Back to Search Results

Description
Details
Sub-Projects
Publications
Patents
Outcomes
Clinical Studies
News and More
History
Similar Projects

Pathogenesis of Jeilongvirus

Project Number	Contact PI/Project Leader	Awardee Organization
5R01AI128924-03	HE, BIAO	UNIVERSITY OF GEORGIA

Description

Abstract Text

PROJECT SUMMARY J paramyxovirus (JPV) was first isolated from rodents in the early 1970s in Australia. Its genome structure was determined In 2005. The JPV genome has eight genes in the order of 3'-N-P/V/C-M-F-SH-TM-G-L-5'. JPV encodes a TM (transmembrane) protein that has no homology to any known proteins and does not exist in any other classified paramyxoviruses. In 2006, Beilong virus (BeiPV) was isolated from human kidney mesangial cells (HMCs) as a contaminant from a rat cell line. BeiPV has the same genome structure as JPV. Studies indicate that BeiPV is a rodent virus. Because of their unique genome structure, a new genus, Jeilongvirus, was proposed to classify JPV and BeiPV within the paramyxovirus family. Tailam virus (TlmPV), isolated from the kidney of a Sikkim rat in Hong Kong in 2011, has an identical genome structure as JPV and BeiPV, indicating that it is a member of Jeilongvirus genus. In 2014, a likely member of Jeilongvirus genus was identified from the primary culture of grey squirrel kidney cells from the UK. In addition, RNA sequences of JPV-like viruses have been identified in rodents and **bats** in Africa, Europe, and China (personal communication) since 2012, indicating that Jeilongvirus is widely distributed and infects a variety of mammals. At present, very little is known about this new and emerging class of viruses. Antibodies against JPV have been detected in rodents, pigs, and humans, suggesting that JPV has a broad host range and zoonotic potential. The fact that Jeilongviruses have been identified in **bats** illustrates their zoonotic potential, since **bats** are thought to be the natural reservoirs for many emerging zoonotic viruses such as SARS-CoV, Hendra and Nipah viruses and Ebola virus. In every genus of mammalian paramyxoviruses, there are important human pathogens. Thus, it is reasonable to expect that one of the viruses in the Jeilongvirus genus is pathogenic in humans. It is important to study JPV for following reasons: (1) in case a pathogenic human Jeilongvirus emerges, we will have knowledge about this class of viruses; (2) JPV can be used as a model for the study of the functions of the small hydrophobic (SH) protein of paramyxoviruses; and (3) TM of JPV is unique in that it is the only viral protein in the paramyxovirus family that plays a critical role in cell-to-cell fusion, but it is not essential for virus-to-cell fusion. We have chosen JPV as a prototype of Jeilongvirus, because we have identified a strain of JPV that is pathogenic in laboratory mice. In this proposal, we plan to carry out a comprehensive analysis of JPV, focusing on understanding the functions of SH and TM and their roles in pathogenesis in animals. Towards these goals, we have established an animal model for in vivo pathogenesis studies and a reverse genetics system for manipulating the RNA genome of JPV. In addition, we have generated polyclonal and monoclonal antibodies for all JPV proteins. In this proposal, we will focus on following specific aims: (1) Elucidating the functions of SH and the mechanisms of its functions and (2) Understanding the functions of TM in vitro and in vivo. JPV represents a new class of viruses that have not been studied. Our proposed work will guide us in developing potential countermeasures in case one of them is pathogenic in humans and provide new knowledge regarding viral protein functions and entry processes.

Public Health Relevance Statement

PROJECT NARRATIVES J paramyxovirus (JPV) represents a new class of viruses that have not been studied. This class of viruses has been identified in bats. Furthermore, human exposure to this class of viruses has been proposed due to detection of the viral antibody in humans. In this work, we will study pathogenesis of JPV in a mouse model that JPV naturally infects and causes diseases.

NIH Spending Category

Biotechnology | Emerging Infectious Diseases | Infectious Diseases | Rare Diseases

Back to Search Results

Description

Details

Sub-Projects

Publications

Patents

Outcomes

Clinical Studies

News and More

History

Similar Projects

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Read More

Details

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MICROBIOLOGY/IMMUN/VIROL(

Organization Type
SCHOOLS OF VETERINARY MEDICINE

State Code
GA

Congressional District
10

Other Information

FOA
PA-16-160

Study Section
Special Emphasis Panel[ZRG1-IDM-W(02)M]

Fiscal Year
2019

Award Notice Date
28-June-2019

Administering Institutes or Centers
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

DUNS Number
004315578

CFDA Code
855

Project Start Date
01-July-2017

Project End Date
30-June-2022

Budget Start Date
01-July-2019

Budget End Date
30-June-2020

Project Funding Information for 2019

Total Funding
$471,179

Direct Costs
$350,818

Indirect Costs
$120,361

Year	Funding IC	
2019	NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES	$471,179

Thank you for your feedback!

Back to Search Results

Description

Details

Sub-Projects

Publications

Patents

Outcomes

Clinical Studies

News and More

History

Similar Projects

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UNIVERSITY OF GEORGIA

Emerging Infectious Diseases; Infectious Diseases; Rare Diseases;

Sub Projects

No Sub Projects information available for 5R01AI128924-03

Publications

No Publications available for 5R01AI128924-03

Patents

No Patents information available for 5R01AI128924-03

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 5R01AI128924-03

Clinical Studies

No Clinical Studies information available for 5R01AI128924-03

News and More

Related News Releases

No news release information available for 5R01AI128924-03

History

Back to Search Results

Description

Details

Sub-Projects

Publications

Patents

Outcomes

Clinical Studies

News and More

History

Similar Projects

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Project Number	Contact PI/Project Leader	Awardee Organization
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