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# Genomic Basis of Susceptibility to COVID-19 Infection and its Complications

| Project Number | Former Number | Contact PI/Project Leader | Awardee Organization |
|---|---|---|---|
| 3U01HG006379-09S1 | 3U01HG006379-08S1 | KULLO, IFTIKHAR JOther PIs | MAYO CLINIC ROCHESTER |

## Description

### Abstract Text

PROJECT SUMMARY In addition to causing millions of cases and hundreds of thousands of deaths, the Coronavirus disease 2019 (**COVID**-19) pandemic has brought life and economic activity to a near standstill in many parts of the world. A coordinated scientific effort is necessary to mitigate the widespread misery, morbidity and mortality inflicted by the pandemic. The goal of this supplemental application is to contribute to informatics and genomics efforts to identify the genomic basis of susceptibility to and complications of **COVID**-19. The wide spectrum of disease severity with **COVID**-19 is only partially explained by age and medical comorbidities and genetic factors are likely to play a key role. Identifying genomic factors impacting **COVID**-19 case status and complications is important for risk stratification, identifying new pathophysiologic pathways for drug development/repurposing, and improved understanding of the biology of SARS-CoV-2 infection and its complications. As part of the electronic Medical Records and Genomics (eMERGE) since its inception in 2007, Mayo investigators have considerable experience in using the electronic health record (EHR) for genomics research. We will develop electronic phenotyping algorithms to ascertain **COVID**-19 case status, complications and fatality, to identify genomic variants associated with adverse outcomes. Using DNA samples linked to the EHR, we will perform genomic analyses to identify common and rare variants associated with case status, case severity and case mortality. We will collaborate with health systems and consortia in the US and around the world to increase the power and rapidity of the genomic studies. Our specific aims are: Specific Aim 1: Develop and validate electronic phenotyping algorithms to ascertain **COVID**-19 related phenotypes including case control status, i.e., individuals tested and those were identified to be positive for **COVID**-19, and disease severity, in particular cardiovascular complications including myocardial injury/infarction, arrhythmias, coagulopathy as well as large vessel thrombosis. Specific Aim 2: Perform genomic association analyses to identify variants associated with susceptibility to infection with SARS-CoV-2 and its complications. We will compare test +ve vs test -ve individuals, mild vs hospitalized cases of **COVID**-19 and among the latter those who develop severe disease or die. In addition to genome-wide association studies (GWAS), we will conduct association studies of the HLA region and burden tests using sequence data.

### Public Health Relevance Statement

PROJECT NARRATIVE A coordinated scientific effort is necessary to mitigate the widespread misery, morbidity and mortality inflicted by the COVID-19 pandemic. The goal of this supplemental application is to identify the genetic factors that predispose individuals develop severe complications after COVID-19 infection. Identifying such factors is important for risk stratification, finding new pathways for drug development/repurposing, and to improve our understanding of the biology of SARS-CoV-2 infection and its complications.

### NIH Spending Category

Biotechnology Cardiovascular Clinical Research Coronaviruses Emerging Infectious Diseases Genetics Hematology Human Genome Infectious Diseases

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Electronic Medical Records and Genomics Network Genes Genetic Genomic approach Genomics Goals HLA Antigens Health system Individual Infarction Infection Inflammasome Informatics Life Link

Read More

## Details

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MAYO CLINIC ROCHESTER

City
ROCHESTER

Country
UNITED STATES (US)

Department Type
Unavailable

Organization Type
Other Domestic Non-Profits

State Code
MN

Congressional District
01

### Other Information

FOA
PA-18-591

Study Section
ZHG1(J2)

Fiscal Year
2020

Award Notice Date
16-September-2020

Administering Institutes or Centers
NATIONAL HUMAN GENOME RESEARCH INSTITUTE

DUNS Number
006471700

CFDA Code
172

Project Start Date
15-August-2011

Project End Date
30-April-2025

Budget Start Date
16-September-2020

Budget End Date
30-April-2021

### Project Funding Information for 2020

| Total Funding | Direct Costs | Indirect Costs |
|---|---|---|
| $282,848 | $177,892 | $104,956 |

| Year | Funding IC | FY T |
|---|---|---|
| 2020 | NATIONAL HUMAN GENOME RESEARCH INSTITUTE | $282,848 |

### 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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Genome; Infectious Diseases;

## Sub Projects

No Sub Projects information available for 3U01HG006379-09S1

## Publications

No Publications available for 3U01HG006379-09S1

## Patents

No Patents information available for 3U01HG006379-09S1

## 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 3U01HG006379-09S1

## Clinical Studies

No Clinical Studies information available for 3U01HG006379-09S1

## News and More

### Related News Releases

No news release information available for 3U01HG006379-09S1

## History

No Historical information available for 3U01HG006379-09S1

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Thank you for your feedback!