BUZZ CHRONICLES > CVFUNDING Saved by @TXstillWatching See On Twitter

# Twitter Thread by EF





Who's face so I need to shove this into? Add HANDLES please in comment. Here are COVID19 Funding From 2014 to 2021

**Delaware and New York** 

China was always working fauci and the NIH ON THIS PROJECT

Delaware and New York ring a bell..... MONSTER ISLAND? PLUM ISLAND?

Award Number: R01AI110964 ORCAVEZATIONE NATIONAL INSTITUTE OF OPDIV: NIH AWARD CLASS: DISCRETIONARY AWARD ACTIVITY TYPE: SCIENTIFIC/HEAL												
Group Awards By Issue Date Pf or Funding Pf: ●	Issue Date FY Funding FY										VIEW AWARD ARSTRACT	
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#### But ukraine biolabs smh.. don't worry I'll drop the source at the end of the thread this needs to be addressed seriously

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Award Information

#### UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE

Award Number: R01AI110964 ORGANIZATION: NATIONAL INSTITUTE OF ALLERGY & INFECTIOUS DISEASES OPDIV: NIH AWARD CLASS: DISCRETIONARY

AWARD ACTIVITY TYPE: SCIENTIFIC/HEALTH RESEARCH (INCLUDES SURVEYS)

Issue

Date
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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 (Alm 3). Alm 2. Community, and clinic-based syndromic, surveillance to capture SARSr-CoV spillover, routes of

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	Legal Entity Name:	ECOHEALTH ALLIANCE INC
	Legal Entity Address:	1200 LINCOLN AVENUE
	Legal Entity City:	PROSPECT PARK
	Legal Entity State:	PA
	Legal Entity Zip Code:	19076
	Legal Entity COUNTY:	DELAWARE
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Legal Entity City:	PROSPECT PARK
Legal Entity State:	PA
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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 SARS-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 dose to bat habitats are the primary risk groups for spillover, that at one site diverses SARS-COVs exist that contain every genetic element of the SARS-COV genome, and identified serological evidence of human exposure among people innone and erview in Cell. Vet sallent queetositons remain on the origin, diversity, catacity to cause illness, and risk of grillover of these viruses. In this R01 address these issues through 3 specific anis: km 1. Characterize natural SARS-COV diversity in southern China. We will septentes to light proteins to lidentify viruses with the highest potential for spillover of views viruses. In this R01 address these issues through 3 specific anis: km 1. Characterize natural SARS-COV siglilover, routes of exposure and potential public health consequences. We will conduct biological-behavioral surveillance to capture SARS-COV siglilover, routes of exposure and potential gonalins (km 1), and clinic-based syndromic surveillance to capture SARS-COVs: & 2) assess possible health effects of SARS-COV sin flection in people. We will analyze bat-COV serology against human-willidle contact and exposure data to quantify risk factors for serological and PCR evidence of bat SARS-COVs: & 2) assess possible health effects of SARS-COV sinfection in people. We will analyze bat-COV serology against human-willefe contact and exposure data to quantify risk factors and health impacts of SARS-COV spillover, risk analts for receptor bioling