**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)

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

April 2019 - Sept 2021

**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

1. 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
2. **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