

International Vaccine Design Center

Division of Systems Immunology (Human Immune-Profiling Team)

ヒト免疫プロファイリング系・数理免疫学分野

| Professor Kei Sato, Ph.D.

| 教授 博士(医学) 佐藤 佳

The aim of this laboratory is to launch an interdisciplinary research network to “quantitatively” understand the behaviors of pathogens and the immune reaction against pathogen infection. Our study will connect microbiology and immunology, which will lead to the development of novel vaccines in the future.

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.

Publications

Taguchi, J., Kikuchi, M., Jeon, H., Shimizu, R., Mori, H., Ikawa, M., Yamada, Y., Sato, K., Ikeda, T., Yamazaki, S., & Ozawa, M. A scalable two-step genome editing strategy for generating full-length gene-humanized mice at diverse genomic loci. *Nat Commun.*, in press.

Kaku, Y., Fujiwara, M., Uriu, K., Yo, M. S., Kawakubo, S., Ito, J., Itoh, N., Uwamino, Y., Saito, F., Satoh, H., The Genotype to Phenotype Japan (G2P-Japan) Consortium & Sato, K. Humoral immunity after LP.8.1 monovalent vaccines against a broad range of SARS-CoV-2 variants including XEC, LP.8.1,

- NB.1.8.1, XFG, and BA.3.2. **Lancet Infect Dis.**, in press.
- Nakata, Y., Yamasaki, M., Watanabe, Y., Uriu, K., Hashimoto, R., Yamamoto, T., The Genotype to Phenotype Japan (G2P-Japan) Consortium, Sato, K., Saito, A., & Takayama, K. Mpox virus OPG175 negatively regulates viral replication by controlling Wnt signaling. **iScience**, in press.
- Tsujino, S., Tsuda, M., Deguchi, S., Ito, J., Taha, T. Y., Nasser, H., Wang, L., Rosecrans, J., Suzuki, R., Suzuki, S., Yoshimatsu, K., Ott, M., Ikeda, T., Sato, K., Takayama, K., Tanaka, S., Tamura, T., Fukuhara, T., & Genotype to Phenotype Japan (G2P-Japan) Consortium. A non-spike nucleocapsid R204P mutation in SARS-CoV-2 Omicron XEC enhances inflammation and pathogenicity. **Nat Commun.**, in press.
- Hirano, R., Yoshimi, K., Asano, K., Takeshita, K., Ishii, K. J., Sato, K., & Mashimo, T. Sustainable and portable CRISPR-based diagnostics for high-sensitivity Mpox detection. **npj Biosensing**, in press.
- Nakata, Y., Uriu, K., Hashimoto, R., Yamamoto, T., The Genotype to Phenotype Japan (G2P-Japan) Consortium, Saito, A., Sato, K., & Takayama, K. Mpox virus replicates in lung organoids without significantly affecting their cellular function. **Biochem Biophys Rep.**, 44:102326, 2025.
- Sato K. Systems virology as a cornerstone for pandemic responsiveness: A G2P-Japan perspective. **Cell Host Microbe**, 33(11), 1807–1810, 2025.
- Tsujino, S., Tsuda, M., Nao, N., Okumura, K., Wang, L., Oda, Y., Mimura, Y., Li, J., Hashimoto, R., Matsumura, Y., Suzuki, R., Suzuki, S., Yoshimatsu, K., Nagao, M., Ito, J., Takayama, K., Sato, K., Matsuno, K., Tamura, T., Tanaka, S., Fukuhara, T. & Genotype to Phenotype Japan (G2P-Japan) Consortium. Evolution of BA.2.86 to JN.1 reveals that functional changes in non-structural viral proteins are required for fitness of SARS-CoV-2. **J Virol.**, 99(10), e0090825, 2025.
- Chen, L., Hinay, A. A. Jr., Fujita, S., Ito, J., Asakura, H., Nagashima, M., Sadamasu, K., Yoshimura, K. and Sato, K. The spike S2 substitution, P804L, drives the adaptation of BANAL-20–236 to a broad range of Rhinolophus bat ACE2. **Front. Virol.**, 5:1612630, 2025.
- Kosugi, Y., Matsumoto, K., Lytras, S., Plianchaisuk, A., Tolentino, J. E., Fujita, S., Yo, M. S., Luo, C., Kim, Y., Shihoya, W., Ito, J., Nureki, O., & Sato, K. Molecular basis of sarbecovirus evolution and receptor tropism in natural hosts, potential intermediate hosts, and humans. **Cell Rep.**, 44(9), 116220, 2025.
- Pan, L., Kaku, Y., Tolentino, J. E., Kosugi, Y., & Sato, K. Cross-neutralization ability of anti-MERS-CoV monoclonal antibodies against a variety of merbecoviruses. **Front Microbiol.**, 16, 1593095, 2025.
- Uriu, K., Okumura, K., Uwamino, Y., Chen, L., Tolentino, J. E., Asakura, H., Nagashima, M., Sadamasu, K., Yoshimura, K., Ito, J., Sato, K., & Genotype to Phenotype Japan (G2P-Japan) Consortium. Virological characteristics of the SARS-CoV-2 NB.1.8.1 variant. **Lancet Infect Dis.**, 25(8), e443, 2025.
- Uriu, K., Kaku, Y., Kihara, M., Genotype to Phenotype Japan (G2P-Japan) Consortium, & Sato, K. Antiviral humoral immunity against SARS-CoV-2 omicron JN.1 subvariants induced by JN.1 recombinant protein vaccine. **Vaccine**, 54, 127129, 2025.
- Kobiyama, K., Utsumi, D., Kaku, Y., Sasaki, E., Yasui, F., Okamura, T., Onodera, T., Tobuse, A. J., Sakakour, A., Amiry, A. F., Hayashi, T., Temizoz, B., Liu, K., Negishi, H., Toyama-Sorimachi, N., Kohara, M., Sawasaki, T., Takagi, J., Sato, K., Takahashi, Y., Yasutomi, Y. & Ishii, K. J. Immunological analysis of LC16m8 vaccine: preclinical and early clinical insights into mpox. **EBioMedicine**, 115, 105703, 2025.
- Tolentino, J. E., Lytras, S., Ito, J., & Sato, K. Beyond MERS: Merbecovirus receptor plasticity calls for emergence preparedness. **Cell Host Microbe**, 33(4), 453–456, 2025.
- Mayer, J., Blanco-Melo, D., Coffin, J. M., Gifford, R. J., Johnson, W. E., Lindemann, D., Peeters, M., Sato, K., Stoye, J., Tachedjian, G., & Hatziioannou, T. 2024 taxonomy update for the family Retroviridae. **Arch Virol.**, 170(8), 164, 2025.
- Ito, J., Strange, A., Liu, W., Joas, G., Lytras, S., Genotype to Phenotype Japan (G2P-Japan) Consortium, & Sato, K. A protein language model for exploring viral fitness landscapes. **Nat Commun.**, 16(1), 4236, 2025.
- Chen, L., Kaku, Y., Okumura, K., Uriu, K., Zhu, Y., Genotype to Phenotype Japan (G2P-Japan) Consortium, Ito, J., & Sato, K. Virological characteristics of the SARS-CoV-2 LP.8.1 variant. **Lancet Infect Dis.**, 25(4), e193, 2025.
- Lytras, S., Lamb, K. D., Ito, J., Grove, J., Yuan, K., Sato, K., Hughes, J., & Robertson, D. L. Pathogen genomic surveillance and the AI revolution. **J Virol.**, 99(2), e0160124, 2025.
- Uriu, K., Kaku, Y., Uwamino, Y., Fujiwara, H., Saito, F., Genotype to Phenotype Japan (G2P-Japan) Consortium, & Sato, K. Antiviral humoral immunity induced by JN.1 monovalent mRNA vaccines against SARS-CoV-2 omicron subvariants including JN.1, KP.3.1.1, and XEC. **Lancet Infect Dis.**, 25(2), e61, 2025.