Rafael Massahiro Yassue

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RESEARCH INTERESTS

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, 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

Virginia Tech **2021 – Present**
Visiting scholar *Blacksburg, United States*
Luiz de Queiroz College of Agriculture - University of São Paulo **2018 – Present**
Ph.D., Genetics and Plant Breeding *Piracicaba, Brazil*
Luiz de Queiroz College of Agriculture - University of São Paulo **2016 – 2018**
M.S., Genetics and Plant Breeding *Piracicaba, Brazil*
Western Paraná State University - Unioeste **2011 – 2015**
B.Sc. Agronomic Engineering *Mal. C. Rondon, Brazil*

SKILLS

- Quantitative genetics
- Plant breeding
- Statistical modeling
- Image processing
- Phenomics
- Genomics
- R, Python, and Julia
- Markdown, GitHub, and LaTeX

LANGUAGES

- Portuguese (native)
- English (advanced)
- Spanish (Basic)

EXPERIENCE

Coordinator of plant breeding study group, Gvenck **2019**
Coordinated the group's activities *Piracicaba, Brazil*
Member of plant breeding study group, Gvenck **2016 – 2019**
Promote discussions on relevant plant breeding issues, and soft skills improvement *Piracicaba, Brazil*
Academic internship, Soybean breeding, Esalq **2015**
Field experimentation, scientific discussion, and data analysis *Piracicaba, Brazil*
Intern, Soybean breeding, Coodetec **2013-2014**
Hands-on experience in an industry breeding program *Cascavel, Brazil*
Undergraduate Research, Plant breeding, Unioeste **2011 – 2015**
Learning in methods of research and development of scientific thought *Mal. C. Rondon, Brazil*

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

PRESENTATIONS

- An assessment of the predictive ability of plant growth-promoting bacteria inoculation status and shoot dry mass using hyperspectral images in tropical maize. ASA, CSSA, and SSSA International Annual Meetings. Virtual – 2021
- A low-cost greenhouse-based high-throughput phenotyping platform for genetic studies in maize under inoculation with plant growth-promoting bacteria. NAPB Annual Meeting. Virtual – 2021
- Melhoramento do Milho. Aula da disciplina: Introdução à Engenharia Agronômica. ESALQ. Virtual – 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. Virtual – 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.Virtual – 2021

PUBLICATIONS

- Galli G, et al. Automated Machine Learning: a case study of genomic "image-based" prediction in maize hybrids. Frontiers in Plant Science, 2022. doi
- 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, 2021. doi
- 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), 2021. doi
- Yassue RM, et al. CV-α: designing validations sets to increase the precision and enable multiple comparison tests in genomic prediction studies. Euphytica. 2021. doi
- Souza RS, et al. Combining ability for the improvement of vegetable soybean, Agronomy Journal. 2020. doi
- Espolador FG, et al. Assessing tolerance to Asian soybean rust in soybean inbred lines from exotic and adapted crosses. Euphytica, 2020. doi
- Yassue RM, et al. Uni and multivariate approaches for diallel analysis in early generation trials for soybean tolerance to rust. Bragantia. 2019. doi

REFERENCES

- Prof. Dr. Gota Morota – Assistant Professor of quantitative genetics at Virginia Polytechnic Institute and State University – morota@vt.edu
- Prof. Dr. Roberto Fritsche-Neto - Senior Scientist at International Rice Research Institute – r.fritscheneto@irri.org
- Prof. Dr. James Chen - Assistant Professor of Animal Data Sciences at Virginia Tech – niche@vt.edu