

# Yu Sugihara

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

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

## Education

---

2020 - Present	<b>Ph. D student</b> Graduate School of Agriculture, Kyoto University, Japan Advisor: Prof. Ryohei Terauchi
2020	<b>MSc</b> Graduate School of Agriculture, Kyoto University, Japan Advisor: Prof. Ryohei Terauchi
2018	<b>BSc</b> 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

## Publication

---

1. 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
2. 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
3. **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
  4. **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
  5. 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
  6. **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

3. 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) [Apoplastic CBM1-interacting proteins bind conserved carbohydrate binding module 1 motifs in fungal hydrolases to counter pathogen invasion](#). *bioRxiv*. DOI: 10.1101/2021.12.31.474618

## 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