Yuya Kiguchi
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PROFILE

[Nationality]	Japan
[Affiliation]	Division of Hematology, Medicine, Stanford University
[Degree]	Ph.D.

EDUCATION

Waseda University Tokyo, Japan
Ph.D. 2022
Cooperative Major of Advanced Health Science
Supervisor: Masahira Hattori

The University of Tokyo Chiba, Japan
Master of Science 2014
Department of Computational Biology, the Graduate School of Frontier Sciences
Supervisor: Masahira Hattori

Hosei University Tokyo, Japan
Bachelor of Science 2012
Faculty of Bioscience and Applied Chemistry
Supervisor: Kaneyoshi Yamamoto

WORK EXPERIENCE

Stanford University October 2024~Present
Postdoctoral Fellow
Division of Hematology, Medicine
Prof. Ami S. Bhatt group

The University of Tokyo April 2022~September 2024

Postdoctoral Fellow

Department of Computational Biology and Medical Sciences

Prof. Yutaka Suzuki group

RIKEN Center for Integrative Medical Sciences May 2020~Present

Visiting Researcher

Laboratory for Microbiome Sciences

Waseda University April 2020~February 2022

Research Associate

Research Institute for Science and Engineering

National Institute of Advanced Industrial Science and Technology May 2017~March2020

Research Assistant

Computational Bio Big-Data Open Innovation Laboratory

Takara Bio Inc. April 2014~March 2017

Scientific Researcher

Biomedical Center

FELLOWSHIP

1. Stanford Medicine Children's Health Center for IBD and Celiac Disease Postdoctoral and Early Career Support Award, Stanford University, 2024
2. Competitive Scholarship for Young Doctoral Students from Waseda University, 2019
3. Competitive Scholarship for Young Doctoral Students from Waseda University, 2018
4. Competitive Scholarship for Young Doctoral Students from Waseda University, 2017

AWARDS

1. Poster Award for Excellence The 51st Naito Conference, The Naito Foundation, 2024
2. Seminar on Research Planning of Advanced Health Science (Best Presentation Award), Waseda University, 2017

GRANT

1. Grant-in-Aid for Early-Career Scientists, Discovery of the extrachromosomal elements in the human microbiome, 2024-2026, 24K18092, **Principal Investigator**
2. Grant-in-Aid for Scientific Research (B), Elucidation of the full picture of mobile genetic

elements and their defense systems in the intestinal microbiota, 2024-2027, 24K01676
3. Fund for the Promotion of Joint International Research (International Collaborative Research), Research for infection immunity against global viral infections with a new bioinformatic approach, 2023-2027, 23KK0176
4. Japan Agency for Medical Research and Development(AMED), Study of the antibiotic-resistant bacteria pathophysiology and control from gut ecosystem dynamics, 2023
5. Institute for Fermentation, Osaka (Y-2022-1-010), 2022, **Principal Investigator**

PUBLICATIONS

1. **Yuya Kiguchi†*.,** Nagisa Hamamoto†., Yukie Kashima., et al. Giant extrachromosomal element "Inocle" potentially expands the adaptive capacity of the human oral microbiome. *Nature Communications* 16, 7397 (2025). **†co-first author, *Corresponding author**
2. Maghini, Dylan G*., **Yuya Kiguchi***, Aaron E. Darling, Leigh G. Monahan, Aaron L. Halpern, Catherine M. Burke, Erich Jaeger, et al. 2025. "Illumina Complete Long Read Assay Yields Contiguous Bacterial Genomes from Human Gut Metagenomes." *mSystems*, no. e01531-24 (July): e0153124. ***co-first author**
3. Daiki Takewaki*, **Yuya Kiguchi***, Hiroaki Masuoka, Mallahalli S. Manu, Ben J. E. Raveney, Seiko Narushima, Rina Kurokawa, et al. 2024. "Tyzzerella Nexilis Strains Enriched in Mobile Genetic Elements Are Involved in Progressive Multiple Sclerosis." *Cell Reports* 43 (10): 114785. ***co-first author**
4. Masuda, Sachiko, Pamela Gan, **Yuya Kiguchi**, Mizue Anda, Kazuhiro Sasaki, Arisa Shibata, Wataru Iwasaki, Wataru Suda, and Ken Shirasu. 2024. "Uncovering Microbiomes of the Rice Phyllosphere Using Long-Read Metagenomic Sequencing." *Communications Biology* 7 (1): 1–13.
5. Rina Kurokawa, Hiroaki Masuoka, Lena Takayasu, **Yuya Kiguchi**, Yusuke Ogata, Ryoko Miura-Kawatsu, Masahira Hattori, and Wataru Suda. 2023. "Recovery of Microbial DNA by Agar-Containing Solution from Extremely Low-Biomass Specimens Including Skin." Scientific Reports 13 (1): 19666.
6. Lena Takayasu, Eiichiro Watanabe, Taichi Umeyama, Rina Kurokawa, Yusuke Ogata, **Yuya Kiguchi**, Hiroaki Masuoka, Masahiro Umezaki, Masahira Hattori, and Wataru Suda. 2022. "Lifelong Temporal Dynamics of the Gut Microbiome Associated with Longevity in Mice." *bioRxiv*. https://doi.org/10.1101/2022.11.07.515511.
7. Suguru Nishijima, Naoyoshi Nagata, **Yuya Kiguchi**, Yasushi Kojima, Tohru Miyoshi-Akiyama, Moto Kimura, Mitsuru Ohsugi, Kohjiro Ueki, Shinichi Oka, Masashi Mizokami, Takao Itoi, Takashi Kawai, Naomi Uemura, Masahira Hattori, Extensive Gut Virome Variation and Its Associations with Host and Environmental Factors in a Population-Level Cohort, *Nature Communications*, 13 (1): 1–14, 2022.
8. **Yuya Kiguchi**, Suguru Nishijima, Naveen Kumar, Masahira Hattori, Wataru Suda, Long-read metagenomics of multiple displacement amplified DNA of low-biomass human gut phageomes by SACRA preprocessing chimeric reads, *DNA Research*, Volume 28, Issue 6, December 2021, dsab019
9. Koji Atarashi, Wataru Suda, Chengwei Luo, Takaaki Kawaguchi, Iori Motoo, Seiko Narushima, **Yuya Kiguchi**, Keiko Yasuma, Eiichiro Watanabe, Takeshi Tanoue, Christoph A. Thaiss, Mayuko Sato, Kiminori Toyooka, Heba S. Said, Hirokazu

Yamagami, Scott A. Rice, Dirk Gevers, Ryan C. Johnson, Julia A. Segre, Kong Chen, Jay K. Kolls, Eran Elinav, Hidetoshi Morita, Ramnik J. Xavier, Masahira Hattori, Kenya Honda, Ectopic colonization of oral bacteria in the intestine drives TH1 cell induction and inflammation, *Science*, Vol. 358, Issue 6361, pp. 359-365, 2017.

10. Tatsuaki Kurata, Akira Katayama, Masakazu Hiramatsu, **Yuya Kiguchi**, Masamitsu Takeuchi, Tomoyuki Watanabe, Hiroshi Ogasawara, et al. 2013. "Identification of the Set of Genes, Including Nonannotated morA, under the Direct Control of ModE in Escherichia Coli." *Journal of Bacteriology* 195 (19): 4496–4505.

CONFERENCES (2018~)

1. Giant extrachromosomal element "Inocle" potentially expands the adaptive capacity of the human oral microbiome, 2024, 34th Microbiome Virtual International Forum, (Selected Talks).
2. Inocles are novel extrachromosomal genetic element in the oral microbiome associated with blood cell populations, 2024, 51th Naito Conference, Hokkaido, Japan, Poster session and Oral session (Selected Talks).
3. Dysbiosis of the bacteriophage-bacteria interactions exacerbate the pathology of multiple sclerosis, 2023, The human microbiome, EMBL Heidelberg, Poster Session
4. Dysbiosis of the human gut bacteria-phage interactions associate with propionate reduction in multiple sclerosis, 2022, 9th International Human Microbiome Consortium Meeting (IHMC), Kobe, Japan, Poster Session
5. Dysbiosis of the human gut bacteriophage community in Multiple Sclerosis, 2021, 44th Annual Meeting of the Molecular Biology Society of Japan, Yokohama, Oral Session
6. Long-read metagenomics of multiple displacement amplification-treated phageome uncovers cluster specific characteristics of human gut *Microviridae*, 2021, 8th International Human Microbiome Consortium Meeting (IHMC), Barcelona, Spain, Poster Session
7. The structure of human gut virome, 2020, International Workshop on Eukaryotic Microbiome, The University of Tokyo, Oral Session
8. Comprehensive reconstruction of human gut full-length phage genomes using a long-read sequencer, 2019, The 42nd Annual Meeting of the Molecular Biology Society of Japan, Fukuoka, Oral Session
9. Development of a bioinformatic tool for long-read metagenomic sequencing of the human gut virome, 2019, Meeting on MICROBIOME, Cold Spring Harbor Laboratory, USA, Poster Session
10. Assessment of fecal storage condition for human gut virome analysis, 2018, 7th International Human Microbiome Consortium Meeting (IHMC), Killarney, County Kerry, Ireland, Poster Session