Potential pandemic bird flu modified to be more dangerous in new risky NIH research

By **Dilyana Gaytandzhieva** - January 24, 2022

Dr. Anthony Fauci, director of the US National Institute of Allergy and Infectious Diseases (NIAID), putting his protective suit. Photo: NIH

The US National Institutes of Health (NIH) has continued funding risky gain-of-function research (GoF) on potential pandemic pathogens, newly disclosed information reveals. The US government medical research agency has funded scientists to study avian influenza (bird flu) which does not transmit among humans. However, the NIH projects aim to make avian influenza viruses able to transmit among mammals and assess their pandemic potential as a possible threat to humans.

Gain-of-function (GOF) studies improve the ability of a pathogen to cause disease by increasing its virulence and transmissibility. These dangerous experiments have not been terminated even though COVID-19 has been suspected to be the result of such NIH-funded GoF research in the Wuhan Institute of Virology.

Instead of terminating all GoF research since the pandemic started NIH and its sub agency – the National Institute of Allergy and Infectious Diseases (NIAID), have continued their financial support for the following GoF studies: Transmissibility of Avian Influenza Viruses in Mammals (NIAID support ended in **August 2021**); Centers of Excellence for Influenza Research and Surveillance (CEIRS) (NIAID support ended in **March 2021**). The third one: Mimicking evolution to define mechanisms of airborne transmission of H7N9 viruses, started on 2nd September 2021 and is **ongoing**.

Transmissibility of avian influenza viruses in mammals

Project Number	Former Number	Contact PI/Project Leader	Awardee Organization
4R01AI069274-09	5R01AI069274-09	KAWAOKA, YOSHIHIRO	UNIVERSITY OF WISCONSIN-MADISON

Description

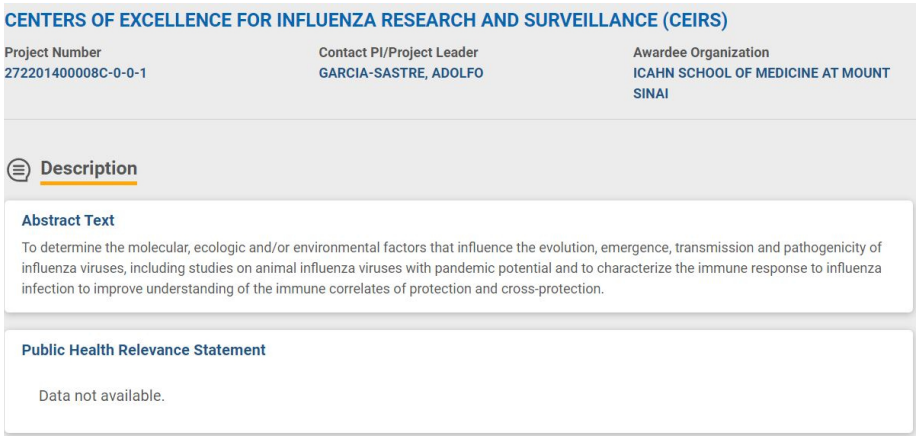
Abstract Text

DESCRIPTION (provided by applicant): Since 1997, highly pathogenic avian influenza viruses of the H5N1 subtype have infected humans with high case fatality rates, although no sustained human-to-human transmission has yet been reported. Currently, the molecular features and mechanisms that would result in human-to-human transmission of H5N1 viruses are not fully understood. Indeed, several attempts in the past to select transmissible H5 viruses (which typically do not transmit among mammals) were not successful, suggesting that influenza virus transmissibility is determined by several currently unknown factors. Recently, we screened H5 virus libraries possessing random mutations in the globular head region of the hemagglutinin (HA) protein and identified mutant H5 HAs that acquired the ability to bind to human-type receptors. These mutant H5 HAs did not support virus transmission among ferrets (an established influenza virus transmission model) via respiratory droplets, but acquired this ability after two passages of the virus in these animals, which resulted in the selection of additional mutations in HA. This marks the first conversion of an H5 virus that does not transmit among ferrets into one with efficient respiratory droplet transmission. Based on this finding, we propose to decipher the determinants of H5N1 virus transmission in mammals. In Aim 1, we plan "To Identify the Mechanisms That Control H5N1 Virus Transmissibility in Mammals". To gain a better understanding of the mutations in HA that result in transmissible viruses, we will select transmissible viruses based on H5 HA proteins derived from different subclades that have caused human infections. Our recent study suggested that HA stability may contribute to virus transmissibility. To test this concept, we also plan to identify mutations in HA that increase HA stability and then test these mutations for their significance in virus transmissibility. The HA proteins of all ferret-transmissible H5N1 viruses will then be characterized for their receptor-binding specificity, their structural consequences, their effects in other genetic backgrounds, and their pathogenicity in mice and ferrets. Mutations in HA that allow avian influenza viruses to bind to human-type receptors are most likely a prerequisite for transmission among mammals; however, findings by us and others indicate that human-type receptor binding is not sufficient for respiratory droplet transmission among ferrets, and that other viral genes also contribute to transmissibility. In Aim 2 ("To Characterize the Contribution of Viral Genes Other than HA to H5N1 Virus Transmissibility", we plan to passage non-transmissible viruses of different genetic backgrounds in ferrets to select transmissible mutants. Selected mutations will be characterized for their biological effects, using established assays for internalization, intracellular transport replication and transcription, assembly and budding, and interferon antagonism. Collectively, these studies are expected to generate critical information about the molecular determinants and mechanisms of H5N1 virus transmissibility in mammals.

Project 4R01AI069274-09 – Total funding: $605,206

H5N1, a highly pathogenic avian influenza virus, does not transmit among mammals. The researchers aim to make the virus able to transmit in order to assess its pandemic potential.

According to the project's description, "no sustained human-to-human transmission has yet been reported. Several attempts in the past to select transmissible H5 viruses (which typically do not transmit among mammals) were not successful". That is why the researchers "plan to passage non-transmissible viruses of different genetic backgrounds in ferrets (an established influenza virus transmission model) to select transmissible mutants". Selected mutations will be characterized for their biological effects and the potential of H5N1 to transmit in mammals.



CENTERS OF EXCELLENCE FOR INFLUENZA RESEARCH AND SURVEILLANCE (CEIRS)

Project Number	Contact PI/Project Leader	Awardee Organization
272201400008C-0-0-1	GARCIA-SASTRE, ADOLFO	ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI

Description

Abstract Text

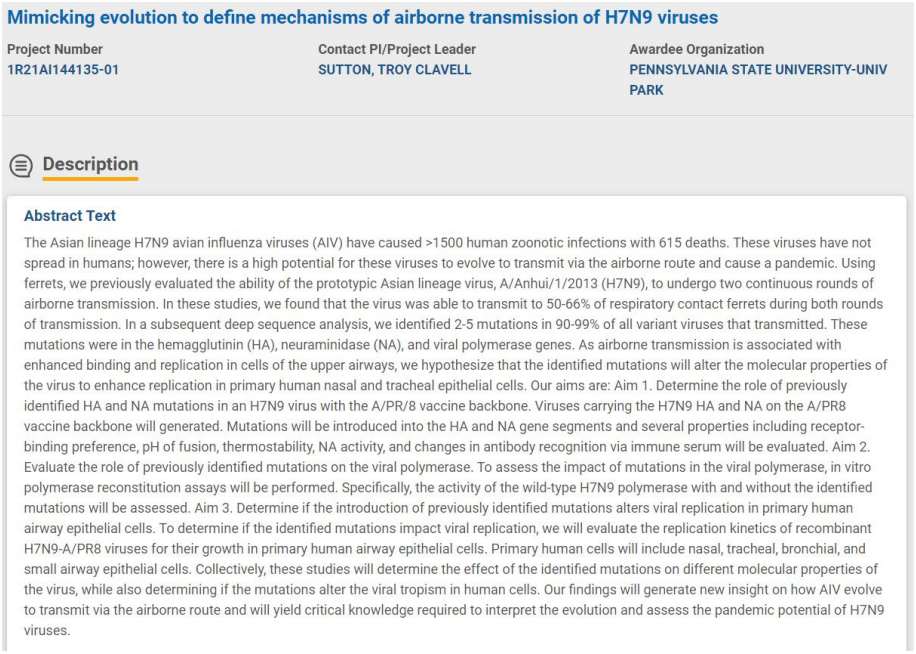
To determine the molecular, ecologic and/or environmental factors that influence the evolution, emergence, transmission and pathogenicity of influenza viruses, including studies on animal influenza viruses with pandemic potential and to characterize the immune response to influenza infection to improve understanding of the immune correlates of protection and cross-protection.

Public Health Relevance Statement

Data not available.

Project 272201400008C-0-0-1 – Total funding: $7,336,466

The project includes studies on animal influenza viruses with pandemic potential. No further information has been provided.



Mimicking evolution to define mechanisms of airborne transmission of H7N9 viruses

Project Number	Contact PI/Project Leader	Awardee Organization
1R21AI144135-01	SUTTON, TROY CLAVELL	PENNSYLVANIA STATE UNIVERSITY-UNIV PARK

Description

Abstract Text

The Asian lineage H7N9 avian influenza viruses (AIV) have caused >1500 human zoonotic infections with 615 deaths. These viruses have not spread in humans; however, there is a high potential for these viruses to evolve to transmit via the airborne route and cause a pandemic. Using ferrets, we previously evaluated the ability of the prototypic Asian lineage virus, A/Anhui/1/2013 (H7N9), to undergo two continuous rounds of airborne transmission. In these studies, we found that the virus was able to transmit to 50-66% of respiratory contact ferrets during both rounds of transmission. In a subsequent deep sequence analysis, we identified 2-5 mutations in 90-99% of all variant viruses that transmitted. These mutations were in the hemagglutinin (HA), neuraminidase (NA), and viral polymerase genes. As airborne transmission is associated with enhanced binding and replication in cells of the upper airways, we hypothesize that the identified mutations will alter the molecular properties of the virus to enhance replication in primary human nasal and tracheal epithelial cells. Our aims are: Aim 1. Determine the role of previously identified HA and NA mutations in an H7N9 virus with the A/PR/8 vaccine backbone. Viruses carrying the H7N9 HA and NA on the A/PR8 vaccine backbone will generated. Mutations will be introduced into the HA and NA gene segments and several properties including receptor-binding preference, pH of fusion, thermostability, NA activity, and changes in antibody recognition via immune serum will be evaluated. Aim 2. Evaluate the role of previously identified mutations on the viral polymerase. To assess the impact of mutations in the viral polymerase, in vitro polymerase reconstitution assays will be performed. Specifically, the activity of the wild-type H7N9 polymerase with and without the identified mutations will be assessed. Aim 3. Determine if the introduction of previously identified mutations alters viral replication in primary human airway epithelial cells. To determine if the identified mutations impact viral replication, we will evaluate the replication kinetics of recombinant H7N9-A/PR8 viruses for their growth in primary human airway epithelial cells. Primary human cells will include nasal, tracheal, bronchial, and small airway epithelial cells. Collectively, these studies will determine the effect of the identified mutations on different molecular properties of the virus, while also determining if the mutations alter the viral tropism in human cells. Our findings will generate new insight on how AIV evolve to transmit via the airborne route and will yield critical knowledge required to interpret the evolution and assess the pandemic potential of H7N9 viruses.

Project 1R21AI144135-01 – Total funding: $226,169

Source: NIAID

According to the description provided for Project 1R21AI144135-01: "The Asian lineage H7N9 avian influenza viruses (AIV)… have not spread in humans; however, there is a high potential for these viruses to evolve to transmit via the airborne route and cause a pandemic… Viruses carrying the H7N9 HA and NA on the A/PR8 vaccine backbone will be generated. Mutations will be introduced into the HA and NA gene segments…we will evaluate the replication kinetics of recombinant H7N9-A/PR8 viruses for their growth in primary human airway epithelial cells. Primary human cells will include nasal, tracheal, bronchial, and small airway epithelial cells." The researchers want to make the virus able to transmit via the airborne route in order to assess the pandemic potential of H7N9 viruses.

These last NIH-funded experiments are just a small part of many controversial lab studies approved by the agency. One of them was the risky bat coronavirus research in China which is under investigation in the US for a possible link to the COVID-19 pandemic.

Despite repeated denials from NIAID director Dr. Antony Fauci including before Congress, NIH finally acknowledged last year that US did fund GoF research on bat coronaviruses in Wuhan from where the pandemic started and spread across the world. The $3.7 million grant was awarded to the US non-profit organization EcoHealth Alliance. In a letter to U.S. House of Representatives NIH states that EcoHealth Alliance violated Terms and Conditions of NIH grant AI110964 and failed to report all its activities in China. According to the NIH letter, a "limited experiment" was conducted in order to test if "spike proteins from naturally occurring bat coronaviruses circulating in China were capable of binding to the human ACE2 receptor in a mouse model."

This is much bigger than Dr. Fauci – it involves the entire US government: US Congressman

Following the release of a House Intelligence Committee report stating that "significant circumstantial evidence" supports the lab leak hypothesis, Rep. Mike Gallagher urged members

of Congress and members of the media to more closely scrutinize additional US funding streams that sent taxpayer dollars to EcoHealth Alliance. According to the congressman, "If you start to do basic research, it quickly becomes apparent that this is much bigger than Dr. Fauci – it involves the entire US government".

EcoHealth Alliance has received **$112.1 million** in total in US government funding since 2003, according to information obtained from the US federal contracts registry. Among its main sponsors are NIH through NIAID and the Pentagon through the Defense Threat Reduction Agency (DTRA). The projects' objectives are discovery and assessment of viruses with pandemic potential mainly in Africa and Asia.

NIH grants:

Federal Grant Awards for Ecohealth Alliance Inc.

Name	Awardee	Dollars Obligated	Award Date	Updated At
U01AI153420	Ecohealth Alliance Inc.	$1.2m	9/15/2020	7/1/2021
STUDY OF NIPAH VIRUS DYNAMICS AND GENETICS IN ITS BAT RESERVOIR AND OF HUMAN EXPOSURE TO NIV ACROSS BANGLADESH TO UNDERSTAND PATTERNS OF HUMAN OUTBREAKS				
U01AI151797	Ecohealth Alliance Inc.	$3.1m	6/17/2020	6/11/2021
UNDERSTANDING RISK OF ZOONOTIC VIRUS EMERGENCE IN EID HOTSPOTS OF SOUTHEAST ASIA				
R01AI110964	Ecohealth Alliance Inc.	$3.7m	6/1/2014	9/14/2021
UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE				
R56TW009502	Ecohealth Alliance Inc.	$300.0k	9/17/2012	9/14/2012
COMPARATIVE SPILLOVER DYNAMICS OF AVIAN INFLUENZA IN ENDEMIC COUNTRIES				
R01AI079231	Ecohealth Alliance Inc.	$2.6m	9/18/2008	8/7/2012
RISK OF VIRAL EMERGENCE FROM BATS				
K08AI067549	Ecohealth Alliance Inc.	$442.8k	9/15/2007	9/14/2010
RISK FOR FUTURE OUTBREAKS OF HENIPAVIRUSES IN SOUTH ASIA				
R01TW005869	Ecohealth Alliance Inc.	$3.7m	8/1/2002	7/27/2012
THE ECOLOGY, EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH				

Pentagon grants:

Federal Grant Awards for Ecohealth Alliance Inc.

Name	Awardee	Dollars Obligated	Award Date	Updated At
HDTRA12110023	Ecohealth Alliance Inc.	$253.3k	7/20/2021	7/19/2021
PREDICTING BIOTHREAT IMPACTS FROM EARLY-STAGE DATA VIA TRANSFER LEARNING.				
HDTRA12010029	Ecohealth Alliance Inc.	$3.0m	9/29/2020	9/29/2020
REDUCING THE THREAT OF MIDDLE EAST RESPIRATORY SYNDROME CORONAVIRUS AND AVIAN INFLUENZA IN JORDAN & STRENGTHENING REGIONAL DISEASE SURVEILLANCE CAPACITY				
HDTRA12010026	Ecohealth Alliance Inc.	$3.0m	9/25/2020	9/24/2020
BIOSURVEILLANCE FOR SPILLOVER OF HENIPAVIRUSES AND FILOVIRUSES IN RURAL COMMUNITIES IN INDIA.				
HDTRA12010018	Ecohealth Alliance Inc.	$5.0m	7/1/2020	6/30/2020
CRIMEAN-CONGO HEMORRHAGIC FEVER: REDUCING AN EMERGING HEALTH THREAT IN TANZANIA.				
HDTRA12010016	Ecohealth Alliance Inc.	$4.9m	6/1/2020	5/27/2020
REDUCING THE THREAT FROM HIGH-RISK PATHOGENS CAUSING FEBRILE ILLNESS IN LIBERIA				
HDTRA11910033	Ecohealth Alliance Inc.	$5.0m	8/19/2019	3/24/2020
REDUCING THE THREAT OF RIFT VALLEY FEVER THROUGH ECOLOGY, EPIDEMIOLOGY AND SOCIO-ECONOMICS				
HDTRA11710064	Ecohealth Alliance Inc.	$6.5m	10/2/2017	3/23/2020
UNDERSTANDING THE RISK OF BAT-BORNE ZOONOTIC DISEASE EMERGENCE IN WESTERN ASIA				
HDTRA11710037	Ecohealth Alliance Inc.	$1.6m	5/1/2017	5/25/2018
SEROLOGICAL BIOSURVEILLANCE FOR SPILLOVER OF HENIPAVIRUSES AND FILOVIRUSES AT AGRICULTURAL AND HUNTING HUMANANIMAL INTERFACES IN PENINSULAR MALAYSIA				
HDTRA11410029	Ecohealth Alliance Inc.	$4.9m	5/28/2014	5/25/2018
UNDERSTANDING RIFT VALLEY FEVER IN THE REPUBLIC OF SOUTH AFRICA				

Source: govtribe.com

Coronavirus research in controversial Pentagon biolab in Georgia

EcoHealth Alliance has implemented a number of military biological research programs for the Pentagon. In 2017 the US Defense Threat Reduction Agency (DTRA) tasked EcoHealth Alliance with a $6.5 million project to collect and isolate coronaviruses in 5,000 bats in Western Asia. The duration of the program is 5 years (2017-2022) with the Lugar Center, the Pentagon biolaboratory in the Republic of Georgia, being the local laboratory for this genetic research.

The project's objectives are: 1. Capture and non-lethally sample 5,000 bats; 2. Collect 20,000 samples (i.e. oral, rectal swabs and/or feces, and blood) and screen for CoVs using consensus PCR at regional labs in Georgia and Jordan. According to the project presentation, Eco Health Alliance already sampled 270 bats of 9 species in three Western Asian countries: 90 individual bats in Turkey (Aug 2018), Georgia (Sept 2018), and Jordan (Oct 2018).

EcoHealth Alliance and Georgian scientists processing bats for a $6.5 million Pentagon project in Western Asia (photo: Facebook, Kendra Phelps, Eco Health Alliance, October 2018)

The Lugar Center which is the partner laboratory for this research is a $180 million Pentagon biolaboratory in Georgia's capital Tbilisi. It has been operated by a special US Army Unit – USAMRU-G, whose personnel have been given diplomatic immunity to research viruses without being diplomats.

The Lugar Center is the $180 million Pentagon-funded biolaboratory in Georgia's capital Tbilisi.

A diplomatic car with a registration plate of the US Embassy to Tbilisi in the car park of the Lugar Center. US scientists working at the Pentagon laboratory in Georgia drive diplomatic vehicles as they have been given diplomatic immunity. Photos: Dilyana Gaytandzhieva

The Lugar Center has become notorious in the last years for controversial activities, laboratory incidents and scandals surrounding the US drug giant Gilead's Hepatitis C program in Georgia which has resulted in at least 248 deaths of patients. The cause of death in the majority of cases has been listed as unknown, internal documents have shown.

There is no public information about the results of the research performed by EcoHealth Alliance at the Lugar Center for the Pentagon neither what viruses have been discovered and what genome experiments have been performed.

$5,000 for bat on the black market

The State Security Committee of South Ossetia raised awareness about the EcoHealth Alliance bat research project in neighboring Georgia after a Georgian national Khvicha Mgebrishvili was detained on 3 July 2020 near the village of Adzisar in the Tskhinvali region of South Ossetia for violating the state border. During the interrogation by South Ossetian KGB border officers, he explained that he

was interested in a colony of bats in the villages of Artseu and Grom in the Tskhinvali region. According to Mgebrishvili, he intended to capture the so-called "Bat cocoons" and sell them in Georgia for $5,000 each. These species are listed in the Red Book and hunting them is punishable by prison in South Ossetia.

Local authorities accused neighboring Georgia of suspicious activities stating that "the Lugar Center for Public Health Research has shown increased interest in the population of South Ossetian bats since 2012". As always the Lugar Center and the US Embassy in Tbilisi denied all allegations as fake news and a conspiracy theory.

In response to all scandals surrounding the Lugar Center and the growing distrust among Georgians the US Embassy in Tbilisi has launched a propaganda campaign to educate the local population with animated movies on social media and Georgian TV channels. All information concerning the Lugar Center apart from the official government narrative has been branded as "fake news", "disinformation" and "conspiracy theories". The Lugar Center has been given by Western media as an example in the fight against the novel coronavirus even though COVID-ravaged Georgia ranks seventh in the world among the countries with the highest number of deaths per million as of this month.

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