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Tropism, pathogenicity, and potential for zoonotic spillover of emergent henipa- and henipa-like viruses

Project Number	Contact PI/Project Leader	Awardee Organization
5R01AI123449-04	LEE, BENHUR	ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI

Description

Abstract Text

ABSTRACT Nipah (NiV) and Hendra (HeV) viruses are highly pathogenic type species of the Henipavirus (HNV) genus within the Paramyxovirinae. Zoonotic transmission of NiV and HeV from their natural fruit bat reservoirs to humans can result in mortality rates in excess of 90%. Originally thought to be limited to Southeast Asia and Australia, the recent discovery of numerous divergent clades of HNVs across Africa, and of Henipa-like viruses (HNLV) in China such as the Mojiang paramyxovirus (MojPV), qualitatively changes the risk- calculus associated with the possible global emergence of these zoonotic viruses. Indeed, we recently found evidence for HNV spillover into human populations at high-risk for zoonotic transmission in Cameroon, which raise urgent questions about potential spillover events that may have remained undetected or misdiagnosed. The recent Ebola epidemic in West Africa underscores the importance of understanding the mechanisms of zoonotic spillover and transmission of highly pathogenic emerging viruses. HNVs use EphrinB2 and EphrinB3, highly conserved cellular proteins, as viral entry receptors. The recent discovery of novel HNVs with differential usage of EphrinB2 and B3 provides new opportunities to study how receptor usage contributes to the pathogenicity and potential for zoonotic spillover of these emergent HNVs. Our overall goal is to elucidate the envelope-receptor interactions of HNVs and HNLVs that contribute to viral tropism, pathogenicity, transmissibility, and the potential for zoonotic spillover. Our primary objective is to understand the structure-function correlates of envelope- receptor interactions in the pathobiology of HNV/HNLV zoonotic infections. A secondary objective is to leverage that understanding to interrogate the rational basis for a vaccine design that might elicit antibodies that are more broadly neutralizing and effective against an ever-expanding spectrum of diverse HNVs. Our driving hypothesis is: the structural plasticity of HNV-Gs accounts for the differential efficiency and choice of receptor usage exhibited by divergent HNVs, and that this contributes to a virulence spectrum among these zoonotic viruses that is equally diverse. To achieve our objectives and interrogate our driving hypothesis, we propose the following Specific Aims: (1) Investigate the role of receptor usage and choice in virus pathogenicity. (2) Evaluate how attachment protein-receptor interactions contribute to transmissibility and the potential for zoonotic spillover. (3) Examine the implications of the structural and phylogenetic diversity of HNVs on vaccine design.

Public Health Relevance Statement

NARRATIVE Henipaviruses (HNVs) are emerging paramyxoviruses that are classified as BSL4 select agents due to their extreme pathogenicity. They are zoonotic viruses that can cause severe disease in humans and livestock when spillover occurs from the natural animal reservoirs. We seek to understand the viral envelopereceptor interactions that contribute to viral pathogenicity and the potential for zoonotic spillover.

NIH Spending Category

Biodefense	Emerging Infectious Diseases	Infectious Diseases	Rare Diseases
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Project Terms

Africa	Animals	Antibodies	Australia	Automobile Driving	Binding Sites	
Brain Stem	Calculi	Cameroon	China	Chiroptera	Complex	Disease
Ebola virus	Encephalitis	Epidemic	Event	Exhibits	Fruit	Ghana

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Project Number 5R01AI123449-04	Contact PI/Project Leader LEE, BENHUR	Awardee Organization ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI
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Details

Contact PI/ Project Leader	Other PIs	Program Official
Name LEE, BENHUR 	Not Applicable	Name PARK, EUN-CHUNG
Title PROFESSOR OF MICROBIOLOGY		Contact epark@niaid.nih.gov
Contact BENHURL@MICROBIO.UCLA.EDU		

Organization

Name ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI	Department Type MICROBIOLOGY/IMMUN/VIROLOG	State Code NY
City NEW YORK	Organization Type SCHOOLS OF MEDICINE	Congressional District 13
Country UNITED STATES (US)		

Other Information

FOA PA-13-302	Administering Institutes or Centers NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES	Project Start Date 26-September-2016
Study Section Virology - B Study Section[VIRB]	DUNS Number CFDA Code 078861598 855	Project End Date 31-August-2021
Fiscal Year 2019	Award Notice Date 06-August-2019	Budget Start Date 01-September-2019
		Budget End Date 31-August-2020

Project Funding Information for 2019


Total Funding \$584,782	Direct Costs \$463,139	Indirect Costs \$121,643
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Year	Funding IC	
2019	NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES	\$584,782


NIH Categorical Spending	Click here for more information on NIH Categorical Spending	
Funding IC	FY Total Cost by IC	NIH Spending Category


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Project Number 5R01AI123449-04	Contact PI/Project Leader LEE, BENHUR	Awardee Organization ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI
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Sub Projects

No Sub Projects information available for 5R01AI123449-04



Publications

No Publications available for 5R01AI123449-04



Patents

No Patents information available for 5R01AI123449-04



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 5R01AI123449-04



Clinical Studies

No Clinical Studies information available for 5R01AI123449-04



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Related News Releases

No news release information available for 5R01AI123449-04












History

No Historical information available for 5R01AI123449-04

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