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Understanding the Risk of Bat Coronavirus Emergence

Project Number
2R01AI110964-06

Contact PI/Project Leader
DASZAK, PETER

Awardee Organization
ECOHEALTH ALLIANCE, INC.

Description

Abstract Text

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.

Public Health Relevance Statement

Program Director/Principal Investigator: Daszak, Peter 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.

NIH Spending Category

Biodefense Biotechnology Clinical Research Emerging Infectious Diseases Infectious Diseases Lung Pneumonia Pneumonia & Influenza Prevention Rare Diseases

Project Terms

Acute Acute Diarrhea Address Amino Acid Sequence Animals Behavior Behavioral Biological Cells China Chiroptera Clinic Clinic Visits Clinical Communities Coronavirus Coronavirus Infections Coupled Data Data Analyses Development Disease Outbreaks Epithelial Cells Exposure to Family suidae Future Genome

Geographic Distribution Geography Habitats Health Human In Vitro Individual Infection Influenza Investigation Lead Maps Middle East Respiratory Syndrome Coronavirus Modeling Molecular Monoclonal Antibodies Nature Paper Patients Phylogenetic Analysis

Read More

Details

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Not Applicable

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Country
UNITED STATES (US)

Department Type
Unavailable

Organization Type
Other Domestic Non-Profits

State Code
NY

Congressional District
12

Other Information

FOA
PA-18-484

Study Section
Clinical Research and Field Studies of Infectious Diseases Study Section[CRFS]

Fiscal Year
2019

Award Notice Date
24-July-2019

Administering Institutes or Centers
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

DUNS Number
077090066

CFDA Code
855

Project Start Date **01-June-2014**

Project End Date **30-June-2026**

Budget Start Date **24-July-2019**

Budget End Date **30-June-2022**

Project Funding Information for 2019

Total Funding
$661,980

Direct Costs
$538,926

Indirect Costs
$123,054

Year	Funding IC	FY Total Cost by IC
2019	NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES	$661,980

NIH Categorical Spending

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Funding IC	FY Total Cost by IC	NIH Spending Category
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES	$661,980	Biodefense; Biotechnology; Clinical Research; Emerging Infectious Diseases; Infectious Diseases; Lung; Pneumonia; Pneumonia & Influenza; Prevention; Rare Diseases;

Sub Projects

No Sub Projects information available for 2R01AI110964-06

Publications

No Publications available for 2R01AI110964-06

Patents

Thank you for your feedback!

No Patents information available for 2R01AI110964-06

Outcomes

The Project Outcomes shown here are displayed verbatim as submitted by the Principal Investigator (PI) for this award. Any opinions, findings, and conclusions or recommendations expressed are those of the PI and do not necessarily reflect the views of the National Institutes of Health. NIH has not endorsed the content below.

No Outcomes available for 2R01AI110964-06

Clinical Studies

No Clinical Studies information available for 2R01AI110964-06

News and More

Related News Releases

No news release information available for 2R01AI110964-06

History

No Historical information available for 2R01AI110964-06

Similar Projects

No Similar Projects information available for 2R01AI110964-06

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