**Goal2** Realization of ultra-early disease prediction and intervention by 2050.

Understanding and Control of Virus-Human Interaction Networks

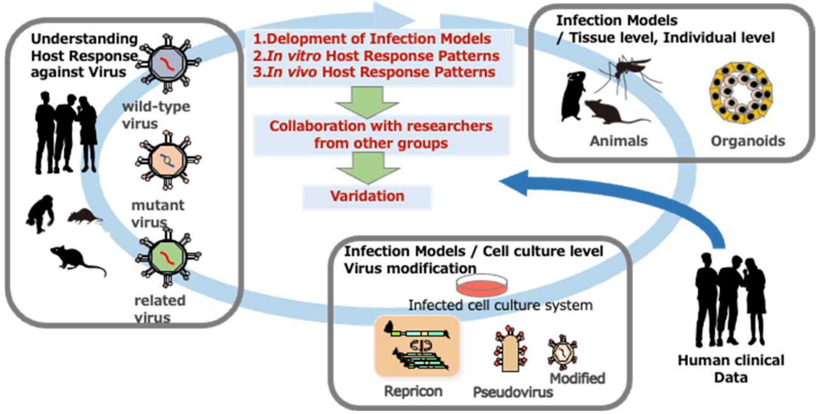
R&D item

# 1. Analysis of virus infection networks

## Progress until FY2023

### 1. Outline of the Project

We establish in vitro and in vivo models for various viral infections, create a database of host response networks after viral infection using various omics analyses, and extract host response patterns in collaboration with researchers in immunology and mathematical sciences. Then, we aim to identify biomarkers that can predict profound pathological changes at an extremely early stage and target molecules that enable therapeutic intervention. Furthermore, through mutual feedback analysis with human clinical data, the results obtained using animal models will be scientifically verified with human clinical data, and human clinical data will be scientifically verified with animal models.



Understanding Host Response against Virus

1.Delopment of Infection Models
2.*In vitro* Host Response Patterns
3.*In vivo* Host Response Patterns

Collaboration with researchers from other groups

Varidation

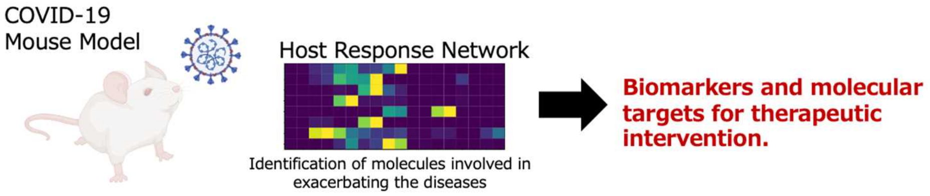
Infection Models / Tissue level, Individual level

Infection Models / Cell culture level
Virus modification

### 2. Research Achievements

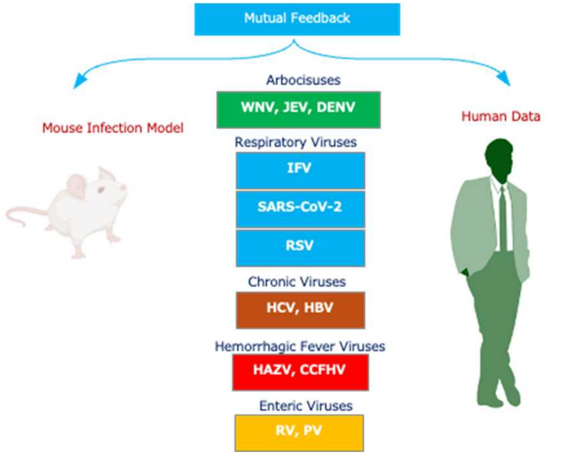
Respiratory diseases like influenza virus (IFV) and coronavirus are the most likely to cause pandemics. In this project, we focused on the SARS-CoV-2 infection model and worked with researchers from Project 3 to identify key molecules involved in severe cases. We identified several molecules involved in severe cases. We examined the therapeutic effects of the inhibitors against these molecules in mouse models and found that treatment with some inhibitors ameliorates the severity of mice infected with SARS-CoV-2.

We also established mouse infection models for respiratory syncytial virus (RSV), Japanese encephalitis virus (JEV), rotavirus, hemorrhagic fever viruses, and hepatitis C virus (HCV). Collaborating with Project3 researchers, we analyzed omics to extract host response networks.



### 3. Future Plans

By 2023, we have conducted comprehensive omics analyses on various virus infection models to identify molecular targets and biomarkers for early prevention and intervention of viral infectious diseases. We also performed cross-sectional analyses to define new virus classifications and develop tailored prevention and treatment methods. Data from animal models are being cross-referenced with human data to facilitate the application of our research findings to human health.



Japan Science and Technology Agency