

Rafael Massahiro Yassue

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I am a Ph.D. candidate with experience in plant breeding, field experimentation, quantitative genetics, statistical modeling, phenomics, and genomics. My line of research is connecting genomics, high-throughput phenotyping, machine learning, and quantitative genetics to plant breeding. My goal is to solve challenges by applying multidisciplinary approaches. Furthermore, I continuously improve myself in communication, teamwork, and leadership.

Education

- 2018: Ph.D. (in progress), Genetics and Plant Breeding, Luiz de Queiroz College of Agriculture - University of São Paulo, SP, Brazil
 - ✓ Dissertation: “Genetic architecture of tropical maize for interaction with plant growth-promoting bacteria via high-throughput phenotyping”
 - ✓ Advisor: Prof. Dr. Roberto Fritsche-Neto
- 2016-2018: M.S., Genetics and Plant Breeding, Luiz de Queiroz College of Agriculture - University of São Paulo SP, Brazil
 - ✓ Thesis: “Tolerance of soybean to Asian rust in multivariate diallel and contrasting environments of fungicides”
 - ✓ Advisor: Prof. Dr. Natal Antonio Vello
- 2011-2015: B.Sc. Agronomic Engineering, Western Paraná State University, PR, Brazil

Experience

- 2016-2019: Member of plant breeding study group, GVENCK
 - ✓ Organizing scientific events, promote discussions on relevant genetic and plant breeding issues, and soft skills improvement
- 2015: Academic internship, Soybean breeding, ESALQ
 - ✓ Field experimentation, scientific discussion, and data analysis
- 2013-2014: Intern, Soybean breeding, Coodetec
 - ✓ Hands-on experience in an industry breeding program
- 2011-2015: Undergraduate Research, Plant breeding, Unioeste
 - ✓ Learning in methods of research and development of scientific thought

Skills

- Soft Skills: Teamwork, leadership, and communication
- Languages: English and Portuguese
- Quantitative genetics: Population structure, GWAS, and genomic prediction
- Computer Skills: R programming (asreml, caret, BGLR), Python (OpenCV, Keras, Numpy, Pandas), and Julia (JWAS)
- High throughput phenotype: Shovelomics, data acquisition, mosaicking assembly, and data analysis
- Statistical modeling: Machine learning, mixed models, multivariate models, and Bayesian methods
- Image processing: RGB, multispectral, thermal, and hyperspectral images

Additional training

- Introdução ao aprendizado de máquinas com Python (2021)
- Workshop on Analysis of Breeding Experiments using ASReml-R (2020)
- Workshop on Crop Growth Models Applied for Plant Breeding (2020)
- Treinamento genotype to phenotype models in plant breeding. (2019)
- System biology and gene networks inference: application to livestock. (2019)
- IV Workshop on Longitudinal and Incomplete Data (2018)
- Quantitative Genetics and Genomics (2018)
- New methodologies for high-resolution mapping and development of molecular (2017)

Invited presentations

- Cultura do Milho: Melhoramento do Milho. Aula da disciplina: Introdução à Engenharia Agrônômica. ESALQ. Online. 2021.
- Investigating the genetic architecture of the interaction between tropical maize and plant growth-promoting bacteria via high-throughput phenotyping. Translation Plant Science-Discussion Group (TPS-DG). Virginia Tech. Online. 2021.
- Genetic architecture of the interaction between tropical maize and plant growth-promoting bacteria via high-throughput phenotyping. Genomics and machine learning discussion group. Virginia Tech. Online. 2021.

Participation in events

- National Association of Plant Breeders 2021 Annual Meeting (Virtual conference)
- International Meeting on Plant Breeding: New approaches on plant breeding: insights into artificial intelligence. 2019 (Meeting)
- 10º Brazilian Plant Breeding Congress. 2019 (Congress)
- 9º Brazilian Plant Breeding Congress. 2017 (Congress)
- II Latin-American Conference on Plant Phenotyping and Phenomics for Plant Breeding. 2017. (Conference).

Publications

- Yassue RM, et al. On the genetic architecture in a public tropical maize panel of the symbiosis between corn and plant growth-promoting bacteria aiming to improve plant resilience. *Molecular Breeding*. <https://doi.org/10.1007/s11032-021-01257-6>
- Galli G, et al. Automated Machine Learning: a case study of genomic “image-based” prediction in maize hybrids. *Research Square* (Preprint). <https://doi.org/10.21203/rs.3.rs-840380/v2>
- Yassue RM et al. A low-cost greenhouse-based high-throughput phenotyping platform for genetic studies: a case study in maize under inoculation with plant growth-promoting bacteria *bioRxiv* (Preprint). <https://doi.org/10.1101/2021.08.12.456112>
- Yassue RM, et al. CV- α : designing validation sets to increase the precision and enable multiple comparison tests in genomic prediction studies. *Euphytica*. 2021. <https://doi.org/10.1101/2020.11.11.376343>
- Souza RS, et al. Combining ability for the improvement of vegetable soybean, *Agronomy Journal*. 2020. <https://doi.org/10.1002/agj2.20322>
- Espolador FG, et al. Assessing tolerance to Asian soybean rust in soybean inbred lines from exotic and adapted crosses. *Euphytica*, 2020. <https://doi.org/10.1007/s10681-020-02597-8>
- Yassue RM, et al. Uni and multivariate approaches for diallel analysis in early generation trials for soybean tolerance to rust. *Bragantia*. 2019. <http://dx.doi.org/10.1590/1678-4499.20190037>.