Yu Sugihara

Division of Genomics & Breeding,
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Education

2023	**Ph. D**	
	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

Apr. 2024 – present	Postdoc at Division of Genomics & Breeding, Iwate Biotechnology Research Center, Japan
Apr. 2023 – Mar. 2024	Postdoc at The Sainsbury Laboratory, UK (Sophien Kamoun group)
Oct. 2021 – Mar. 2023	Internship at The Sainsbury Laboratory, UK (Sophien Kamoun group)
Apr. 2019 – Sep. 2021	Visiting Researcher at Division of Genomics & Breeding, Iwate Biotechnology Research Center, Japan

Publications

1. Huang C-Y, Huang Y-S, **Sugihara Y**, Wang H-Y, Huang L-T, Lopez-Agudelo JC, Chen Y-F, Lin K-Y, Chiang B-J, Toghani A, Kourelis J, Wang C-H, Derevnina L, Wu C-H (2024) Subfunctionalization of NRC3 altered the genetic structure of the Nicotiana NRC network. *PLOS Genetics* 20:e1011402. DOI:10.1371/journal.pgen.1011402

2. Sugimura Y, Oikawa K, **Sugihara Y**, Utsushi H, Kanzaki E, Ito K, Ogasawara Y, Fujioka T,

Takagi H, Shimizu M, Shimono H, Terauchi R, Abe A (2024) Impact of rice GENERAL REGULATORY FACTOR14h (GF14h) on low-temperature seed germination and its application to breeding. *PLOS Genetics*, 20:e1011369. DOI: 10.1371/journal.pgen.1011369

3. Barragan AC*¹, Latorre SM*¹, Malmgren A, Harant A, Win J, **Sugihara Y**, Burbano HA, Kamoun S*², Langner T*² (2024) Multiple horizontal mini-chromosome transfers drive genome evolution of clonal blast fungus lineages. *Molecular Biology and Evolution,* 41:msae164. DOI: 10.1093/molbev/msae164 *¹Authors contributed equally, *²Corresponding authors

4. **Sugihara Y**, Abe Y, Takagi H, Abe A, Shimizu M, Ito K, Kanzaki E, Oikawa K, Kourelis J, Langner T, Win J, Białas A, Lüdke D, Contreras MP, 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. *PLOS Biology*, 21:e3001945. DOI: 10.1371/journal.pbio.3001945 *Corresponding authors

5. 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

6. Saiga S, Tada M, Segawa T, **Sugihara Y**, Nishikawa M, Makita N, Sakamoto M, Tanaka K, Wada T, Takagi H (2023) 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

7. 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 *Corresponding authors

8. 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

9. 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

10. **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

11. **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 *Authors contributed equally

12. 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

13. **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 Koeyer 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 *Corresponding authors

Preprints

1. **Sugihara Y**, Kourelis J, Contreras MP, Pai H, Selvaraj M, Toghani A, Martinez-Anaya C*, Kamoun S* (2024) Helper NLR immune protein NRC3 evolved to evade inhibition by a cyst nematode virulence effector. *bioRxiv*. DOI:10.1101/2024.06.16.598756 *Corresponding authors

2. Selvaraj M, Toghani A, Pai H, **Sugihara Y**, Kourelis J, Yuen ELH, Ibrahim T, Zhao H, Xie R, Maqbool A, Concepcion JCD la, Banfield MJ, Derevnina L, Petre B, Lawson DM, Bozkurt TO, Wu C-H, Kamoun S*, Contreras MP* (2023) Activation of plant immunity through conversion of a helper NLR homodimer into a resistosome. *bioRxiv*. DOI: 10.1101/2023.12.17.572070 *Corresponding authors

3. 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**, Kourelis J, Contreras MP, Pai H, Selvaraj M, Toghani A, Martinez-Anaya C, Kamoun S. Helper NLR immune protein NRC3 evolved to evade inhibition by a cyst nematode virulence effector. *The 26th Annual Meeting of Society for Evolutionary Studies, Japan*. Kanagawa, Japan. Aug. 2024

2. **Sugihara Y**, Białas A, Langner T, Barragan AC, Kourelis J, Abe Y, Fujisaki K, Banfield MJ, Terauchi R, Kamoun S. The NLR immune receptor Pik-1 evolved to respond to fungal effectors of the AVR-Mgk family early in the evolution of Oryza and prior to rice domestication. *2023 IS-MPMI*. Rhode Island, PA. July 2023

3. **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

4. **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

5. **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

Awards

1. Postdoctoral oral presentation award, *The 26th Annual Meeting of Society for Evolutionary Studies, Japan*. Aug. 2024

Peer reviews

- New Phytologist (3)
- Genetics (1)
- Ecology and Evolution (1)
- Scientific Reports (1)