding coronavirus cellular permissivity, in vitro replication kinetics, and therapeutic treatment options within the Baric laboratory.

Relevant publications: My most relevant work to date focuses on using primary human lung cells as culture models for human and human-like bat coronavirus strains.

1. Menachery VD, Yount BL, Sims AC, Agnihothram S, Gralinski LE, Plante JA, Graham RL, Scobey T, Royal S, Pickles RJ, Randell SH, Lanzavecchia A, Marasco WA, Shi Z, Baric RS (2016). SARS-like WIV1-CoV poised for human emergence. **Proceedings of the National Academy of the Sciences** 15:113(11): 3048-53. PMC4801244
2. Becker MM, Graham RL, Donaldson EF, Rockx B, Sims AC, Timothy Sheahan, Raymond Pickles, Davide Corti, Robert E. Johnston, Ralph S. Baric, Mark R. Denison (2008). Platforms for the Synthetic Reconstitution of Noncultivable Zoonotic Viruses. **Proceedings of the National Academy of the Sciences** PMC2588415
3. Sims AC, Baric RS, Yount B, Burkett SE, Jeffers L, Pickles RJ (2005). SARS-CoV infection of human ciliated airway epithelium: the role of the ciliated cell in viral spread in the conducting airways of the lung. **Journal of Virology** 79(24):15511-15524, 2005. PMC1316022
4. Scobey T, Yount BL, Sims AC, Donaldson EF, Agnihothram SS, Menachery VD, Graham RL, Swanstrom J, Bove PF, Kim JD, Grego S, Randell SH, Baric RS. Reverse genetics with a full-length infectious cDNA of the Middle East respiratory syndrome coronavirus.**Proceedings of the National Academy of the Sciences** U S A. 2013 Oct 1;110(40):16157- 62. PMID: 24043791. PMC3791741
5. Sims AC, Sheahan TP, Graham RL, Menachery VD, Gralinski LE, Case JB, Leist SR, Pyrc K, Feng JY, Trantcheva I, Bannister R, Park Y, Babusis D, Clarke MO, Mackman RL, Siegel D, Ray AS, Cihlar T, Jordan R, Denison MR, Baric RS (2017). Broad-spectrum antiviral GS-5734 inhibits both epidemic and zoonotic coronaviruses. **Science Translational Medicine** 28;9(396). PMC5567817

Obtained via FOIA by Judicial Watch, Inc.

B. Positions and Honors

1993 American Society of Microbiology Undergraduate Research Award, University of Alabama
1994 Albert Einstein College of Medicine Summer Student Award
1996 - 01 Graduate Student, Laboratory of Mark Denison, Vanderbilt University, Nashville, TN
1999 Dissertation Enhancement Award, Vanderbilt University
2001 - 02 Postdoctoral Fellow, Laboratory of Jack Keene, Duke University, Durham, NC
2002 - 05 Postdoctoral Fellow, Laboratory of Ralph Baric, UNC at Chapel Hill
2002 - 04 Infectious Disease Pathogenesis Training Grant Fellow (NIH/NIAID 5T32AI07151-27)
2005 - 17 Research Assistant Professor, Department of Epidemiology, UNC, Chapel Hill, NC
2017 - Research Associate Professor, Department of Epidemiology, UNC, Chapel Hill, NC

C. Contributions to Science

1. *In vitro* models for viral infection. Finding suitable in vitro models for studying newly identified or emerged human respiratory viruses can be a challenge. Primary cells isolated from the human conducting airway can be cultured at an air liquid interface and following maturation recapitulate the morphology of the airway epithelium. These cultures provide a unique in vitro model and for one human coronavirus, HKU1, provide the only in vitro model for studying this virus.

a) Sims AC, Pyrc K, Dijkman R, Jebbink M, Long C, Deming D, Donaldson E, Vabret A, Baric RS, van der Hoek L, Pickles R (2010). Culturing the unculturable: human coronavirus HKU1 infects, replicates, and produces progeny virions in human ciliated airway epithelial cell cultures. **Journal of Virology**, 84(21): 11255-63. PMC2953148

b) Sims AC, Baric RS, Yount B, Burkett SE, Jeffers L, Pickles RJ (2005). SARS-CoV infection of human ciliated airway epithelium: the role of the ciliated cell in viral spread in the conducting airways of the lung. **Journal of Virology**, 79(24): 15511-15524. PMC1316022

2. Gene pathways to regulate viral replication. In collaboration with researchers at the University of Wisconsin Madison and Pacific Northwest National Laboratories, I have been working to identify specific host gene networks and pathways that regulate lethal human respiratory virus replication and pathogenesis. Specifically, I was interested in determining genes that regulate SARS-CoV and MERS-CoV replication in human cell lines, models of the human conducting airway and mouse models.

a) Sims AC, Tilton SC, Menachery VD, Gralinski LE, Schäfer A, Matzke MM, Webb-Robertson BM, Chang J, Luna ML, Long CE, Shukla AK, Bankhead AR, Burkett SE, Zornetzer G, Tseng CK, Metz TO, Pickles R, McWeeney S, Smith RD, Katze MG, Waters KM, and Baric RS (2013). Release of SARS-CoV Nuclear Import Block Enhances Host Transcription in Human Lung Cells. Journal of Virology, 87(7): 3885-902. PMC3624188

b) Mitchell HD, Eisfeld AJ, Sims AC, Waters KM. A Network Integration Approach to Identify Highly Conserved Regulatory Targets Related to Pathogenicity for Influenza and SARS-CoV Respiratory Viruses. **PLoS ONE** 8(7): e69374. PMC3723910

c) Menachery VD, Eisfeld AJ, Josset L, Sims AC, Schaefer A, Proll S, Fan S, Li C, Neumann G, Tilton SC, Chang J, Gralinski LE, Long C, Green R, Matzke MM, Webb-Robertson BJ, Shukula AK, Burkett S, Metz TO, Pickles R, Smith RD, Waters KM, Katze M, Kawaoka Y, Baric RS (2014) Pathogenic influenza and coronaviruses utilize similar and contrasting approaches to control global ISG responses. mBio, 5(3). PMC4030454

d) Aevermann BD, Pickett BE, Kumar S, Sims AC, Sova P, Tam VC, Tchitchek N, Thomas PG, Tilton SC, Totura A, Wang J, Webb-Robertson B, Wen J, Weiss J, Yang J, Yount B, Zhang Q, McWeeney S, Smith RD, Waters KM, Kawaoka Y, Baric RS, Aderem A, Katze MM, Scheuermann R (2014). A Comprehensive Collection of Systems Biology Data Characterizing the Host Response to Viral Infection. **Nature's Scientific Data**,1(10). 1038/sdata.2014.33. PMC4410982

Complete List of Published Work in NCBI MyBibliography:

Obtained via FOIA by Judicial Watch, Inc.

http://www.ncbi.nlm.nih.gov/myncbi/collections/bibliography/49189460/

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

U19-AI106772-01 (PI: Kawaoka) 06/01/13-05/31/19 Univ. of Wisconsin/NIH
MERS-CoV Supplement for OMICs Proposal
The proposed studies will provide a more detailed look at the intracellular environment by taking “snapshots” of the lipids, metabolytes, and proteins present during viral infection time courses.These assays will allow us to determine the innate immune response occurring immediately following virus infection and to determine how the virus and cell interact over a 72 hour window.
Role: Project PI

U19 AI 109680 CETR (PI: Whitley) 03/01/14-02/28/19 UAB/NIH/NIAID
Antiviral Drug Discovery and Development Center
The specific aims of the proposal will identify small molecule inhibitors of CoV fidelity and RNA capping, define their mechanism of action, and determine their efficacy against SARS-CoV and across CoV families using in vivo mouse models of acute and persistent CoV disease.
Role: Investigator

U19 AI109761 CETR (PI: Lipkin) 03/01/14-02/28/19 Columbia/NIH/NIAID
Diagnostic and Prognostic Biomarkers for Viral Severe Lung Disease
The overall goal of this program is to develop new platform technologies that use functional genomics as diagnostic and prognostic indicators of severe end stage lung disease following virus infection of the lung.
Role: Investigator

R01 AI110700 (PI: Baric) 04/01/15-03/31/20 NIH
Mechanisms of MERS-CoV Entry, Cross-species Transmission and Pathogenesis
The overall goal is to build a comprehensive understanding of the molecular mechanisms guiding group 2c CoV receptor recognition, entry and pathogenesis.
Role: Investigator

1R01 AI132178-01 (MPI:Sheahan/Baric) 08/06/17-07/31/22 NIH
Broad-spectrum antiviral GS-5734 to treat MERS-CoV and related emerging CoV
In partnership with Gilead Sciences, we aim to accelerate the preclinical development of GS-5734 and promote IND licensure. We define the pharmacokinetics, pharmacodynamics, resistance profile, efficacy breadth and mechanism of action of GS-5734 against MERS-CoV and related emerging CoV.
Role: Investigator

Completed Research Support

Contract 576652 (PI:Katze) 09/26/08-09/25/13 University of Washington/NIAID
Systems Biology of Lethal and Attenuated SARS-CoV Infection
The overall hypothesis is that highly pathogenic respiratory viruses use common and unique strategies to mechanistically remodel the intracellular environment to enhance virus replication, regulate disease severity and promote virus transmission.Using SARS-CoV and H1N1 2009 and a comparative systems biology approach with H5N1 avian influenza virus we will identify unique and common signaling circuitry that is essential for promoting severe disease profiles in the lung.
Role: Co-Investigator

Supplement to OMIC Pilot Award (PI: Kawaoka) 6/1/14-5/31/16 Univ. of Wisconsin/NIH/NIAID
Epigenetic Regulation of Interferon-Stimulated Genes Following MERS-CoV Infection
The overriding hypothesis of this supplemental application is that MERS-CoV and H5N1 manipulate host epigenetic programs to specifically down-regulate certain classes of ISGs, which likely antagonize virus replication efficiency in vitro.The goal is to develop systems biology datasets and unbiased modeling algorithms to deconvolute the complex pathogen-host interactions that regulate severe disease outcomes following infection and identify common host pathways/genes that can be exploited for therapeutic control.

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Role: Project PI

U19-AI100625 (PI: Baric) 8/05/12-07/31/17 NIH/NIAID
Systems Immunogenetics of Biodefense Pathogens in the Collaborative Cross
Specific Aims:In this proposal, we are utilizing the Collaborative Cross (CC), a novel panel of reproducible, recombinant inbred (RI) mouse lines to identify genes and gene interactions, which regulate the induction, kinetics, and magnitude of the innate, inflammatory and adaptive arms of the immune response following virus infection.Specifically, we will develop novel modeling algorithms to predict and validate the causal relationships between natural genetic variation and host signaling networks, immune cell recruitment, and immune function.
Role: Investigator and Co-Education Director

Supplement to OMIC (PI: Kawaoka) 6/1/16-5/31/17 Univ. of Wisconsin/NIH/NIAID
Systems Virology for MERS-CoV in vivo
The goal is to develop systems biology datasets and unbiased modeling algorithms to deconvolute the complex pathogen-host interactions that regulate severe disease outcomes following infection and identify common host pathways/genes that can be exploited for therapeutic control.These studies will build on our current data set by collecting data sets for MERS-CoV in vivo.
Role: Project PI

(b) (4)

The overall goal of this project is to test (b) (4) protease inhibitor/interferon cocktails in comparison to and with nucleoside analog compounds to determine the best course of treatment for patients infected with highly pathogenic human coronaviruses.

Not Assigned (PI: Baric) 08/01/17-06/30/18 Emory/NIH
Elucidating the potential of nucleoside analog, EIDD-1931, as a broad-spectrum antiviral against highly pathogenic human coronavirus strains
To define the activity, potency and mechanism of action of EIDD-1931 against highly pathogenic human coronaviruses for development as potential therapeutic.
Role: Investigator

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BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Emily Ann Hagan	Research Scientist
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YYYY	FIELD OF STUDY
Hiram College	BA	05/2008	Biol. Biomed. Humanities
Columbia Univ. Mailman Sch. Public Health	MPH	05/2013	Epidemiology
Columbia Univ. Mailman Sch. Public Health	CPH	08/2013	Public Health

A. Personal Statement

I have a background in laboratory science, veterinary science, epidemiology, and human behavioral health. My main focus in the current proposed R01 work is on the human behavioral work in Aim 2. My experience in understanding the implications of laboratory testing, in conducting and analyzing quantitative and qualitative human behavioral risk assessment and mixed-methods data analysis are exactly the tools required to conduct this work. As assistant to the Senior Behavioral Risk Scientist on the USAID-EPT-PREDICT project I have regularly applied behavioral analytical skills to research data from 28 countries. I have also conducted my own focused work in Bangladesh, analyzing the results of 2 years of survey work on zoonotic viral spillover risk – directly applicable to the current proposal.

B. Positions and Honors

Positions and Employment

2006-2007 Researcher, Hiram College, Hiram College, Cellular and Molecular Lab, Hiram, OH
2007 NSF REU Research Intern, University of Akron, Polymer Department, Akron, OH
2007-2008 Teaching Assistant, Hiram College, Organic Chemistry Department, Hiram, OH
2008-2012 RA, Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, MA
2011-2012 Team Manager, Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, MA
2013-2015 RA, EcoHealth Alliance, New York, NY
2015-2016 Research Coordinator, EcoHealth Alliance, New York, NY
2016-2018 Research Scientist and PREDICT Bangladesh Country Liaison, EcoHealth Alliance, NY

Other Experience and Professional Memberships

2013- *EcoHealth*, reviewer
2016- WHO Bulletin, reviewer
2018- *PLOS Neglected Tropical Diseases*, reviewer

Honors

2008 Biology Departmental Honors, Hiram College

C. Contribution to Science

1. **Human behavioral risk analysis.** I have helped design, coordinate training for, and conduct on-the-ground human behavioral work for the USAID-EPT-PREDICT project. This work focuses on the risk of zoonotic spillover of novel viruses from wildlife to people at high-risk interfaces in developing countries, and is therefore directly applicable to the research proposed for this R01. I have conducted field survey work in

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China and Bangladesh and have published two papers directly from this work. I am currently drafting 4 manuscripts concerning behavioral risk discoveries in multiple countries.

a) Wang N, Li S, Yang X, Huang H, Zhang Y, Guo H, Luo C, Miller M, Zhu G, Chmura AA, Hagan E, Zhou J, Zhang Y, Wang L, Daszak P, Shi Z (2018). Serological evidence of bat SARS-related coronavirus infection in humans, China. **Virologica Sinica**, 33(1), 104-107.

b) Miller M, Hagan E (2017). Integrated biological–behavioural surveillance in pandemic-threat warning systems. **Bulletin of the World Health Organization**, 95(1), 62.

2. **Research collaboration in developing countries.** I have worked to provide support in analyzing and reporting novel serological, quantitative, and qualitative findings from in-country staff in developing countries. This has taken the form of training local anthropologists, physicians, clinicians, and social scientists in ethical data collection, methods of quantitative and qualitative data analysis, usage of the R statistical software, usage of the MAXQDA qualitative analysis software, and understanding the norms of scientific journal article preparation and submission. My scientific training and interdisciplinary professional experiences will be useful in the current proposed work through coordinating survey and sample collection work in China.

a) Miller M, Hagan E (2017). Integrated biological–behavioural surveillance in pandemic-threat warning systems. **Bulletin of the World Health Organization**, 95(1), 62.

b) Wang N, Li S, Yang X, Huang H, Zhang Y, Guo H, Luo C, Miller M, Zhu G, Chmura AA, Hagan E, Zhou J, Zhang Y, Wang L, Daszak P, Shi Z (2018). Serological evidence of bat SARS-related coronavirus infection in humans, China. **Virologica Sinica**, 33(1), 104-107.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

R01 AI110964 Daszak (PI) 06/01/14-05/31/19
NIAID: Understanding the Risk of Bat Coronavirus Emergence
Bat ecological, human risk behavioral and virological studies to understand the risk of bat coronavirus emergence
Role: Research Scientist

USAID EPT PREDICT-2 Mazet (PI) 10/01/14 – 09/30/19
Conducting surveillance for novel pathogens in wildlife, livestock and people; characterizing human risk behavior; modeling risk of novel disease emergence; identifying mitigation strategies
The goal of this project is to assist focal countries in monitoring viruses with pandemic potential, as well as the behaviors, practices, and conditions that are associated with viral evolution, spillover, amplification, and spread.
Role: Research Scientist

Completed Research Support

USAID EPT PREDICT-1 Mazet (PI) 10/01/09 – 09/30/14
Modeling hotspots for disease emergence and conducting surveillance in wildlife in hotspots for new emerging zoonoses

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This project preceded PREDICT-2, described above. $75 million award to identify hotspots of emerging diseases of pandemic potential and to help guide surveillance activities and disease control and prevention strategies across several countries.
Role: Research Scientist

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Guangjian Zhu	Co-Investigator
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
East China Normal University, Shanghai, China	BS	07/03	Biology Science
Hainan Normal University, Haikou, China	MS	07/03	Ecology
East China Normal University, Shanghai, China	PHD	6/12	Biochemistry/Mol. Biol.

A. Personal Statement

Throughout my graduate studies and work with East China Normal University, I have carried out molecular biology and field ecological research focused on bat genetics and viral diversity. I have co-authored multiple publications in the field of viral genetics and bat ecology under the mentorship of Drs. Daszak (EcoHealth Alliance) and Shi (Wuhan Inst. Virol.). For the past 9 years I have been the in-country coordinator for all EcoHealth Alliance work in China on USAID- EPT-PREDICT, as well as for the previous NIAID R01 on bat CoVs. During this time I have been responsible for the identification of high-risk interfaces between wildlife and people, where close contact might allow for zoonotic pathogen spillover. I have also led wildlife surveys which involved bat and rodent capture and sampling for viral discovery. Through this work I have led site-selection and wild and domestic animal sampling in Guangxi, Yunnan, Guangdong and Shanghai, and have compiled archived and current samples from birds in Shanghai Chongming Reserve for H7N9 avian influenza analyses. Under the USAID PREDICT program I collected over 1,000 bat samples which have been tested for coronaviruses and other viral families at the Wuhan Institute of Virology. Under our previous NIAID award (R01AI110964), I am responsible for developing and leading a wildlife team to sample bats, rodents, and other small mammals in the live animal markets of southern China. I will continue these efforts in our renewal proposal as we focus our efforts on centers of CoV diversity in southern China. Through my graduate and professional work I have developed expertise in collecting high-quality, non-destructive samples from wildlife as well as expertise in molecular diagnostics.

B. Positions and Honors

Positions and Employment

2007- Assistant Researcher, Guangdong Entomological Institute, China

Other Experience and Professional Memberships

Honors

2009 Biology Prize of the 2009 Ig Nobel Prize (Tan *et al.* 2009, PLoS One)

C. Selected peer-reviewed publications most relevant to the current application

Ge XY, Li JL, Yang X-L, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang YJ, Luo CM, Tan B, Wang N, Zhu Y, Crameri G, Zhang SY, Wang LF, Daszak P, Shi Z (2013). Isolation and characterization of a bat SARS-like Coronavirus that uses the ACE2 receptor. **Nature** 503: 535-538.

Obtained via FOIA by Judicial Watch, Inc.

Zhu G, Han N, Hong T, Tan M, Yu D, Zhang L (2008). Echolocation Call, Roost and ND 1 Sequence Analysis of New Record of *Nyctalus plancyi* (Chiroptera: Vespertilionidae) on Hainan Island. **Zoological Research**, 29(4): 447-451.

Zhu G, Li D, Ye J, Hong T, Zhang L (2008). New Record of *Ia io* in Hainan Island, its Echolocation Pulses and ND1 Analysis. **Chinese Journal of Zoology**, 43(5): 69-75.

Sun Y, Yu D, Zhu G, Liu X, Zhang SY, Chen J (2009). Isolation and characterization of 11 microsatellite loci in *Scotophilus kuhlii* (Lesser Asiatic Yellow House Bat). **Conservation Genetics**, 10: 1857-1859.

Mao X, Zhu G, Zhang SY, Rossiter SJ (2010). Pleistocene climatic cycling drives intra-specific diversification in the intermediate horseshoe bat (*Rhinolophus affinis*) in Southern China. **Molecular Ecology**, 19(13): 2754-2769.

Hua P, Zhang L, Zhu G, Jones G, Zhang SY, Rossiter SJ (2011). Hierarchical polygyny in multiparous lesser flat-headed bats. **Molecular Ecology**, 20(17): 3669-3680.

Additional recent publications of importance to the field (in chronological oder)

Mazet JAK, Wei Q, Zhao G, Cummings DAT, Desmond JS, Rosenthal J, King CH, Cao W, Chmura AA, Hagan EA, Zhang S, Xiao X, Xu J, Shi Z, Feng F, Liu X, Pan W, Zhu G, Zuo G, Daszak P (2015). Joint China-Us Call for Employing a Transdisciplinary Approach to Emerging Infectious Diseases. **EcoHealth** 12(4): 555-559.

Hu B, Chmura AA, Li J, Zhu G, Desmond JS, Zhang YJ, Zhang JS, Epstein JH, Daszak P, Shi Z (2014). Detection of Diverse Novel Astroviruses from Small Mammals in China. **Journal of General Virology** 95: 2442-2449.

Zhu G, Wang R, Xuan F, Daszak P, Anthony SJ, Zhang SY, Zhang L, He G (2013). Characterization of Recombinant H9n2 Influenza Viruses Isolated from Wild Ducks in China. **Veterinary Microbiology** 166(4): 327-336.

Zhu G, Chmura AA, Zhang L (2011). Morphology, echolocation calls and diet of *Scotophilus kuhlii* (Chiroptera: Vespertilionidae) on Hainan Island, south China. **Acta Chiropterologica**, 14(1): 175-181.

Ma J, Jones G, Zhu G, Metzner W (2010). Echolocation behaviours of the Japanese pipistrelle bat *Pipistrellus abramus* during foraging flight. **Acta Theriologica**, 55(4): 315-332.

Tan M, Jones G, Zhu G, Ye J, Hong T, Zhou S, Zhang S, Zhang L (2009). Fellatio by fruit bats prolongs copulation time. **PLOS One**, 4(10), e7595.

Zhang L, Zhu G, Jones G, Zhang SY (2009). Conservation of bats in China: problems and recommendations. **ORYX**, 43(2): 179-182.

Zhu G, Tang Z, Liang B, Zhang X (2007). Diet and Roost Site of *Cynopterus sphinx* in Winter in Haikou. **Chinese Journal of Zoology**, 42(4): 22-27.

D. Research Support

Ongoing Research Support

USAID	EPT PREDICT-1	Mazet (PI)	10/01/09 – 09/30/14

Obtained via FOIA by Judicial Watch, Inc.

Modeling hotspots for disease emergence and conducting surveillance in wildlife in hotspots for new emerging zoonoses
Amount: $18 million subcontract on a $75 million award
Role: Lead Field Scientist

1R01AI110964 Daszak (PI) 06/01/14 – 05/31/19
NIAID: Understanding the Risk of Bat Coronavirus Emergence
Bat ecological, human risk behavioral and virological studies to understand the risk of bat coronavirus emergence
Amount: $2.5 million
Role: Lead Field Scientist

Completed Research Support

USAID EPT PREDICT-1 Mazet (PI) 10/01/09 – 09/30/14
Modeling hotspots for disease emergence and conducting surveillance in wildlife in hotspots for new emerging zoonoses
Amount: $18 million subcontract on a $75 million award
Role: Lead Field Scientist

1 R01AI079231 Daszak (PI) 09/18/08 – 08/31/13
NIAID Non-Biodefense Emerging Infectious Diseases
Risk of viral emergence from bats.
To model hotspots for bat viral diversity, identify & characterize new bat viruses & understand their pathology
Role: Research Scientist

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Linfa Wang	Co-Investigator
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
East China Normal University, Shanghai	BS	01/1982	Biology
University of California, Davis	PHD	07/2086	Biochemistry

A. PERSONAL STATEMENT

My 20+ years of research focused on designing and applying novel testing platforms to discover zoonotic pathogens has direct applicability to the current proposal. I am trained as a biochemist and molecular biologist, and have been working in the field of virology and infectious diseases for more than 20 years, playing a key role in identification of animal links with several high profile zoonotic agents, including Hendra virus in Australia, Nipah virus in Malaysia and SARS virus in China. During this time, I've directed largescale laboratory diagnostic studies based on serological and PCR surveys of wildlife, domestic animals and people; and worked with multidisciplinary lab, field and modeling teams, including those at EcoHealth Alliance, to interpret the results. In my current role as director of the Program in Emerging Infectious Diseases at Duke-NUS Graduate Medical School, I have initiated major projects to continue this work, and to analyze bat genomics and basic bat biology to better understand bat-unique biological features such as longevity and co-existence with pathogens with no or minimal clinical disease. This work has led to a number of patented techniques, as well as novel reagents that I have made available to collaborators and the greater scientific community. Over the years, I have established an extensive collaborative network with scientists all around the world, covering research and surveillance work into infections of human, animal and wildlife in a truly One Health approach, including many of the collaborators on the current proposal.

Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, McEachern J, Field H, Daszak P, Eaton BT, Zhang S, Wang LF (2005) Bats are natural reservoir of SARS-like coronaviruses. **Science** 310: 676-679.

Ge XY, Li JL, Yang X-L, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang YJ, Luo CM, Tan B, Wang N, Zhu Y, Crameri G, Zhang SY, Wang LF, Daszak P, Shi Z (2013). Isolation and characterization of a bat SARS-like Coronavirus that uses the ACE2 receptor. **Nature** 503: 535-538.

Zhang G, Cowled C, Shi Z, Huang Z, Bishop-Lilly KA, Fang X, Wynne JW, Xiong Z, Baker ML, Zhao W, Tachedjian M, Zhu Y, Zhou P, Jiang X, Ng J, Yang L, Wu L, Xiao J, Feng Y, Chen Y, Sun X, Zhang Y, Marsh GA, Crameri G, Broder CC, Frey KG, Wang LF Wang J (2013) Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. **Science** 339: 456-60.

Zhou P, Fan H, Lan T, Yang XL, Shi WF, Zhang W, Zhu Y, Zhang YW, Xie QM, Mani S, Zheng XS, Li B, Li JM, Guo H, Pei GQ, An XP, Chen JW, Zhou L, Mai KJ, Wu ZX, Li D, Anderson DE, Zhang LB, Li SY, Mi ZQ, He TT, Cong F, Guo PJ, Huang R, Luo Y, Liu XL, Chen J, Huang Y, Sun Q, Zhang XL, Wang YY, Xing SZ, Chen YS, Sun Y, Li J, Daszak P, Wang LF, Shi ZL, Tong YG, Ma JY (2018). Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. **Nature** 556: 255–258

Patents: A protease deficient Bacillus subtilis mutant strain US patent No. 5,585,253; Bacillus subtilis expression and secretion system. US patent No. 7,238,560; Footrot antigens, vaccines and diagnostic assays.

Obtained via FOIA by Judicial Watch, Inc.

Australian Patent No. 38377/93; A novel epitope tagging system for protein surveillance and purification.
Australian Patent No. PM7419/94; Assay for the Parallel Detection of Biological Material Based on PCR.
PCT/SG2013/000455; A Chimeric Animal Comprising Stably Transplanted Bat Cells. IMC/P/10031/00/SG

B. POSITIONS AND HONORS

Positions and Employment

1986 - 89 Post-doctoral Fellow, Department of Biochemistry, University of California, Davis, USA
1990 Senior Research Officer, Centre for Molecular Biology and Medicine, Monash University, Australia
1990 - 92 Research Scientist, CSIRO Australian Animal Health Laboratory (AAHL), Geelong, Australia
1992 - 96 Senior Research Scientist, CSIRO AAHL, Geelong, Australia
1996 - 04 Principal Research Scientist, CSIRO AAHL, Geelong, Australia
2004 - 08 Senior Principal Research Scientist, CSIRO AAHL, Geelong, Australia
2008 - 15 OCE Science Leader, CSIRO AAHL, Geelong, Australia
2012 - Professor & Director, Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore

Other Experience and Professional Memberships

1996 - Editorial Board, *Asia Pacific J. Mol. Biol. Biotech.*
2003 WHO SARS Scientific Research Advisory Committee
2005 - Honorary Professor, Wuhan Institute of Virology, Chinese Academy of Sciences
2006 - Editorial Board, *Chinese J. Virol.*; *Zoonoses & Publ. Hlth.*
2006 - 7 NH & MRC Grant Review Panel
2008 - Chair, ICTV Study Group, Paramyxoviridae
2009 - Honorary Professor, University of Melbourne, Australia
2010 - Editorial Board, *Frontiers Virol.*
2012 - Editor-in-Chief, *Virol. J.*
2012 - Board of Directors, Singapore Eye Research Institute
2012 - Executive Committee, Australasian Society of Virology
2013 - WHO International Health Regulations, Roster of Experts
2017 - World Economic Forum, Global Health Threat Advisory Board

Selected Awards/Honors:

2006 CSIRO Award for Excellence in Partnership
2007 Finalist, Eureka Prize for Scientific Research
2008 CSIRO CEO Science Leader Award
2010 Elected fellow of the Australian Academy of Technological Sciences and Engineering
2011 Gardner Lecture Award, European Society of Clinical Virologist
2013 CSIRO Chairman's Medal for Research
2014 Winner, Eureka Prize for Infectious Disease Research
2014 Finalist, Prime Minister's Science Award, Australia

C. CONTRIBUTION TO SCIENCE

1. **Application of both molecular and serological platforms to pathogen discovery**

   My work at CSIRO AAHL, and now at Duke-NUS has focused on the development and use of PCR and serological assays to identify novel pathogens in wildlife, livestock and people, often under outbreak conditions. This includes the discovery of bats as a reservoir for SARS-CoV, using novel serological assays and PCR techniques I developed.

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a. Bossart KN, McEacherna JA, Hickey AC, Choudhry V, Dimitrov DS, Eaton BT, Wang LF (2007) Neutralization assays for differential henipavirus serology using Bio-Plex Protein Array Systems. **Journal of Virological Methods,** 142: 29-40.

b. Thalmann CM, Cummins DM, Yu M, Lunt R, Pritchard LI, Hansson E, Crameri S, Hyatt A, Wang LF (2010) Broome virus, a new fusogenic Orthoreovirus species isolated from an Australian fruit bat. **Virology** 402:26-40.

c. Cui J, Tachedjian G, Tachedjian M, Holmes EC, Zhang SY, Wang LF (2012) Identification of diverse groups of endogenous gammaretroviruses in mega- and microbats. **Journal of General Virology** 93:2037-2045.

d. Wang J, Selleck P, Yu M, Ha W, Rootes C, Gales R, Wise T, Crameri S, Chen H, Broz I, Hyatt A, Woods R, Meehan B, McCullough S, Wang LF (2014) Novel Phlebovirus with Zoonotic Potential Isolated from Ticks, Australia. **Emerging Infectious Diseases** 20:1040-1043.

2. Identification of bats as major reservoir of emerging zoonotic viruses

I have used surveillance in wildlife, livestock and humans, coupled with experimental infections under BSL-2, -3, and -4, and laboratory assays to identify evidence that bats are the reservoir for a series of emerging viruses in people, including Hendra virus, Nipah virus, SARS-CoV, and others. This work has been one of the foundations for current interest in bats in emerging infectious disease research.

a. Eaton BT, Broder CC, Middleton D, and Wang LF, (2006). Hendra and Nipah viruses: different and dangerous. **Nature Reviews Microbiology**, 4: 23-35.

b. Chua KB, Crameri C, Hyatt A, Yu M, Tompang MR, Rosli J, McEachern J, Crameri S, Kumarasamy V, Eaton BT, Wang LF (2007). A previously unknown reovirus of bat origin is associated with an acute respiratory disease in humans. **Proceedings of the National Academy of Sciences**, 27: 11424-11429.

c. Mahalingam S, Herrero LJ, Playford G, Spann K, Herring B, Rolph R, Middleton D, McCall B, Field H, Wang LF (2012) Hendra virus: an emerging paramyxovirus in Australia. **Lancet Infectious Diseases** 12: 799-807.

d. Clayton BA, Middleton D, Arkinstall R, Frazer L, Wang LF, Marsh GA (2016) The Nature of Exposure Drives Transmission of Nipah Viruses from Malaysia and Bangladesh in Ferrets. **PLOS Neglected Tropical Diseases,** 10(6): e0004775.

3. Establishment of bats as a new mammalian model system to study virus-host interaction and evolutionary biology

Working with collaborators around the world, my lab has amassed an unprecedented collection of serological, tissue and other samples from bat surveillance programs. I have used these to develop and disseminate primary and immortalized bat cell lines, and a host of reagents which my team and collaborators are using to test hypotheses about why bats are able to host so many distinct viruses. Current projects include bat genomics and proteomics; examining the bat MHC, using gene knockout technology to identify links between flight, viral resistance, and longevity.

a. Wynne JW, Shiell BJ, Marsh G, Boyd V, Monaghan P, Zhou P, Klein R, Todd S, Mok L, Green D, Tachedjian M, Baker M, Matthews D, Wang LF (2014). Proteomics informed by transcriptomics reveals Hendra virus sensitizes bat cells to TRAIL mediated apoptosis. **Genome Biology** 15: 532.

b. Zhou P, Tachedjian M, Wynne JW, Boyd V, Cui J, Smith I, Cowled C, Ng JH, Mok L, Michalski WP, Mendenhall IH, Tachedjian G, Wang LF, Baker ML (2016). Contraction of the type I IFN locus and unusual constitutive expression of IFN-α in bats. **Proceedings of the National Academy of Sciences**, 113: 2696-2701.

Obtained via FOIA by Judicial Watch, Inc.

c. Xie J, Li Y, Shen X, Goh G, Zhu Y, Cui J, Wang LF, Shi Z, Zhou P (2018). Dampened STING-Dependent Interferon Activation in Bats. **Cell Host and Microbe**, 23(3):297-301.

d. Yong KSM, Ng JHJ, Her Z, Hey YY, Tan SY, Tan WWS, Irac SE, Liu M, Chan XY, Gunawan M, Foo RJH, Low DHW, Mendenhall IH, Chionh YT, Dutertre CA, Chen Q, Wang LF (2018). Bat-mouse bone marrow chimera: a novel animal model for dissecting the uniqueness of the bat immune system. **Science Reports**, 8(1):4726.

D. RESEARCH SUPPORT

Ongoing research support

NRF2012NRF-CRP001-056 Wang (PI) 01/11/13-31/10/18
National Research Foundation (NRF, Singapore)
Learning from bats: from genomics to controlling viral infection and combating cancer
Using bats as model to study immunology, inflammation and other cellular/molecular mechanisms which are responsible for the unique biological features of bats, such as longevity and infection with no or less diseases.
Role: Leading PI

AI212961 Crump (PI) 01/02/16-31/01/21
NIH
Investigating Febrile Deaths in Tanzania (INDITe)
To identify actionable patient management and health system interventions that could avert fatal outcomes among patients with severe febrile illness in low-resource areas.
Role: Co-PI

(b) (4)

Development of multiple serological platforms for differentiation of Zika and dengue virus infections

Using multiple multiplex serological platforms to develop antibody tests which can differentiation infections of Zika virus from Dengue virus and other closely related flaviviruses.
Role: PI

Completed

(b) (4)

Establishment of serological diagnostic capability for highly virulent zoonotic viral infections in Singapore

Using most advanced technological platforms to enhance the capability in diagnosing and responding to future zoonotic disease outbreaks in Singapore.
Role: PI

(b) (4)

Understanding the host pathogen relationships of Hendra Virus in bats, horses and humans
Examines why bats can be infected with Hendra Virus with no apparent symptoms, yet the virus causes severe disease in other mammals including humans. We hope this information can be used to design new drugs or vaccines to Hendra Virus.
Role: Co-PI

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(b) (4)

Improving the management of an emerging viral disease In Australia: determination of the mechanisms of neuroinvasion by Hendra Virus and their control, leading to optimization of post-exposure therapy following contact with Hendra Virus
Using a recently established mouse infection model, this study aims to elucidate the mechanism of Hendra Virus neuroinvasion and to optimize the post-exposure therapy strategies.
Role: Chief Investigaor

(b) (4)

New targets in antiviral therapies
Development of novel antiviral strategies based on the interruption of nuclear localization process of key virus proteins in the families of *Paramyxoviridae* and *Rhabdoviridae*.
Role: Co-PI

AI077995 Broder (PI) 01/06/07-31/05/13
NIH/NIAID
Vaccines and therapeutics for Nipah and Hendra Virus
Establish virus infection, lethal dose, and detection parameters of Nipah virus in a ferret model. 2. Evaluate the protective efficacy of recombinant sG as a subunit vaccine for Nipah virus in the ferret. 3. Determine the passive protective efficacy of neutralizing, anti-G, fully-human monoclonal antibody therapy for Nipah virus infection in the cat and ferret. 4. Determine the solution structure of Nipah sG and in complex with its receptor ephrinB2.
Role: Co-PI

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Lili Ren	Co-Investigator
eRA COMMONS USER NAME (credential, e.g., agency login) (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
Norman Bethune Univ. Med. Sci., China	BS	07/1998	Clinical medicine
Medical College, Jilin university	MS	07/2002	Pathology, pathophysiol.
Ctr. Disease Control & Prevention, China	Ph.D	07/2005	Immunology

A. Personal Statement

I have expertise in the pathogenesis and evolution of respiratory viruses. Using systems biological concepts and technical systems, my group has identified several new emerging respiratory virus epidemics in China, clarifying new causative viral agents of severe pneumonia, providing insights into the pathogenic mechanisms of viruses, and improving clinical pathogen diagnostics. My group has also conducted a longitudinal study to analyze evolution of known common respiratory viruses since 2005 – the largest and the longest continuous study of its type in China. My multiple pathogen detection system approach has been transferred to more than 300 national sentinel sites. In addition, my group has established several platforms to identify the serological epidemiology of common respiratory viruses including human CoVs. This will be a critical reference for the proposed R01 work, and have implications on the design of our serological screening platform. I have also established a collaborative group with clinicians in China to study the ecology of emerging viral pathogens. My extensive experience in this type of study will greatly assist in my role overseeing clinical sample collection, and screening by PCR and serological methods in southern China.

B. Positions and Honors.

Positions and Employment

2005-2010 Research assistant, Institute of Pathogen Biology, Chinese Academy of Medical Sciences/Peking Union Medical College, China

2010-2016, Research scientist, Institute of Pathogen Biology, Chinese Academy of Medical Sciences/Peking Union Medical College, China

2016- Senior Scientist, Institute of Pathogen Biology, Chinese Academy of Medical Sciences/Peking Union Medical College, China

Other Experience and Professional Memberships

2016-2019 Member, Expert Committee on Biosafety Assessment of the National Health and Family Planning Commission

2014-2020 Member, Youth Committee of the Chinese Medical Association Medical Virology Branch

2016-2021 Member, China Research Hospital, Space Microbiology and Infection Committee Branch

2017- Editorial board, *Chinese Journal of Experimental & Clinical Virology*

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Honors

2008 - 10	Outstanding Young Talents of New Century (NCET-07-0506), granted by Ministry of Education, China. Principal Investigator.
2015	2nd prize of the advanced science and technology progress award, second author, granted by Ministry of Education, China.
2016	1st prize of the advanced science and technology progress award, second author, granted by Ministry of Education, China.
2017	Excellent teacher of Peking Union Medical College (PUMC), China

C. Selected peer-reviewed publications most relevant to the current application

* = Co-corresponding or first authors

Ren L*, Richard G*, Wang Z*, Xiang Z*, Wang Y*, Zhou H, Li J, Xiao Y, Yang Q, Zhang J, Chen L, Wang W, Li Y, Li T, Meng X, Zhang Y, Guy V, Chen J, Jin Q, Wang J (2009) Prevalence of human respiratory viruses in adults with acute respiratory tract infections in Beijing, 2005–2007. **Clinical Microbiology and Infection**,15(12): 1146-1153.

Ren L, Gonzalez R, Xu X, Li J, Zhang J, Vernet G, Paranhos-Baccalà G, Jin Q, Wang J (2009) WU polyomavirus in fecal specimens of children with acute gastroenteritis, China. **Emerging Infectious Diseases**, 15(1): 134-135.

Ren L, Gonzalez R, Xiao Y, Xu X, Chen L, Vernet G, Paranhos-Baccalà G, Jin Q, Wang J (2009) Saffold cardiovirus in children with acute gastroenteritis, Beijing, China. **Emerging Infectious Diseases** 15(9): 1509-1511.

Ren L, Gonzalez R, Xu J, Xiao Y, Li Y, Zhou H, Li J, Yang Q, Zhang J, Chen L, Wang W, Vernet G, Paranhos-Baccalà G, Wang Z, Wang J (2011). Prevalence of human coronaviruses in adults with acute respiratory tract infections in Beijing, China. **Journal of Medical Virology** 83(2): 291-297.

Yang J*, Yang F*, Ren L*, Xiong Z, Wu Z, Dong J, Sun L, Zhang T, Hu Y, Du J, Wang J, Jin Q (2011). Unbiased parallel detection of viral pathogens in clinical samples by use of a metagenomic approach. **Journal of Clinical Microbiology**, 49(10): 3463-3469.

Guo L*, Zhang X*, Ren L*, Yu X*, Chen L*, Zhou H, Gao X, Teng Z, Li J, Hu J, Wu C, Xiao X, Zhu Y, Wang Q, Pang X, Jin Q, Wu F, Wang J (2014). Human antibody responses to avian influenza A(H7N9) virus, 2013. **Emerging Infectious Diseases**, 20(2): 192-200.

Ren L*, Yu X*, Zhao B*, Wu F, Jin Q, Zhang X, Wang J (2014). Infection with possible precursor of avian influenza A(H7N9) virus in a Child, China, 2013, **Emerging Infectious Diseases**, 20(8): 1362-1365.

Ren L*, Zhang Y*, Li J, Xiao Y, Zhang J, Wang Y, Chen L, Paranhos-Baccalà G, Wang J (2015). Genetic drift of human coronavirus OC43 spike gene during adaptive evolution. **Scientific Reports**, 5:11451. doi.org/10.1038/srep11451

Zhang Y, Li J, Xiao Y, Zhang J, Wang Y, Chen L, Paranhos-Baccalà G, Ren L*, Wang J* (2015). Genotype shift in human coronavirus OC43 and emergence of a novel genotype by natural recombination. **Journal of Infection**, 70(6): 641-650.

Yan F, Xiao Y, Li M, Zhang H, Zhang R, Zhou H, Shen H, Wang J, Li W*, Ren L* (2017). Metagenomic analysis identified human rhinovirus B91 infection in an adult suffering from severe pneumonia. **American Journal of Respiratory and Critical Care Medicine**, 195(11):1535-1536.

Obtained via FOIA by Judicial Watch, Inc.

Ren L*, Yang D*, Ren X*, Li M, Mu X, Wang Q, Cao J, Hu K, Yan C, Fan H, Li X, Chen Y, Wang R, An F, An S, Luo M, Wang Y, Xiao Y, Xiang Z, Xiao Y, Li L, Huang F, Jin Q, Gao Z, Wang J (2017). Genotyping of human rhinovirus in adult patients with acute respiratory virus infections identified predominant infections of genotype A21. **Scientific Reports**, 7:41601.

Ren L*, Zhang R*, Rao J, Xiao Y, Zhang Z, Yang B, Cao D, Zhong H, Ning P, Shang H, Li M, Gao Z, Wang J (2018). Transcriptionally Active Lung Microbiome and Its Association with Bacterial Biomass and Host Inflammatory Status. **mSystems**, 3:e00199-18.

D. Research Support

Ongoing Research Support

1. 2017ZX10103004, Key project of infectious diseases 01/01/2017-12/31/2020
Viral etiology and spectrum of respiratory tract infections and the mutations characteristics
The goal of this project is to identify the etiology of community acquired pneumonia in China and the epidemic and mutations of the important respiratory viruses.
Role: PI

Completed Research Support

1. 2012ZX10004-206 Key project of infectious diseases 01/01/2012-12/31/2015
Viral etiology and spectrum of respiratory tract infections and the mutations characteristics
The goal of this project is to investigate the etiology of acute respiratory tract infections in China and the sero-epidemiological of important respiratory viruses.
Role: PI

2. 2009ZX10004-206 Key project of infectious diseases 01/01/2009-12/31/2010
Viral etiology and spectrum of respiratory tract infections and the mutations characteristics
The goal of this project is to establish the surveillance network and to investigate the etiology of acute respiratory tract infections in China.
Role: PI

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BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Li Guo	Co-Investigator
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
Bengbu Medical College, China	B.S.	07/1997	Clinical Medicine
Anhui Medical University, China	M.S.	07/2002	Microbiology
Chinese Center for Disease Control & Prevention	M.D.	07/2006	Immunology

A. Personal Statement

I have direct expertise in the proposed work described in this R01. I have been working on the etiology and immunology of respiratory viruses since 2003. I have evaluated cross-reactivity of NP among HCoVs and developed a competitive ELISA (cELISA) for detecting anti-N IgG antibodies against HCoV -229E, -OC43, -NL63, and -HKU1. These data indicate differential transmission of HCoVs in the Chinese population and that anti-N IgG may serves as an index for susceptibility to HCoV infections. In addition, I have evaluated human antibody responses to A(H7N9) influenza virus, differential seroprevalence of human bocavirus species 1-4 in China, and found bocavirus in children with respiratory tract infections.

B. Positions and Honors.

Positions and Employment

1997 - 99 Teaching Assistant, Bengbu Medical College
2002 - 09 Assistant Professor, Chinese Center for Disease Control and Prevention
2009 - 15 Associate Professor, Institute of Pathogen Biology (IPB), Chinese Academy of Medical Science (CAMS) /Peking Union Medical College.
2015 - Professor, Institute of Pathogen Biology (IPB), Chinese Academy of Medical Science (CAMS) /Peking Union Medical College

C. Selected peer-reviewed publications

* = Co-corresponding or first author

Guo L, Wang D, Zhou H, Wu C, Gao X, Xiao Y, Ren L, Paranhos-Baccalà G, Shu Y, Jin Q, Wang J (2016). Cross-reactivity between avian influenza A (H7N9) virus and divergent H7 subtypic and heterosubtypic influenza A viruses. **Scientific Reports**, 6, 22045.

Gao X, Zhou H, Wu C, Xiao Y, Ren L, Paranhos-Baccalà G, Guo L*, Wang J* (2015). Antibody against nucleocapsid protein predicts susceptibility to human coronavirus infection. **Journal of Infection** 71(5): 599-602.

Chen Z*, Wang J*, Bao L*, Guo L*, Zhang W, Xue Y, Zhou H, Xiao Y, Wang J, Wu F, Deng Y, Qin C, Jin Q (2015). Human monoclonal antibodies targeting the haemagglutinin glycoprotein can neutralize H7N9 influenza virus. **Nature Communications**, 6:6714.

Obtained via FOIA by Judicial Watch, Inc.

Yang J*, Zhang T*, Guo L*, Hu YF, Li JL, Su HX, Xiao Y, Ren XW, Dong J, Sun LL, Xiao Y, Li Li, Yang F, Wang JW, Yuan H, Jin Q (2014). Mutations of Novel Influenza A(H10N8) Virus in Chicken Eggs and MDCK Cells. **Emergining Infectious Diseases**, 20(9):1541-1543.

Zhou Z, Gao X, Wang Y, Zhou H, Wu C, Paranhos-Baccalà G, Vernet G, Guo L*, Wang J* (2014). Conserved B-Cell Epitopes among Human Bocavirus Species Indicate Potential Diagnostic Targets. **PLOS One**, 9(1): e86960.

Guo L, Zhang X, Ren L, Yu X, Chen L, Zhou H, Gao X, Teng Z, Li J, Hu J, Wu C, Xiao X, Zhu Y, Wang Q, Pang X, Jin Q, Wu F, Wang J (2014). Human antibody responses to avian influenza A(H7N9) virus. **Emerging Infectious Diseases**, 20(2): 192-200.

Guo L, Wu C, Zhou H, Wu C, Paranhos-Baccalà G, Vernet G, Jin Q, Wang J, Hung T (2013). Identification of a nonstructural DNA-binding protein (DBP) as an antigen with diagnostic potential for human adenovirus. **PLOS One**, 8(3): e56708.

Guo L, Wang Y, Zhou H, Wu C, Song J, Li J, Paranhos-Baccalà G, Vernet G, Wang J, Hung T (2012). Differential seroprevalence of human bocavirus species 1-4 in Beijing, China. **PLOS One**, 7(6): e39644.

Guo L, Gonzalez R, Zhou H, Wu C, Vernet G, Wang Z, Wang J (2012). Detection of three human adenovirus species in adults with acute respiratory infection in China. **European Journal of Clinical Microbiology and Infectious Disease**, 31(6): 1051-1058.

Guo L, Gonzalez R, Xie Z, Zhou H, Liu C, Wu C, Paranhos-Baccalà G, Vernet G, Shen K, Jin Q, Wang J (2011). Bocavirus in children with respiratory tract infections. **Emerging Infectious Diseases**, 17(9): 1775-1777.

Wang Y, Gonzalez R, Zhou H, Li J, Li Y, Paranhos-Baccalà G, Vernet G, Guo L*, Wang J* (2011). Detection of human bocavirus 3 in China. **European Journal of Clinical Microbiology and Infectious Disease**, 30(6): 799-805.

Guo L, Gonzalez R, Wang W, Vernet G, Paranhos-Baccalà G, Wang J (2010). Complete genome sequence of human astrovirus genotype 6. **Virology Journal**, 7: 29.

Guo L, Xu X, Song J, Wang W, Wang J, Hung T (2010). Molecular Characterization of Astrovirus Infection in Children with Diarrhea in Beijing, 2005-2007. **Journal of Medical Virology**, 82(3): 415-423.

Guo L, Zhou H, Wang M, Song J, Han B, Shu Y, Ren L, Si H, Qu J, Zhao Z, Wang J, Hung T (2009). A recombinant adenovirus prime-virus-like particle boost regimen elicits effective and specific immunities against norovirus in mice. **Vaccine**, 27(38): 5233-5238.

Guo L, Song J, Xu X, Ren L, Li J, Zhou H, Wang M, Qu J, Wang J, Hung T (2009). Genetic analysis of norovirus in children affected by acute gastroenteritis in Beijing, 2004-2007. **Journal of Clinical Virology** 44(1): 94-98.

Guo L, Wang J, Zhou H, Si H, Wang M, Song J, Han B, Shu Y, Ren L, Qu J, Hung T (2008) Intranasal administration of a recombinant adenovirus expressing the norovirus capsid protein stimulates specific humoral, mucosal, and cellular immune responses in mice. **Vaccine**, 26(4): 460-468.

D. Research Support

Ongoing Research Support

2018ZX10734404-006 01/01/2018-12/31/2020

Obtained via FOIA by Judicial Watch, Inc.

Key technologies for the identification and identification of important respiratory viruses and establishment of reference libraries
Role: Co-PI

Completed Research Support

(b) (4)

Study on the immunoprotection of recombinant adenovirus vaccine against Norovirus by using virus-like particles as a control
Role: PI

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Peng Zhou	Co-Investigator
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
College of Life Science, Henan University, China	BS	07/04	Bioengineering
Wuhan Inst. Virol., Chinese Acad. Sci., China	PHD	01/11	Virology
Australian Animal Health Laboratory, CSIRO	Postdoc	07/14	Viral Immunology
Singapore Duke-NUS Medical School, Singapore	Postdoc	02/16	Viral Immunology

A. Personal Statement

My virological expertise is directly related to the proposed work in this R01 renewal, including next generation diagnostic tool development for monitoring bat virus spillover, bat pathogen discovery and bat viral immunology. I have worked on bat virology since 2004, and participated in the work that led to the discovery of SARS-like coronaviruses in Mainland China. I worked on bat viral immunology to explore reasons why bats can coexist with high viral diversity and viral loads. My findings show that in bats, a constitutively expressed interferon and a dampened STING-dependent interferon production pathway exists, which may explain why bats can control viral replication and tolerate viral diseases. My most recent work on Swine Acute Diarrhea Syndrome (SADS) characterized the spillover of CoV from bats to swine causing a large-scale pandemic. I have worked closely with Dr. Linfa Wang from Singapore Duke-NUS medical school, on developing next-generation viral nucleotide, serological and isolation tools for coronavirus from bats and other animals. I have also collaborated with, and published papers with Dr. Daszak and other staff at EcoHealth Alliance. I will be in charge of diagnostics, genomics, and virus isolation in this project.

B. Positions and Honors.

Positions and Employment

2016- Principle Investigator, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China

Other Experience and Professional Memberships

2009 - 10 Joint PhD study in Australia Animal Health Laboratory, CSIRO

Honors

2009 Scholarship for China-Australia Joint PhD study, China Scholarship Council.
2017 Natural Science Award (the first rank) of Hubei province, China.
2018 National Science Fund for Excellent Young Scholars, China.

C. Selected peer-reviewed most relevant to the current application

* = Co-corresponding or first authors

1. Zhou P, Fan H, Lan T, Yang XL, Shi WF, Zhang W, Zhu Y, Zhang YW, Xie QM, Mani S, Zheng XS, Li B, Li JM, Guo H, Pei GQ, An XP, Chen JW, Zhou L, Mai KJ, Wu ZX, Li D, Anderson D, Zhang LB, Li SY, Mi ZQ, He TT, Cong F, Guo PJ, Huang R, Luo Y, Liu XL, Chen J, Huang Y, Sun Q, Zhang XLL, Wang YY, Xing SZ, Chen YS, Sun Y, Li J, Daszak P, Wang LF, Shi ZL, Tong YG, Ma JY (2018) Fatal swine acute diarrhea syndrome

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caused by an HKU-2 related coronavirus of bat origin. **Nature**, 556: 255-258. doi.org/10.1038/s41586-018-0010-9

2. Xie J, Li Y, She X, Goh G, Zhu Y, Cui J, Wang LF, Shi Z, Zhou P (2018) Dampened STING-dependent interferon activation in bats. **Cell Host and Microbes** 23(3): 297-301. doi.org/10.1016/j.chom.2018.01.006
3. Zhou P, Tachedjian M, Wynne JW, Boyd V, Cui J, Smith I, Cowled C, Ng JH, Mok L, Michalski WP, Mendenhall IH, Tachedjian G, Wang LF, Baker ML (2016). Contraction of the type I IFN locus and unusual constitutive expression of IFN-α in bats. **Proceedings of the National Academy of Sciences**, 113(10): 2696-701. doi.org/10.1073/pnas.1518240113
4. Wu L*, Zhou P*, Ge XY, Wang LF, Baker ML, Shi Z (2013). Deep RNA Sequencing Reveals Complex Transcriptional Landscape of a Bat Adenovirus. **Journal of Virology**, 87(1): 503-511. doi.org/10.1128/JVI.02332-12
5. Zhou P, Li H, Wang H, Wang LF, Shi Z (2012). Bat severe acute respiratory syndrome-like coronavirus ORF3b homologues display different interferon antagonist activities. **Journal of General Virology**, 93: 275-281. doi.org/10.1099/vir.0.033589-0
6. Zhou P, Cowled C, Todd S, Crameri G, Virtue ER, Marsh GA, Shi ZL, Wang LF, and Baker ML (2011). Type III Interferons in pteropid bats: differential expression patterns provide evidence for distinct roles in antiviral immunity. **Journal of Immunology**,186(5): 3138-3147. doi.org/ 10.4049/jimmunol.1003115
7. Zhou P, Han Z, Wang LF, Shi Z (2009). Immunogenicity difference between the SARS coronavirus and the bat SARS-like coronavirus spike (S) proteins. **Biochemal Biophysical Research Communications**, 387(2): 326-329. doi.org/10.1016/j.bbrc.2009.07.025

D. Research Support

Ongoing Research Support

(b) (4)

Combating the next SARS- or MERS-like emerging infectious disease outbreak by improving active surveillance
Role: PI

(b) (4)

Interferon responses in SARS-Like Coronavirus infected Bat cells
Role: PI

(b) (4)

Bat virology
Role: PI

Completed Research Support

(b) (4)

Immune responses and transcriptome analysis of bat adenovirus infected bat cells
Role: Co-PI

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Ben Hu	Co-Investigator
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
Huazhong Agricultural University, China	BS	2007	Veterinary medicine
Huazhong Agricultural University, China	MS	2010	Preventive vet. med.
Wuhan Inst. Virology, Chinese Acad. Sci.	PHD	2015	Microbiology

A. Personal Statement

I obtained my PhD degree in 2015 and have been working as a Research Assistant in Dr. Zhengli Shi's laboratory for over 3 years. My research is focused on the discovery and characterization of viruses in small mammals, especially in bats and rodents. My work forms the basis for some of the key findings built on in the current R01 proposal, in particular: 1) the identification of diverse bat SARSr-CoVs at cave sites in Yunnan, China; 2) the potential recombination origin of SARS-CoV; and 3) characterization of spillover risk for bat SARSr-CoVs. I have also reported genetically diverse novel astroviruses in bats, rodents, and shrews in China. I have collaborated with EcoHealth Alliance scientists on multiple research projects for the past 3 years.

B. Positions and Honors.

Positions and Employment

2015- Assistant Researcher, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China

Honors

C. Selected peer-reviewed publications most relevant to the current application

Note: * = Corresponding Author

1. Ge X, Li J, Yang X, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang YJ, Luo CM, Tan B, Wang N, Zhu Y, Crameri G, Zhang SY, Wang LF, Daszak P*, Shi Z (2013). Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. **Nature**, 503: 535-538. doi.org/10.1038/nature12711
2. Hu B, Chmura AA, Li J, Zhu G, Desmond JS, Zhang Y, Zhang W, Epstein JH, Daszak P, Shi Z (2014). Detection of diverse novel astroviruses from small mammals in China. **Journal of General Virology** 95, 2442-2449. doi.org/10.1099/vir.0.067686-0
3. Hu B, Ge X, Wang LF, Shi Z (2015). Bat origin of human coronaviruses. **Virology Journal**, 12(1): 221. doi.org/10.1186/s12985-015-0422-1
4. Ge XY, Wang N, Zhang W, Hu B, Li B, Zhang YZ, Zhou JH, Luo CM, Yang XL, Wu LJ, Wang B, Zhang Y, Li ZX, Shi Z (2016). Coexistence of multiple coronaviruses in several bat colonies in an abandoned mineshaft. **Virologica Sinica**, 31(1): 31-40. doi.org/10.1007/s12250-016-3713-9

Obtained via FOIA by Judicial Watch, Inc.

5. Wang MN, Zhang W, Gao YT, Hu B, Ge XY, Yang XL, Zhang YZ, Shi Z (2016). Longitudinal surveillance of SARS-like coronaviruses in bats by quantitative real-time PCR. **Virologica Sinica**, 31(1): 78-80. doi.org/ 10.1007/s12250-015-3703-3

6. Yang XL, Hu B, Wang B, Wang MN, Zhang Q, Zhang W, Wu LJ, Ge XY, Zhang YZ, Daszak P, Wang LF, Shi Z (2016). Isolation and Characterization of a Novel Bat Coronavirus Closely Related to the Direct Progenitor of Severe Acute Respiratory Syndrome Coronavirus. **Journal of Virology**, 90(6): 3253-3256. doi.org/ 10.1128/JVI.02582-15

7. Waruhiu C, Ommeh S, Obanda V, Agwanda B, Gakuya F, Ge XY, Yang XL, Wu LJ, Zohaib A, Hu B, Shi Z (2017). Molecular detection of viruses in Kenyan bats and discovery of novel astroviruses, caliciviruses, and rotaviruses. **Virologica Sinica**, 32(2):101-114. doi.org/ 10.1007/s12250-016-3930-2

8. Hu B, Zeng LP, Yang XL, Ge XY, Zhang W, Li B, Xie JZ, Shen XR, Zhang YZ, Wang N, Luo DS, Zheng XS, Wang MN, Daszak P, Wang LF, Cui J, Shi Z (2017). Discovery of A Rich Gene Pool of Bat SARS-related Coronaviruses Provides New Insights into the Origin of SARS Coronavirus. **PLOS Pathogens**, 13(11): e1006698.

9. Luo CM, Wang N, Yang XL, Liu HZ, Zhang W, Li B, Hu B, Peng C, Geng QB, Zhu GJ, Li F, Shi Z (2018). Discovery of Novel Bat Coronaviruses in South China That Use the Same Receptor as Middle East Respiratory Syndrome Coronavirus. **Journal of Virology**, 92(13): e00116-18.

10. Luo Y, Li B, Jiang RD, Hu BJ, Luo DS, Zhu GJ, Hu B, Liu HZ, Zhang YZ, Yang XL, Shi ZL (2018). Longitudinal Surveillance of Betacoronaviruses in Fruit Bats in Yunnan Province, China during 2009-2016. **Virologica Sinica**, 33(1):87-95. doi.org/ 10.1007/s12250-018-0017-2

D. Research Support

Ongoing Research Support

31800142 Hu (PI) 01/01/2019-12/31/2021
National Natural Science Foundation of China
Pathogenicity studies of two novel bat SARSr-CoVs on transgenic mice expressing human ACE2
Role: PI

R01 AI110964 Daszak (PI) 06/01/14-05/31/19
Understanding Risk of Bat Coronaviruses
The goal of this study is to analyze the risk of coronavirus spillover from bats to humans in Southern China
Role: Research Scientist

Emerging Pandemic Threat Program, USAID Mazet (PI) 10/01/14-09/30/19
PREDICT 2
The goal of this project is to create and implement a global virus surveillance system in animals and humans and analyze spillover risk.
Role: Laboratory Scientist

Completed Research Support

USAID EPT PREDICT-1 Mazet (PI) 10/01/09 – 09/30/14
Modeling hotspots for disease emergence and conducting surveillance in wildlife in hotspots for new emerging zoonoses
Amount: $18 million subcontract on a $75 million award
Role: Laboratory Scientist

Obtained via FOIA by Judicial Watch, Inc.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Aleksei A. Chmura	Research Scientist
eRA COMMONS USER NAME (b) (6)	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
Columbia University	BS	06/2004	Biology
School of Life Sciences, Kingston University (UK)	PhD	08/2018	Biology

A. Personal Statement

Dr. Chmura has an interdisciplinary background in ecology, wildlife biology, virology, and extensive on-the-ground experience conducting wildlife sampling in China. Fluent in spoken and written Mandarin, for the past decade, Dr. Chmura has acted as a key coordinator among EcoHealth Alliance headquarters staff, and laboratory and field teams in China. Dr. Chmura's personal research involves the wildlife origins of SARS-CoV, wildlife paramyxovirus diversity and evolution, and human-wildlife contact behavior in southern China. His work has been funded by USAID EPT/PREDICT since 2009. As part of his doctoral work, he spent over a year in the Wuhan Institute of Virology laboratory in China under the direction of Dr. Zhengli Shi and Dr. Peter Daszak.

B. Positions and Honors.

Positions and Employment

2001-2004, Volunteer Curator, Dept. of Mammalogy, American Museum of Natural History, USA
2001-2005, Program Assistant, Ctr. Environmental Research and Conservation, Columbia University, USA
2002-2005, Instructor, Columbia University Tropical Field Ecology Programs, USA/Domician Republic/Brazil
2005-Present, Program Coordinator, EcoHealth Alliance, USA
2006-Present, Managing Editor, *EcoHealth*, New York, USA

Other Experience and Professional Memberships

2000-2005 The Explorers Club
2002-present American Museum of Natural History
2005-present International Association for Ecology and Health
2009-present Society for Applied Microbiology

C. Selected peer-reviewed publications most relevant to the current application

Monagin C, Ning L, Schneider B, Chmura AA, Epstein JH, Wu D, Paccha B, Ke C, Daszak P, Rabinowitz P (2018) Serologic and behavioral risk survey of workers with wildlife contact in China. **PLOS ONE**, 13(4): e0194647.

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

Zeng L, Ge X, Peng C, Yang X, Tan B, Gao Y, Chen J, Chmura AA, Daszak P, Shi Z (2016) Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response. **Journal of Virology**, 90(14): 6573–6582.

Mazet JAK, Wei Q, Zhao G, Cummings DAT, Desmond JS, Rosenthal J, King CH, Cao W, Chmura AA, Hagan EA, Zhang S, Xiao X, Xu J, Shi Z, Feng F, Liu X, Pan W, Zhu G, Zuo G, Daszak P (2015). Joint China-Us Call for Employing a Transdisciplinary Approach to Emerging Infectious Diseases. **EcoHealth** 12(4): 555-559.

Obtained via FOIA by Judicial Watch, Inc.

Hu B, Chmura AA, Li J, Zhu G, Desmond JS, Zhang YJ, Zhang JS, Epstein JH, Daszak P, Shi Z (2014). Detection of Diverse Novel Astroviruses from Small Mammals in China. **Journal of General Virology** 95: 2442-2449.

Ge XY, Li JL, Yang X-L, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang YJ, Luo CM, Tan B, Wang N, Zhu Y, Crameri G, Zhang SY, Wang LF, Daszak P, Shi Z (2013). Isolation and characterization of a bat SARS-like Coronavirus that uses the ACE2 receptor. **Nature** 503: 535-538.

Zhu G, Chmura AA, Zhang L (2011). Morphology, echolocation calls and diet of *Scotophilus kuhlii* (Chiroptera: Vespertilionidae) on Hainan Island, south China. **Acta Chiropterologica**, 14(1): 175-181.

Kilpatrick AM, Chmura AA, Gibbons DW, Fleischer RC, Marra PP, Daszak P (2006). Predicting the global spread of H5N1 avian influenza. **PNAS** 103: 19368-19373.

D. Research Support

Ongoing Research Support

R01 AI110964 — Daszak (PI) — 06/01/14-05/31/19
Understanding Risk of Bat Coronaviruses
The goal of this study is to analyze the risk of coronavirus spillover from bats to humans in Southern China
Role: Research Scientist

Emerging Pandemic Threat Program, USAID — Mazet (PI) — 10/01/14-09/30/19
PREDICT 2
The goal of this project is to create and implement a global virus surveillance system in animals and humans and analyze spillover risk.
Role: Program Coordinator

Completed Research Support

USAID EPT PREDICT-1 — Mazet (PI) — 10/01/09 – 09/30/14
Modeling hotspots for disease emergence and conducting surveillance in wildlife in hotspots for new emerging zoonoses
Role: Program Coordinator

2 R01TW005869 — Daszak (PI) — 09/01/08 – 08/31/13
NIH Ecology of Infectious Diseases (Fogarty International Center)
The Ecology, Emergence and Pandemic Potential of Nipah virus in Bangladesh
To conduct mathematical modeling and fieldwork to understand the dynamics of Nipah virus in Bangladesh
Role: Research Scientist

NSF DEB-1257513 — Daszak (PI) — 08/15/12-07/31/13
US-China Ecology and Evolution of Infectious Diseases Collaborative Workshop; Kunming, China 2012
Role: Program Coordinator

1 R01AI079231 — Daszak (PI) — 09/18/08 – 08/31/13
NIAID Non-Biodefense Emerging Infectious Diseases
Risk of viral emergence from bats.
To model hotspots for bat viral diversity, identify & characterize new bat viruses & understand their pathology
Role: Research Scientist

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 1

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 0770900660000

Budget Type*: ● Project ○ Subaward/Consortium

Enter name of Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period:** 1

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	PETER		DASZAK		PD/PI							(b) (4), (b) (6)
2 .	Dr.	Kevin	J	Olival		Co-Investigator							
3 .	Dr.	Leilani	V	Francisco		Co-Investigator							
4 .	Dr.	Noam		Ross		Co-Investigator							
5 .	Ms.	Hongying		Li		Research Scientist							
6 .	Dr.	Alice		Latinne		Research Scientist							
7 .	Ms.	Emily	A	Hagan		Research Scientist							
8 .	Dr.	Aleksei	A	Chmura		Research Scientist							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person **223,713.00**

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**
						Total Salary, Wages and Fringe Benefits (A+B)	**223,713.00**

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 1

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ❍ Subaward/Consortium
Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period: 1**

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	9,440.00
2. Foreign Travel Costs	29,958.00
Total Travel Cost	**39,398.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 1

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period:** 1

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	20,850.00
2. Publication Costs	
3. Consultant Services	79,750.00
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	190,649.00
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**291,249.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**554,360.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . EcoHealth Alliance Indirect Cost	32.74	363,710.00	119,079.00
2 . EcoHealth Alliance Indirect Cost on 3 Subawards (IPB, UNC, WIV)	32.74	75,000.00	24,555.00
3 . University of North Carolina at Chapel Hill Indirect Cost	55.5	50,000.00	27,750.00
4 . IPB and WIV Subawards (2) Indirect Costs	8.0	140,649.00	11,252.00
		Total Indirect Costs	**182,636.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**736,996.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	736,996.00

L. Budget Justification*	File Name: EHA_NIAID_COV_BUDGET_JUSTIFICATION_FINAL.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 2

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 0770900660000

Budget Type*: ● Project ○ Subaward/Consortium

Enter name of Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period: 2**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	PETER		DASZAK		PD/PI							(b) (4), (b) (6)
2 .	Dr.	Kevin	J	Olival		Co-Investigator							
3 .	Dr.	Leilani	V	Francisco		Co-Investigator							
4 .	Dr.	Noam		Ross		Co-Investigator							
5 .	Ms.	Hongying		Li		Research Scientist							
6 .	Dr.	Alice		Latinne		Research Scientist							
7 .	Ms.	Emily	A	Hagan		Research Scientist							
8 .	Dr.	Aleksei	A	Chmura		Research Scientist							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person **223,713.00**

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**
						Total Salary, Wages and Fringe Benefits (A+B)	**223,713.00**

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 2

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ❍ Subaward/Consortium
Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period: 2**

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	9,440.00
2. Foreign Travel Costs	29,958.00
Total Travel Cost	**39,398.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 2

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period:** 2

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	14,850.00
2. Publication Costs	6,000.00
3. Consultant Services	79,750.00
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	190,649.00
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**291,249.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**554,360.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . EcoHealth Alliance Indirect Cost	32.74	363,710.00	119,079.00
2 . University of North Carolina at Chapel Hill Indirect Cost	55.5	50,000.00	27,750.00
3 . IPB and WIV Subawards (2) Indirect Costs	8.0	140,649.00	11,252.00
		Total Indirect Costs	**158,081.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**712,441.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	712,441.00

L. Budget Justification*	File Name: EHA_NIAID_COV_BUDGET_JUSTIFICATION_FINAL.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 3

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 0770900660000

Budget Type*: ● Project ○ Subaward/Consortium

Enter name of Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period: 3**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	PETER		DASZAK		PD/PI							(b) (4), (b) (6)
2 .	Dr.	Kevin	J	Olival		Co-Investigator							
3 .	Dr.	Leilani	V	Francisco		Co-Investigator							
4 .	Dr.	Noam		Ross		Co-Investigator							
5 .	Ms.	Hongying		Li		Research Scientist							
6 .	Dr.	Alice		Latinne		Research Scientist							
7 .	Ms.	Emily	A	Hagan		Research Scientist							
8 .	Dr.	Aleksei	A	Chmura		Research Scientist							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person **223,713.00**

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**
						Total Salary, Wages and Fringe Benefits (A+B)	**223,713.00**

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 3

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ❍ Subaward/Consortium
Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period: 3**

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	9,440.00
2. Foreign Travel Costs	29,958.00
Total Travel Cost	**39,398.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 3

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period:** 3

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	14,850.00
2. Publication Costs	6,000.00
3. Consultant Services	79,750.00
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	190,649.00
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**291,249.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**554,360.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . EcoHealth Alliance Indirect Cost	32.74	363,710.00	119,079.00
2 . University of North Carolina at Chapel Hill Indirect Cost	55.5	50,000.00	27,750.00
3 . IPB and WIV Subawards (2) Indirect Costs	8.0	140,649.00	11,252.00
		Total Indirect Costs	**158,081.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**712,441.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	712,441.00

L. Budget Justification*	File Name: EHA_NIAID_COV_BUDGET_JUSTIFICATION_FINAL.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 4

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 0770900660000

Budget Type*: ● Project ○ Subaward/Consortium

Enter name of Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period: 4**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	PETER		DASZAK		PD/PI							(b) (4), (b) (6)
2 .	Dr.	Kevin	J	Olival		Co-Investigator							
3 .	Dr.	Leilani	V	Francisco		Co-Investigator							
4 .	Dr.	Noam		Ross		Co-Investigator							
5 .	Ms.	Hongying		Li		Research Scientist							
6 .	Dr.	Alice		Latinne		Research Scientist							
7 .	Ms.	Emily	A	Hagan		Research Scientist							
8 .	Dr.	Aleksei	A	Chmura		Research Scientist							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person **223,713.00**

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**
						Total Salary, Wages and Fringe Benefits (A+B)	**223,713.00**

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 4

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ❍ Subaward/Consortium
Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period:** 4

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	9,440.00
2. Foreign Travel Costs	29,958.00
Total Travel Cost	**39,398.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 4

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period:** 4

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	14,850.00
2. Publication Costs	6,000.00
3. Consultant Services	79,750.00
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	190,649.00
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**291,249.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**554,360.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . EcoHealth Alliance Indirect Cost	32.74	363,710.00	119,079.00
2 . University of North Carolina at Chapel Hill Indirect Cost	55.5	50,000.00	27,750.00
3 . IPB and WIV Subawards (2) Indirect Costs	8.0	140,649.00	11,252.00
		Total Indirect Costs	**158,081.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**712,441.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	712,441.00

L. Budget Justification*	File Name: EHA_NIAID_COV_BUDGET_JUSTIFICATION_FINAL.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 5

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 0770900660000

Budget Type*: ● Project ○ Subaward/Consortium

Enter name of Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period: 5**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	PETER		DASZAK		PD/PI							(b) (4), (b) (6)
2 .	Dr.	Kevin	J	Olival		Co-Investigator							
3 .	Dr.	Leilani	V	Francisco		Co-Investigator							
4 .	Dr.	Noam		Ross		Co-Investigator							
5 .	Ms.	Hongying		Li		Research Scientist							
6 .	Dr.	Alice		Latinne		Research Scientist							
7 .	Ms.	Emily	A	Hagan		Research Scientist							
8 .	Dr.	Aleksei	A	Chmura		Research Scientist							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person **223,713.00**

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**
						Total Salary, Wages and Fringe Benefits (A+B)	**223,713.00**

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 5

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ❍ Subaward/Consortium
Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period: 5**

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	**Funds Requested ($)***
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	9,440.00
2. Foreign Travel Costs	29,958.00
Total Travel Cost	**39,398.00**

E. Participant/Trainee Support Costs		**Funds Requested ($)***
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 5

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: ECOHEALTH ALLIANCE, INC.

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period:** 5

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	14,850.00
2. Publication Costs	6,000.00
3. Consultant Services	79,750.00
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	190,649.00
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**291,249.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**554,360.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . EcoHealth Alliance Indirect Cost	32.74	363,710.00	119,079.00
2 . University of North Carolina at Chapel Hill Indirect Cost	55.5	50,000.00	27,750.00
3 . IPB and WIV Subawards (2) Indirect Costs	8.0	140,649.00	11,252.00
		Total Indirect Costs	**158,081.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**712,441.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	712,441.00

L. Budget Justification*	File Name: EHA_NIAID_COV_BUDGET_JUSTIFICATION_FINAL.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

ECOHEALTH ALLIANCE BUDGET JUSTIFICATION

A. Senior/Key personnel:

The PD/PI, Dr. Peter Daszak, will commit (b) (4), (b) (6) per year in each year of this budget. He will be primarily responsible for overseeing the project, general management, communication and collaboration with subaward partners, as well as contributing to data analysis and manuscript writing.

Co-Investigator, Dr. Kevin Olival, will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Olival will lead the design and implementation of the bat sampling fieldwork (Aim 1); facilitate overall project management; and train and oversee field teams. Dr. Olival will also oversee modeling and analyses under Aims 1 & 3, participate in regular conference calls, and help write manuscripts and reports.

Co-Investigator, Dr. Leilani Francisco, will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Francisco will lead the implementation of the community and clinic-based surveillance (Aim 2), including adherence to study design, sampling methodology, and ethics in human subjects research; data collection instrument development; data management, cleaning, and analysis; and, findings dissemination.

Co-Investigator, Dr. Noam Ross, will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Ross will lead modeling work and assist in with data analyses and manuscript writing. He will also advise on data management, statistical approaches, and computational work.

B. Other Personnel

Research Scientist, Ms. Hongying Li, will commit (b) (4), (b) (6) per year in each year of this budget. Ms. Li will coordinate the field and laboratory activities in China, maintaining the financial administration, results reporting, and data management, as well as work closely with Dr. Lili Ren at the Institute of Pathogen Biology to refine protocols, oversee field data collection, and perform data analysis for human study.

Research Scientist, Dr. Alice Latinne, will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Latinne will assist in with phylogenetic and phylogeographic analyses and manuscript writing. She will also advise on data management and field activities.

Research Scientist, Dr. Aleksei Chmura, will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Chmura will coordinate regular calls, reports, maintain EcoHealth Alliance and subaward budgets and both project and financial reporting, draft subcontracts, and set-up project databases, advise field activities, assist with statistical analysis, and manuscript writing.

Research Scientist, Ms. Emily Hagan, will commit (b) (4), (b) (6) per year in each year of this budget. Ms. Hagan will assist with the development of human data collection instruments, testing, and implementation; advise on data storage, data analyses, and manuscript writing. She will also provide training for field teams conducting human subjects research.

Fringe benefits for Year 1 are calculated for EcoHealth Alliance's federally approved rate of 31.5% of base salary and is included in all subsequent years.

C. Equipment

No Equipment costing more than $5,000 will be purchased

D. Travel

Domestic Travel

$9,440 is requested annually for Years 1 through 5 for the PD/PI, 3 Co-Investigators, and 1 Research Scientist to attend and present on research results at the annual American Society for Tropical Medicine and Hygiene and the American Public Health Association meetings. 2 night and 3 day travel to Washington, DC is

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calculated as follows: $205 for hotels ($251 x 2 nights x 5 people x 2 trips = $5,020); $76 for meals and incidentals ($76 x 2.5 days x 5 people x 2 trips = $1,900); and $252 for round-trip train ($252 x 5 x 2 = $2,520).

International Travel
$11,998 is requested annually in Years 1 to 5. This will support round-trip flights from New York to Beijing and Wuhan for the field annual meetings for 3 Senior/Key Personnel and 1 for the PD/PI (Daszak) at $1,055 each. Five nights and six days of hotels, meals, and incidentals for 3 Senior/Key Personal and 1 PD/PI are calculated at $1,944.50 per year: hotels at $258 per night (x 5 nights and 4 personnel = $5,160) and meals and incidentals at $119 per day (x 5.5 days and 4 personnel = $2,856).

$17,960 is requested annually in Years 1 to 5 for EHA Research Scientists (Ms. Li and Ms. Hagan) who will travel to China for two field training and supervising visits per year for duration of 21 days each. Support for this request, annually, is $17,960 and is calculated as follows: 2 round trip flights = $4,400; hotel $258 x 20 nights x twice a year = $4,732; meals and incidentals at $119 per day x 20.5 days x twice a year = $3,570

E. Participant/Trainee Support Costs
There are no participant/trainee support costs.

F. Other Direct Costs
Materials & Supplies
We request $7,000 in Year 1 for sample collection materials to be shipped to China including bat catching equipment ($1,000); PPE ($2,000); and 1 liquid nitrogen dry shipper ($1,000) for Wuhan Institute of Virology in China to be used by Dr. Guanjian Zhu for field work.

In Years 2 through 5, field and human sampling will be completely underway; we request support for PPE ($2,000) and other sample collection materials ($2,000) in each of these years.

Publication Costs
We request $6,000 per year for only Years 2 to 5 for publication fees required to publish research findings in peer-reviewed journals such as *Nature*, *Public Library of Science*, and other journals

Subawards/Consortium/Contractual Costs
We are requesting consortium/contractual support for our three partners: Wuhan Institute of Virology (WIV), Institute of Pathogen Biology (IPB), and University of North Carolina (UNC). We have fully detailed these direct and indirect costs in their respective sub-award budgets.

Computers, Software, Reference Materials and Dataset Acquisition
We request support of $6,000 to permit two Research Scientists to purchase 1 laptop each (2 x $3,000 including insurance and software). We also request $1,000 per year in each year to cover software and reference materials, and an additional $1,000 per year in each year for acquisition of datasets.

Shipping
We will be shipping the materials and supplies detailed above to our subaward institutions in China (IPB and WIV). Shipping box and all taxes are estimated at $1,667 per shipment. We estimate 3 shipments of supplies and materials will be sent every year through the duration of this project.

Consultants
Dr. Linfa Wang, Co-Investigator/Consultant We request (b) (4), (b) (6) per year for each year of the project for a consultancy for Dr. Linfa Wang who will focus on PCR development, serological testing strategy and virus characterization, and will also participate in regular meetings with collaborators. Dr. Wang has more than 20 years of research experience in designing and applying novel testing platforms to discover zoonotic pathogens.

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Dr. Guangjian Zhu, Co-Investigator/Consultant In total, we request $368,000 for the consultancy of Dr. Guangjian Zhu from Year 1 to Year 5 of the project including: $204,390 for field personnel, $124,750 for field travel; $33,548 for field supplies and materials, and $5,255 for other costs. Detailed expenses are calculated as the follows:

Personnel ($204,390)
Dr. Guangjian Zhu Co-Investigator/Consultant will oversee all field sampling activities in China by coordinating with local partners and stakeholders to lead the specimen collection and bats population monitoring at selected surveillance sites. Dr. Zhu is a zoologist and ecologist specializing in bats surveillance in southern and western China and has been leading EcoHealth Alliance's field surveillance work in China for more than 15 years. We request (b) (4), (b) (6) annual stipend for Zhu, who will commit (b) (4), (b) (6) per year to this project in years 1-3 and increase time to (b) (4), (b) (6) per year for in years 4-5, since he will allocate more time to collaborating on peer-reviewed publications in the last two years of the project.

Research Assistant (TBD) will assist the Co-PI and Field Coordinator (Zhu) for project data management, reporting, and administration. We request (b) (4), (b) (6) p.a. salary for this Research Assistant who will dedicate 2 months p.a. on this project from Years 1-5.

Field Assistants (2 in each province, TBD) will assist all field surveillance activities including specimen collection and data entry and management. The assistants will commit a total of 50 days per year to this project from years 1-5. We request (b) (4), (b) (6) per year to support each assistant for the field surveillance work.

Travel ($124,750)
Inter-Province Travel. We request 1) $1,200 per year for all five years of this project to cover 3-per-year round-trip flights/trains each from Shanghai, to Yunnan, Guangdong, Guizhou, and Guangxi for Dr. Zhu to meet with collaborating institutions, train field teams, and ensure sample collection, storage, and shipments. Each round-trip flight is estimated at $400, in total $6,000 for 5 years; 2) $2,400 per year for all five years of this project to cover 2-per-year round-trip flights/trains for 2 field assists traveling to the field sites in Yunnan, Guangdong, Guizhou, and Guangxi for sampling work. Each round-trip flight is estimated at $400, in total $12,000 for 5 years.

Field Transportation. Field work will take place for 50 days per year for 5 years, the expenses of local transportation include 1) car rental at the rate of $79/car/day, with 1 car for 50 days, in total of $3,950 per year, and $19,750 for 5 years; 2) Gas and toll fee at the rate of $32/car/day, with 1 car for 50 days, in total of $1,600 per year, and $8,000 for 5 years.

Meal and Lodging. We request 1) $6,400 to cover the expense of meals for 4 field team members in the field for 50 days per year, at the rate of $32/person/day, totaling $32,000 in 5 years; 2) $9,400 for lodging expenses of 4 field team members in the field for 50 days at the rate of $47/person/night, totaling $247,000 in 5 years.

Supplies and Materials ($33,548)
Biological sampling supplies ($25,165) We request $25,165 to purchase supplies for biological sampling during the 5 years of the project, including 1) puritan calcium alginate swabs $8,800 (5,000 IND); 2) viral sample collection tubes $6,875 (15,000 IND); 3) heparinized glass hematocrit tubes $190 (~4,000IND); 4) mist nets for bats trapping $2,200 (~500IND); 5) cloth bags for bats trapping $2,400 (~1,000IND); 6) Viral Transport Media $4,700 (~7,000 mL).

Personal Protection Equipment ($4,336): We request 1) $3,440 for 3M N95 respirators (~1,600IND) for field work across Year 1-5; 2) $470 for eye protection glasses (~100 IND) for

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the use in field across Year 1-5; 3) $426 for nitrile gloves (~3,000IND) for sampling work for Year 1-5.

Cold Chain Maintenance ($4,047): We request $4,047 to purchase 3 liquid nitrogen dry shippers for preserve biological samples in the field before transported an ultra-low temperature freezer. The expense is calculated at the rate of $1,349 each, with 1 purchased per year from Year 1-3, totaling $4,047.

Equipment ($0)
No equipment over $5,000 will be purchased.

Other Costs ($6,399)
We request 1) a total of $1,275 for specimen transportation or delivery from the field to partners' labs from Year 1-5, at the rate of $85/delivery with 1,000 tubes, with three times per year; and 2) a total of $3,980 for rabies and tetanus vaccination 4 field team members from Year 1-5, at the rate of $199/year/person.

H. Indirect Costs

We are requesting the EcoHealth Alliance federally approved indirect cost rate of 32.74% on all applicable direct costs. Indirect is taken only on the first $25,000 for each consortium/contractual agreement in each year. As there are 3 (Wuhan Institute of Virology, Institute of Pathogen Biology, and University of North Carolina), a total of $24,555 ($8,185 x 3) is requested as indirect costs on consortium/contractual/subaward agreements. This is not included as part of direct cost calculations and is only requested for year 1. In years 2-5 no indirect will be taken on consortium/contractual agrrement subcontracts.

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - Cumulative Budget

	Totals ($)	
Section A, Senior/Key Person		1,118,565.00
Section B, Other Personnel		0.00
Total Number Other Personnel	0	
Total Salary, Wages and Fringe Benefits (A+B)		1,118,565.00
Section C, Equipment		0.00
Section D, Travel		196,990.00
1. Domestic	47,200.00	
2. Foreign	149,790.00	
Section E, Participant/Trainee Support Costs		0.00
1. Tuition/Fees/Health Insurance	0.00	
2. Stipends	0.00	
3. Travel	0.00	
4. Subsistence	0.00	
5. Other	0.00	
6. Number of Participants/Trainees	0	
Section F, Other Direct Costs		1,456,245.00
1. Materials and Supplies	80,250.00	
2. Publication Costs	24,000.00	
3. Consultant Services	398,750.00	
4. ADP/Computer Services	0.00	
5. Subawards/Consortium/Contractual Costs	953,245.00	
6. Equipment or Facility Rental/User Fees	0.00	
7. Alterations and Renovations	0.00	
8. Other 1	0.00	
9. Other 2	0.00	
10. Other 3	0.00	
Section G, Direct Costs (A thru F)		2,771,800.00
Section H, Indirect Costs		814,960.00
Section I, Total Direct and Indirect Costs (G + H)		3,586,760.00
Section J, Fee		0.00
Section K, Total Costs and Fee (I + J)		3,586,760.00

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 1

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 6081952770000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period:** 1

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Ralph	S	Baric		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Amy		Sims		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Laboratory Technician						(b) (4), (b) (6)
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 1

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period:** 1

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	
Total Travel Cost	**0.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 1

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period:** 1

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	15,960.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**15,960.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**50,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . All Direct Costs	55.5	50,000.00	27,750.00
		Total Indirect Costs	**27,750.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**77,750.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	77,750.00

L. Budget Justification*	File Name: NIAID_COV_2019_UNC_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 2

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 6081952770000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period: 2**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Ralph	S	Baric		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Amy		Sims		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Laboratory Technician						(b) (4), (b) (6)
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 2

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period:** 2

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	
Total Travel Cost	**0.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 2

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period:** 2

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	15,960.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**15,960.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**50,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . All Direct Costs	55.5	50,000.00	27,750.00
		Total Indirect Costs	**27,750.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**77,750.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	77,750.00

L. Budget Justification*	File Name: NIAID_COV_2019_UNC_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 3

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 6081952770000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period: 3**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Ralph	S	Baric		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Amy		Sims		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Laboratory Technician						(b) (4), (b) (6)
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 3

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period:** 3

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	
Total Travel Cost	**0.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 3

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period:** 3

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	15,960.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**15,960.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**50,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . All Direct Costs	55.5	50,000.00	27,750.00
		Total Indirect Costs	**27,750.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**77,750.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	77,750.00

L. Budget Justification*	File Name: NIAID_COV_2019_UNC_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 4

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 6081952770000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period: 4**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Ralph	S	Baric		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Amy		Sims		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Laboratory Technician						(b) (4), (b) (6)
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 4

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period:** 4

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	
Total Travel Cost	**0.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 4

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period:** 4

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	15,960.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**15,960.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**50,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . All Direct Costs	55.5	50,000.00	27,750.00
		Total Indirect Costs	**27,750.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**77,750.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	77,750.00

L. Budget Justification*	File Name: NIAID_COV_2019_UNC_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 5

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 6081952770000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period: 5**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Ralph	S	Baric		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Amy		Sims		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Laboratory Technician						(b) (4), (b) (6)
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 5

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period:** 5

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	
Total Travel Cost	**0.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 5

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period:** 5

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	15,960.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**15,960.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**50,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . All Direct Costs	55.5	50,000.00	27,750.00
		Total Indirect Costs	**27,750.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**77,750.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	77,750.00

L. Budget Justification*	File Name: NIAID_COV_2019_UNC_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL BUDGET JUSTIFICATION, SUBAWARD

A. Senior/Key Personnel

Ralph Baric, PhD Co-Investigator (b) (4), (b) (6) Dr. Baric is a known expert in coronavirus cross species transmission and pathogenesis and has studied this group of viruses for over 30 years. His group developed the first reverse genetic systems for epidemic and zoonotic SARS-like coronaviruses and they have studied the ability of these viruses to replicate efficiently in various primary human airway epithelial cell cultures as well as other key primary cell types. His group has also studied the sensitivity of these viruses to be controlled by existing vaccines and therapeutics both in vitro and in vivo. Dr. Baric will lead the studies at the University of North Carolina at Chapel Hill. He will design research strategies, interpret findings and review research outcomes with Dr. Sims and Mr. Yount. At a regular basis, Dr. Baric will report the results of the teams research to Dr. Daszak and Dr. Shi and together, they will use this information to identify additional research priorities and design downstream studies. Drs. Daszak, Shi and Baric have published together in the past and participated on research project applications. Dr. Baric recently spent several days in Wuhan, China, where he discussed research strategies and collaborations with Dr. Daszak and Dr. Shi. He will work closely with Dr. Sims and Mr. Yount to prepare timely reports, share research and discuss future research directions with the group.

Amy Sims, PhD Co-Investigator (b) (4), (b) (6) Dr. Sims has over 22 years of research studying coronavirus molecular biology, replication and pathogenesis. She has published over 50 papers including seminal papers on characterizing host response patterns of primary human lung airway epithelial cells and other cell types after infection with SARS-CoV, MERS-CoV, influenza and various SARS-like bat coronaviruses. She is not only well versed in the preparation, cultivation and maintenance of primary human lung cells but also proficient at studying virus infection outcomes, in the presence and absence of antiviral therapeutics. In consultation with Dr. Baric, Dr. Sims will design experiments, perform infections and characterize epidemic and bat SARS-like coronavirus replication in human cells. She will compile data and share these results with the research team. Dr. Sims will also interface and work closely with Mr. Yount, who will assist in these studies, including infections, cell preparations and characterizing virus growth efficiency in these cultures. Dr. Sims has over 15 years of experience working in a BSL3 laboratory and oversees the management of these facilities. She has select agent clearance.

B. Other Personnel

Mr. Boyd Yount, Laboratory Technician (b) (4), (b) (6). Mr. Yount has published over 50 papers on coronaviruses and developed the first reverse genetic platforms for SARS-CoV, MERS-CoV and various SARS-like bat coronaviruses. He will work closely with Drs. Barics, Shi and Daszak to design and recover select bat SARS-like coronaviruses for downstream studies in the Baric and Shi laboratories, including characterizing virus phenotypes in primary cells as well as cells expressing various human, civet and bat ACE2 receptors. He will prepare virus stocks, Mr. Yount will work closely with Drs. Baric and Sims to design and implement experiments in the BSL3 laboratory, prepare reports and research outcomes during the course of the program. Mr. Yount has over 15 years of experience in a BSL3 setting and is well versed in all the techniques used in this proposal. He has select agent clearance.

Fringe Benefits. Benefits are for faculty, staff and postdoctoral research associates are calculated as follows:
Faculty and Staff – 24.519% Social Security and retirement and $6,104 for health insurance,
Supplies and Reagents. $15,960

C. Equipment

No equipment over $5,000 will be purchased.

D. Travel

No travel will be requested for this subaward. Travel to EcoHealth Alliance and other collaborators will be covered from other UNC funding.

Obtained via FOIA by Judicial Watch, Inc.

F. Other Direct Costs

Materials and Supplies. A variety of culture media and serum ($3,000), primary cell procurement ($2500), recombinant enzymes ($1500) and antibodies ($1500), synthetic DNAs ($2,500) and an assortment of miscellaneous supplies (e.g., gloves, chemicals, plasticware, etc.)($2460) are needed during the course of the program to recover recombinant viruses and maintain cells in culture, perform virus growth curves and identify virus tropisms by immunohistochemistry. In addition, personnel protective equipment (PPE), portal breathing apparati (PAPR), globes and protective clothing are used in the BSL3 setting ($2500).

H. Indirect Costs

In an agreement with DHHS dated 11/23/2016 the indirect cost rate for The University of North Carolina is 55.5% of MTDC, excluding equipment and tuition.

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - Cumulative Budget

	Totals ($)	
Section A, Senior/Key Person		104,095.00
Section B, Other Personnel		66,105.00
Total Number Other Personnel	5	
Total Salary, Wages and Fringe Benefits (A+B)		170,200.00
Section C, Equipment		0.00
Section D, Travel		0.00
1. Domestic	0.00	
2. Foreign	0.00	
Section E, Participant/Trainee Support Costs		0.00
1. Tuition/Fees/Health Insurance	0.00	
2. Stipends	0.00	
3. Travel	0.00	
4. Subsistence	0.00	
5. Other	0.00	
6. Number of Participants/Trainees	0	
Section F, Other Direct Costs		79,800.00
1. Materials and Supplies	79,800.00	
2. Publication Costs	0.00	
3. Consultant Services	0.00	
4. ADP/Computer Services	0.00	
5. Subawards/Consortium/Contractual Costs	0.00	
6. Equipment or Facility Rental/User Fees	0.00	
7. Alterations and Renovations	0.00	
8. Other 1	0.00	
9. Other 2	0.00	
10. Other 3	0.00	
Section G, Direct Costs (A thru F)		250,000.00
Section H, Indirect Costs		138,750.00
Section I, Total Direct and Indirect Costs (G + H)		388,750.00
Section J, Fee		0.00
Section K, Total Costs and Fee (I + J)		388,750.00

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 1

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 5290274740000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Wuhan Institute of Virology

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period:** 1

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Zhengli		Shi		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Peng		Zhou		Co-Investigator							
3 .	Dr.	Ben		Hu		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person **17,567.00**

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**
						Total Salary, Wages and Fringe Benefits (A+B)	**17,567.00**

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 1

ORGANIZATIONAL DUNS*: 5290274740000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Wuhan Institute of Virology

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period: 1**

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	**Funds Requested ($)***
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	4,314.00
Total Travel Cost	**4,314.00**

E. Participant/Trainee Support Costs		**Funds Requested ($)***
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 1

ORGANIZATIONAL DUNS*: 5290274740000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Wuhan Institute of Virology

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period:** 1

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	48,668.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**48,668.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**70,649.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Direct Costs	8.0	70,648.00	5,652.00
		Total Indirect Costs	**5,652.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**76,301.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	76,301.00

L. Budget Justification*	File Name: NIAID_COV_2019_WIV_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 2

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 5290274740000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: Wuhan Institute of Virology

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period: 2**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Zhengli		Shi		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Peng		Zhou		Co-Investigator							
3 .	Dr.	Ben		Hu		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person **17,567.00**

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**
						Total Salary, Wages and Fringe Benefits (A+B)	**17,567.00**

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 2

ORGANIZATIONAL DUNS*: 5290274740000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Wuhan Institute of Virology

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period:** 2

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	4,314.00
Total Travel Cost	**4,314.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 2

ORGANIZATIONAL DUNS*: 5290274740000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Wuhan Institute of Virology

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period:** 2

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	48,668.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**48,668.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**70,649.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Direct Costs	8.0	70,648.00	5,652.00
		Total Indirect Costs	**5,652.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**76,301.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	76,301.00

L. Budget Justification*	File Name: NIAID_COV_2019_WIV_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 3

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 5290274740000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: Wuhan Institute of Virology

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period: 3**

A. Senior/Key Person

Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 . Dr.	Zhengli		Shi		Co-Investigator							(b) (4), (b) (6)
2 . Dr.	Peng		Zhou		Co-Investigator							
3 . Dr.	Ben		Hu		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person **17,567.00**

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**
						Total Salary, Wages and Fringe Benefits (A+B)	**17,567.00**

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 3

ORGANIZATIONAL DUNS*: 5290274740000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Wuhan Institute of Virology

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period:** 3

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	4,314.00
Total Travel Cost	**4,314.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 3

ORGANIZATIONAL DUNS*: 5290274740000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Wuhan Institute of Virology

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period:** 3

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	48,668.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**48,668.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**70,649.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Direct Costs	8.0	70,648.00	5,652.00
		Total Indirect Costs	**5,652.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**76,301.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	76,301.00

L. Budget Justification*	File Name: NIAID_COV_2019_WIV_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 4

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 5290274740000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: Wuhan Institute of Virology

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period: 4**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Zhengli		Shi		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Peng		Zhou		Co-Investigator							
3 .	Dr.	Ben		Hu		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person **17,567.00**

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**
						Total Salary, Wages and Fringe Benefits (A+B)	**17,567.00**

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 4

ORGANIZATIONAL DUNS*: 5290274740000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Wuhan Institute of Virology

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period:** 4

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	4,314.00
Total Travel Cost	**4,314.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 4

ORGANIZATIONAL DUNS*: 5290274740000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Wuhan Institute of Virology

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period:** 4

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	48,668.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**48,668.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**70,649.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Direct Costs	8.0	70,648.00	5,652.00
		Total Indirect Costs	**5,652.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**76,301.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	76,301.00

L. Budget Justification*	File Name: NIAID_COV_2019_WIV_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 5

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 5290274740000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: Wuhan Institute of Virology

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period: 5**

A. Senior/Key Person

Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 . Dr.	Zhengli		Shi		Co-Investigator							(b) (4), (b) (6)
2 . Dr.	Peng		Zhou		Co-Investigator							
3 . Dr.	Ben		Hu		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person **17,567.00**

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**
						Total Salary, Wages and Fringe Benefits (A+B)	**17,567.00**

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 5

ORGANIZATIONAL DUNS*: 5290274740000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Wuhan Institute of Virology

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period:** 5

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	4,314.00
Total Travel Cost	**4,314.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 5

ORGANIZATIONAL DUNS*: 5290274740000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Wuhan Institute of Virology

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period:** 5

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	48,668.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**48,668.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**70,649.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Direct Costs	8.0	70,648.00	5,652.00
		Total Indirect Costs	**5,652.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**76,301.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	76,301.00

L. Budget Justification*	File Name: NIAID_COV_2019_WIV_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

WUHAN INSTITUTE OF VIROLOGY BUDGET JUSTIFICATION, SUBAWARD

A. Senior/Key Personnel:

Dr. Zhengli Shi, Co-Investigator. Senior Research Scientist at Wuhan Institute of Virology (WIV) Chinese Academy of Sciences, will commit (b) (4), (b) (6) per year (b) (4), (b) (6) to this project to oversee the laboratory implementation at WIV. At a regular basis, Dr. Shi will meet with other Co-PIs to refine study protocols, report back results, and prepare publications. Dr. Shi has been working on the discovery and characterization of novel viruses from bats and other wildlife since 2004. This included the discovery that Chinese horseshoe bats are the natural reservoir of SARSr-CoVs and the likely origin of SARS-CoV. Her lab at WIV isolated SARSr-CoVs from bats sharing high homology with human SARS-CoV and demonstrated their interspecies transmission risk, largely confirming bats as the source of SARs. She will lead her team to carry out then systematic studies on the epidemiology, genetic evolution, interspecies infection mechanism and pathogenesis of a series of bat-borne CoVs on this R01 renewal proposal.

Dr. Peng Zhou, Co-Investigator. Research Scientist at Wuhan Institute of Virology (WIV) Chinese Academy of Sciences, will commit will commit (b) (4), (b) (6) per year (b) (4), (b) (6) to this project to be in charge of the diagnostics, genomics, and virus isolation work at WIV. Dr. Zhou have been working on bat virology since 2004, who will contribute his expertise in next generation diagnostic tool development for monitoring bat virus spillover, bat pathogen discovery, and bat viral immunology to this R01 renewal proposal.

Dr. Ben Hu, Co-Investigator. Research Associate and coordinator of Shi's laboratory at WIV, will commit (b) (4), (b) (6) (b) (4), (b) (6) per year (b) (4), (b) (6) to this project to directly supervisor the lab technicians, and coordinate with our collaborators in this R01 proposal for communication, reporting, and or organizing meetings. Dr. Hu has been working on discovery and characterization of viruses in small mammals in bats and rodents since 2010 at WIV, and had extensive experience managing international collaborative projects.

B. Equipment

No equipment over $5,000 will be purchased.

C. Travel

We are requesting $4,314 per year for all years for Dr. Shi to travel to the United States to meet with EcoHealth Alliance (Daszak, Francesco, Olival, Ross) and University of North Carolina at Chapel Hill (Baric, Sims) collaborators. Travel is calculated at one round trip airfare from Wuhan to New York City ($1,000), nine-night hotel in New York City ($288 per night), and 10 days per diem at $76 per day except for first and last day, which have a reduced per diem of $57.

D. Other Direct Costs

We are requesting support for laboratory experiments and related testing costs with a minimum base of 2,000 samples from 1,000 animals per year.

RNA Extractions

We will be running RNA Extractions for 1,000 bats per year (two samples per bat: rectal and blood) in each year of the project. This will cost $6,214 per year (QIAamp ViralRNA Mini Kit with Axygen Pipette Tips and Filter Tubes at $3.11 per sample).

RT-PCR

Costs for 1-Step RT-PCR assays for Coronavirus conducted on 2,000 samples per year for each year of the project total $6,358 and are detailed as follows: Superscript III one step kit ($2.31 per sample); Platinum Tag DNA Polymerase ($0.25 per sample); nuclease-free water ($0.07 per sample); and Axygen Pipette Tips and Filter Tubes ($0.54 per sample).

DNA Sequencing

In each year of the project, DNA Sequencing will be performed on 1,500 samples at a cost of $4.34 per reaction. We request a total of $6,503 per year in each year.

Obtained via FOIA by Judicial Watch, Inc.

In vitro Infection Experiment

We are requesting support for *in vitro* infection experiments using pseudoviruses carrying the spike proteins (wild type or mutants) or live viruses in cell lines of different origins, binding affinity assays between the spike proteins (wild type or mutants) and different cellular receptor molecules, and humanized mouse experiments. In each year of the project, we request $1,040 for Lipofectamine3000 transfection reagent; $3,612 for GIBCO Fetal Bovine Serum, $517 for GIBCO antibiotic antimycotic, and 2,601 for GIBCO medium that will be used in the *in vitro* infection experiments that will be used for *in vitro* infection experiment, as well as $6,000 for cell lines, in total of $8,639 per year.

Luciferase Immunoprecipitation System (LIPS) Assay

We are requesting $18,642 to support the in each year of the project to develop LIPS assay for bat CoV antibody detection, with detailed cost as follows: $9,827 for Protein A/G UltraLink Resin; $434 for Monoclonal ANTI-FLAG(R) M2 antibody; $5,636 for Renilla Luciferase Assay System; $2,168 for Merck-Millipore MSBVN1B50 MultiScreen HTS; $578 for Axygen Polypropylene PCR Tube Strips.

The Enzyme-Linked Immunosorbent Assay (ELISA)

We also request $2,312 to support the serological testing of 1,000 bat serum samples per year with ELISA plates, at the cost of $2.31 per sample.

E. Indirect Costs

We are requesting an extremely low indirect cost of 8% on all direct costs.

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - Cumulative Budget

	Totals ($)	
Section A, Senior/Key Person		88,335.00
Section B, Other Personnel		0.00
Total Number Other Personnel	0	
Total Salary, Wages and Fringe Benefits (A+B)		88,335.00
Section C, Equipment		0.00
Section D, Travel		21,570.00
1. Domestic	0.00	
2. Foreign	21,570.00	
Section E, Participant/Trainee Support Costs		0.00
1. Tuition/Fees/Health Insurance	0.00	
2. Stipends	0.00	
3. Travel	0.00	
4. Subsistence	0.00	
5. Other	0.00	
6. Number of Participants/Trainees	0	
Section F, Other Direct Costs		243,340.00
1. Materials and Supplies	243,340.00	
2. Publication Costs	0.00	
3. Consultant Services	0.00	
4. ADP/Computer Services	0.00	
5. Subawards/Consortium/Contractual Costs	0.00	
6. Equipment or Facility Rental/User Fees	0.00	
7. Alterations and Renovations	0.00	
8. Other 1	0.00	
9. Other 2	0.00	
10. Other 3	0.00	
Section G, Direct Costs (A thru F)		353,245.00
Section H, Indirect Costs		28,260.00
Section I, Total Direct and Indirect Costs (G + H)		381,505.00
Section J, Fee		0.00
Section K, Total Costs and Fee (I + J)		381,505.00

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 1

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 5281563570000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: Institute of Pathogen Biology

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period:** 1

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Lili		Ren		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Li		Guo		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	0.00

Total Salary, Wages and Fringe Benefits (A+B) (b) (4), (b) (6)

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 1

ORGANIZATIONAL DUNS*: 5281563570000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Institute of Pathogen Biology

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period: 1**

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	**Funds Requested ($)***
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	4,314.00
Total Travel Cost	**4,314.00**

E. Participant/Trainee Support Costs		**Funds Requested ($)***
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 1

ORGANIZATIONAL DUNS*: 5281563570000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Institute of Pathogen Biology

Start Date*: 06-01-2019 **End Date*:** 05-31-2020 **Budget Period:** 1

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	48,686.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**48,686.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**70,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Direct Costs	8.0	70,000.00	5,600.00
		Total Indirect Costs	**5,600.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**75,600.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	75,600.00

L. Budget Justification*	File Name: NIAID_COV_2019_IPB_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 2

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 5281563570000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: Institute of Pathogen Biology

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period: 2**

A. Senior/Key Person

Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 . Dr.	Lili		Ren		Co-Investigator							(b) (4), (b) (6)
2 . Dr.	Li		Guo		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	0.00

Total Salary, Wages and Fringe Benefits (A+B) (b) (4), (b) (6)

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 2

ORGANIZATIONAL DUNS*: 5281563570000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Institute of Pathogen Biology

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period: 2**

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	**Funds Requested ($)***
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	4,314.00
Total Travel Cost	**4,314.00**

E. Participant/Trainee Support Costs		**Funds Requested ($)***
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 2

ORGANIZATIONAL DUNS*: 5281563570000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Institute of Pathogen Biology

Start Date*: 06-01-2020 **End Date*:** 05-31-2021 **Budget Period:** 2

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	48,686.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**48,686.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**70,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Direct Costs	8.0	70,000.00	5,600.00
		Total Indirect Costs	**5,600.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**75,600.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	75,600.00

L. Budget Justification*	File Name: NIAID_COV_2019_IPB_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 3

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 5281563570000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: Institute of Pathogen Biology

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period: 3**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Lili		Ren		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Li		Guo		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	0.00

Total Salary, Wages and Fringe Benefits (A+B) (b) (4), (b) (6)

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 3

ORGANIZATIONAL DUNS*: 5281563570000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Institute of Pathogen Biology

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period:** 3

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		**Funds Requested ($)***
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		
2. Foreign Travel Costs		4,314.00
	Total Travel Cost	**4,314.00**

E. Participant/Trainee Support Costs		**Funds Requested ($)***
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 3

ORGANIZATIONAL DUNS*: 5281563570000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Institute of Pathogen Biology

Start Date*: 06-01-2021 **End Date*:** 05-31-2022 **Budget Period:** 3

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	48,686.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**48,686.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**70,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Direct Costs	8.0	70,000.00	5,600.00
		Total Indirect Costs	**5,600.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**75,600.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	75,600.00

L. Budget Justification*	File Name: NIAID_COV_2019_IPB_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 4

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 5281563570000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: Institute of Pathogen Biology

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period: 4**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Lili		Ren		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Li		Guo		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	**0.00**

Total Salary, Wages and Fringe Benefits (A+B) (b) (4), (b) (6)

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 4

ORGANIZATIONAL DUNS*: 5281563570000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Institute of Pathogen Biology

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period:** 4

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	4,314.00
Total Travel Cost	**4,314.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 4

ORGANIZATIONAL DUNS*: 5281563570000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Institute of Pathogen Biology

Start Date*: 06-01-2022 **End Date*:** 05-31-2023 **Budget Period:** 4

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	48,686.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**48,686.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**70,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Direct Costs	8.0	70,000.00	5,600.00
		Total Indirect Costs	**5,600.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**75,600.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	75,600.00

L. Budget Justification*	File Name: NIAID_COV_2019_IPB_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 5

Obtained via FOIA by Judicial Watch, Inc.

ORGANIZATIONAL DUNS*: 5281563570000

Budget Type*: ❍ Project ● Subaward/Consortium

Enter name of Organization: Institute of Pathogen Biology

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period: 5**

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Lili		Ren		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Li		Guo		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
0	**Total Number Other Personnel**					**Total Other Personnel**	0.00

Total Salary, Wages and Fringe Benefits (A+B) (b) (4), (b) (6)

RESEARCH & RELATED Budget {A-B} (Funds Requested)

Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 5

ORGANIZATIONAL DUNS*: 5281563570000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Institute of Pathogen Biology

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period:** 5

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		
2. Foreign Travel Costs		4,314.00
	Total Travel Cost	**4,314.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 5

ORGANIZATIONAL DUNS*: 5281563570000
Budget Type*: ❍ Project ● Subaward/Consortium
Organization: Institute of Pathogen Biology

Start Date*: 06-01-2023 **End Date*:** 05-31-2024 **Budget Period:** 5

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	48,686.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5. Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**48,686.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**70,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Direct Costs	8.0	70,000.00	5,600.00
		Total Indirect Costs	**5,600.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**75,600.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	75,600.00

L. Budget Justification*	File Name: NIAID_COV_2019_IPB_BUDGET_JUSTIFICATION.pdf (Only attach one file.)

RESEARCH & RELATED Budget {F-K} (Funds Requested)

Obtained via FOIA by Judicial Watch, Inc.

WUHAN INSTITUTE OF VIROLOGY BUDGET JUSTIFICATION, SUBAWARD

A. Senior/Key Personnel:

Dr. Lili Ren, PhD Co-Investigator [redacted] (b) (4), (b) (6) Dr. Ren is an expert in the pathogenesis and evolution of respiratory viruses. She will refine study protocols, coordinate research, oversee implementation of all activities, analyze data, lead regular meetings with other Co-Investigators and Other Senior/Key Personnel as well as draft papers.

Dr. Li Guo, PhD Co-Investigator and Senior Research Technician [redacted] (b) (4), (b) (6) per year to perform all laboratory work. She has been working on etiology and immunology research on respiratory viruses since 2003 and has evaluated the cross-reactivities of N among HCoVs and developed a competitive ELISA (cELISA) for detecting anti-N IgG antibodies against HCoV -229E, -OC43, -NL63, and -HKU1.

B. Other Personnel

No other Personnel will be required for this subaward. All Institute of Pathogen Biology salaries include the US benefits, so benefits are not calculated separately.

C. Equipment

No equipment over $5,000 will be purchased.

D. Travel

We are requesting $4,314 per year for all years for Dr. Ren or Dr. Guo to travel to the United States to meet with EcoHealth Alliance (Daszak, Francesco, Olival, Ross) and University of North Carolina at Chapel Hill (Baric, Sims) collaborators. Travel is calculated at one round trip airfare from Beijing to New York City ($1,000), nine-night hotel in New York City ($288 per night), and 10 days per diem at $76 per day except for first and last day, which have a reduced per diem of $57.

F. Other Direct Costs

We are requesting support for laboratory experiments and related costs with a minimum base of 1,000 samples expected per year.

RNA Extractions

We will be running 1,000 RNA Extractions per year in each year of the project. This will cost $10,450 per year for QIAamp ViralRNA Mini Kit with an additional $2,023 per year for Axygen Pipette Tips and Filter Tubes at $1.08 per sample.

1-STEP RT-PCR

Costs for 1-Step RT-PCR assays for Coronavirus conducted on 1,000 samples per year for each year of the project total $6,358 and are detailed as follows: Superscript III one step kit ($4.62 per sample); Platinum Tag DNA Polymerase ($0.51 per sample); nuclease-free water ($0.15 per sample); and Axygen Pipette Tips and Filter Tubes ($1.08 per sample).

DNA Sequencing

In each year of the project, DNA Sequencing will be performed on 3,200 samples at a cost of $2.62 per reaction. We request a total of $2,601 per year in year.

Cell Culture

We request a total of $4,913 in year one; $6,647 in year two (upon expectation of 35% increase in positive samples); and $8,671 (a 30% increase) per year for the remaining years (3-5) of the project to cover costs for cell culturing. This will require GIBCO Fetal Bovine Serum, antibiotic antimycotic, growth medium, and cell culture plates and flasks. Flask costs are estimated at $1.45 per plate/flask.

Obtained via FOIA by Judicial Watch, Inc.

Protein Expression and Purification
For protein expression and purification, we request a total of $6,590 in year 1, $6,705 in year 2, and $5,260 in each year of years 3-5. Details of protein expression and purification costs include histidine and sepharose tagged protein purification fast flow columns ($116 each), Q sepharose fast flow media ($116 each), protease inhibitor ($289 each), eStain Protein staining kits ($145 each), protein G sepharose 4 fast flow ($145 each), Q and SP sepharose fast flow ($723 each), and bacterial culture plates ($116 each). It is expected that more samples will be processed in year 1, so costs are estimated to reduce by 20% in years 2-5

Serological Tests
We request support for serology assays. None will be conducted in year one until we have samples. Costs are estimated for years 2-5 with $9,220 in year 2 and due to additional IgM and IgG secondary antibodies costs and increase in estimate to $9,436 in years 3-5. Cost estimates include IgM and IgG secondary antibodies at $72.25; mouse and rabbit IgG antibodies at $434; mouse and rabbit IgM antibodies at $434; and ELISA plates at $2.90 each.

Lab Supplies
Funding is requested to support laboratory supplies including three (3) -80˚C freezers ($4,340 each); reagents including agarose, sodium chloride, yeast extract, phosphate buffer, Tris and other biochemical reagents (average of $307 per year); centrifuge tube costs are estimated to increase in years 2-5 (average of $665 per year); disposable personnel protective equipment (PPE), portal breathing apparati (PAPR), globes and protective clothing to be used in BSL settings are estimated at $723 per year; cell lines will be required in years 1 and 2 ($867 each); and *in vitro* culture (lipofectamine2000) will be required at cost of $434 in year 1 and $2,168 per year in years 2-5.

H. Indirect Costs
We are requesting an extremely low indirect cost of 8% on all direct costs.

Obtained via FOIA by Judicial Watch, Inc.

RESEARCH & RELATED BUDGET - Cumulative Budget

	Totals ($)	
Section A, Senior/Key Person		85,000.00
Section B, Other Personnel		0.00
Total Number Other Personnel	0	
Total Salary, Wages and Fringe Benefits (A+B)		85,000.00
Section C, Equipment		0.00
Section D, Travel		21,570.00
1. Domestic	0.00	
2. Foreign	21,570.00	
Section E, Participant/Trainee Support Costs		0.00
1. Tuition/Fees/Health Insurance	0.00	
2. Stipends	0.00	
3. Travel	0.00	
4. Subsistence	0.00	
5. Other	0.00	
6. Number of Participants/Trainees	0	
Section F, Other Direct Costs		243,430.00
1. Materials and Supplies	243,430.00	
2. Publication Costs	0.00	
3. Consultant Services	0.00	
4. ADP/Computer Services	0.00	
5. Subawards/Consortium/Contractual Costs	0.00	
6. Equipment or Facility Rental/User Fees	0.00	
7. Alterations and Renovations	0.00	
8. Other 1	0.00	
9. Other 2	0.00	
10. Other 3	0.00	
Section G, Direct Costs (A thru F)		350,000.00
Section H, Indirect Costs		28,000.00
Section I, Total Direct and Indirect Costs (G + H)		378,000.00
Section J, Fee		0.00
Section K, Total Costs and Fee (I + J)		378,000.00

Obtained via FOIA by Judicial Watch, Inc.

Total Direct Costs less Consortium F&A

NIH policy (NOT-OD-05-004) allows applicants to exclude consortium/contractual F&A costs when determining if an application falls at or beneath any applicable direct cost limit. When a direct cost limit is specified in an FOA, the following table can be used to determine if your application falls within that limit.

Category	Budget Period 1	Budget Period 2	Budget Period 3	Budget Period 4	Budget Period 5	TOTALS
Total Direct Costs less Consortium F&A	515,358	515,358	515,358	515,358	515,358	**2,576,790**

Obtained via FOIA by Judicial Watch, Inc.

PHS 398 Cover Page Supplement

OMB Number: 0925-0001

Expiration Date: 03/31/2020

1. Vertebrate Animals Section

Are vertebrate animals euthanized? ○ Yes ● No

If "Yes" to euthanasia

Is the method consistent with American Veterinary Medical Association (AVMA) guidelines?

○ Yes ○ No

If "No" to AVMA guidelines, describe method and provide scientific justification

2. *Program Income Section

*Is program income anticipated during the periods for which the grant support is requested?

○ Yes ● No

If you checked "yes" above (indicating that program income is anticipated), then use the format below to reflect the amount and source(s). Otherwise, leave this section blank.

*Budget Period	*Anticipated Amount ($)	*Source(s)

Tracking Number: GRANT12743073 Funding Opportunity Number: PA-18-484 . Received Date: 2018-11-05T16:31:22.000-05:00

Obtained via FOIA by Judicial Watch, Inc.

PHS 398 Cover Page Supplement

3. Human Embryonic Stem Cells Section

*Does the proposed project involve human embryonic stem cells? ○ Yes ● No

If the proposed project involves human embryonic stem cells, list below the registration number of the specific cell line(s) from the following list: http://grants.nih.gov/stem_cells/registry/current.htm. Or, if a specific stem cell line cannot be referenced at this time, check the box indicating that one from the registry will be used:

❑ Specific stem cell line cannot be referenced at this time. One from the registry will be used.

Cell Line(s) (Example: 0004):

4. Inventions and Patents Section (Renewal applications)

*Inventions and Patents: ○ Yes ● No

If the answer is "Yes" then please answer the following:

*Previously Reported: ○ Yes ○ No

5. Change of Investigator/Change of Institution Section

❑ Change of Project Director/Principal Investigator

Name of former Project Director/Principal Investigator

Prefix:

*First Name:

Middle Name:

*Last Name:

Suffix:

❑ Change of Grantee Institution

*Name of former institution:

Obtained via FOIA by Judicial Watch, Inc.

PHS 398 Research Plan

OMB Number: 0925-0001
Expiration Date: 03/31/2020

Introduction	
1. Introduction to Application (for Resubmission and Revision applications)	
Research Plan Section	
2. Specific Aims	NIAID_COV_2019_SPECIFIC_AIMS_final.pdf
3. Research Strategy*	NIAID_COV_2019_RESEARCH_STRATEGY_final.pdf
4. Progress Report Publication List	NIAID_COV_2019_PROGRESS_REPORT_PUBLICATION_LIST.pdf
Other Research Plan Section	
5. Vertebrate Animals	NIAID_COV_2019_VERTEBRATE_ANIMALS_Final.pdf
6. Select Agent Research	NIAID_COV_2019_SELECT_AGENTS_Final.pdf
7. Multiple PD/PI Leadership Plan	
8. Consortium/Contractual Arrangements	NIAID_COV_2019_CONSORTIUM_CONTRACTUAL_Final.pdf
9. Letters of Support	NIAID_COV_2019_LOS_Final.pdf
10. Resource Sharing Plan(s)	NIAID_COV_2019_RESOURCE_SHARING_PLAN_Final.pdf
11. Authentication of Key Biological and/or Chemical Resources	NIAID_COV_2019_AUTHENTICATION_OF_KEY_BIO_RSCS.pdf
Appendix	
12. Appendix	

Obtained via FOIA by Judicial Watch, Inc.

SPECIFIC AIMS

Zoonotic coronaviruses are a significant threat to global health, as demonstrated with the emergence of Severe Acute Respiratory Syndrome coronavirus (SARS-CoV) in 2002, and the continuing spread of Middle East Respiratory Syndrome (MERS-CoV). The wildlife reservoirs of SARS-CoV were identified by our group as bat species, and since then we have sequenced dozens of novel SARS-related CoV (SARSr-CoV) strains. Our previous R01 work demonstrates that bats in southern China harbor an extraordinary diversity of SARSr-CoVs, some of which are able to use human ACE2 to enter into human cells, can infect humanized mouse models to cause SARS-like illness, and evade available therapies or vaccines. We found that the bat hosts of SARSr-CoVs appear to no longer be traded in wildlife markets, and that people living close to bat habitats are the primary risk groups for spillover. At one of these sites, we found diverse SARSr-CoVs containing every genetic element of the wild-type SARS-CoV genome, and serological evidence of human exposure among people living nearby. Thus, there is significant potential for future spillover of SARSr-CoVs, and of public health impacts. *Yet salient questions remain: Are there specific bat communities and sites that harbor CoV strains with higher risk for bat-to-human spillover? Which human behaviors drive risk of bat SARSr-CoV exposure that could lead to infection? Does human exposure to these viruses cause SARS-like or other illness? Can we characterize viral strain diversity, bat traits and human behaviors to assess risk of potential future CoV spillover?* **The proposed work in this renewal R01 builds on these findings** to address these issues by conducting: **1)** focused sampling of bats in southern China to **identify viral strains with high predicted risk of spillover**; **2)** community-based, and clinic-based syndromic, sampling of people to **identify spillover, and assess behavioral risk factors and evidence of illness**; and **3)** conduct *in vitro* and *in vivo* viral characterization and analyze epidemiological data **to identify hotspots of future CoV spillover risk**. This work will follow 3 specific aims:

Aim 1: Characterize the diversity and distribution of high spillover-risk SARSr-CoVs in bats in southern China. We will conduct targeted bat sampling at sites where we predict that undiscovered high risk SARSr-CoV strains exist. Bat sampling will be targeted geographically and by host species to test predictions about evolutionary diversity of SARSr-CoV. We will analyze RdRp and S protein sequences to test their capacity for spillover to people in Aim 3.

Aim 2: Community- and clinic-based surveillance to capture SARSr-CoV spillover, routes of exposure and potential public health consequences. We will conduct focused, targeted human surveys and sampling to identify key risk factors for SARSr-CoV spillover and evidence of illness. To maximize our opportunity of capturing human exposure to bat CoVs, we will conduct community-based surveillance in regions with high SARSr-CoV prevalence and diversity, and individuals having contact with bats. We will assess bat-CoV seropositive status against a small number of questions about human-wildlife contact and exposure. We will conduct clinic-based syndromic surveillance close to these sites to identify patients presenting with influenza-like illness and severe acute respiratory illness, assess their exposure to bats via a questionnaire, and test samples for PCR- and serological evidence of SARSr-CoV infection. We will conduct follow-up sampling to capture patients who had not yet seroconverted at the time of clinic visit.

Aim 3: *In vitro* and *in vivo* characterization of SARSr-CoV spillover risk, coupled with spatial and phylogenetic analyses to identify the regions and viruses of public health concern. We will characterize the propensity of novel SARSr-CoVs to infect people *in vitro* using primary human airway epithelial cells and *in vivo* using the transgenic hACE2 mouse model. We will use mAb and vaccine treatments to test our hypothesis that SARSr-CoVs with 10-25% divergence in S protein sequences from SARS-CoV are likely able to infect human cells, and to evade mAb therapeutics and vaccines. We will then map the geographic distribution of their bat hosts and other ecological risk factors to identify the key 'hotspots' of risk for future spillover.

Overall, our SARSr-CoV program serves as a model platform to integrate virologic, molecular and ecologic factors contributing to CoV emergence while informing high impact strategies to intervene and prevent future pandemics. This includes providing critical reagents, therapeutic interventions and recombinant viruses for future SARSr-CoV pandemic and public health preparedness.

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1. RESEARCH STRATEGY

A. Significance:

Severe Acute Respiratory Syndrome coronavirus (SARS-CoV) emerged in China threatening public health and global economies (*1, 2*). Like most other emerging pathogens (*3*), it originated in animal reservoir hosts, initially thought to be carnivores (*4*), and later shown by our group to be bats (*5*). Bats harbor a high diversity of β-coronaviruses, including those related to Middle Eastern Respiratory Syndrome coronavirus (MERS-CoV) (*6-9*) and the newly emerged Swine Acute Diarrhea Syndrome coronavirus (SADS-CoV) (*10*), and may be the progenitor hosts of all *Coronaviridae* (*5, 11-15*). SARS-CoV uses the angiotensin-converting enzyme 2 (ACE2) receptor to gain entry to human cells (*16*). In 2012, we isolated and characterized two bat SARS-related coronaviruses (SARSr-CoVs) in China that use the ACE2 receptor and are closely related to SARS-CoV (*17*). Since then, under an R01 awarded in 2014, we have discovered >50 bat SARSr-CoVs in southern China. Some of these strains can bind to and infect human cells, cause SARS-like clinical signs in a humanized mouse model, and evade therapeutic and vaccine candidates against SARS-CoV (*18*). The *Rhinolophus* spp. bat hosts of these viruses are abundant across southern China, where hunting and consumption of wildlife is common and human population growth high, and where we have now identified serological evidence of exposure to SARSr-CoVs and other bat CoVs (*19*). Thus, there is significant potential for future spillover of SARSr-CoVs, and of their subsequent spread. *Yet salient questions remain: Are there specific bat communities and sites that harbor CoV strains with higher risk for bat-to-human spillover? Which human behaviors drive risk of bat SARSr-CoV exposure that could lead to infection? Does human exposure to these viruses cause SARS-like or other illness? Can we characterize viral strain diversity, bat traits and human behaviors to assess risk of potential future CoV spillover?* **This R01 renewal** proposal aims to address these critical issues by conducting: **1)** focused sampling of bats in southern China to **identify viral strains with high predicted risk of spillover**; **2)** community-based, and clinic-based syndromic, sampling of people to **identify spillover, and assess behavioral risk factors and evidence of illness**; and **3)** conduct *in vitro* and *in vivo* viral characterization and analyze epidemiological data **to identify hotspots of future CoV spillover risk**.

B. Progress report: R01 AI110964, Daszak PI, Project Period: 06/01/2014 – 05/31/2019

The aims of our previous R01 were to: 1) Assess bat SARSr-CoV spillover potential at high risk human-wildlife interfaces, e.g. the wildlife trade, as reported for the 2003 outbreak (*4, 20*); 2) Analyze how viral diversity and phylogeny relates to host range and risk of emergence; and 3) Use binding assays, cell culture and mouse models to test the propensity of different SARSr-CoVs to infect humans. We made significant discoveries leading to **18 published peer-reviewed papers (*18, 19, 21-33*), including two papers in *Nature* (*10, 34*), and a review in *Cell* (*35*)** (see Progress Report Publication List). These findings include:

Diversity and distribution of bat β- and SARSr-CoVs in Southern China.

We sampled and PCR-screened >16,000 individual bats from 6 families (16 genera) in southern China, finding 9 species positive (5,730 individuals screened) for SARSr-CoVs **(Table 1, Fig. 1)**. We identified 178 novel β-CoVs, of which 172 were novel (52 novel SARSr-CoVs). This includes members of a new β-CoV clade, "lineage E" (*26*), and diverse HKU3-related CoVs (179 sequences) within a 'sister' clade to the SARS-CoV lineage.

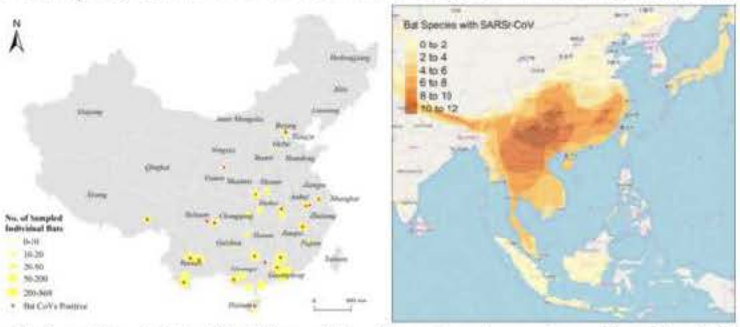


Fig. 1 (left): Bat sampling at 47 sites in China under our previous R01. Yellow = sampling effort, red = CoV +ve bats. **Fig. 2 (right)**: Map of bat species found positive for SARSr-CoVs in our previous R01, highlighting S. China (particularly Yunnan Province) as a center of diversity for SARSr-CoV reservoir host species.

We found 6.7% mean PCR prevalence of SARSr-CoVs across bat hosts, with a small number of *Rhinolophus* spp. horseshoe bats having significantly higher PCR prevalence than other species sampled **(Table 1)**. These bats are widely distributed, diverse, abundant, and roost and feed close to people and livestock, suggesting high potential for future SARSr-CoVs spillover. Distribution data for SARSr-CoV bat hosts suggest viral strain diversity is likely highest in southern China, particularly Yunnan Province **(Fig. 2)**.

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Table 1: Species found PCR-positive for SARSr-CoVs in our R01, with sample sizes and prevalence estimates.

Bat Species	Individuals tested	# positive	SARSr-CoV mean prev.	SARSr-CoV prev. range
Rhinolophus sinicus	1,328	113	8.5%	7.1 – 10.1%
R. macrotis	70	3	4.3%	0.9 - 12%
R. ferrumequinum	406	12	3.0%	1.5 – 5.1%
R. spp.	331	10	3.0%	1.5 – 5.5%
R. affinis	792	7	0.9%	0.4 – 1.8%
R. pusillus	1,023	8	0.8%	0.3 – 1.5%
Aselliscus stoliczkanus	269	2	0.7%	0.1 – 2.7%
Hipposideros pratti	323	2	0.6%	0.1 – 2.2%
H. armiger	1,188	1	0.1%	0.0 – 0.5%

We identified one cave system (the "Jinning Cave") in Yunnan Province that harbors *Rhinolophus* spp. bats with diverse SARSr-CoVs, including some with S proteins able to use human ACE2 as entry receptors. Bats in this cave carried SARSr-CoVs with **all unique genetic elements of the SARS-CoV outbreak virus**, suggesting that this site may be a potential public health risk (*29*).

We used a novel phylogeographic analysis, Maximum Clade Credibility (MCC) tree, to reconstruct the geographic areas of evolutionary origin for β-CoVs that we sequenced. Results suggest that: 1) Guangdong Province is the ancestral center of diversity of β-CoVs (data not shown); 2) Guizhou is the likely origin of the HKU3-related clade (lineage 1); and 3) Guangdong and Guangxi are the likely ancestral origins of the SARS-CoV outbreak sequences (lineage 2) **(Fig. 3)**. Despite our intensive sampling at some sites, around half of the 20 *Rhinolophus* spp. we identified were captured at sample sizes below the minimum required to detect SARSr-CoVs at prevalences we found (n=110, power 80%), and 5 others were SARSr-CoV negative in our study. To estimate sampling gaps, we used a viral 'mark-recapture' approach we previously published (*36, 37*). Results suggest we are approaching saturation of CoV strain discovery at some sites, whereas other sites contain rich pools of SARSr-CoVs that remain undiscovered **(Fig. 4)**. **In the current proposal,** we have used these analyses to estimate geographic and species-specific sampling targets **to more effectively identify new strains and CoV lineages needed to support experimental infection studies and risk assessment.**

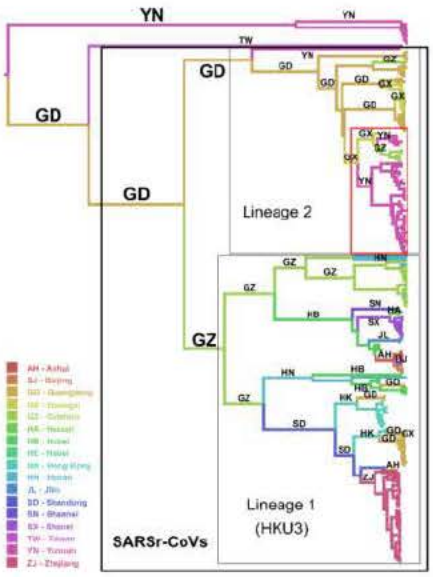


Fig.3 (left): MCC phylogeny of lineage B β-CoVs, including SARSr-CoVs (black box). Lineage 1 includes HKU3-related CoVs, lineage 2 includes SARS-CoV outbreak strains and close relatives (red box). Branches colored according to province of inferred ancestral origin (Guangdong GD, Yunnan YN, Guizhou, GZ).

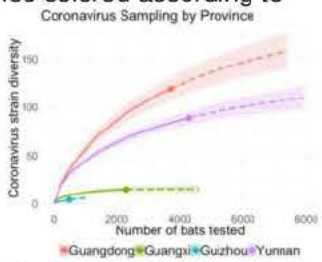


Fig. 4 (right): Estimates of SARSr-CoV strain diversity in the bats we sampled (strain defined as >10% sequence divergence in RdRp gene). GD and YN harbor highest CoV diversity, but discovery has not yet saturated. We estimate proposed additional sampling of 5,000 bats will identify >80% of remaining β-CoV strains in bat hosts from these regions.

<u>In vitro & in vivo *characterization of SARSr-CoV potential for human infection*</u>

We conducted *in vitro* and *in vivo* experiments to characterize the pathogenic potential of novel SARSr-CoVs. We isolated three SARSr-CoVs from bat feces: WIV1, WIV16 and Rs4874, with S protein sequences that diverged from SARS-CoV by 3% to 7% (*17, 22, 29*). We conducted full-length genome sequencing of 12 other novel SARSr-CoVs from the Jinning Cave, some highly similar to outbreak SARS-CoV in the most variable genes: N-terminal domain and receptor binding domain (RBD) of the S gene, ORF8 and ORF3 (*29*). Using our reverse genetics system, we constructed chimeric viruses with SARSr-CoV WIV1 backbone and the S gene of different variants, including WIV1-Rs4231S and WIV1-Rs7327S. All 3 SARSr-CoV isolates and the two chimeric viruses replicated efficiently in Vero E6 cells and in HeLa cells expressing hACE2, but not in HeLa cells that don't express ACE2 (*17, 22, 29*) **(Fig. 5a)**. In collaboration with Ralph Baric (UNC), we used the SARS-CoV reverse genetics system (*38*) to generate a chimeric virus with a mouse-adapted SARS-CoV

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backbone expressing SHC014 S protein with 10% sequence divergence from SARS-CoV S. This chimera replicated in primary human airway epithelium, using the human ACE2 receptor to enter into cells (*18*) (**Fig. 5b**). Thus, **SARSr-CoVs with diverse variants of SL-CoV S protein without deletions in their RBD can use human ACE2 as receptor for cell entry.**

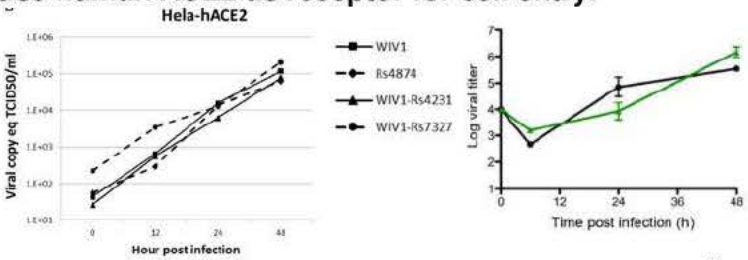


Fig. 5a (left): RT-PCR shows that bat SARSr-CoVs WIV1, Rs4874, and chimeras WIV1-Rs4231S, WIV1-Rs7327S grow in HeLa cells expressing human ACE2. **Fig. 5b (right):** Viral replication of SARS-CoV Urbani (black) and SARS-SHC014S (green) primary air-liquid interface human airway epithelial cell cultures at an MOI of 0.01.

We infected transgenic mice expressing hACE2 with 10^5 pfu of full-length recombinant WIV1 and three chimeric viruses (WIV1 backbone with SHC014S, WIV16S and Rs4231S). hACE2 transgenic mice challenged with rWIV1-SHC014S experienced ~20% body weight loss by 6dpi; rWIV1 and rWIV-4231S produced less body weight loss, and rWIV1-WIV16S led to no body weight loss **(Fig. 6a)**. At 2 and 4 dpi, viral loads in lung tissues of mice challenged with all three chimeras reached > 10^6 genome copies/g, significantly higher than rWIV1 infection **(Fig. 6b)**. This demonstrates that pathogenicity of SARSr-CoVs in humanized mice differs with divergent S proteins, **confirming the value of this model in assessing novel SARSr-CoV pathogenicity**.

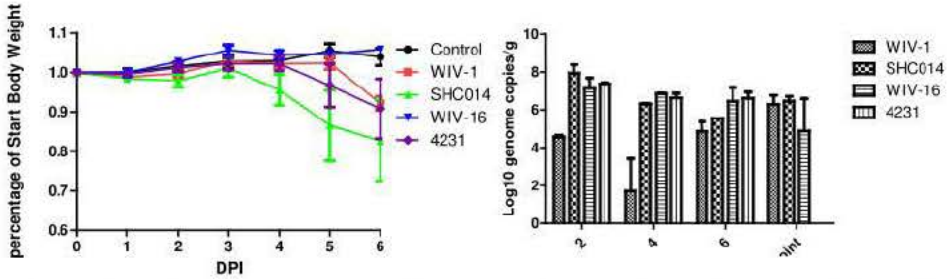


Fig. 6: *In vivo* infection of SARSr-CoVs in hACE2 transgenic mice. **6a (left)** Body weight change after infection; **6b (right)** Viral load in lung tissues.

Infection of rWIV1-SHC014S caused mild SARS-like clinical signs in the transgenic hACE2 mouse model **that weren't reduced by immune-therapeutic monoclonals that attenuate SARS-CoV pathogenecity.** Vaccination against SARS-CoV did not reduce severity of clinical signs in mice subsequently infected with rSARS-SHC014S (*18*). We found 2/4 broad human mAbs against SARS-CoV RBD cross-neutralized WIV1, but none could efficiently neutralize SHC014 which is less similar to SARS-CoV in the RBD (*39*). We repeated this virus characterization approach with chimeras using HKU3r-CoV S proteins that are ~25% divergent from SARS-CoV S, **and found that they are unable to use the ACE2 receptor**. Additionally, we were unable to culture HKU3r-CoVs in Vero E6 cells, or human cell lines. **The ability of HKU3r-CoVs to infect people, and their receptor binding target, remain unknown.**

This work has three implications for our R01 renewal: 1) some SARSr-CoVs currently circulating in bats in southern China **are likely able to infect and replicate within people**; 2) clinical outcomes of infection may include SARS-like illness that is currently **not treatable with mAb nor preventable with experimental vaccines**; 3) SARSr-CoV ability to bind human ACE2 is lost with S protein divergence between 10% (SHC014) and 25% (HKU3r-CoVs). **Although no viruses within this range have so far been described, these strains likely use hACE2 but could escape existing vaccines and immunotherapeutics and represent significant public health threats**. In our R01 renewal proposal, we will actively seek to identify viruses with this level of S protein divergence, characterize their binding targets *in vitro*, and their capacity to produce SARS-like disease that evades immunotherapy and vaccination *in vivo*.

Discovery of a novel bat-origin α-CoV associated with pig die-offs

Coronaviruses have a well-described propensity to jump the species barrier and cause new outbreaks (*40*). In 2016-17, we analyzed fecal samples from pigs at 5 farms in Guangdong Province (GD) affected by a fatal diarrheal disease. We discovered an α-CoV closely related to HKU2, and used PCR, serological and pathological data, followed by infection experiments to demonstrate that this novel virus, Swine Acute Diarrheal Syndrome coronavirus (SADS-CoV), caused the death of more than 20,000 pigs at these farms (*10*). We

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identified SADSr-CoVs in *Rhinolophus* spp. bats in GD, and analyzed >30 full-length genomes to provide phylogenetic evidence that SADS-CoV originated in these bats (**Fig. 7**).

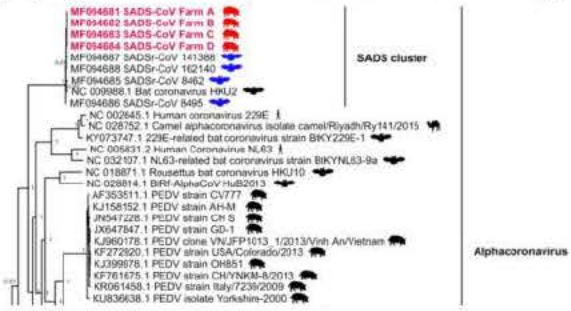


Fig. 7: Bayesian phylogenetic tree of the full-length genome sequences of SADS-CoV (red), bat SADSr-CoVs (blue), and related α-coronaviruses. Host species represented by symbol.

SADS-CoV replicates in Vero cells (*10, 41, 42*), but its capacity to replicate in human cell lines, and its zoonotic potential remains unknown. We developed a novel Luciferase Immunoprecipitation Systems (LIPS) antibody assay for SADS-CoV and found no evidence of spillover to pig farm workers at affected farms (0/33 people seropositive) (*10*). In the current proposed work we will include SADS-CoV diagnostic reagents in our serological panel to opportunistically screen human samples for evidence of spillover into people exposed to bats in southern China

Mapping bat viral emergence risk

We analyzed host and viral data for all known mammalian viruses and used a generalized additive models to correct for underlying sampling and reporting biases (*34*). This approach allowed us to predict the relative number of yet-to-be-described or 'missing' viruses that a species likely harbors. For China, there are distinct hotspots of unknown bat viral diversity in Yunnan Province **(Fig. 8)**.

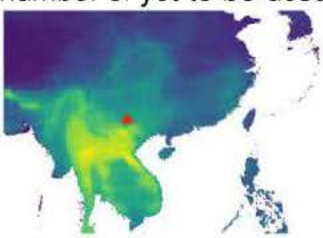


Fig. 8: Spatial distribution of predicted 'missing' or as-yet undiscovered viruses, from (*34*). Yellow = highest diversity, red triangle = Jinning Cave, Yunnan (*29*).

In a separate paper, we found that bat host diversity and climatic variability are correlates of viral diversity within bats, and that human population density, bushmeat hunting, and livestock production are correlates of the risk of transmission for viruses that spillover (*26*). The risk of spillover and spread differ spatially, suggesting that locations where bat viruses are most diverse may not be the most strategic sites for public health intervention (*21*). Work in the current proposal will improve on both approaches to identify hotspots of CoV emergence risk, by **using data from the high-risk locations and interfaces identified in our previous R01**, including better characterization of SARSr-CoV diversity in bats, and the potential of these viruses to cause infection.

Human risk behavior, the wildlife trade, and evidence of bat SARSr-CoV spillover.

Qualitative Study: Our previous R01 hypothesis was that SARSr-CoV spillover would most likely occur through the trade in bats for food, via the same market chains that to the emergence of SARS (*20*). To test this, we conducted an exploratory study using standardized one-on-one semi-structured ethnographic interviews and observational data in southern China among 88 people involved in trading wild bats, to assess local social and cultural norms and individual attitudes underlying contact with bats (publication in prep.). Our results suggest that in the 11 years since the emergence of SARS, there have been substantial changes to the wildlife trade: 1) Former wildlife markets are now predominantly selling captive-bred species (poultry, livestock, farmed wildlife); and 2) few bats are now sold through markets. We identified other risk factors for spillover, including people living near to bat roosts, and those visiting bat caves for hunting or recreation.

Human Questionnaire & Sero-surveillance: We used qualitative study findings to develop a human behavioral risk questionnaire on the type and frequency of animal contact, wildlife observed in daily life, and unusual illnesses reported over the past 12 months. We conducted a cross-sectional study among populations that live near bat caves or roosts where we had detected bat SARSr-CoVs. Study participants provided biological samples, and bats were concurrently captured and sampled. Questionnaires and biological samples (oropharynx swab, serum, plasma) were collected from 1,585 participants from 7 sites in Yunnan, Guangxi, and Guangdong provinces **(Fig. 9)**.

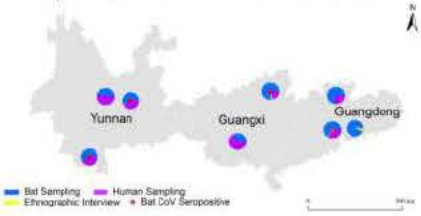


Fig. 9: Concurrent sampling in bats and target human population in communities in Yunnan, Guangxi, and Guangdong provinces. Pie-charts indicate sampling effort (bat sampling = blue, Human questionnaire and sampling = purple, Ethnographic interview = yellow, bat CoV seropositive = red)

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Serological Evidence of Exposure: We developed serological assays for HKU9 CoVs (β), SARSr-CoV Rp3 (β), HKU10 CoV (α), and MERS-CoV (β) and used ELISA and Western blot to test serum samples collected in 2016/17. **We found 7 individuals (7/733, 0.95%) living within a 6 km radius of the Jinning Cave, and 6/209 people (2.87%) at one site, with evidence of exposure to bat SARSr-CoVs (Table 2; Fig. 8).**

Site	# tested	Bat CoV + (%)	SARSr-CoV Rp3 + (%)	HKU10 + (%)	HKU9 + (%)	MERS-CoV+ (%)
Jinning, Yunnan	209	6 (2.87)	6 (2.87)	-	-	-
Mengla, Yunnan	168	1 (0.6)	1 (0.6)	-	-	-
Jinghong, Yunnan	212	-	-	-	-	-
Lufeng, Yunnan	144	-	-	-	-	-
Guangdong	420	-	-	-	-	-
Guangxi	412	2 (0.48)	-	2 (0.48)	-	-

Table 2 (left): ELISA and Western blot confirmed testing of human sera for antibodies to 4 bat CoVs.

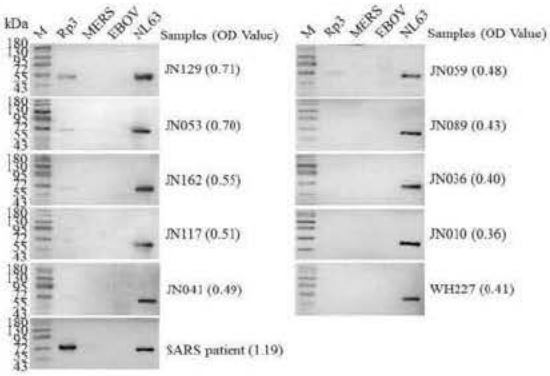


Fig. 10: Western blot reactivity of human sera to SARSr-CoV Rp3 NP.

We found evidence among human populations in Guangxi Province of people with prior exposure to the bat α-CoV HKU10 (2/412, 0.48%). This is of potential public health interest because HKU10 is known to be able to jump host species within bats, and therefore may have high propensity for emergence (*43*).

Behavioral Risk Factors: Questionnaire response and demographic data suggest specific risk factors included type of occupation, keeping of pets and visiting wet markets. Seropositive individuals were mostly farmers/peasants (8/9), living in Yunnan province (7/9), 41-60 yrs old (7/9), with domestic contact with rodents (6/9), and are male (6/9). However, these characteristics were common and occurred in ~40% of survey respondents. Although these results are preliminary and don't provide detailed information on routes of exposure, they suggest that further refining use serological tests coupled with qualitative and questionnaire data will identify likely routes of exposure to novel CoVs in China. In Aim 2 of this R01 renewal proposal, we identify strategies to better target at-risk people, and conduct focused **questionnaires and serosurveys to produce statistically significant findings.**

Analysis of self-reported illness: We analyzed data on self-reported symptoms of fever with cough and shortness of breath or difficulty breathing (severe acute respiratory illness - SARI), and fever with muscle aches, cough, or sore throat (influenza-like illness - ILI) from study participants. We used a least absolute shrinkage and selection operator (LASSO) regression to identify associations between ILI and/or SARI symptoms and contact with animals in the last year. Salient predictors or combination of predictors were, in descending order of odds ratio: 1) having eaten raw or undercooked carnivores; 2) having slaughtered poultry and being a resident of Guangxi province; 3) having had contact with cats or bats in the house; and 4) being a male who has raised poultry **(Fig. 11).**

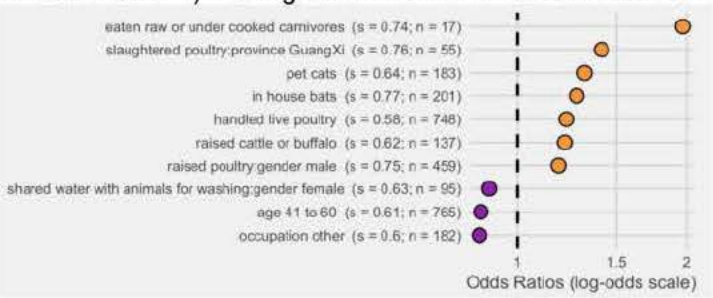


Fig. 11: Predictors of self-reported ILI and/or SARI in prior 12 months (s = bootstrap support; n = number +ve out of 1,585 respondents). Orange circles = odds ratios > 1 (positively associated with the outcome); purple = odds ratios <1 (negatively associated with the outcome).

2. APPROACH

Rationale and Innovation : Our previous R01 work demonstrates that bats in southern China harbor an extraordinary diversity of SARSr-CoVs, some of which are able to use human ACE2 to enter into human cells, can infect humanized mouse models to cause SARS-like illness, and evade available therapies or vaccines. We found that the bat hosts of SARSr-CoVs appear to no longer be traded in wildlife markets, and that people living close to bat habitats are the primary risk groups for spillover. At one of these habitats, we found diverse SARSr-CoVs containing every genetic element of the wild-type SARS-CoV genome, and serological evidence of human exposure among people living nearby. The proposed work in this renewal R01 builds on these

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findings:. **In Aim 1, we will conduct targeted bat sampling at sites where we predict that undiscovered high risk SARSr-CoV strains exist**. Bat sampling will be targeted geographically and by host species to test predictions about evolutionary diversity of SARSr-CoV. We will analyze RdRp and S protein sequences to test their capacity for spillover to people in Aim 3. **In Aim 2,** will conduct focused, targeted human surveys and sampling **to identify key risk factors for SARSr-CoV spillover and evidence of illness**. To maximize our opportunity of capturing human exposure to bat CoVs, we will conduct community-based surveillance in regions with high SARSr-CoV prevalence and diversity, and individuals having contact with bats. We will assess bat-CoV seropositive status against a small number of questions about human-wildlife contact and exposure. We will conduct clinic-based syndromic surveillance close to these sites to identify patients presenting with influenza-like illness and severe acute respiratory illness, assess their exposure to bats via a questionnaire, and test samples for PCR- and serological evidence of SARSr-CoV infection. We will conduct follow-up sampling to capture patients who had not yet seroconverted at the time of clinic visit. **In Aim 3,** we will characterize the propensity of novel SARSr-CoVs to infect people *in vitro* using primary human airway epithelial cells and *in vivo* using the transgenic hACE2 mouse model. We will use mAband vaccine treatments to test our hypothesis that SARSr-CoVs with 10-25% divergence in S protein sequences from SARS-CoV are **likely able to infect human cells, and to evade mAb therapeutics and vaccines**. We will then map the geographic distribution of their bat hosts and other ecological risk factors to **identify the key 'hotspots' of risk for future spillover.** Our SARSr-CoV program serves as a model platform to integrate virologic, molecular and ecologic factors contributing to CoV emergence while informing high impact strategies to intervene and prevent future pandemics. This includes providing critical reagents, therapeutic interventions and recombinant viruses for future SARSr-CoV pandemic and public health preparedness.

Research team and management: We have reinforced our original collaboration between EcoHealth Alliance (EHA), a global leader in field investigations of emerging viruses from wildlife and modeling/analysis of viral risk, and Wuhan Institute of Virology, a global leader in bat viral investigations **(Fig. 12)**. First, we have included senior behavioral risk scientists Co-I Francisco (EHA) and Ren (Inst. Pathogen Biol., Beijing) to oversee human survey and sampling work in Aim 2. Second, Prof. Linfa Wang (Duke-NUS), a world leader in understanding the role of bats as hosts of emerging viruses, will act as a consultant by advising and assisting in the development of PCR and serological tests and virus characterization. Prof. Wang has developed a unique array of bat immunological reagents that enrich the serological arms of the proposal. Third, Prof Ralph Baric (UNC) will use his expertise in CoV characterization to conduct primary human epithelial airway cell infections to identify high risk strains that are poised for human emergence. He will oversee and participate in animal experiments in Aim 3. This expanded team will work on a more focused set of goals, based on the results of our previous R01. PI Daszak has collaborated with all partners for between 3 and 15 yrs and will host monthly calls, annual in-person meetings, conduct quarterly adaptive management to refine research lines of work.

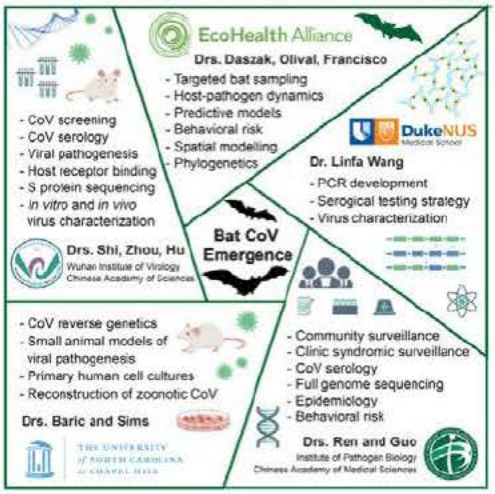


Fig. 12: Interdisciplinary team & roles in the proposed R01 renewal work.

Aim 1: Characterize the diversity and distribution of high spillover-risk SARSr-CoVs in bats in southern China

1.1 Rationale/Innovation: Our previous R01 work identified diverse SARSr-CoVs with high propensity for human infection (*18, 19, 29*). Characterization of these suggests SARSr-CoVs that are up to 10%, but not 25% different in the spike glycoprotein use human and bat ACE2 receptors for docking and entry. Uneven sampling gaps (e.g., no strains were found with 10-25% spike variation) prevent a thorough understanding of the transition point where the most divergent strains lose human ACE2 receptor usage. Our viral discovery curves **(Fig. 4)** suggest further sampling will reveal a rich diversity of as-yet-undiscovered SARSr-CoVs. In this aim we will use phylogenetic and viral discovery analysis to specifically target bat species and regions that are undersampled to allow sufficient power to identify and characterize missing SARSr-CoV strain diversity. Our

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previous work also suggests that SARSr-CoVs with S proteins that are ~10% divergent from SARS-CoV resist neutralization by therapeutic mAbs and escape SARS-CoV vaccines (*17, 18, 23*), suggesting that . However, viruses with 10-25% divergence in S proteins may bind to human cell receptors, but completely evade therapeutic and vaccine effects, and could therefore be a higher risk for public health. We will sequence the S proteins of novel SARSr-CoVs to prioritize viruses for experimental work in Aim 3 to test this hypothesis.

1.2 General Approach: We will use sampling, testing, and CoV sequence data from our previous R01 to pinpoint sites and host species needing additional sampling. We will work in 4 provinces (Yunnan, Guangxi, Guizhou and Guangdong) that we have identified phylogenetically as having the highest diversity of as-yet-undiscovered SARSr-CoVs and with competent natural hosts. Precise sampling site locations will be refined in Y1. We will target at least 5,000 individual bats over 5 years from 15 currently undersampled species of *Rhinolophus* bats, which we calculate will allow us to almost fully characterize the expected natural diversity of SARSr- and other β-CoVs in the region. Bats will be captured, sampled, and released at the site. Specimens will be transported in liquid N_2 to Wuhan Inst. Virology (WIV) for PCR screening, and positive samples selected for further molecular characterization and S Protein sequencing. EHA will lead the study design, field sampling, and data analysis for this Aim; and WIV will lead the testing and viral sequencing.

1.3 Sampling and testing of bats: 1.3.a Site selection & sample sizes: In Y1 we will use our bat host and viral trait modeling, phylogeographic analyses of RdRp and S Protein sequences, and geographic and host species-based viral discovery curve analyses to identify SARSr-CoV diversity hotspot regions for bat sampling. We will sample at 8 new sites in four provinces. We will use cave site data (*44*), and demographic information to identify two sites in each of Yunnan, Guangxi, Guangdong, and Guizhou where humans likely have contact with bats. In Yunnan, we will identify two unsampled caves close to, but distinct from, the Jinning cave (*29*). This will provide adequate coverage of lineage 1 and 2 SARSr-CoVs, including a rich source of new HKU3r-CoVs, which have unknown potential for zoonotic spillover. Sampling will begin towards the end of Y1. We will use survey data from our previous R01 and host-specific viral accumulation curve data to target an additional 10 under-sampled *Rhinolophus* spp., 5 that were SARSr-CoV negative in our study, and a small number of related bat genera (including *Hipposideros* spp. and *Aselliscus* spp.) we previously found PCR positive for SARSr-CoVs **(Table 1)**. We will sample at least 5,000 bats from these 4 provinces (~1250 per province). Given ~5-12% prevalence of SARSr-CoVs in *Rhinolophus* spp. at our previous sites, **this sample size would give us 425 (±175) positive individual bats, and ~125 novel strains.**

1.3.b CoV screening, isolation: Viral RNA will be extracted from bat fecal pellets/anal swabs with High Pure Viral RNA Kit (Roche). RNA will be aliquoted, and stored at -80C. One-step hemi-nested RT-PCR (Invitrogen) will be used to detect the presence of CoV sequences using primers that target a 440-nt fragment in the RNA-dependent RNA polymerase gene (RdRp) of all known α- and β-CoVs (*45*). PCR products will be gel purified and sequenced with an ABI Prism 3730 DNA analyzer. We will attempt isolation on samples with diverse and interesting novel CoVs, using Vero E6 cells and bat primary cell culture.

1.3.c Sequencing S proteins: For all novel SARSr-CoV strains, we will sequence the complete S gene by amplifying overlapping fragments using degenerate primers as shown previously (*17, 29*). Full-length genomes of selected SARSr-CoV strains (representative across subclades) will be sequenced via high throughput sequencing method followed by genome walking. The sequencing libraries will be constructed using NEBNext Ultra II DNA Library Prep Kit for Illumina and sequenced on a MiSeq sequencer. PCR will be performed to fill gaps in the genome. The full length S gene sequences, including the amount of variation in the S receptor binding residues that bind the ACE2 receptor, will be used to select strains for Aim 3 experiments.

1.3.d Host ACE2 receptors: We will sequence host ACE2 receptors of different bat species or different bat populations from a single species (e.g. *Rhinolophus sinicus*) to identify relative importance of different hosts of high risk SARSr-CoVs and the *intra*specific scale of host-CoV coevolution. Of particular interest is homology across 18 bat and human orthologue ACE2 contact interface residues that engage the SARS RBD as a potential indicator of SARSr-CoV cross species transmission potential and growth in human cells (*46*).

1.4 Analyses: 1.4.a Bat-CoV evolution and distribution: We will use Bayesian and Maximum Likelihood phylogenetic analyses of RdRp, Spike, and full genome sequence (when available) data to reconstruct the evolutionary history of the novel bat SARSr-CoVs we identify. We will rerun MCC analyses **(Fig. 3)** to

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reconstruct β-CoV evolutionary origins using our expanded dataset. Ecological niche models will be used to predict spatial distribution of PCR-positive species, identify target sites for additional bat sampling, and analyze overlap with people. We will use our viral discovery/accumulation curve approach **(Fig. 4)** to monitor progress towards discovery of >80% of predicted diversity of SARSr-CoVs (lineage 1 & 2) within species and sites, halting sampling when this target is reached, and freeing up resources for work other work (*37, 47*).

1.4.b Viral strain prioritization: Of the expected 100-200 novel SARSr-CoV strains, we will down-select to prioritize for further characterization based on S genes that are: i) different from SHC014, WIV1, SARS-CoV with diversity ranges of 10-25%; ii) have virus S RBD that could use human/bat receptors; iii) have recombinant chimeric spikes indicative of gene flow between clade I and II strains; iv) have bat ACE2 receptors that might select for spike RBDs that can use human receptors for entry (15/18 conserved residues in human/bat ACE2 molecules that bind SARSs-CoV S RBD domains are likely more efficient receptors than 3/18 conserved sites). Using structural models based on the SARS S glycoprotein, the extent and location of antigenic variation will be annotated onto the structure, further resolving the locations of highly evolving and conserved structural motifs/epitopes that function in protective immunity (*48-51*).

1.5 Potential problems/alternative approaches: Permission to sample bats in sites or provinces we select. We have a >15-year track record of successful field work in southern China and have worked with local authorities and communities to ensure access. We have existing permissions in place which will be renewed at the start of this project. Due to the abundance of distinct caves in the region, if access to a site is withdrawn, we will rapidly identify a suitable, complementary site with similar bat species composition and abundance. **We may not identify β-CoVs in our sample bat species due to seasonality of viral shedding.** The sampling regions we have selected are subtropical, and our previous data, and even published studies in temperate regions (*52*), do not suggest a strong pattern of seasonality in SARSr-CoV shedding. Nonetheless to account for this we will conduct sampling evenly on quarterly basis within each province.

Aim 2: Community and clinic-based surveillance to capture SARSr-CoV spillover, routes of exposure and potential public health consequences.

2.1 Rationale: Our previous R01 study identified serological evidence of exposure to SARSr-CoVs in certain communities in S. China **(Table 2, Fig. 10)** (*19*). However, the low seroprevalence (0.6%-2.7% at positive sites) suggests we need a larger sample size, and a focused, targeted study to maximize the likelihood of identifying seropositive cases. In Aim 2, we will use combined biological-behavioral risk surveillance in targeted populations within the community and clinical settings to 1) identify risk factors correlated with seropositivity (exposure to) and PCR positive status (infection with) bat SARSr-CoVs; and 2) assess possible health effects of SARSr-CoVs infection in people. Obtaining this information could be a significant step in understanding the likelihood of recent 'hidden' spillover events and their public health impacts, as well as the risk of future emergence of SARS-like diseases. It will also support the development of risk-mitigation strategies by public health authorities within China and other countries with bats that harbor these viruses (e.g. most of SE Asia).

2.2 General Approach/Innovation: We will use a dual study design to gain in depth understanding of exposure and risk factors for SARSr-CoV spillover **(Fig. 13)**. We will conduct community-based surveillance, with more focused questionnaires and biological sampling to determine the seroprevalence of SARSr-CoVs in at-risk human populations, and to identify risk-factors for SARS-CoV spillover in these communities. We will conduct clinic-based syndromic surveillance and biological sampling at sites that include the community-based surveillance sites within their catchment. This will include follow-up sampling to capture seroconversion of recently infected people and the full course of symptoms. We will also use PCR to test for present of active SARSr-CoV replication. Both community-based and clinic-based syndromic surveillance programs are case-control studies designed with the sample sizes necessary to statistically quantify (with a power of 80%) risk factors and health impacts for SARSr-CoV spillover, linked to serological status and symptoms.

2.3 Target population & sample size: We will target sites in the same four provinces, and close to those for bat sampling, based on: 1) sites of likely divergence of SARSr-CoVs; 2) a high diversity of SARSr-CoVs within the S protein sequence divergence of 5-25%; and 3) high rates of human-wildlife interactions. Community-based surveillance will be conducted at 2 sites in each of the 4 provinces, a total of 8 sites. From our previous work we anticipate that 10-30% of the community population will have had exposure to bats allowing us to

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capture highly exposed and non-exposure individuals at each site. Individuals living or working around bat roosts, who hunt wildlife, work with wildlife or livestock farming, transportation, selling, or slaughtering wildlife in the surveyed areas will be targeted so that they make up ≥30% of the sampled population in each community. We will stratify sampling to ensure appropriate representation of sex, demographic, and socio-economic factors at each community site. We will initiate active clinic-based syndromic surveillance at 2 county-level hospitals and 1 provincial-level hospital in each of the 4 provinces, in total 12 hospital sites, all within the catchment areas for bat sampling, and which are used by people in our community-based surveillance. Patients ≥ 12 years old presenting at the health facility who meet the syndromic and clinical case definitions for SARI and ILI will be recruited into the study. We will enroll a total of at least 2,750 individuals for clinical studies, which accounts for up to 40% loss from follow-up. Study data will be pooled across sites, as clinical patients are limited by the number of individuals presenting at hospitals. For community-based surveillance, we will enroll 1,650 individuals per province, pooled across two sites for each province, allowing us to make province-level comparisons of differing effects. Estimating 5% overall seroprevalence in these high-exposure populations, these sample sizes are sufficient to estimate effect sizes of behavioral risk factors of 2X or greater with 80% power.

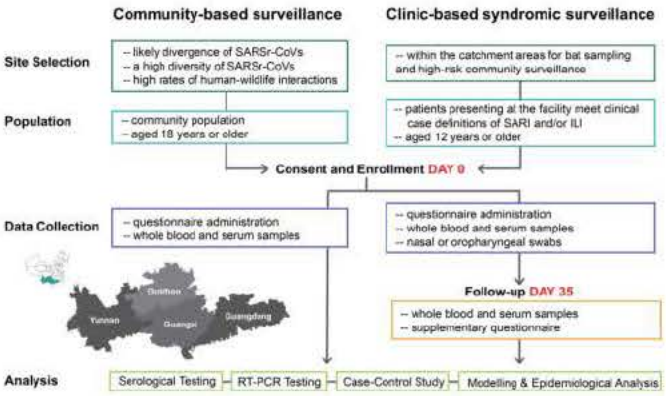


Fig. 13: Human survey and sampling study design overview

2.4 Data & sample collection: At both community and clinical settings, following enrollment with signed consent form, biological specimens (two whole blood samples, one max. 500 µL; two 500 µL serum samples) will be collected from all eligible participants, and a questionnaire will be administered. We will investigate five risk factors, so as to maximize the power of the analyses, all related to high risk wildlife exposure, based on continuing analysis of our previous work, and will include: 1) occupation; 2) observed or reported interactions with bats in/around house; 3) proximity to nearby bat roosts; 4) working or regular visit to animal markets; 5) self-reported ILI/SARI. An additional two nasal or oropharyngeal swabs will be collected from patients enrolled in the clinic-based syndromic study. With permission from each clinic, and consent from participants, we will review clinical records to collect data on medical history, clinical syndromes, and patient etiology.

2.5 Clinic enrollment and follow-up: We will recruit inpatients and outpatients after initial screening to meet the clinical case definition of 1) severe/acute respiratory illness (SARI/ARI) of unknown etiology; or 2) Influenza-like illness (ILI) of unknown etiology. Once enrolled, biological samples will be collected and a questionnaire administered by trained hospital staff that speak appropriate local dialects. Samples will be taken concurrently when collecting samples for normative diagnostics. For inpatients, samples will be collected within 10 days of reported onset of illness to increase the chance of PCR CoV detection (*53*). We will follow up 35 days after enrollment to collect an additional two 500 µL serum samples conduct a standardized questionnaire supplement to collect additional data on the course of symptoms in the interim period. 35 days gives adequate time for development of IgG, which occurs <28 days after onset of symptoms for SARS patients (*54*).

2.6: Laboratory analysis: 2.6.a Serological testing: In our previous R01, we expressed his-tagged nucleocapsid protein (NP) of SARSr-CoV Rp3 in *E.coli* and developed a SARSr-CoV specific ELISA for serosurveillance using the purified Rp3 NP. The specificity of this assay was evaluated using polyclonal antibodies against HKU1, OC43, 229E, NL63, MERS-CoV and EBOV and no significant cross-activity was detected (*19*). **While this shows it is a specific test for Rp3, it suggests that if we can expand our serology tests to cover other bat CoVs, we may identify many more seropositive individuals.** In this renewal, we will therefore use two serological testing approaches. First, we will expand test all human sera collected from both community- and clinic- based sampling for a panel of bat CoVs that will include SARS-CoV (outbreak strain), a range of lineage 2 SARSr-CoVs (including WIV1 and SHC014), lineage 1 HKU3r-CoVs, MERS-CoV, and the α-CoVs SADS-CoV and HKU10. We previously found serological evidence of human exposure to HKU10 (*19*), but HKU10 is known to jump from one host bat species to another (*43*) and is

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therefore likely to have infected people more widely. Incoporating serological testing for SHC014 is also likely to yield higher seroprevalence because it is readily divergent from SARS-CoV wildtype and therefore unlikely to have been picked up in our earlier testing. It is possible that non-neutralizing cross reactive epitopes exist that afford an accurate measure of cross reactivity between clade1 and clade 2 strains which would allow us to target exposure to strains of 15-25% divergence from SARS-CoV. Additionally, we will test samples for antibodies to common human CoVs (HCoV NL63, OC43 – see potential pitfalls/solutions below). Secondly, we recognize that CoVs have a high propensity to recombine. To serologically target 'novel' recombinant virus exposure, we will conduct 1) ELISA screening with SARSr-CoV S or RBD; 2) confirm these results by Western blot; then 3) use NP based ELISA and LIPS assays with a diversity of SARSr-CoV NP. For NP ELISA, micro-titer plates will be coated with 100 ng/well of recombinant batCoV NP and incubated with human sera in duplicates followed by detection with HRP labeled goat anti-human IgG antibodies. For confirmation, all ELISA positive samples will be subjected to Western blot at a dilution of 1:100 by using batCoV-NP as antigen. We will use an S protein-based ELISA to distinguish the lineage of SARSr-CoV. As new SARSr-CoVs are discovered, we will rapidly design specific Luciferase immunoprecipitation system (LIPS) assays targeting the S1 genes of bat-CoV strains for follow-up serological surveillance, as per our previous work (*10*).

2.6.b RT-PCR testing. Specimens will be screened using RT-PCR for the RdRp gene (See section 1.3.b for details). Positive samples will be subjected to full genome sequencing and RT-PCR amplification of the S glycoprotein gene. Samples from the clinic-based syndromic surveillance will also be tested using RT-PCR for Influenza A & B, HCoV NL63, OC43, HKU1, SARS-CoV & 229E as rule-outs, and SADS-CoV and HKU10 as an opportunistic survey for potential spillover these CoVs as proposed above.

2.7 Epidemiological analysis: We will conduct a case-control study to identify risk factors for SARSr-CoVs spillover. "Cases" are defined as participants whose samples tested positive for SARSr-CoVs by serological tests. "Controls" will be selected from the pool of participants admitted to the studies but testing negative. We will use nearest neighbor matching to pair cases demographically with controls at a 1-to-3 ratio or greater. We will use generalized linear models to analyze correlation between serological/PCR status and risk factors including: Activities with likely exposure to 1) bats; 2) livestock; and 3) locations of residence and work. We will use the same procedure to determine how clinical presentation differs between SARSr-COVs-exposed and unexposed enrollees, in the time course of illness, severity of symptoms, and type of symptoms.

2.8 Potential problems/alternative approaches: Rarity of spillover events means it may be difficult to identify sufficient seropositives to statistically analyze risk behavior or illness. First, we are now targeting our community-based surveillance to subpopulations with high-levels of bat exposure, at sites selected for diverse and prevalent SARSr-CoVs, and are adding clinic-based syndromic surveillance of SARI and ILI cases in these same regions – both will increase likelihood of finding positive individuals. Second, our serology testing will include a panel of assays for a large diversity of lineage 1 and 2 SARSr-CoVs as well as SADS-CoV, HKU10 and other bat-borne CoVs. *Rhinolophus* spp. bats host all of these (overall bat CoV PCR prevalence, 11.8%; β-CoV, 3.4%; α-CoV, 9.1%). Thus, using this broad serological panel to screen individuals in likely contact with these species increases the potential for detecting spillover with enough power for statistical analyses, and will shed light on behaviors that predispose to CoV spillover from bats. Third, we will include common human CoVs in our panel, so that even if low prevalence of bat CoVs is found, we will be able to conduct a valuable cross-sectional study of the seroprevalence of human CoVs. Finally, we will be able to assess relative measures of human-wildlife contact from our survey work. We will analyze intensity of contact against other risk factors and clinical outcomes to provide useful proxy information for spillover risk. **Patients visiting clinics may have cleared virus, but not yet developed IgG antibodies, reducing seropositive cases.** Our 35 day follow-up sampling should avoid this because the maximum lag time between SARS infection and IgG development was ~28 days (*53*). We also expect that patients in rural communities will only visit clinics when symptoms have progressed, likely coinciding with late illness and onset of IgG. We will also have data from our community study, so won't be completely reliant on hospital data to identify PCR- or seropositives. Finally, the risk is outweighed by the potential public health importance of discovering active spillover of a new SARSr-CoV. **Serological testing may not match known CoVs due to recombination events.** We will use the three-tiered serological testing system outline in **2.6.a** to try to identify these 'novel' CoVs, however, we will also remain flexible on interpretation of data to ensure we account for recombination.

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Aim 3: *In vitro* and *in vivo* characterization of SARSr-CoV spillover risk, coupled with spatial and phylogenetic analyses to identify the regions and viruses of public health concern

3.1 Rationale/Innovation: In **Aim 1**, we aim to expand the known diversity of SARSr-CoVs by over 125 strains, targeting 10-25% S protein divergence that we predict infers high spillover risk and evasion of immune therapeutic and vaccine efficacy. In **Aim 3**, we will further characterize the zoonotic potential of a selected group of these novel SARSr-CoVs, using infectious clone technology, *in vitro* and *in vivo* infection experiments and analysis of HKU3r-CoV receptor binding to test the hypothesis that S protein % sequence divergence thresholds predict spillover potential (*18, 55*). We will analyze data from these viral characterization and infection experiments, coupled with bat host distribution, viral diversity and phylogeny, human survey of risk behaviors and illness, and human serology to assess spillover risk of SARSr-CoVs in different bat species across southern China. This will enable future development of public health interventions and enhanced surveillance to prevent the emergence of a novel SARSr-CoV.

3.2 General Approach: We will use S protein sequences to select a range of viral strains that cover the 10-25% S protein divergence we predict as high public health potential and construct chimeric SARSr-CoVs using the WIV1 backbone and these S genes as done previously (*12, 18, 38*). We will rescue of full-length clones and assess infection of non-permissive cells expressing human, bat and civet ACE2 receptors, Vero cells, primary human airway epithelial cells, and CaCo cells for HKU3r-CoVs (which have not been cultured and may use intestinal epithelium in nature). We will conduct experimental infections in hACE2 transgenic mice to assess pathogenicity and clinical signs (*18*). Finally, using a panel of mAbs that neutralize SARS-CoV infection *in vitro* and *in vivo*, and vaccine against SARS-CoV S protein, we will examine the capacity of strains with divergent S protein sequences to evade therapeutics, revealing strains with high public health potential. We will also conduct limited experiments to analyze HKU3r-CoV receptor binding and assess spillover potentia. Using these results, and data from Aims 1 and 2, we will use spatial modeling techniques to identify geographic hotspots in southern China where bat species that harbor high risk SARSr-CoVs inhabit, where communities that have high exposure to bats exist, where serological or PCR evidence of spillover has been identified, and where underlying demographic or environmental trends suggest high risk of future emergence.

3.3 Virus characterization: 3.3.a Construction of chimeric SARSr-CoV viruses: Infectious clones with the S gene of novel SARSr-CoVs and the SARSr-CoV WIV1 genome backbone using the reverse genetic system developed in our previous R01 (*24*). The correct infectious BAC clones will be screened by BAC DNA digestion with appropriate restriction enzyme or PCR amplification. The chimeric viruses will be rescued in Vero cells and then verified by sequence analyses. Our research group is well versed in coronavirus reverse genetics.

3.3.b Cell entry analysis: HeLa cells expressing human ACE2 are cultured on coverslips in 24-well plates incubated with the chimeric bat SARSr-CoVs with different spike proteins at a multiplicity of infection (MOI) = 1.0 for 1h. The inoculum is removed and the cells are washed twice with PBS and supplemented with medium. HeLa cells without ACE2 are used as negative control. Twenty-four hours after infection, cells are rinsed with PBS and fixed with 4% formaldehyde in PBS (pH7.4) at 4℃ for 20 min. ACE2 expression is detected by using goat anti-human ACE2 immunoglobulin followed by FITC-labelled donkey anti-goat immunoglobulin. Virus replication is detected by using rabbit antibody against the nucleocapsid protein of bat SARSr-CoV followed by Cy3-conjugated mouse anti-rabbit IgG. In parallel with the immunofluorescence assay, plaque assay will be conducted to determine the viral titers and growth kinetics in the infected cells at different times post-infection.

3.3.b Primary human airway epithelial cell culture: Primary human ciliated airway epithelial cells (HAE) cultures from the lungs of transplant recipients represent highly differentiated human airway epithelium containing ciliated and non-ciliated epithelial and goblet cells, grown on an air-liquid interface for several weeks prior to use (*18, 55, 56*). We will prepare HAE cultures from three different patient codes in triplicate in collaboration with the tissue procurement facility at the Cystic Fibrosis Center at UNC. Cultures will be inoculated with chimeric bat SARSr-CoVs to assess efficient replication. At 72 hpi, cultures will be fixed for immunofluorescent staining using antisera to the SARS-CoV conserved nucleocapsid protein (N) (*57, 58*). SARSr-CoVs that differ significantly in S protein sequence (11-24%) from epidemic SARS-CoV yet replicate *in vitro*, will also be evaluated for sensitivity to neutralization in Vero cells by PRNT50 assays using broadly SARS-CoV cross reactive human mAbs S227.14, S230.15, S215.17, and S109.8 (*49, 55*). As controls, the S

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genes of novel SARSr-CoV will be inserted into VEE 3526 replicon vectors (VRP3526-S), packaged and used to vaccinate mice (*59*). Polyclonal sera will be harvested and tested for ability to cross neutralize SARS-CoV, GD03, WIV-1, SHC014, WIV-16, other novel SARSr-CoV and HKU3-SRBD by PRNT50 assay (*55, 60, 61*). Using PRNT50 titers with sera (n=4 each) among these viruses, antigenic cartography (*62*) will allow comparison of antigenic vs. phylogenetic distance, identifying the transition at which SARSr-CoV strains escape SARS-CoV based vaccines, informing immunotherapeutic and vaccine design strategies (*63-65*).

3.3.c Humanized mouse infection experiments: Briefly, in BSL3, n=5 10- to 20-week old hACE2 transgenic mice will be intranasally inoculated with 1 x 10^4 PFU of wildtype WIV-1 or chimeric bat SARSr-CoVs with different spike proteins, then monitored daily for weight loss, morbidity, and clinical signs of disease. Mice will be euthanized at 2, 4, and 6 dpi (endpoint of 14 dpi), organs harvested and virus quantified by SARS-CoV NP RT-PCR. After 7 days in formalin, tissues for histopathology will be removed from the BSL3 and stained with H&E, and for immunohistochemistry using polyclonal antibodies against the N protein. We will conduct limited evaluation of existing countermeasures using therapeutic monoclonal antibodies *in vitro* and *in vivo*. Existing SARSr-CoV mAbs will be diluted in DMEM starting at 1:20, and serial 2-fold dilutions mixed with an equal volume of 50 PFU of chimeric bat SARSr-CoVs with different spike proteins, then incubated on Vero E6 cells at 37°C for 1 h, then changed to a semi-solid medium (DMEM containing 1% methylcellulose and 2% FBS). Antibody neutralization titers will be evaluated by plaque quantification at 4-5dpi. hACE2 transgenic mice will be injected with SARS-CoV mAbs, and infected with chimeric bat SARSr-CoVs. Clinical signs and morbidity will be assessed and tissue pathology examined and compared with mice without treatment of mAbs to determine the therapeutic effect on SARSr-CoV infection, and protection of SARSr-CoV by wildtype SARS-S based vaccines assessed as described (*56, 66*). We will sequence full length genomes of high risk strains that are antigenically distinct and escape SARS cross neutralization, synthetically reconstruct a small subset (1-2) and evaluate the ability of nucleoside analogues to inhibit growth in HAE cultures and/or *in vivo* (*55, 56*).

3.3.d HKU3 clade cellular receptor: We will screen potential receptor molecules by pull-down analysis on membrane proteins interacting with the spike protein, initially using bat primary intestinal epithelial cell lines and lysates to extract protein, isolate membranes, and proteomically sequence intestinal proteins. The fusion protein of the HKU3 and HKU3r-CoV S proteins containing human Immunoglobulin Fc fragment will be eukaryotically expressed and purified. SARSr-CoV S will be incubated as bait protein with the membrane proteins extracted from *Rhinolophus sinicus* intestinal cells, to capture and precipitate membrane proteins that interact with the S protein. Mass Spectrometry will be performed to screen for the candidate receptor molecules and Co-Immunoprecipitation assay to confirm binding of the SARSr-CoV S protein to the candidate receptor. Alternatively, retroviruses pseudotyped with the SARSr-CoV S protein will be constructed and used to infect cells trans-expressing the candidate receptor molecule. Luciferase activity will be measured to test whether the S protein can bind to the receptor. If successful, this work will allow future research to clone and study human HKU3 receptor ortholog's ability to function as a receptor for other clade 2 strains and will allow better assessment of risk of clade 2 SARSr-CoV spillover to humans.

3.4 Combined spatial risk 'hotspot' analyses: We will use data from **3.3** to identify rank SARSr-CoV strains most likely to infect people and evade therapeutic and vaccine modalities. We will use bat survey and zoological data (*44*) to build species distribution models (*67*) and predict the distribution of bat species that harbor low, medium and high risk viral strains. Stacking these modeled distributions for the ~20-30 *Rhinolophus* and related species that occur in the region will allow estimates of SARSr-CoV diversity for a given locality. We will use machine learning models (boosted regression trees) and spatial 'hotspot' mapping approaches to identify the ecological, socio-economic and other correlates of SARSr-CoV diversity and spillover (from serosurveys) (*21, 68, 69*). We will include data from our human behavioral surveys and sampling to give a direct measure of where risk of spillover to people is likely to be highest in the region.

Potential problems/alternative approaches: We may not be able to glean further information about the **capacity of HKU3r-CoVs to infect human cells, or bind to human cell surface receptors.** If attempts at culture are unsuccessful, and efforts to identify the receptor too costly or time-consuming, we will cease this line of work. In that event, we will focus entirely on filling out the gaps in the 10-25% S protein sequence divergence from SARS-CoV, by working on a greater diversity of lineage 2 SARSr-CoVs.

Obtained via FOIA by Judicial Watch, Inc.

Progress report publication list: R01 AI110964, Daszak PI, Project Period: 06/01/2014 – 05/31/2019

The following are peer-reviewed papers published from work funded by this NIAID R01 during the project period (*1-18*). Other manuscripts on behavioral risk, phylogenetic and viral risk characterization are in prep and awaiting submission prior to the end date of the grant.

1. B. Hu *et al.*, Detection of diverse novel astroviruses from small mammals in China. *Journal of General Virology* **95**, 2442-2449 (2014). PMID: 25034867
2. B. Hu, X. Y. Ge, L. F. Wang, Z. L. Shi, Bat origin of human coronaviruses. *Virology journal* **12**, (2015). PMID: 26689940
3. V. D. Menachery *et al.*, A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. *Nature Medicine* **21**, 1508-+ (2015). PMID: 26552008
4. J. N. Mandl *et al.*, Reservoir Host Immune Responses to Emerging Zoonotic Viruses. *Cell* **160**, 20-35 (2015). PMID: 25533784
5. M. N. Wang *et al.*, Longitudinal surveillance of SARS-like coronaviruses in bats by quantitative real-time PCR. *Virologica Sinica* **31**, 78-80 (2016). PMID: 26920711
6. L. Brierley, M. J. Vonhof, K. J. Olival, P. Daszak, K. E. Jones, Quantifying Global Drivers of Zoonotic Bat Viruses: A Process-Based Perspective. *American Naturalist* **187**, E53-E64 (2016). PMID: 26807755
7. X. Y. Ge *et al.*, Coexistence of multiple coronaviruses in several bat colonies in an abandoned mineshaft. *Virologica Sinica* **31**, 31-40 (2016). PMID: 26920708
8. L.-P. Zeng *et al.*, Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response. *Journal of Virology* **90**, 6573-6582 (2016). PMID: 27170748
9. X. L. Yang *et al.*, Isolation and Characterization of a Novel Bat Coronavirus Closely Related to the Direct Progenitor of Severe Acute Respiratory Syndrome Coronavirus. *Journal of Virology* **90**, 3253-3256 (2016). PMID: 26719272
10. K. J. Olival *et al.*, Host and viral traits predict zoonotic spillover from mammals. *Nature* **546**, 646-650 (2017). PMID: 28636590
11. L. P. Zeng *et al.*, Cross-neutralization of SARS coronavirus-specific antibodies against bat SARS-like coronaviruses. *Science China-Life Sciences* **60**, 1399-1402 (2017). PMID: 29134417
12. X. L. Yang *et al.*, Genetically Diverse Filoviruses in Rousettus and Eonycteris spp. Bats, China, 2009 and 2015. *Emerging Infectious Diseases* **23**, 482-486 (2017). PMID: 28221123
13. B. Hu *et al.*, Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. *PLoS pathogens* **13**, (2017). PMID: 29190287
14. N. Wang *et al.*, Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. *Virologica Sinica*, (2018). PMID: 29500691
15. C. M. Luo *et al.*, Discovery of Novel Bat Coronaviruses in South China That Use the Same Receptor as Middle East Respiratory Syndrome Coronavirus. *Journal of Virology* **92**, (2018). PMID: 29669833
16. Y. Luo *et al.*, Longitudinal Surveillance of Betacoronaviruses in Fruit Bats in Yunnan Province, China During 2009-2016. *Virologica Sinica* **33**, 87-95 (2018). PMID: 29500692
17. Z. Wu *et al.*, Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. *Microbiome* **6**, 178 (2018). PMID: 30285857
18. P. Zhou *et al.*, Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. *Nature* **556**, 255-258 (2018). PMID: 29618817

Obtained via FOIA by Judicial Watch, Inc.

PHS Human Subjects and Clinical Trials Information

OMB Number: 0925-0001 and 0925-0002

Expiration Date: 03/31/2020

Are Human Subjects Involved	● Yes ○ No
Is the Project Exempt from Federal regulations?	○ Yes ● No
Exemption Number	❑ 1 ❑ 2 ❑ 3 ❑ 4 ❑ 5 ❑ 6 ❑ 7 ❑ 8
Other Requested Information	

Obtained via FOIA by Judicial Watch, Inc.

Human Subject Studies

Study#	Study Title	Clinical Trial?
1	Understanding the Risk of Bat Coronavirus Emergence: Community and clinic-based surveillance to capture SARSr-CoV spillover, routes of exposure and potential public health consequences	No

Obtained via FOIA by Judicial Watch, Inc.

Section 1 - Basic Information (Study 1)

OMB Number: 0925-0001 and 0925-0002

Expiration Date: 03/31/2020

1.1. Study Title *

Understanding the Risk of Bat Coronavirus Emergence: Community and clinic-based surveillance to capture SARSr-CoV spillover, routes of exposure and potential public health consequences

1.2. Is this study exempt from Federal Regulations * ○ Yes ● No

1.3. Exemption Number ❑ 1 ❑ 2 ❑ 3 ❑ 4 ❑ 5 ❑ 6 ❑ 7 ❑ 8

1.4. Clinical Trial Questionnaire *

1.4.a. Does the study involve human participants?	● Yes	○ No
1.4.b. Are the participants prospectively assigned to an intervention?	○ Yes	● No
1.4.c. Is the study designed to evaluate the effect of the intervention on the participants?	○ Yes	● No
1.4.d. Is the effect that will be evaluated a health-related biomedical or behavioral outcome?	○ Yes	● No

1.5. Provide the ClinicalTrials.gov Identifier (e.g. NCT87654321) for this trial, if applicable

Obtained via FOIA by Judicial Watch, Inc.

Section 2 - Study Population Characteristics (Study 1)

2.1. Conditions or Focus of Study

- Emerging zoonotic disease from bat Coronavirus

2.2. Eligibility Criteria

Participants to be enrolled in this study will be people living, working, or visiting the high-risk sites: 1) of likely divergence of SARSr-CoVs; 2) with a high diversity of SARSr-CoVs within the S protein sequence divergence of 5-25%; and 3) with high rates of human-wildlife interactions in four provinces of Yunnan, Guangxi, Guizhou, and Guangdong in China, who meet the inclusion criteria outlined below. Study sites are prioritized according to ecological and epidemiological conditions associated with a high risk for SARSr-CoVs spillover.

Research participants will be enrolled in two settings of community and hospital or clinic.

Community
People living, working, or visiting targeted high-risk communities (as defined above) who have close contact with bats, we anticipate interviewing and collecting biological samples from individuals with a range of exposure to bats. Enrolled research participants will be asked to provide biological samples and complete a questionnaire that is designed to obtain information about living circumstances (e.g. distance between the living house and closest bat roost, observed bats in house), income or livelihood, experience with SARI and ILI-like illness and involvement in activities with direct or indirect (e.g. via livestock) contact with bats.

Additional inclusion criteria for community participants
- Adults (18 years of age or older) who provide informed consent
- Pregnant women will be considered eligible for inclusion

Exclusion criteria for community participants
- Adults (18 years of age or older) who are unable to provide informed consent, including individuals with physiologically or medically induced cognitive impairments
- Individuals under 18 years of age
- Prisoners

Hospital or clinic
Patients at clinics or hospitals presenting with clinically defined symptoms of severe/acute respiratory illness (SARI/ARI) and/or influenza-like illness (ILI) with unknown origin. As with the community-based group, biological samples will be collected from the patients, and the patients or his/her designate will complete a questionnaire. We will follow up with these participants 35 days after enrollment to collect another biological sample to assess the development of IgG and collect additional data on the course of symptoms in the interim period.

Additional inclusion criteria for hospital or clinic participants
- Adults (18 years of age or greater) who provide informed consent
- Children aged 12 years or older with an accompanying parent or guardian who is able to provide informed consent, with the assent of children 12 years or older also required
- Pregnant women will be considered eligible for inclusion

Exclusion criteria for hospital or clinic participants
- Individuals over the age of 12 years who refuse to provide informed consent
- Adults unable to provide informed consent, including individuals with physiologically or medically induced cognitive impairments
- Children, aged 12-17, without an accompanying parent or guardian who is able to provide informed consent, or a child aged 12 to 17 who is unable or unwilling to provide assent
- Children < 12 years of age
- Prisoners

2.3. Age Limits	Min Age: 12 Years	Max Age: N/A (No limit)
2.4. Inclusion of Women, Minorities, and Children	NIAID_COV_2019_Inclusion_of_Women_Minorities_Children_Final.pdf	
2.5. Recruitment and Retention Plan	NIAID_COV_2019_Recruitment_Retention_Final.pdf	
2.6. Recruitment Status	Not yet recruiting	
2.7. Study Timeline	NIAID_COV_2019_Study_Timeline_Final.pdf	
2.8. Enrollment of First Subject	06/01/2020	Anticipated

Obtained via FOIA by Judicial Watch, Inc.

INCLUSION OF WOMEN AND MINORITIES:

This proposal will enroll men and women as study participants without regard to ethnicity.

- At community sites, exposure to bats in working and living environments will be the primary criteria for identifying participants in community. We will make every effort to have men and women equally represented in this study and no individuals will be excluded based on ethnicity.

- At clinic sites, only patients who present at the health facility who meet the clinical case definition of 1) severe/acute respiratory illness (SARI/ARI) of unknown origin; or 2) Influenza-like illness (ILI) of unknown origin will be recruited for this study, and no patients will be excluded (or included) based on ethnicity or gender.

INCLUSION OF CHILDREN:

Children aged 12 years or older will be included in the clinical syndromic study.

- Previous clinic-based studies have shown that children are one of the major populations who are affected by the severe/acute respiratory illness (SARI/ARI) and/or Influenza-like illness (ILI).
- Children aged 12 years or older are post-primary school and are able to respond to the questionnaire on their own which increases the reliability of responses.
- Our human research team at the Institute of Pathogen Biology are all well-trained and have extensive experience working with children at this age, as well as their parents, in a clinical setting since 2009.
- Every effort will be made to protect the privacy, dignity, and well-being of children who participate in this study.
- Inclusion of children in the study would increase the sample size to allow for the estimation of effect sizes of behavioral risk factors by two-fold (2X) or greater with 80% power.

We will not include children in the community-based surveillance because children in target communities are mainly school children who have very limited exposures to bats or other wild animals under the scenarios of interest to the study, prolonged time spent in the forests or markets.

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RECRUITMENT AND RETENTION PLAN

In order to improve recruitment within target communities, introductory visits will be made by project staff to each of the selected sites. These visits will be advertised through word of mouth and a project description letter to town/city leaders that can be posted in a central community location. The letter will inform the community that a team will be coming on a particular day(s) to discuss health issues related to animal contact. The letter will not be advertised for recruitment purposes. It will only be used to inform the community of the research visits. The project description letter will be written in the local language with a Flesch–Kincaid readability score equivalent to a 7th grade and up level (post-primary in China), to assure that potential community participants understand the study purpose, eligibility, and inclusion guidelines.

During community visits, discussions and meetings will be held firstly with local authorities and community leaders to introduce our project, and when appropriate and following approval from local authorities, the study team will post flyers to inform the community when the team will be coming back to speak about enrollment. This “town hall” style meeting will be completely voluntary, and, based on our experience, those interested would likely attend. Although local authorities may be present to introduce the study team members, they will not be involved in the recruitment and/or consent of the participants for the study. If research visits or recruitment are held at a workplace, subjects will be clearly informed during this recruitment process that their participation in the study is voluntary and will not impact their employment, nor will information discussed be shared with employers. With the local permission and accompanied will local authorities or community leaders, study team members will also engage in community ‘walkabouts’ during which they will discuss study details, as well as dates, times, and locations for enrollment and participation in the study.

Participation in the study will be strictly voluntary and will require signed informed consent for all participants and signed assent for clinical participants aged 12-17 along with parent or guardian consent. Participants will be given a consent form prior to being asked to participate in this study. Our research staff will read the consent form to potential participants, and they will review the consent form with the research staff and be given time to ask questions. After reviewing the consent form, study staff will explain details of the study including: why they were selected, what the study procedures are and what will be expected from them, potential risks and benefits of their participation, that their participation is completely voluntary, and that they can withdraw their participation at any time. Responses will be kept strictly confidential. Measures will be taken to assure the privacy, dignity, and respect of each participant. During training of research staff, we will emphasize the importance of avoiding coercion and protecting the privacy of participants.

Community-based recruitment: Participants from the community will be recruited through town hall meetings and community ‘walkabouts’ as described above. Meeting dates, times, and locations for enrollment and participation will be shared during these activities, and participants who wish to enroll can volunteer to participate at these times and locations.

Clinic-based recruitment: Patients eligible for enrollment will be identified at intake areas or in the emergency room, ward, or intensive care unit of each participating clinic and hospital by clinic staff, according to standard operating procedures at collaborating sites. Employed staff at each location will identify potential participants meeting the clinical case definition of severe/acute respiratory illness (SARI/ARI) and/or influenza-like illness (ILI) with unknown origin. Patients will be screened for eligibility according to the inclusion/exclusion criteria based on available clinical information. For larger provincial-level hospitals, interval sampling will be implemented by selecting every Nth case at the site among those individuals who meet enrollment criteria. The interval will be determined by local implementing partners based on an evaluation of the expected number of cases presenting at the site within a given year in order to best meet study design and sample size criteria. In terms of retention, we will express our gratitude to subjects for their participation and discuss the importance of the follow-up data collection. Nonetheless, we expect to have an approximate 40% loss to follow up and have included this in our sample size calculations.

Obtained via FOIA by Judicial Watch, Inc.

STUDY TIMELINE

Patients/participants will be asked to volunteer approximately 1 hour of their time for participation in the study, including providing biological samples and completing the questionnaire at each sampling time point.

This will be an ongoing, five-year project (June 01, 2019 -- May 31, 2024). We anticipate to starting human subject enrollment on June 01, 2020, and completion of preliminary analyses is expected in 2024.

Obtained via FOIA by Judicial Watch, Inc.

Inclusion Enrollment Reports

IER ID#	Enrollment Location Type	Enrollment Location
Study 1, IER 1	Foreign	Local community and hospital/clinic in Yunnan, Guangdong, Guangxi, Guizhou Provinces

Obtained via FOIA by Judicial Watch, Inc.

Inclusion Enrollment Report 1

Using an Existing Dataset or Resource* : ○ Yes ● No

Enrollment Location Type* : ○ Domestic ● Foreign

Enrollment Country(ies): CHN: CHINA

Enrollment Location(s): Local community and hospital/clinic in Yunnan, Guangdong, Guangxi, Guizhou Provinces

Comments: This is a renewal, the cumulative enrollment from the previous funding period 5R01AI110964-05 is 980 females and 616 males, in total 1,596 Asians.
We don't plan to use the existing dataset.

Planned

Racial Categories	Ethnic Categories				Total
	Not Hispanic or Latino		Hispanic or Latino		
	Female	Male	Female	Male	
American Indian/ Alaska Native	0	0	0	0	0
Asian	4675	4675	0	0	9350
Native Hawaiian or Other Pacific Islander	0	0	0	0	0
Black or African American	0	0	0	0	0
White	0	0	0	0	0
More than One Race	0	0	0	0	0
Total	4675	4675	0	0	9350

Cumulative (Actual)

Racial Categories	Ethnic Categories									Total
	Not Hispanic or Latino			Hispanic or Latino			Unknown/Not Reported Ethnicity			
	Female	Male	Unknown/ Not Reported	Female	Male	Unknown/ Not Reported	Female	Male	Unknown/ Not Reported	
American Indian/ Alaska Native	0	0	0	0	0	0	0	0	0	0
Asian	0	0	0	0	0	0	0	0	0	0
Native Hawaiian or Other Pacific Islander	0	0	0	0	0	0	0	0	0	0
Black or African American	0	0	0	0	0	0	0	0	0	0
White	0	0	0	0	0	0	0	0	0	0
More than One Race	0	0	0	0	0	0	0	0	0	0
Unknown or Not Reported	0	0	0	0	0	0	0	0	0	0
Total	0	0	0	0	0	0	0	0	0	0

Obtained via FOIA by Judicial Watch, Inc.

Section 3 - Protection and Monitoring Plans (Study 1)

3.1. Protection of Human Subjects	NIAID_COV_2019_Protection_Human_Subjects_Final.pdf
3.2. Is this a multi-site study that will use the same protocol to conduct non-exempt human subjects research at more than one domestic site?	○ Yes ● No ○ N/A
If yes, describe the single IRB plan	
3.3. Data and Safety Monitoring Plan	
3.4. Will a Data and Safety Monitoring Board be appointed for this study?	○ Yes ● No
3.5. Overall structure of the study team	

Obtained via FOIA by Judicial Watch, Inc.

PROTECTION OF HUMAN SUBJECTS:

1. Risks to Human Subjects

1.1 Human Subjects Involvement, Characteristics, and Design

This project is a study of human exposure to animal coronaviruses in southern China. Subjects will be enrolled on a voluntary basis and informed consent will be obtained from all participants. Consenting participants will provide biological samples and complete a questionnaire. Subjects will be individuals: 1) who are highly exposed to bats in community settings, including through hunting, butchering, or general handling within the context of their living or working environment (≥ 18 years old); and 2) patients admitted to hospitals and clinics presenting with disease symptoms of clinically-defined severe/acute respiratory illness (SARI/ARI) or Influenza-like illness (ILI) of unknown origin (≥ 12 years old).

The study population will be selected from the Yunnan, Guangxi, Guangdong, and Guizhou provinces of China. We will aim to enroll: 1) in 12 clinic sites across the four provinces, 2,750 individuals (accounting for an estimated 40% loss from follow-up); and 2) in 8 community sites, 1,650 individuals per each of the four provinces, pooled across two sites for each province for a total of 6,660 (1,650*4) participants, allowing us to make province-level comparisons of differing effects (one time data collection, no follow-up among community participants). The community and clinical sites are further defined in **"Specific Aim 2: Using community-based and clinical biological-behavioral surveys to identify SARSr-CoV spillover, routes of exposure and public health consequences of human infection"**.

There are no data to suggest a gender or ethnic bias for coronavirus exposure or infection, therefore subjects will be enrolled based on exposure criteria, and subjects will not be excluded based on ethnicity or gender. We will also stratify sampling to ensure representation of sex, demographic, and socio-economic factors in each community site.

1.2 Sources of Materials

Samples to be collected and screened for coronaviruses include whole blood and nasal/oropharyngeal swabs. Samples will be collected and a questionnaire will be administered by trained medical personnel from the local CDC, hospitals, and clinics. In community sites, whole blood samples (only) will be collected once during Years 2-4 of the study, and samples will be screened for coronaviruses using developed ELISA at the Institute of Pathogen Biology and the Wuhan Institute of Virology. In clinic sites, both whole blood samples and nasal/oropharyngeal swabs will be collected at enrollment, and samples will be screened for coronaviruses using ELISA and consensus PCR (cPCR). Patients who test positive for coronavirus or antibodies to coronavirus will be followed up 35 days after enrollment, when additional blood samples will be collected for serological testing with ELISA.

At the enrollment, a standardized questionnaire will be administered at both community and clinic sites to collect data on living circumstances (e.g. distance between the living house and closest bat roost, observed bats in house), income or livelihood, experience with SARI and ILI-like illness and involvement in activities with direct or indirect (e.g. via livestock) contact with bats. During the follow-up with clinic study participants, a standardized questionnaire supplement will be administered to collect additional data on the course of symptoms in the interim period. All electronic data will be password protected, and all hardcopy files and biological samples will be stored in secure storage facilities. All consent forms will be stored separately from any data in separated locked filing cabinets.

1.3 Potential Risks

The potential risks to study participants resulting from study participation are minimal. The volume of blood being collected is within normal safety limits. The questionnaire will be designed to assess exposure risk, and may ask personal questions, but they will conducted in private and confidentially to protect privacy. There may be some stress to subjects who are informed that they have been exposed to an animal virus, but counseling will be available and options for medical care will be included in the discussion.

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2. Adequacy of Protection against Risks

2.1 Recruitment and Informed Consent

Potential study participants at each site will be identified by well-trained in-country research team in partnership with local CDC staff (for community participants) and medical personnel (for clinic participants). The team will be thoroughly trained on communicating the research objectives, what is being asked of participants, any risks or benefits, and will be able to address any questions that potential subjects may have. Both written and oral descriptions of the study details will be provided in Chinese Mandarin (or orally via an interpreter in local dialects if necessary) as part of the informed consent process. Contact details of the collaborators at the local CDC or hospital and the study PI will be provided to all subjects, and CDC or hospital personnel on the research team will be available onsite to answer questions from the study subjects. Test results will be communicated to each subject and counseling offered to minimize stress.

2.2 Protection against Risks

After the informed consent process, the questionnaire will be conducted in private, ensuring that others cannot overhear responses. Individual sessions will be held in areas where there are no other individuals within a 10-foot distance. A barrier will be created so that no other individuals can view the participants during their interview. Depending on the location, this could be a private room, behind a building or fence, or behind a line of trees, obstructing view so that confidentiality may be maintained. The interview team will take care to pair interviewers and respondents by sex to the best of their ability to increase the level of comfort of the participant and the team will ensure the privacy and confidentiality of responses. Children will not be interviewed in the absence of a parent or guardian. This study will not involve greater than minimal risk, and every effort will be made to ensure the privacy, dignity, and well-being of children who participate in this study.

3. Potential Benefits to Subjects and Others

There are potential benefits to the study subjects including receiving a physical exam/health check from a medical officer and the potential benefit of identifying a health hazard. At the conclusion of the study, we will deliver an educational workshop for high risk individuals (open to study subjects and non-study subjects) describing the health benefits of using PPE and hand-washing during animal handling activities throughout the day, as well as to share other prevention interventions that emerge from the research data.

4. The Importance of Knowledge to be Gained

There are valuable potential benefits to the general public from the knowledge to be gained by this study, as it may identify sources of zoonotic coronaviruses in the market system or through hunting. Avoidance of these animals or extra care when handling them may substantially reduce the risk of CoVs (and other zoonotic pathogen) transmission.

Obtained via FOIA by Judicial Watch, Inc.

Section 4 - Protocol Synopsis (Study 1)

4.1. Brief Summary

4.2. Study Design

4.2.a. Narrative Study Description

4.2.b. Primary Purpose

4.2.c. Interventions

Type	Name	Description

4.2.d. Study Phase

Is this an NIH-defined Phase III Clinical Trial? ❍ Yes ❍ No

4.2.e. Intervention Model

4.2.f. Masking ❍ Yes ❍ No

❑ Participant ❑ Care Provider ❑ Investigator ❑ Outcomes Assessor

4.2.g. Allocation

4.3. Outcome Measures

Type	Name	Time Frame	Brief Description

4.4. Statistical Design and Power

4.5. Subject Participation Duration

4.6. Will the study use an FDA-regulated intervention? ❍ Yes ❍ No

4.6.a. If yes, describe the availability of Investigational Product (IP) and Investigational New Drug (IND)/ Investigational Device Exemption (IDE) status

4.7. Dissemination Plan

Obtained via FOIA by Judicial Watch, Inc.

Delayed Onset Studies

Delayed Onset Study#	Study Title	Anticipated Clinical Trial?	Justification
The form does not have any delayed onset studies			

Obtained via FOIA by Judicial Watch, Inc.

VERTEBRATE ANIMALS:

1. **Detailed description of animal use.**

Work with vertebrate animals will be conducted at Wuhan University at the School of Medicine in Wuhan, China and the University of North Carolina, Chapel Hill, USA.

Capture and sampling techniques for all wild animals (bats) described in this study have been previously approved by multiple Institutional Animal Care and Use Committees (IACUCs) for projects led by EcoHealth Alliance. These institutions include: UC Davis IACUC (Mazet and Epstein; UC Davis 15898; current); and The Cummings School of Veterinary Medicine at Tufts University (Olival and Epstein, current), Animal Welfare Assurance (#A4059-01) on file with the Office of Laboratory Animal Welfare at the National Institutes of Health. We have prepared a draft IACUC application for this project, and will submit it within 1 month of the project's start date (to Tufts University) to minimize delays in beginning Year 1 field sampling.

Experimental work using humanized mice will be conducted at the Center for Animal Experiment Biosafety 3 lab of Wuhan University at the School of Medicine in Wuhan, China and the University of North Carolina at Chapel Hill, the Institute for Pathogen Biology. The Wuhan laboratory is AAALAC accredited and has both an Institutional Biosafety Committee and an Institutional Animal Care and Use Committee. We will submit our protocols for IACUC approval should this proposal be funded. Conditions for animal use are described below. Both laboratories (Wuhan and UNC) have Internal Biosafety Committees and are accredited BSL-2 and BSL 3 laboratories. Animals will be housed in a BSL-3 facility and will be under the care of a full-time veterinarian. All experimental work using infectious material will be conducted under appropriate biosafety standards. Disposal of hazardous materials will be conducted according to the institutional biosafety regulations.

Note: The majority of wild bats captured and sampled will be done using non-destructive, techniques. In a small number of instances (~ 2 bats per species for previously unsampled *Rhinolophus* sp.), where intestine and lung tissue is required to establish cell lines, animals will be humanely euthanized and a necropsy performed according to accepted protocols (see euthanasia section)

Bat capture. Free-ranging bats will be captured using either a mist net or harp trap. The net system is manned by two people during the entire capture period, and bats are removed from the net as soon as they become entangled to minimize stress and prevent injury. In the Co-PI's (Dr. Olival) experience, a maximum of 20-30 bats can be safely held and processed by a team of three people per trapping period. Duration of trapping will depend on the capture rate. Bats are placed into a pillowcase or small cloth bag and hung from a branch or post until samples are collected. Bats are held for a maximum of six hours (typically less than 3 hours), and released after sampling.

Laboratory mice. Lab mice will be sourced commercially by the Wuhan Center for Animal Experiment at Wuhan University.

Sample Collection:

Bats: Bats will be manually restrained during sampling. Depending on the species and size of bat, swabs will be taken from the oropharynx, urogenital tract, and rectum. Fresh feces will be collected if available, in which case a rectal swab will not be collected. Blood will be collected from fruit bats either from the cephalic vein or from the radial artery or vein using a 25 gauge needle and 1cc syringe. Blood

Obtained via FOIA by Judicial Watch, Inc.

will be collected from bats weighing less than 100g according to published techniques (*126*).
Rodents: Anesthesia for captive small rodents will be conducted using plastic tubes, with the animals transferred directly from the traps to the tubes containing a cotton swab soaked in ether, isoflurane, or methoxyflurane for anesthetic induction. For larger rodents, chemical restraint and anesthesia (ketamine alone, or ketamine combined with xylazine) will be applied either through the squeeze cages by syringe if applicable. Once anesthetized a small blood sample will be collected using a capillary tube placed into the retro-orbital sinus. Only trained technicians will perform retro-orbital bleeding and it will only be performed on anesthetized rodents. Femoral or jugular venipuncture may be used for larger rodents (e.g. rats). In all rodents, blood volumes of no more than 1% of body weight will be withdrawn. (example 0.2 ml blood from a 20 gram rodent).

Laboratory Mice. Humanized mice will be bred at the University of Wuhan and University of North Carolina at Chapel Hill. Mice will be inoculated with a specific dose (e.g. $1x10^6$ TCID50) of virus through different routes (intranasally and intraperitoneally). Mouse body temperature will be monitored with implanted temperature sensing microchips (LifeChip Bio-thermo, Destron Fearing), and mice will be weighed daily. Animals will be observed daily for clinical signs of illness. Moribund mice will be euthanized, according to AVMA recommendations. Live animals will be euthanized at three weeks post-inoculation and organs harvested. We will collect sera on days 10, 15 and 21 to test for neutralizing antibodies against bat CoVs. We will collect nasal washes, oral swabs, and rectal swabs, and urine every two days. These are minimally invasive procedures, and will be performed by experienced lab technicians under the supervision of a full-time veterinarian.

2. Justify use of animals, choice of species, numbers to be used. Species and number used in study: The purpose of this study is to conduct targeted, but extensive surveillance of bat populations in Southern China to detect coronaviruses that may pose a risk to the health of both humans and animals. The experimental work is designed to understand the ability of bat coronaviruses to bind to human receptors. In this renewal application, we propose a total bat sample size comparable to our initial R01 effort of ~5000 animals. These animals will be sampled from ~15-20 species collected across 4 provinces. Given ~5-12% prevalence of SARSr-CoVs in *Rhinolophus* spp. at our previous sites during our initial R01, this sample size would give us 425 (±175) positive individual bats, and allow us to identify ~125 novel strains. Assuming a conservative prevalence rate, a sample size of n=110 individuals per species will allow us to detect SARSr-CoV using PCR with a power of 80%. **Wild bats**: We will sample a minimum of 110 individuals from ~15-20 different bat species from sites across four provinces in Southern China (Yunnan, Guangxi, Guizhou and Guangdong). Sampling will focus on species in the family *Rhinolophidae,* genus *Rhinolophus.,* but will also include individuals in the related genera *Hipposideros* and *Aselliscus.* In every situation, sampling of wildlife will be conducted in the most humane manner while minimizing the impacts on individual animals and their wild populations. In all instances, the fewest number of animals will be sampled that will provide valid information and statistical inference for the pathogen and disease of interest and every effort will be made to minimize stress and discomfort for the animal.

A small number of bats (maximum 2 per species) representing each of the species in this study may be euthanized in order to collect lung and intestinal tissue required for characterizing coronavirus receptors. Voucher specimens may also be collected at the discretion of the team leader for the accurate identification of species using molecular methodology.

Humanized mice for experimental infection for Specific Aim 3: In order to understand whether select strains of bat-borne CoVs utilize receptors found in people have the potential to infect people, we will use Swiss albino mice (standard breed at Wuhan University) that have been genetically modified to have

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human receptors. We'll infect them with cultured bat coronaviruses and determine which organs become infected and whether these mice are capable of shedding infectious virus. Humanized mice will be genetically modified to carry human ACE2 gene will be used to evaluate pathogenesis of CoVs. We cannot anticipate exactly how many viruses we will find that are candidates for experimental models, however will likely identify approximately 5-6 bat SARSr-CoV strains that will be used for mouse infection experiments. We will use 15-20 adult mice per virus strain, and therefore will require a maximum of 120 mice over the study period.

3. **Provide information on veterinary care.** For wild caught animals, **t**here is no specific veterinary care that is appropriate, nor will clinical veterinary facilities be available. Animals that are injured during the capture or sampling process will be assessed by an experienced team leader, and if the animal is determined to be unlikely to survive if released, it shall be euthanized humanely (see euthanasia section). Animals will be released within hours of capture.

Laboratory mice will be housed in BSL-3 small animal facilities at the Center for Animal Experiment at Wuhan University and University of North Carolina at Chapel Hill, the Institute for Pathogen Biology. Experimental animals will be regularly monitored by experienced staff and a supervising veterinarian. The animal facility operates 24 hours a day and has full-time veterinarians on staff. All animals will be provided with food and water ad libitum and will otherwise receive standard care.

4. **Procedures for ensuring animal comfort, lack of distress, pain, or injury:** Wild bats will not be held longer than 6 hours during the sampling process. Co-PI Olival has extensive experience in capture, anesthesia, and sampling wildlife, especially bats. In our team's experience, bats tolerate the described procedure well. Mist nets will be attended continuously during capture periods, and bats will be extracted from the net as soon as they become entangled. This will minimize stress and injury from entanglement. Bats will be placed individually in cotton bags and hung from tree branches while awaiting processing and during recovery. The bags are sufficiently porous as to allow for ventilation and are designed for bat capture. The enclosed environment seems to calm the bats, as they do not struggle once inside, but they hang quietly – this is a standard and accepted practice in the bat research world and best way to minimize stress to the animal. Animals will be monitored by a veterinarian or experienced field team member during all stages of capture, processing, and release. Animals will be kept in a cool place while in the pillowcases.

The procedures used in this experiment (blood draw, nasal, oral, and rectal swabs) are minimally invasive. Mice that show signs of morbidity post-infection will be examined and euthanized according to AVMA standards (see below).

5. **Euthanasia:** In the event of injury to an animal that results in pain and suffering, and reasonable veterinary care is unavailable, the animal will be euthanized by a veterinarian or trained field team member using ketamine injected intramuscularly 37.5mg/kg and sodium pentobarbital injected intravenously at a dose of 1.0ml per 5kg injected intravenously. This protocol is in accordance with the AVMA euthanasia report (2007). Any animal that is euthanized using a chemical agent will be disposed such that it will not be permitted to enter the food supply either through markets or hunting.

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SELECT AGENT RESEARCH/BIOHAZARDS. No select agent research.

Agents: SARS-related bat coronaviruses (SARSr-CoV), like WIV1, WIV16 and SHC014. These bat viruses are distantly related to the epidemic human SARS-CoV which emerged in 2003 and caused 8,000 cases and 800 deaths worldwide. While the epidemic human SARS-CoV is a BSL3 select agent, the SARSr-CoV are BSL3 pathogens in the US and not select agents. The proposal will use a SARSr-CoV molecule clone designated WIV1 during the course of these studies, which is NOT a select agent. This strain has not been shown to cause human disease or be transmissible between humans. All recombinant DNA work will use the bat SARSr-CoV WIV1 molecular clone. At the University of North Carolina (US Government select agent certified laboratory), some virus growth studies will be conducted in primary human airways, comparing wildtype SARS-CoV, WIV1 and various SARSr-CoV WIV1 chimeric virus growth kinetics. Wildtype SARS-CoV strain research will not be conducted at the Wuhan Institute of Virology.

Registration status of all entities where select agent(s) will be used. Wildtype SARS-CoV is a select agent. UNC-Chapel Hill is currently registered with the CDC for select agent use, including SARS-CoV, as required by select agent regulations (42 CFR 73). The UNC SARS select agent laboratories are routinely inspected by the environmental health and safety department at UNC and by the CDC. Workers receive select agent and BSL3 training focused on SARS-CoV safety, procedures and protective clothing/PAPR training each year.

Introduction and Background. SARS-CoV caused outbreaks with significant case fatality rates, and there are no vaccines available for this agent. SARS-CoV is classified as a BSL-3 select agent. Wildtype SARS-CoV is currently thought extinct in the wild. The work proposed in this application will involve two aspects: field work and laboratory work, focusing on distantly SARS-like bat coronaviruses (SARSr-CoV). Fieldwork involves the highest risk of exposure to SARSr-related or other bat CoVs, while working in caves with high bat density overhead and the potential for fecal dust to be inhaled. There is also some risk of exposure to pathogens or physical injury while handling bats, civets, rodents or other animals, their blood samples or their excreta. The Co-PIs and field team have extensive experience and certification working with wildlife species and high-biosecurity pathogens (Nipah virus, ebolavirus, SARS), and great care will be taken in the field to limit the risk of accidental exposure to known or unknown animal pathogens. We have strict procedures for handling bats and working with samples from them as they are secured in the field and transported to the lab. Field team members handling animals will be trained to utilize personal protective equipment (PPE) and practice proper environmental disinfection and biosafety techniques. This includes wearing coveralls or dedicated clothing, nitrile gloves, eye protection, and a P95 or P100 respirator during bat handling and sampling. Fully Tyvek suits and HEPA-filtered Powered Air Purifying and Supplied Air Respirator Systems (PAPRs) will additionally be worn in cave systems where there is a higher risk of contact with aerosolized bat feces. All field clothing and equipment will be disinfected using Virkon disinfectant. All biological waste from field surveys will be disposed of in the appropriate container (sharps box or an autoclave bag) and will be autoclaved at local hospitals or university labs. All personnel will be vaccinated against rabies and have a neutralizing antibody titer, in accordance with WHO and CDC recommendations. Field teams will carry rabies boosters in the field and will receive a booster in the event of a potential rabies exposure.

Field safety protocol: Our procedures to deal with bites, needle-sticks etc. are as follows: The wound is washed thoroughly with soap and water to clean away dirt and debris, then vigorously scrubbed with a sterile gauze bandage and benzalkonium chloride for 5 minutes. If bleeding, pressure is applied with a sterile bandage for until bleeding has stopped. If the wound continues to bleed, medical attention at the nearest hospital is sought. The bat from which the bite or exposure originated is identified, and the samples collected from it labeled on the data sheet that these were involved in an exposure. Our procedures require that the person potentially exposed reports to a major hospital within 24 hours to

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have wound examined and receive a rabies post-exposure booster vaccines as per WHO/CDC protocols. The laboratory work is lower risk, as samples placed in lysis buffer will be non-infectious. Samples placed in viral transport medium and frozen will be stored at ultra-low temperatures (-86˚C) until viral isolation is required. Serum will be heat inactivated at 56˚C for 30 minutes prior to testing.

Lab biosafety: The University of North Carolina at Chapel Hill, the Institute for Pathogen Biology, the Wuhan Institute of Virology, and the Wuhan University Center for Animal Experiment BSL-3 laboratories all have respective Internal Biosafety Committees and are accredited BSL-2 and BSL 3 laboratories. All experimental work using infectious material will be conducted under appropriate biosafety standards. Disposal of hazardous materials will be conducted according to the institutional biosafety regulations.

Available Treatments: No approved treatments are related for SARS and the SARSr-related bat coronavirus infections. However, therapeutic antibodies and nucleoside analogues have been successfully used in SARS-infected rodents and primates, which could be approved for compassionate use in humans exposed to the SARSr-CoV.

UNC Facilities where the select agent(s) will be used. SARS-CoV will be manipulated in research activities including establishment of viral replication curves, infection of rodent animal models and performance of plaque assays in laboratory spaces that meet operational and procedural criteria for BSL-3 activities as outlined in the CDC/NIH “Biosafety in Microbiological and Biomedical Laboratories”, 5th edition, as well as BSL-3 criteria outlined in the NIH Guidelines for Research Involving Recombinant or Synthetic Nucleic Acid Molecules (April 2016). In addition, all mouse studies at UNC-Chapel Hill will be performed in an approved and registered BSL-3/ABSL-3 laboratory equipped with Techniplast Sealsafe^{TM} HEPA-filtered animal housing for rodents. All animal protocols will be approved by the UNC-Chapel Hill IACUC.

UNC BSL-3/ABSL-3/select agent laboratories are equipped with biosafety cabinets, incubators, centrifuges with containment features, cold storage units, an autoclave, sink, eyewash and life safety equipment, and mechanical system monitors and alarms to support effective isolation and containment of operations involving SARS-CoV and SARSr-CoV. The anterooms to the BSL-3 laboratories house PAPR charging stations, laboratory and safety supplies, and a changing area. For both the BSL-2 and BSL-3 select agent spaces, access to select agents is restricted by the door between the hallway and anteroom and the door between the anteroom and BSL-3 space, requiring a combination of swipe card and punch code for entry. All select agent materials (SARS-CoV virus and genome length RNA) are stored in locked freezers and incubators.

UNC Procedures for monitoring possession, use and transfer of select agents. All personnel who will have access to select agent-regulated materials have been added to the Select Agent registration following security risk assessments prescribed by the CDC Select Agent Program. Personnel have completed training in all aspects of select agent compliance requirements and have adopted changes to standard operating procedures as applicable to assure that these requirements are met. Personnel will follow all procedures prescribed for accessing and securing the laboratory, documenting laboratory activities and materials used, and responding to incidents that could result in theft, loss, or release of select agent-regulated materials. Transfers of select agent-regulated materials will be coordinated by the laboratory managers and Responsible Official in accordance with standard operating procedures, including obtaining appropriate permits for shipping select agent materials and observing all regulations for shipping, both under dangerous goods and select agent regulations. Transfer of select agent RNA in TRIzol from registered BSL-3 to registered BSL-2 space and cDNA from registered BSL-2 space to non-registered BSL-2 space is conducted according to current select agent rules, regulations, and guidelines, including the new inactivation policies released in 2017.

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UNC Biosafety, biocontainment, and security of the select agent(s). The Baric laboratories have been operational with BSL-3 core policies and procedures for ~15 years. Standard operating procedures at BSL-3 have been reviewed and approved by the UNC Chapel Hill Institutional Biosafety Committee and undergo both annual review and approval as well as updates as laboratory processes change or biosafety procedures evolve. The content of these documents has been formatted to conform to select agent regulations for the biosafety, security, and incident response plans. Additionally, lab-specific security risk assessments have been completed and recommendations implemented to ensure that security measures and procedures are sufficient to effectively minimize the possibility of unauthorized access to select agent-regulated materials. The UNC Chapel Hill facilities have undergone multiple CDC inspections and are currently in compliance with CDC requirements relating to SARS-CoV and select agent status. Our three-year renewal inspection occurred in June 2018 and we have been renewed for another three years.

UNC Biocontainment resources. All BSL-3 laboratories are under negative pressure, with redundant systems to ensure that negative pressure is maintained. All BSL-3 facilities have autoclaves to decontaminate waste materials as well as approved protocols for treatment or inactivation of any materials leaving the laboratory. All personnel are extensively trained in basic virology and safety protocols before being approved for select agent work and undergo additional extensive training to work with SARS-CoV and related SARSr-CoV as a BSL-3 pathogen. In both laboratories, annual testing is performed to verify that biosafety cabinets, laboratory supply/exhaust systems (including alarms), and other laboratory equipment are functioning as designed. The laboratories are secured at all times, and only personnel who have successfully completed Select Agent clearance and laboratory specific training requirements are permitted to enter without an escort.

P3CO Research. Recognizing the implementation of new gain of function research guidelines under P3CO, SARS-CoV and MERS-CoV are subject to these guidelines, and as such, reverse genetic studies are subject to review. Our group has considerable expertise in interfacing with the appropriate NIH P3CO institutional review boards to review, revise and finalize research designs that have the potential to modify pathogenesis or transmissibility in mammals. **Importantly, we are not proposing to genetically manipulate SARS-CoV** over the course of this proposal. However, we are proposing to genetically manipulate the full length bat SARSr-CoV WIV1 strain molecular clone during the course of the proposal, which is not a select agent, has not been shown to cause human infections, and has not been shown to be transmissible between humans.

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CONSORTIUM/CONTRACTUAL ARRANGEMENTS:

This project is a multi-institutional collaboration led by EcoHealth Alliance, New York (Daszak, PI), which will subcontract funds to three institutions: the Wuhan Institute of Virology (Dr. Shi), the University of North Carolina at Chapel Hill (Dr. Baric), and the Institute of Pathogen Biology (Dr. Ren). In addition, Dr. Linfa Wang from Duke-National University of Singapore (Duke NUS) will act as a senior consultant with no requested subcontract funds, and will primarily advise on the serological and molecular based diagnostic platforms. Dr. Daszak has over 15 years previous experience managing collaborative projects including two R01s on Nipah virus ecology and the current R01 on Coronavirus (AI110964) that involve multiple, separate foreign institutions; a 5-year NSF/NIH Ecology of Infectious Disease award on West Nile virus which involved multiple subcontracts, a NIAID R01 on bat viral discovery that involved multiple international contracts, and a multi-million dollar per year contract from USAID that involves 21 international partners. The applicant organization (EcoHealth Alliance) is justified in taking the lead on this project because it specializes in understanding the ecological, and virological processes underlying zoonotic disease emergence. Dr. Daszak has conducted significant preliminary work on this issue including 15-years of research on the ecological and related factors of the emergence of SARS and 15-years of work in China. The subcontract institutions will work on specific issues and areas in which they have proven expertise. These areas are:

- Human community surveillance, human clinical or hospital syndromic surveillance, CoV serology, full genome sequencing, epidemiology, and behavioral risk (Institute of Pathogen Biology, Dr. Ren)
- CoV screening and serology of non-human samples, viral pathogenesis, serological testing protocol development, host receptor binding, S protein sequencing, *in vitro* and *in vivo* virus characterization (Wuhan Institute of Virology, Dr. Shi)
- Small animal models of viral pathogenesis, primary human cell cultures, CoV reverse genetics, reconstruction of zoonotic CoV (University of North Carolina at Chapel Hill, Dr. Baric).

Dr. Daszak has had inter-institutional contractual agreements with the Wuhan Institute of Virology for over 13 years. Drs. Shi and Daszak have collaborated together since 2002 and have been involved in running joint conferences, collaborating on papers, and shipping samples into and out of China. Drs. Baric, Shi, Wang, and Daszak have collaborated closely for over 10 years on Coronavirus and other emerging disease research. Drs. Shi and Ren have collaborated on viral discovery projects 8 years.

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WUHAN INSTITUTE OF VIROLOGY
THE CHINESE ACADEMY OF SCIENCES

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31 October 2018

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

The Wuhan Institute of Virology, Chinese Academy of Sciences, has an high interest in working with EcoHealth Alliance and its scientists to identify and prevent the transmission of bat coronaviruses to human populations globally. In particular, the NIAID funded R01 renewal proposal entitled "Understanding the risk of bat coronavirus emergence" will provide an excellent opportunity to achieve these goals.

The Wuhan Institute of Virology, Chinese Academy of Sciences, recognizes the mutual benefits to be gained through research cooperation and a successful partnership with EcoHealth Alliance in the field of identification and prevention of zoonotic disease transmission. It is vital to not only identify the diseases themselves, but also identify high-risk human populations and the actions that put them at risk for infection along with evaluating approaches to intervention and disease management.

Understanding and preventing exposure and transmission of zoonotic diseases from wildlife to humans remains a high priority for prevention of pandemics. In our discussion with EcoHealth Alliance, we have agreed to participate in activities that will strengthen the ability of China and other countries in the region to respond to epidemic disease outbreaks – particularly those of animal origin. To assist in this study, we will provide participating laboratories in China with human samples both new and archived and support research in bat coronaviruses.

We at Wuhan Institute of Virology, Chinese Academy of Sciences, look forward to our continued collaborations with the EcoHealth Alliance team and working further on this worthwhile study.

Sincerely,

Dr. Yanyi Wang
Director, Wuhan Institute of Virology
Chinese Academy of Sciences
Xiao Hong Shan, No.44
Wuhan 430071 China
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中国医学科学院
北京协和医学院 病原生物学研究所

01 November 2018

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

The Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College (IPB, CAMS&PUMC) has an high interest in working with EcoHealth Alliance and its scientists to identify and prevent the transmission of bat coronaviruses to human populations globally. In particular, the NIAID funded R01 proposal entitled "Understanding the risk of bat coronavirus emergence" will provide an excellent opportunity to achieve these goals.

The IPB, CAMS&PUMC recognizes the mutual benefits to be gained through research cooperation and a successful partnership with EcoHealth Alliance and long term colleague Dr. Zhang Shu-Yi in the field of identification and prevention of zoonotic disease transmission. It is vital to not only identify the diseases themselves, but also identify high-risk human populations and the actions that put them at risk for infection along with evaluating approaches to intervention and disease management.

Understanding and preventing exposure and transmission of zoonotic diseases from wildlife to humans remains a high priority for prevention of pandemics. In our discussion with EcoHealth Alliance, we have agreed to participate in activities that will strengthen the ability of China and other countries in the region to respond to epidemic disease outbreaks – particularly those of animal origin. To assist in this study, we will provide participating laboratories in China with human samples both new and archived and support research in bat coronaviruses.

We at IPB, CAMS&PUMC look forward to our continued collaborations with the EcoHealth Alliance team and working further on this worthwhile study.

Sincerely,

Lili Ren
Co-Investigator
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UNC
GILLINGS SCHOOL OF
GLOBAL PUBLIC HEALTH

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October 24, 2018

Peter Daszak, PhD
EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

Reference: *Program Announcement number PA-18-484, entitled* NIH Research Project Grant (Parent R01 Clinical Trial Not Allowed), *dated December 6, 2017*

Dear Dr. Daszak,

This letter confirms that the appropriate program and administrative personnel at The University of North Carolina at Chapel Hill (UNC-CH) have reviewed the above referenced program announcement and are committed to enter into a subcontract with the EcoHealth Alliance for the performance period of July 1, 2019 to June 30, 2024. The work to be performed by UNC-CH does not include animal and/or human research subjects. UNC-CH maintains an active and enforced conflict of interest policy meeting the requirements of 42 CFR Part 50, Subpart F and 45CFR Part 94.

EcoHealth Alliance's Principal Investigator on this proposal is Dr. Peter Daszak. The UNC-CH budget, budget justification and scope of work are provided as separate enclosures to this letter. The estimated cost of the proposed subcontract will not exceed $388,750 and includes appropriate direct and indirect costs.

Furthermore, by submission of this commitment letter UNC-CH and its Principal Investigator (PI) certify (1) that the information submitted within the application is true, complete and accurate to the best of the UNC-CH's and PI's knowledge; (2) that any false, fictitious, or fraudulent statements or claims may subject the UNC-CH and PI to criminal, civil, or administrative penalties; and (3) that the PI agrees to accept responsibility for the scientific conduct of the project and to provide the required progress reports if an award is made as a result of UNC-CH's application.

If you have any questions, please contact the undersigned at 919-966-3895.

Sincerely,

Terry Magnuson, PhD
Vice Chancellor for Research

Ralph S Baric, PhD
Professor, Epidemiology, Microbiology and Immunology

Enclosed:
Budget
Budget Justification
Scope of Work

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DukeNUS Medical School

31 Oct, 2018

Dr. Peter Daszak
EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001, **USA**

Dear Peter,

I am writing this letter in strong support of the proposed renewal of the NIH (R01AI110964, Understanding the Risk of Bat Coronavirus Emergence) project led by EcoHealth Alliance.

As you know, I have long experience with EIDs associated with bats, having worked with Hendra virus in Australia, Nipah virus in Malaysia, Singapore and Bangladesh, SARS related viruses in China, Reston ebolavirus in the Philippines. More recently, in collaboration with scientists in EcoHealth and China, I played an important leadership role in coordinating and directing the research which discovered abat HUK2-related coronavirus as the causative agent of a major swine acute diarrhea syndrome (SADS) outbreak in Southern China.

Your current proposal complements and substantially expands this approach in promising novel and more powerful tools to understand how host immune dynamics and heterogeneity in immune response affect the timing, location, and severity of disease outbreaks in wildlife, and risk of spillover from wildlife to human populations.

I very much looking forward to participating in this initiative and should EcoHealth Alliance be successful in its application for renewal, I agree to participate in activities associated with this project, including contributing expertise, helping identify, locate and interpret relevant data, and participating in partner meetings.

This letter conveys my strong interest and commitment to making this initiative a success. I am excited to be part of the initiative to develop tools to better interrogate seroprevalence data and better predict zoonotic disease emergence. I'm confident that the approach will improve our understanding of the dynamics of infectious diseases and have wide application in public health, and I look forward to working with EcoHealth Alliance on this project

Yours sincerely,



Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director, Programme in Emerging Infectious Diseases

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RESOURCE SHARING PLAN

Data Sharing Plan: Data will be available to the public and researchers without cost or registration, and be released under a CC0 license, as soon as related publications are in press. Data will be deposited for in long-term public scientific repositories – all sequence data will be made publicly available via GenBank, species location data via the Knowledge Network for Biodiversity, and other data will be deposited in appropriate topic-specific or general repositories. Computer code for modeling and statistical analysis will be made available on a code-hosting site (GitHub), and archived in the Zenodo repository under an open-source, unrestrictive MIT license. Limited human survey and clinical data will be released following anonymization and aggregation per IRB requirements. Publications will be released as open-access via deposition to PubMed commons.

Viral isolates will remain at the Wuhan Institute of Virology initially. Isolates, reagents and any other products, should they be developed, will be made available to other NIH-funded researchers via applicable Wuhan Institute of Virology and EcoHealth Alliance Material Transfer Agreements and/or licensing agreements.

Sharing Model Organisms: We do not anticipate the development of any model organisms from this study. Should any be developed, they will be made available to other NIH-funded researchers via applicable Wuhan Institute of Virology and EcoHealth Alliance Material Transfer Agreements and/or licensing agreements.

Genomic Data Sharing: We anticipate obtaining genetic sequence data for 100s of novel coronavirus genotypes, including RNA-dependent RNA polymerase (RdRp) and Spike genes for all strains/genotypes. In addition, we will generate full viral genomes for a subset of the bat SARSr-CoVs that we identify. All sequence data will be deposited in the NIH genetic sequence database, GenBank. We will ensure that all meta-data associated with these sequences, including collection locality lat/long, species-level host identification, date of collection, and sequencing protocols will also submitted. The genotype data will be made publicly available no later than the date of initial publication or six months after the receipt of final sequencing data, whichever comes first. We anticipate sequence generation will occur over the 5 year proposed project period.

Genome Wide Association Studies (GWAS): Not applicable.

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Rigor and Authentication of Key Biological and/or Chemical Resources

Our project aims to understand the risk of bat SARS related coronavirus (SARSr-CoV) disease emergence in people, and will use some non-standard biological and chemical resources that require validation and authentication. We will construct chimeric SARSr-CoVs using a WIV1 backbone and the S genes of selected SARSr-CoV strains, and assess capacity to infect hACE2, bACE2 and cACE2 Vero cells, HeLa cells, primary human airway epithelial cells, and potentially CaCo cells for HKU3r-CoVs (which have not yet been cultured in human cell lines and may use intestinal epithelium in nature). We will then conduct experimental infections in hACE2 transgenic mice to assess pathogenicity and clinical signs. Each of these methods have been previously validated and published by our collaborative research team, as highlighted in the research proposal. Each laboratory-based research partner in our project (including University of North Carolina (UNC), Wuhan Institute of Virology (WIV), Institute of Pathogen Biology (IPB) at Chinese Academy of Medical Sciences, and Duke National University of Singapore (DukeNUS)) each have specialized strategies to oversee the authentication of key biological resources, reagents and chemical resources. EcoHealth Alliance will actively engage with each partner to ensure that the highest quality science, public accountability, and social responsibility in the conduct of science are maintained throughout. The overall goal is to ensure that the underlying scientific foundation of the project from conception to completion is scientifically sound. To ensure scientific rigor (e.g., determining group sizes, analyzing anticipated results, reducing bias, ensuring independent and blinded measurements, improving precision and reducing variability including or excluding research subjects, and managing missing data), EcoHealth Alliance will review scientific approaches and outcomes throughout the duration of the award. We will ensure that experimental designs will include considerations of sex as a “Relevant Biological Variables” in all studies involving human subjects or vertebrate animals. Unless otherwise specified and justified, all experiments will include male and females. UNC and WIV will implemented an “audit trail” that tracks animals used in experimental investigations (Aim 3) from parents, through birth, shipment, experimentation, results, QC and analyses, providing outside researchers the ability to track experiments from conception through publication.

Cells.
Early passage primary human airway epithelial cells are a key reagent for the proposed studies. Human lung cells are derived from donors of both sexes and from all ages and ethnic groups. Care is taken during cell isolation to only handle one human organ at a time. Similarly, primary cell populations are handled carefully, only one donor cell type from a single donor at a time to avoid any mixing. The cells are observed to exhibit well-described prototypical characteristics of human primary lung cells in cell type specific medias in culture. For quality control, the cells are cultured in antibiotic free media to test for bacterial and fungal microbial contamination and are subjected to mycoplasma testing. Once the epithelial cells are grown as polarized and differentiated monolayers, a representative sample is subject to quality control histological analysis of cell morphology and Short Terminal Repeat (STR) marker profiling by the UNC Lineberger Cancer Center’s Tissue Culture Facility (TCF). Routine evaluations for mycoplasma contamination are routinely performed in the laboratory.

- Certain experiments also employ immortal cell lines. Cell lines are obtained from the ATCC, or from the TCF. The TCF maintains cell lines, utilizing STR marker profiling and records of authentication are available. New cell lines not available directly from the TCF can be authenticated through the STR marker service provided by the TCF. Cell lines are routinely evaluated for mycoplasma contamination.
- When receiving cell lines, lab members initially maintain isolation and keep them isolated from other authenticated cell lines until mycoplasma testing and STR marker profiling is performed. All cell lines must be authenticated before commencing experimental work with them.
- Records are maintained for each of the cell lines regarding 1) the origin of the cell lines; 2) when they were resuscitated; 3) number of passages; 4) all test results; 5) any unique distinguishing growth behavior; and 6) any known genetic features.
- Cells that have been passaged for 6 months after receipt or from resuscitation will be re-authenticated, or a new vial of the working stock will be thawed.
- Lab members routinely examine cultured cell morphology by phase microscopy and monitor the growth characteristics in culture. New vials of the working stock are thawed if deviation from the baseline is

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observed.
- Mycoplasma contamination is re-checked whenever cells are extensively passaged to create new stocks.

Animals (Mice)
- **Rodent genotyping for mouse strain genetic validation**. Inbred mouse strains are an invaluable tool for biomedical research, and hACE2 transgenic mice represent a key aspect of Aim 3 to assess pathogenicity and clinical signs for SARSr-CoVs. To ensure that the genetic background of all mice used within this program is known and when applicable they are part of a known inbred strains, we will genotype each mouse strain used within this program on the appropriate MUGA platform (Morgan, AP et.al., G3 2016, Dec 18). The most recent iteration of this state of the art genotyping array contains over 140,000 markers and can be used to precisely determine the genetic background at the substrain level and the precise location (at <1 megabase resolution) of genomic regions derived from different mouse inbred strains. In this way, the identity and genomic integrity of all mice used within these studies will be ensured. As new diagnostic assays become available, we will assess their utility and cost effectiveness the different MUGA arrays and implement them as appropriate.
- Furthermore, for each mutant mouse strain used within the project, positive diagnoses of the mutation will be assessed for each cohort of experimental animals with a diagnostic validated PCR assay or Sanger sequencing diagnostic to ensure proper results.

Recombinant and Wildtype Viruses and Mutant Derivatives.
- Recombinant and wildtype viruses contain unique marker mutations that allow for distinguishing strains and mutation profiles, using a combination of full genome sequencing, reverse transcription-polymerase chain reaction (RT-PCR) or RT-PCR restriction fragment length polymorphism analyses (RT-PCR RFLP). Our group has developed defined primer pairs to distinguish between SARS-CoV and SARS-related bat coronaviruses as well as MERS-CoV and MERS-related bat coronaviruses. All viruses will be validated and certified pure of contaminating viruses prior to use or shipment to other laboratories.