

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

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

Publication

1. **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
^{*} Equally contributed to this work
2. 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

3. **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

Preprints

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) Apoplastic CBM1-interacting proteins bind conserved carbohydrate binding module 1 motifs in fungal hydrolases to counter pathogen invasion. *bioRxiv*
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. *bioRxiv*
3. **Sugihara Y**, Young L, Yaegashi H, Natsume S, Shea DJ, Takagi H, Booker H, Innan H, Terauchi R, Abe A (2020) High-performance pipeline for MutMap and QTL-seq. *bioRxiv*

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