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The aim of our laboratory is to expand the knowledge and methodology on virology, which were unable to shed light on by conventional experimental approach alone. To investigate the co-evolutionary relationship between viruses and hosts, we perform bioinformatic and molecular phylogenetic analyses as well as experimental virology. The interdisciplinary investigations based on experimental virology and other scientific fields/methods will pioneer a new science for deeply understanding infectious diseases.

1. Understanding the evolution of SARS-CoV-2

Yu Kaku, Keiya Uriu, Yusuke Kosugi, Shigeru Fujita, Luo Chen, Jarel Elgin Tolentino, Lin Pan, Arnon Plianchaisuk, Ziyi Guo, Alfredo Amolong Hinay, Jr., Kaoru Usui, Wilaiporn Saikruang, Wenye Li, Kaho Okumura, Naoko Misawa, Mai Suganami, Adam Patrick Strange, Naomi Ohsumi, Shiho Tanaka, Mika Chiba, Ryo Yoshimura, Kyoko Yasuda, Keiko Iida, Jumpei Ito, Kei Sato.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a causative agent of coronavirus disease 2019 (COVID-19). SARS-CoV-2 emerged at the end of 2019 and has spread all over the world. Since then, more than 770 million people have been infected with this virus and more than 7 million people have died of COVID-19, meaning that COVID-19 is ongoing pandemic and a most urgent and crucial problem in the current human society. To proceed and accelerate COVID-19-related researches in Japan, we launched a consortium, called “The Genotype to Phenotype Japan (G2P-Japan) Consortium” in January 2021. As of December 2023, more than 10 principal investigators in Japan and Czech Republic join this consortium and proceed fruitful collaboration. We aim to elucidate the virological characteristics of the

SARS-CoV-2 variants continuously emerging in the world.

2. Predicting and understanding virus epidemics and evolution

Jumpei Ito, Arnon Plianchaisuk, Jarel Elgin Tolentino, Mai Suganami, Adam Patrick Strange, Kaho Okumura, Kei Sato

During the COVID-19 pandemic, extensive viral genomic surveillance has been conducted, enabling us to track the epidemic and evolution of SARS-CoV-2 in ultra-high resolution. Leveraging this big data, we are establishing theoretical and technical frameworks to understand and predict the epidemic and evolution of viruses. This year, we have developed a Bayesian hierarchical model to predict the transmissibility of SARS-CoV-2 variants based on mutation patterns in the spike protein (Ito et al., 2023, *Nat. Commun.*). Additionally, we showed that the increased transmissibility observed during the evolution of the Omicron variant can be explained by the acquisition of a small number of mutations in spike protein.

Publications

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