

Yu Sugihara

Laboratory of crop evolution,
Graduate School of Agriculture,
Kyoto University, Kyoto 606-8502, Japan

sugihara.yu.85s@kyoto-u.jp
yu.sugihara@tsl.ac.uk

Education

2020 - Present **Ph. D student**

Graduate School of Agriculture, Kyoto University, Japan
Advisor: Prof. Ryohei Terauchi

2020 **MSc**

Graduate School of Agriculture, Kyoto University, Japan
Advisor: Prof. Ryohei Terauchi

2018 **BSc**

Department of Agriculture, Kyoto University, Japan

Research Experience

Oct 2021 - Present

Internship at The Sainsbury Laboratory, UK
(Sophien Kamoun Group)

April 2019 - Sept 2021

Visiting Researcher at Division of Genomics & Breeding, Iwate
Biotechnology Research Center, Japan

Publications

1. **Sugihara Y**, Abe Y, Takagi H, Abe A, Shimizu M, Ito K, Kanzaki E, Oikawa K, Kourelis J, Langner T, Win J, Bialas A, Ludke D, Mauricio P. Contreras, Chuma I, Saitoh H, Kobayashi M, Zheng S, Tosa Y, Banfield MJ, Kamoun S, Terauchi R, Fujisaki K. (2023) [Disentangling the complex gene interaction networks between rice and the blast fungus identifies a new pathogen effector](#). *bioRxiv*. DOI: 10.1101/2022.07.19.500555. Accepted in *PLOS Biology*

2. Nishiyama C, Sekiguchi S, **Sugihara Y**, Nishikawa M, Makita N, Segawa T, Terasaki M, Takagi H, Koyanagi T. (2023) [Phylogenomic analysis in *Latilactobacillus sakei* by using polymorphisms detected by next-generation sequencing](#). *Bioscience of Microbiota, Food and Health* advpub:2022–017. DOI: 10.12938/bmfh.2022-017.

3. Saiga S, Tada M, Segawa T, **Sugihara Y**, Nishikawa M, Makita N, Sakamoto M, Tanaka K, Wada T, Takagi H. (2022) [NGS-based genome wide association study helps to develop co-dominant marker for the physical map-based locus of PFRU controlling flowering in cultivated octoploid strawberry](#). *Euphytica* 219:6. DOI: 10.1007/s10681-022-03132-7

4. Takeda T, Takahashi M, Shimizu M, **Sugihara Y**, Saitoh H, Fujisaki K, Ishikawa K, Utsushi H, Kanzaki E, Sakamoto Y, Abe A, Terauchi R (2022) [Rice apoplastic CBM1-interacting protein counters blast pathogen invasion by binding conserved carbohydrate binding module 1 motif of fungal proteins](#). *PLOS Pathogens* 18(9): e1010792. DOI: 10.1371/journal.ppat.1010792

5. Natsume S, **Sugihara Y**, Kudoh A, Oikawa K, Shimizu M, Ishikawa Y, Nishihara M, Abe A, Innan H, Terauchi R. (2022) [Genome Analysis Revives a Forgotten Hybrid Crop Edo-dokoro in the Genus *Dioscorea*](#). *Plant and Cell Physiology*, pcac109. DOI: 10.1093/pcp/pcac109

6. Shimizu M, Hirabuchi A, **Sugihara Y**, Abe A, Takeda T, Kobayashi M, Hiraka Y, Kanzaki E, Oikawa K, Saitoh H, Langner T, Banfield MJ, Kamoun S, Terauchi R (2022) [A genetically linked pair of NLR immune receptors show contrasting patterns of evolution](#). *Proceedings of the National Academy of Sciences*, 119(27): e2116896119. DOI: 10.1073/pnas.2116896119

7. **Sugihara Y**, Young L, Yaegashi H, Natsume S, Shea DJ, Takagi H, Booker H, Innan H, Terauchi R, Abe A (2022) [High-performance pipeline for MutMap and QTL-seq](#). *PeerJ*, 10:e13170. DOI: 10.7717/peerj.13170

8. **Sugihara Y***, Kudoh A*, Tamiru-Oli M, Takagi H, Natsume S, Shimizu M, Abe A, Asiedu R, Asfaw A, Adebola P, Terauchi R (2021) [Population genomics of yams: evolution and domestication of *Dioscorea* species](#). In: *Population Genomics*. Springer, Cham. DOI: 10.1007/13836_2021_94 *Equally contributed to this work

9. Segawa T, Nishiyama C, Tamiru-Oli M, **Sugihara Y**, Abe A, Sone H, Itoh N, Asukai M, Uemura A, Oikawa K, Utsushi H, Ikegami-Katayama A, Imamura T, Mori M, Terauchi R, Takagi H (2021) [Sat-BSA: an NGS-based method using local de novo assembly of long reads for rapid identification of genomic structural variations associated with agronomic traits](#). *Breeding Science*, 71(3): 299–312. DOI: 10.1270/jsbbs.20148
10. **Sugihara Y**, Darkwa K, Yaegashi H, Natsume S, Shimizu M, Abe A, Hirabuchi A, Ito K, Oikawa K, Tamiru-Oli M, Ohta A, Matsumoto R, Agre P, De Koeper D, Pachakkil B, Yamanaka S, Muranaka S, Takagi H, White B, Asiedu R, Innan H, Asfaw A, Adebola P, Terauchi R (2020) [Genome analyses reveal the hybrid origin of the staple food crop white Guinea yam \(*Dioscorea rotundata*\)](#). *Proceedings of the National Academy of Sciences*, 17(50): 31987–31992. DOI: 10.1073/pnas.2015830117

Preprints

1. Natsume S, Yaegashi H, **Sugihara Y**, Abe A, Shimizu M, Oikawa K, White B, Kudoh A, Terauchi R (2022) [Whole genome sequencing of a wild yam species *Dioscorea tokoro* reveals a genomic region associated with sex](#). *bioRxiv*. DOI: 10.1101/2022.06.11.495741

Presentations

1. **Sugihara Y**. Genetics approach using whole genome sequencing to rapidly identify the genomic loci involved in biological traits of rice blast fungus. *12th Japan-US Seminar in Plant Pathology*. Zoom workshop. October 2020
2. **Sugihara Y**, Natsume S, Abe A, Shimizu M, Obidiegwu J, Terauchi R. Population genomics of *Dioscorea tokoro*, a wild yam species. *Plant and Animal Genome (PAG) XXVII Conference*. San Diego, CA. January 2019
3. **Sugihara Y**, Abe A, Shimizu M, Yaegashi H, Natsume S, Obidiegwu J, Terauchi R. Application of population genomics and GWAS to *Dioscorea rotundata* (white Guinea yams) for identifying loci controlling agronomically important traits. *Plant and Animal Genome (PAG) XXVII Conference*. San Diego, CA. January 2019

Peer reviews

- New Phytologist (1)