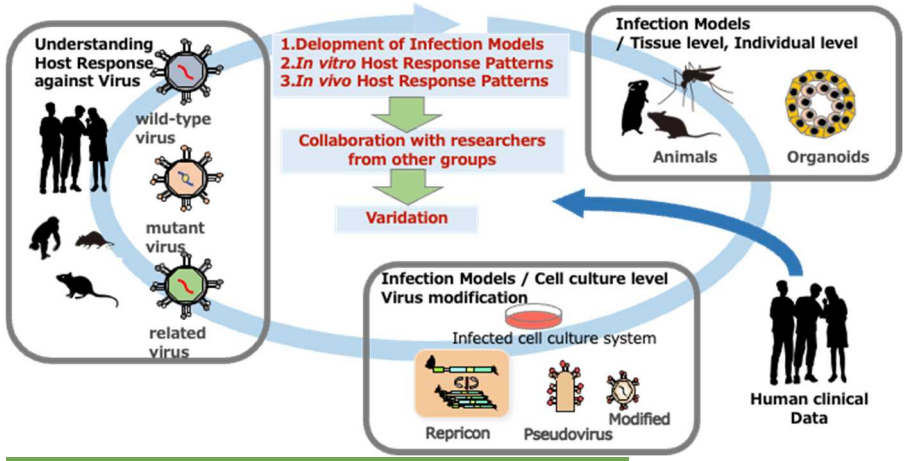
R&D Theme

R & D Project 1: Analysis of virus infection networks

Progress until FY2022

1. Outline of the Project

We establish in vitro or 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 serious 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.

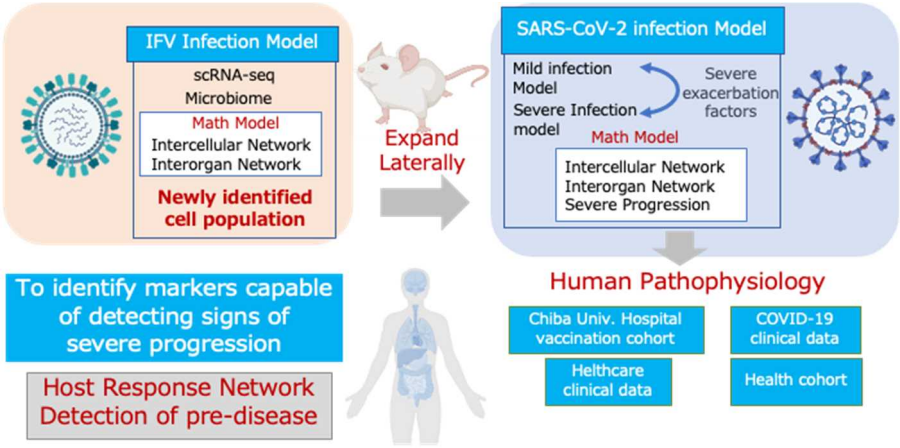


2. Research Achievements

Among viral infections, the most likely to cause pandemics are respiratory viruses such as IFV and coronaviruses. In this project, the analysis of SARS-CoV-2, an urgent issue, was given top priority. A mouse model for SARS-CoV-2 had not been established at the start of the research, and the research progress would take time, such as the need for a BSL3 laboratory. We proceeded with the analysis using the existing IFV mouse model. We efficiently conducted the research by laterally expanding the analysis methods and achievements to the newly established SARS-CoV-2 mouse model. As a result, we found cells and molecules that exhibit characteristic dynamics common to IFV and SARS-CoV-2 infections and identified candidate targets that would enable ultra-early diagnosis and therapeutic intervention.

3. Future Plans

Regarding SARS-CoV-2, researchers in Groups 2 and 3 will acquire human clinical data, and through mutual feedback analyses of animal model data and human clinical data, we aim to implement the research results in humans. In addition, we will apply these analytical results to the RSV infection model for respiratory infections, aiming to extract host response patterns common to acute respiratory infections. In addition, we are making good progress in creating mouse models for hemorrhagic fever viruses, intestinal viruses, arthropod-borne viruses, and persistent infection viruses, and we are trying to classify new viruses based on host response patterns.



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