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Education

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| 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

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|------------------------|---|
| 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 |

Publication

1. 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
2. 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
3. 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 (2021) [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
 4. **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
 5. **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
 6. 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
 7. **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

Preprints

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, Chuma I, Saitoh H, Kobayashi M,

Zheng S, Tosa Y, Banfield MJ, Kamoun S, Terauchi R, Fujisaki K. (2022) [Tangled gene-for-gene interactions mediate co-evolution of the rice NLR immune receptor Pik and blast fungus effector proteins](#). *bioRxiv*. DOI: 10.1101/2022.07.19.500555.

2. 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

Presentation

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