

Department of Microbiology and Immunology

Division of Systems Virology

システムウイルス学分野

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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 coronavirus

Ziyi Guo, Kaoru Usui, Wilaiporn Saikruang, Spyridon Lytras, Keiya Uriu, Shusuke Kawakubo, Mohammad Golam Kibria, Yusuke Kosugi, Shigeru Fujita, Luo Chen, Jarel Elgin Tolentino, Yukun Zhu, Wenye Li, Maximilian Stanley Yo, Yueying Zhang, Mizuka Fujiwara, Mika Chiba, Kaho Okumura, Tsuki Fukuda, Tamaki Yoshihara, Keiko Koizumi, Nanako Kanai, Sakurako Seki, Mizuho Ota, Mai Suganami, Yuka Ozaki, Shiho Tanaka, Eiko Ogawa, Naoko Misawa, Jumpei Ito, Kei Sato.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the causative agent of coronavirus disease 2019 (COVID-19), emerged at the end of 2019 and has spread worldwide. 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. We launched a consortium, called "The Genotype to Phenotype Japan (G2P-Japan) Consortium" in January 2021, and have studied the virological properties of various SARS-CoV-2 variants during the COVID-19 pandemic. This year, we expanded our research to include not only SARS-CoV-2 but also SARS-CoV-2-related coronaviruses derived from

wild animals to understand coronavirus evolution and the mechanisms of cross-species transmission from animals to humans.

2. Predicting viral antigenicity, fitness and evolution from viral genotype

Arnon Planchaisuk, Spyridon Lytras, Shusuke Kawakubo, Luca Nishimura, Ananporn Supataragul, Moonjong Kang, Mai Suganami, Kaho Okumura, Hiroaki Unno, Hinata Yokokawa, Yuka Ozaki, Kyoko Kurihara, Jumpei Ito, Kei Sato.

One of the reasons controlling viral infections is challenging is that viruses evolve and change their characteristics over time. Leveraging the vast viral genome information obtained through genomic epidemiological studies, phenotypic data measured by high-throughput experiments, and state-of-the-art machine learning techniques such as protein language models, it is expected to become possible to model the relationships among viral antigenicity, fitness and evolution directly from their genotypes. We developed PLANT, which projects influenza A/H3N2 viruses onto an antigenic map using HA protein sequences. Using PLANT-based cartography, we show that (i) H3N2 antigenic evolution accelerates during periods of disrupted global circulation, (ii) antigenic

novelty accounts for a substantial portion of viral fitness advantage, and (iii) vaccine strains are often antigenically distant from circulating viruses. We further propose a PLANT-based framework for selecting vaccine strains with improved antigenic match than

the WHO-recommended strains. This study provides a statistical foundation for integrated modeling of viral genotype, antigenicity, and fitness, offering quantitative insights into seasonal influenza virus evolution and supporting rational vaccine design.

Publications

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