Kengo Sakurai

March 2026

CONTACT

113-8657, #327,
Laboratory of Biometry and Bioinformatics,
Department of Agricultural and Environmental Biology,
Graduate School of Agricultural and Life Sciences,
The University of Tokyo
1-1-1 Yayoi, Bunkyo, Tokyo, Japan
E-mail: sakurai@ut-biomet.org
Phone: +81-90-6763-0879

RESEARCH INTERESTS

My research focuses on quantitative genetics and genetic analysis, with a strong interest in developing breeding strategies that integrate genomic prediction and genomic selection. I aim to design efficient, data-driven breeding schemes by leveraging statistical models and genomic information. Ultimately, my goal is to establish breeding strategies that accelerate genetic gain while optimizing long-term breeding efficiency.

EDUCATION

Apr. 2022 – Mar. 2025

Ph.D. course in Department of Agricultural and Environmental Biology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan

・Thesis: A Study on Modeling Measurement Data and Optimizing Breeding Strategies for Data-Driven Breeding

・Laboratory: Lab. of Biometry and Bioinformatics

・Advisor: Assoc. Prof. Dr. Hiroyoshi Iwata

・Committee: Drs. Gota Morota, Takeshi Izawa, Akito Kaga, and Hideki Takanashi

Apr. 2020 - Mar. 2022

Master Course in Department of Agricultural and Environmental Biology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan

・Thesis: “Development of a Drought Tolerance Assessment Method for Soybean Using Multispectral Imaging”

・Laboratory: Lab. of Biometry and Bioinformatics

・Advisor: Assoc. Prof. Dr. Hiroyoshi Iwata

・Committee: Drs. Naohiro Aoki and Hideki Takanashi

Apr. 2018 - Mar. 2020

Major in Applied Biology, Faculty of Agriculture, The University of Tokyo, Japan

・Thesis: “Evaluation of drought stress and biomass-related traits in soybean using a multispectral camera.”

・Laboratory: Lab. of Biometry and Bioinformatics (From the 4th grade)

・Advisor: Assoc. Prof. Dr. Hiroyoshi Iwata (From the 4th grade)

・Bachelor of Agriculture

Apr. 2016 - Mar. 2018

Natural Science I, College of Arts and Science (Junior Division), The University of Tokyo, Japan

Apr. 2012 - Mar. 2015

Kariya High School

EMPLOYMENT

Mar. 2025 – Present

Laboratory of Biometry and Bioinformatics

Department of Agricultural and Environmental Biology
Graduate School of Agricultural and Life Sciences
The University of Tokyo, Bunkyo, Tokyo, Japan
Assistant Professor

Apr. 2022 – Mar. 2025
SPRING GX, Research Fellow of JST (Japan Science and Technology Agency)

Jan. 2019 – Mar. 2025
Ac-Planta Inc., Yushima, Bunkyo, Tokyo, Japan
Research associate (student internship)

PUBLICATIONS

- Sei Kinoshita, **Kengo Sakurai**, Takahiro Tsusaka, Miki Sakurai, Kenta Shirasawa, Sachiko Isobe, Hiroyoshi Iwata. **"Progeny-based genomic selection reveals untapped genetic potential in an underutilized medicinal plant, Perilla frutescens"** bioRxiv, 2025.11.26.690889, 2025. https://doi.org/10.1101/2025.11.26.690889
- Sei Kinoshita, **Kengo Sakurai**, Kosuke Hamazaki, Takahiro Tsusaka, Miki Sakurai, Kenta Shirasawa, Sachiko Isobe, Hiroyoshi Iwata. **"Optimization of crossing strategy based on the usefulness criterion in inter-population crosses considering different genetic effects among populations"** Theoretical and Applied Genetics, 138, 155, 2025. https://doi.org/10.1007/s00122-025-04935-7
- Tung Dang, Yushiro Fuji, Kie Kumaishi, Erika Usui, Shungo Kobori, Takumi Sato, Megumi Narukawa, Yusuke Toda, **Kengo Sakurai**, Yuji Yamasaki, Hisashi Tsujimoto, Masami Yokota Hirai, Yasunori Ichihashi, Hiroyoshi Iwata. **"I-SVVS: Integrative stochastic variational variable selection to explore joint patterns of multi-omics microbiome data"** Briefings in Bioinformatics, 26, 3, bbaf132, 2025. https://doi.org/10.1093/bib/bbaf132
- **Kengo Sakurai**, Kosuke Hamazaki, Minoru Inamori, Akito Kaga, Hiroyoshi Iwata. **"Cross Potential Selection: A Proposal for Optimizing Crossing Combinations in Recurrent Selection Using the Usefulness Criterion of Future Inbred Lines"** G3 Genes|Genomes|Genetics, 14, 11, jkae224, 2024. https://doi.org/10.1093/g3journal/jkae224
- Sei Kinoshita, **Kengo Sakurai**, Kosuke Hamazaki, Takahiro Tsusaka, Miki Sakurai, Terue Kurosawa, Youichi Aoki, Kenta Shirasawa, Sachiko Isobe, Hiroyoshi Iwata. **"Assessing the Potential for Genome-Assisted Breeding in Red Perilla Using Quantitative Trait Locus Analysis and Genomic Prediction"** Genes, 14, 12, 2137, 2023. https://doi.org/10.3390/genes14122137
- **Kengo Sakurai**, Yusuke Toda, Kosuke Hamazaki, Yoshihiro Ohmori, Yuji Yamasaki, Hirokazu Takahashi, Hideki Takanashi, Mai Tsuda, Hisashi Tsujimoto, Akito Kaga, Mikio Nakazono, Toru Fujiwara, Hiroyoshi Iwata. **"Random regression for modeling soybean plant response to irrigation changes using time-series multispectral data"** Frontiers in Plant Science, 14, 1201806, 2023. https://doi.org/10.3389/fpls.2023.1201806
- **Kengo Sakurai**, Yusuke Toda, Hiromi Kajiya-Kanegae, Yoshihiro Ohmori, Yuji Yamasaki, Hirokazu Takahashi, Hideki Takanashi, Mai Tsuda, Hisashi Tsujimoto, Akito Kaga, Mikio Nakazono, Toru Fujiwara, Hiroyoshi Iwata. **"Time-series multi-spectral imaging in soybean for improving biomass and genomic prediction accuracy"** The Plant Genome, 15, e20244, 2022. https://doi.org/10.1002/tpg2.20244
- Kenta Suzuki, Masato S. Abe, Daiki Kumakura, Shinji Nakaoka, Fuki Fujiwara, Hirokuni Miyamoto, Teruno Nakaguma, Mashiro Okada, **Kengo Sakurai**, Shohei Shimizu, Hiroyoshi Iwata, Hiroshi Masuya, Naoto Nihei, Yasunori Ichihashi. **"Chemical-Mediated Microbial Interactions Can Reduce the Effectiveness of Time-Series-Based Inference of Ecological Interaction Networks"** International Journal of Environmental Research and Public Health, 19, 3, 1228, 2022. https://doi.org/10.3390/ijerph19031228

CONFERENCE PRESENTATIONS

ORAL PRESENTATIONS (International Conference)

- **K. Sakurai** 「Random Regression for Modeling Soybean Plant Response to Irrigation Changes Using Time-series Multispectral Data」 Workshop on Plant biology using remote sensing, modelling, genetics and genomics to apply our knowledge for the better future, Zurich, Switzerland, Oct. 2023

ORAL PRESENTATIONS (Domestic Conference)

- T. Abe, S. Kimura, **K. Sakurai**, A. Abe, H. Shimono, H. Iwata, G. Morota, “Genetic trend analysis of historical rice data in Japan using phenotypic, pedigree, and genomic information” The 149th Japanese Society of Breeding Meeting, 109, Tohoku University, Miyagi, Japan, Mar. 2026.
- M. Inamori, **K. Sakurai**, K. Hamazaki, H. Iwata, “Development of BitBreedingSim: A High-Speed Breeding Simulator Executable in R” The 149th Japanese Society of Breeding Meeting, 312, Tohoku University, Miyagi, Japan, Mar. 2026.
- **K. Sakurai**, M. Inamori, R. Okabe, H. Igarashi, N. Yamaguchi, A. Kaga, H. Iwata, “Optimization of Crossing Strategies Considering Multiple Traits Based on Lookahead Simulation in a High-Speed Breeding Simulator” The 149th Japanese Society of Breeding Meeting, 313, Tohoku University, Miyagi, Japan, Mar. 2026.
- M. Watanabe, **K. Sakurai**, S. Kimura, H. Sano, N. Miura, M. Inamori, Y. Unno, W. Guo, S. Isobe, S. Inukai, K. Kusunoki, H. Iwata, “G×E evaluation of growth traits including UAV-based tree height in hybrid larch sibling families” The 149th Japanese Society of Breeding Meeting, 319, Tohoku University, Miyagi, Japan, Mar. 2026.
- **K. Sakurai**, Y. Toda, H. Tsujimoto, A. Kaga, H. Iwata, “Evaluation of Segregation Prediction Accuracy for Aboveground Traits Using Soybean RILs and Subsequent Progeny Populations” The 147th Japanese Society of Breeding Meeting, 306, Tohoku University, Miyagi, Japan, Mar. 2025.
- **K. Sakurai**, L. Moreau, T. Mary-Huard, H. Iwata, A. Charcosset, “Crossing Strategy Considering Multiple Traits Based on The Ability of Future Inbred Lines in Plant Breeding Programs” The 146th Japanese Society of Breeding Meeting, 403, Hiroshima University, Hiroshima, Japan, Sep. 2024.
- S. Kinoshita, **K. Sakurai**, K. Hamasaki, T. Tsusaka, M. Sakurai, K. Shirasawa, S. Isobe, H. Iwata, “Optimization of cross pairs among families with different genetic characteristics to improve multiple traits” The 146th Japanese Society of Breeding Meeting, 404, Hiroshima University, Hiroshima, Japan, Sep. 2024.
- S. Kinoshita, **K. Sakurai**, K. Hamasaki, T. Chen, T. Tsusaka, M. Sakurai, T. Kurosawa, K. Shirasawa, S. Isobe, H. Iwata, “Selection of cross combinations based on predicted breeding value of later generations: application to mating scheme using multiple F3 populations of red perilla” The 143rd Japanese Society of Breeding Meeting, 211, Shizuoka University, Shizuoka, Japan, Mar. 2023.
- H. Iwata, Y. Toda, **K. Sakurai**, Y. Fuji, Y. Ohmori, Y. Yamasaki, H. Takahashi, H. Takanashi, M. Tsuda, H. Kanegae, Y. Hirai, Y. Ichihashi, H. Tsujimoto, M. Nakazono, T. Fujiwara, A. Kaga, “Selection of cross combinations based on genomic-ionomic prediction models: application to the breeding of drought tolerant soybean lines” The 143rd Japanese Society of Breeding Meeting, 430, Shizuoka University, Shizuoka, Japan, Mar. 2023.
- **K. Sakurai**, Y. Toda, Y. Fuji, Y. Ohmori, Y. Yamasaki, H. Takahashi, H. Takanashi, M. Tsuda, Y. Hirai, H. Tsujimoto, M. Nakazono, T. Fujiwara, A. Kaga, H. Iwata, “Estimating genetic correlation between traits and environments based on the analysis of high-dimensional・multi-environmental multiomics data: An application to soybean drought experiment” The 142nd Japanese Society of Breeding Meeting, 123, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan, Sep. 2022
- **K. Sakurai**, Y. Toda, Y. Ohmori, Y. Yamasaki, H. Takahashi, H. Takanashi, M. Tsuda, M. Ishimori, H. Tsujimoto, A. Kaga, M. Nakazono, T. Fujiwara, H. Iwata, “Predict genetic variation in drought tolerance of soybean based on vegetation index and genomic information” The 141st Japanese Society of Breeding Meeting, 527, Online, Mar. 2022
- Y. Toda, K. Hamasaki, M. Okada, **K. Sakurai**, Y. Fuji, Y. Ohmori, Y. Yamasaki, H. Takahashi, H. Takanashi, M. Tsuda, H. Kanegae, Y. Hirai, H. Tsujimoto, A. Kaga, M. Nakazono, T. Fujiwara, Y. Ichihashi, H. Iwata, “Comprehensive genome-wide association analysis of multi-omics data for drought tolerance in soybean” The 141st Japanese Society of Breeding Meeting, 526, Online, Mar. 2022
- **K. Sakurai**, Y. Toda, Y. Ohmori, Y. Yamasaki, H. Takahashi, H. Takanashi, M. Tsuda, M. Ishimori, H. Tsujimoto, A. Kaga, M. Nakazono, T. Fujiwara, H. Iwata, “Evaluating the genetic relationship between vegetation index and drought tolerance in soybean using a multi-trait model.” The 140th Japanese Society of Breeding Meeting, 216, Online, Sep. 2021

POSTER PRESENTATIONS (International Conference)

- **K. Sakurai**, M. Inamori, R. Okabe, H. Igarashi, N. Yamaguchi, A. Kaga, H. Iwata 「Optimization of Crossing Strategies Considering Multiple Traits Based on Lookahead Simulation in a High-Speed Breeding Simulator」 International Symposium on Advancing Soybean Breeding: Genetics, Genomics, Biotechnology and Agronomy, 47, Tokyo, Japan, Feb. 2026
- **K. Sakurai**, L. Moreau, T. Mary-Huard, H. Iwata, A. Charcosset 「Crossing Strategy Considering Multiple Traits Based on The Ability of Future Inbred Lines in Plant Breeding Programs」 7th International Conference of Quantitative Genetics (ICQG7), P-56, Vienna, Austria, Jul. 2024

- **K. Sakurai**, K. Hamazaki, M. Inamori, H. Iwata 「Crossing strategy considering segregation of later generations in a plant breeding program」 International Plant & Animal Genome Conference 2024 (PAG 31), PO0623, San Diego, USA, Jan. 2024
- S. Kinoshita, **K. Sakurai**, K. Hamazaki, T. Tsusaka, M. Sakurai, T. Kurosawa, Y. Aoki, K. Shirasawa, S. Isobe, H. Iwata 「Assessing the potential for genome-assisted breeding in red perilla using quantitative trait locus analysis and genomic prediction」 International Plant & Animal Genome Conference 2024 (PAG 31), PO0257, San Diego, USA, Jan. 2024
- **K. Sakurai**, K. Hamazaki, M. Inamori, H. Iwata 「Crossing Strategy for Plant Breeding」 Symposium University of Tokyo - ETH Zurich - University of Zurich, Switzerland, 8, Oct. 2023 (**Poster Award**)
- S. Kinoshita, **K. Sakurai**, K. Hamazaki, T. Tsusaka, M. Sakurai, T. Kurosawa, K. Shirasawa, S. Isobe, H. Iwata 「Selection of cross combinations based on predicted breeding value of later generations: application to mating scheme using multiple F3 populations of red perilla」 The 4th Asian Horticultural Congress, P1-37, Tokyo, Japan, Aug. 2023

POSTER PRESENTATIONS (Domestic Conference)

- R. Okabe, **K. Sakurai**, M. Inamori, H. Igarashi, N. Yamaguchi, A. Kaga, H. Iwata, “Estimation of Missing Genomic Information in Soybean Crossing Populations and Haplotype-Based Genomic Prediction” The 147th Japanese Society of Breeding Meeting, P011, Tohoku University, Miyagi, Japan, Mar. 2025.
- T. Chen, S. Kinoshita, M. Okada, Y. Imachi, **K. Sakurai**, T. Tsusaka, M. Sakurai, K. Shirasawa, S. Isobe, H. Iwata, “Development of an objective evaluation method for the curling of perilla leaves using a convolutional neural network” The 146th Japanese Society of Breeding Meeting, P104, Hiroshima University, Hiroshima, Japan, Sep. 2024.
- S. Kinoshita, **K. Sakurai**, T. Chen, T. Tsusaka, M. Sakurai, T. Kurosawa, H. Iwata, “Predicting Chromosomal Contributions to Genetic Gain in Medicinal Components of Red Perilla Cross-breeding Populations” The 142nd Japanese Society of Breeding Meeting, P024, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan, Sep. 2022
- **K. Sakurai**, Y. Toda, Y. Ohmori, Y. Yamasaki, H. Takahashi, H. Takanashi, M. Tsuda, M. Ishimori, H. Tsujimoto, A. Kaga, M. Nakazono, T. Fujiwara, H. Iwata, “Prediction of drought tolerance of soybean using multispectral data acquired from a UAV and ground vehicle” The 138th Japanese Society of Breeding Meeting, P055-C, Online, Oct. 2020
- **K. Sakurai**, Y. Toda, Y. Ohmori, Y. Yamasaki, H. Takahashi, H. Takanashi, M. Tsuda, M. Ishimori, H. Tsujimoto, A. Kaga, M. Nakazono, T. Fujiwara, H. Iwata, “Prediction of drought tolerance and growth of soybean genetic accessions using multispectral data” The 137th Japanese Society of Breeding Meeting, P071, The University of Tokyo, Tokyo, Japan, Mar. 2020

OTHER PRESENTATIONS

- **K. Sakurai**, Y. Toda, Y. Ohmori, Y. Yamasaki, H. Takahashi, H. Takanashi, M. Tsuda, M. Ishimori, H. Tsujimoto, A. Kaga, M. Nakazono, T. Fujiwara, H. Iwata, “Relationship analysis between multispectral data, ionome and above-ground phenotypes” The 7th Area Meeting, Research Area “Elucidation of Robustness of Plants against Environmental Change and Creation of Fundamental Technologies for its Application”, 1-25, Online, Sep. 2021

TEACHING EXPERIENCE

Mar. 2025 – Present

The University of Tokyo, Bunkyo, Tokyo, Japan

Co-Instructor

・**Biostatistics**, Faculty of Agriculture, A Semester, 2025

・**Play and Learn! Exploring Genetics and Data Science with the Genome Breeding Game**, College of Arts and Sciences, A Semester, 2025 / A1 Term, 2025

・**Experiments in Advanced Applied Biology** (Oct. 2, 3, 9, 10), Faculty of Agriculture, A Semester, 2025

Topics: Deep learning for image analysis and Plant breeding simulation game

・**Advanced Biometrics**, Graduate School of Agricultural and Life Sciences, S Semester, 2025

Book: Falconer, D. S., and T. F. C. Mackay, 1996 Introduction to Quantitative Genetics, Ed 4. Longmans Green, Harlow, Essex, UK.

・**Practice in Basic Field Agrobiology** (Apr. 16), Faculty of Agriculture, S Semester, 2025

Topic: Design of experiments

- **Experiments in Applied Biology I** (May 16, 22, 29), Faculty of Agriculture, S Semester, 2025
  Topic: Image analysis, QTL mapping, and GWAS

Guest-Instructor

- **Biometrics**, Faculty of Agriculture & Faculty of Science, A Semester, 2025

Apr. 2020 – Mar. 2025
The University of Tokyo, Bunkyo, Tokyo, Japan

Teaching Assistant

- **Biostatistics**, Faculty of Agriculture, A Semester
- **Experiments in Applied Biology**, Faculty of Agriculture, S Semester
- **Experiments in Advanced Applied Biology**, Faculty of Agriculture, A Semester

MEMBERSHIPS

- Japanese Society of Breeding. 2019 – Present

OSS CONTRIBUTIONS

GitHub
https://github.com/Sakuraikengo

MISCELLANEOUS

- Age: 29
- Birthplace: Aichi, Japan
- Languages: Japanese and English
- Computer skills
- Statistical/Numerical computational tools: R
- Content-description languages: LaTeX and Markdown
- Operating systems: Windows

LINKS

ORCID: 0000-0001-7773-289X
Researchmap: https://researchmap.jp/kengosakurai
My website
LinkedIn