

[Back to Search Results](#)

Deciphering the pathogenic potential of Lloviu virus, a novel filovirus

[Description](#)Project Number
5R21AI137793-02Contact PI/Project Leader
MUHLBERGER, ELKE CAwardee Organization
**BOSTON UNIVERSITY
MEDICAL CAMPUS**[Details](#)[Sub-Projects](#)[Publications](#)[Patents](#)[Outcomes](#)[Clinical Studies](#)[News and More](#)[History](#)[Similar Projects](#)[Share](#)

Description

Abstract Text

Recent advances in sequencing technologies have led to the discovery of a multitude of novel zoonotic viruses, some of which are closely related to known human pathogens. In most cases, only partial viral genome sequences were identified, and no infectious viruses were isolated, hampering research aimed at assessing the pathogenic potential of these novel viruses. A prime example of a sequence-based novel virus is Lloviu virus (LLOV), the newest member of the filovirus family. LLOV is closely related to the highly pathogenic ebola- and marburgviruses that cause severe disease in humans with extraordinarily high case fatality rates. The genomic viral RNA of LLOV was isolated from dead **bats** in Spain and is rudimentary. Important sequence elements located at the LLOV genome ends are missing. These include the antigenomic promoter that is essential for viral genome replication. Therefore, studies addressing LLOV genome replication and transcription, or pathogenesis have been impossible to date. In this proposal, we bring together expertise in the field of filoviral replication and transcription, rescue of filovirus clones, filovirus pathogenesis, and statistical modeling to generate infectious LLOV clones for in vitro and in vivo studies. By complementing the missing LLOV sequence with homologous sequences from related filoviruses, we have successfully established a hybrid LLOV minigenome system, enabling studies of LLOV replication and transcription for the first time. Based on this system, we will utilize LLOV minigenome systems in combination with statistical modeling to optimize the complemented promoter sequences (Aim 1). These optimized minigenome systems build the foundation for the generation and rescue of infectious full-length LLOV clones. The generated LLOV clones will then be characterized in in vitro studies. We will determine replication kinetics and host response signatures in primary human cells (Aim 2). Finally, we will perform pathogenesis studies with LLOV using a small animal model of filovirus infection (Aim 3). These studies will be instrumental to get a better understanding of the virulence of LLOV and its potential to cause disease in animals and humans. The platform developed in this project to assess the pathogenic potential of novel viruses can be adapted to other nonsegmented negative-sense RNA viruses and would therefore be of great benefit to the scientific community.

Public Health Relevance Statement

Filoviruses are highly pathogenic viruses with the potential to cause unpredicted outbreaks. Recently, a new filovirus, Lloviu virus, has been discovered. The goal of this project is to gain a better understanding of the virulence of this virus and its pathogenic potential.

NIH Spending Category

Biodefense Biotechnology Emerging Infectious Diseases Genetics
 Infectious Diseases Rare Diseases

Project Terms

Address	Animal Model	Animals	Base Sequence	Biological Assay
Case Fatality Rates	Cell Culture Techniques	Cells	Chiroptera	Communities
Complement	Complementary DNA	Computer Simulation	Disease	
Disease Outbreaks	Ebola virus	Elements	Family	Filoviridae Infections

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[Back to Search Results](#)

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muehlber@bu.edu**Organization**Name
BOSTON UNIVERSITY MEDICAL CAMPUSDepartment Type
MICROBIOLOGY/IMMUN/VIROLOGYState Code
MACity
BOSTONOrganization Type
SCHOOLS OF MEDICINECongressional District
07Country
UNITED STATES (US)**Other Information**

FOA

[PA-16-161](#)

Study Section

[Virology - A Study Section](#)
[\[VIRA\]](#)

Administering Institutes or Centers

Project Start Date
13-February-2018**NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES**Project End Date
31-January-2022Award Notice Date
25-January-2019DUNS Number CFDA Code
604483045 855Budget Start Date
01-February-2019Fiscal Year
2019Budget End Date
31-January-2022**Project Funding Information for 2019**Total Funding
\$247,500Direct Costs
\$150,000Indirect Costs
\$97,500

Year	Funding IC	
2019	NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES	\$247,500

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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[Back to Search Results](#)

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Sub Projects

No Sub Projects information available for 5R21AI137793-02

Publications

No Publications available for 5R21AI137793-02

Patents

No Patents information available for 5R21AI137793-02

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 5R21AI137793-02

Clinical Studies

No Clinical Studies information available for 5R21AI137793-02

News and More

Related News Releases

No news release information available for 5R21AI137793-02

History

No Historical information available for 5R21AI137793-02

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[Back to Search Results](#)

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 [Details](#) [Sub-Projects](#) [Publications](#) [Patents](#) [Outcomes](#) [Clinical Studies](#) [News and More](#) [History](#) [Similar Projects](#)

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