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Risk Assessment of Influenza A Viruses

Project Number
5R21AI135820-02

Contact PI/Project Leader
WAN, XIUFENG HENRY

Awardee Organization
MISSISSIPPI STATE UNIVERSITY

Description

Abstract Text

Title: Risk Assessment of Influenza A Viruses Project Summary Influenza A viruses (IAVs) have caused large losses of life around the world and continue to present a great public health challenge. Risk assessment of influenza viruses is a key component in **pandemic** influenza preparedness (PIP), and it can help optimize resources for influenza surveillance, vaccine development and other control measurements to help minimize losses due to an emerging influenza virus. Risk assessment of influenza viruses includes emergence risk and public health impact of novel influenza viruses. Emergence risk assesses the probability for a novel influenza virus to infect and easily spread among humans; it is the first risk to be evaluated in risk assessment. Although a number of individual mutations or structural/functional motifs have been reported to be associated with influenza infection and transmission, their effects on emergence risk are difficult to predict a priori. Thus, conventional methods for assessment of the emergence risk of a novel IAV often require laboratory generation of reassortants and subsequent measurement of their infectivity, pathogenesis, and transmission, which is often done in a mammalian system. However, this strategy can lead to laboratory mutants with gain of function (i.e., mutants with new or enhanced activity on pathogenesis and/or transmissibility in mammals). Thus, an ideal system for influenza risk assessment should be able to quantify emergence risk for a novel IAV solely by using genomic sequences. Avian influenza A viruses facilitated the emergence of all four known **pandemic** human influenza A viruses: the hemagglutinin genes of 1918, 1957, and 1968 **pandemic** viruses are all of avian origin, and the polymerase PB2 and PA genes of the 2009 **pandemic** virus are of avian origin. Risk assessment of potential reassortants from contemporary endemic human influenza viruses and enzootic avian influenza viruses has been a key component of the **pandemic** influenza preparedness process. The objectives of this study are to develop and validate a machine learning method to assess the emergence risk for a novel IAV using genomic sequences. The study will focus on emergence risk from contemporary endemic human influenza viruses and enzootic avian influenza viruses. We expect to identify genetic features within and across gene segments and ascertain their synergistic effects as emergence risk determinants. We also expect to develop a computational model for estimating the probability of a possible reassortant to emerge, given the genomic sequences of one human influenza virus and one avian influenza virus. The study results should help with understanding the fundamental mechanisms for genetic reassortment and with assessing emergence risk of influenza virus; thus, the results should facilitate **pandemic** influenza preparedness.

Public Health Relevance Statement

Project Narrative This project will develop a computational model for influenza risk assessment, and it will help with understanding the fundamental mechanisms for genetic reassortment and for assessing the emergence risk of influenza viruses, and thus the project will facilitate pandemic influenza preparedness.

NIH Spending Category

Biodefense Biotechnology Emerging Infectious Diseases Genetics Infectious Diseases Influenza Machine Learning and Artificial Intelligence Pneumonia & Influenza Prevention

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MISSISSIPPI STATE UNIVERSITY

Government Hemagglutinin Human In Vitro Individual Influenza Influenza A Virus, H1N1 Subtype Influenza A Virus, H7N9 Subtype Influenza A virus Information Theory Knowledge Laboratories Lead Life Luciferases Machine Learning Mammals Measurement Methods Modeling

Read More

Details

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UNITED STATES (US)

Department Type
VETERINARY SCIENCES

Organization Type
SCHOOLS OF VETERINARY MEDICINE

State Code
MS

Congressional District
03

Other Information

FOA
PA-16-161

Study Section
Biomedical Computing and Health Informatics Study Section[BCHI]

Fiscal Year
2019

Award Notice Date
22-March-2019

Administering Institutes or Centers
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

DUNS Number
075461814

CFDA Code
855

Project Start Date
02-May-2018

Project End Date
15-August-2019

Budget Start Date
01-May-2019

Budget End Date
15-August-2019

Project Funding Information for 2019

Total Funding
$5,173

Direct Costs
$3,555

Indirect Costs
$1,618

Year	Funding IC	
2019	NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES	$5,173

NIH Categorical Spending

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MISSISSIPPI STATE UNIVERSITY

Genetics; Infectious Diseases; Influenza; Machine Learning and Artificial Intelligence; Pneumonia & Influenza; Prevention;

Sub Projects

No Sub Projects information available for 5R21AI135820-02

Publications

No Publications available for 5R21AI135820-02

Patents

No Patents information available for 5R21AI135820-02

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 5R21AI135820-02

Clinical Studies

No Clinical Studies information available for 5R21AI135820-02

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Related News Releases

No news release information available for 5R21AI135820-02

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