

# RAFAEL MASSAHIRO YASSUE

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## RESEARCH INTERESTS

I am a Data Science Analyst at GDM with experience in plant breeding, field experimentation, quantitative genetics, statistical modeling, phenomics, and genomics. My work is to connect 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

*Visiting scholar*

2022

*Blacksburg, United States*

### Luiz de Queiroz College of Agriculture - University of São Paulo

2018 – 2022

*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 | • Statistical modeling | • Phenomics | • R, Python, and Julia                                  |
| • Plant breeding        | • Image processing     | • Genomics  | • Markdown, GitHub, and L <sup>A</sup> T <sub>E</sub> X |

## LANGUAGES

- |                       |                      |                   |
|-----------------------|----------------------|-------------------|
| • Portuguese (native) | • English (advanced) | • Spanish (Basic) |
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## EXPERIENCE

### Data Science Analyst, GDM

2022-present

*Develop algorithms for experimental design and genetic analysis for breeding programs*

*Campinas, Brazil*

### 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

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- 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 Agrônômica. 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

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- Yassue RM, et al. Genome-wide association analysis of hyperspectral reflectance data to dissect the genetic architecture of growth-related traits in maize under plant growth-promoting bacteria inoculation. Plant direct (In press), 2023. [doi](#)
- Bi Ye, et al. Evaluating metabolic and genomic data for predicting grain traits under high night temperature stress in rice. G3: Genes, Genomes, Genetics, 2023. [doi](#)
- Rocha LM, et al. Quantitative trait loci related to growth and wood quality traits in Eucalyptus grandis W. Hill identified through single-and multi-trait genome-wide association studies. Tree Genetics & Genomes, 2022. [doi](#)
- Yassue RM, et al. Classification of plant growth-promoting bacteria inoculation status and prediction of growth-related traits in tropical maize using hyperspectral image and genomic data. Crop Science, 2022. [doi](#)
- 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. The Plant Phenome Journal, 2021. [doi](#)
- Yassue RM, et al. CV- $\alpha$ : designing validation 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

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- Prof. Dr. Gota Morota – Assistant Professor of quantitative genetics at Virginia Tech – [morota@vt.edu](mailto:morota@vt.edu)
- Prof. Dr. Roberto Fritsche-Neto - Senior Scientist at International Rice Research Institute – [r.fritscheneto@irri.org](mailto:r.fritscheneto@irri.org)
- Prof. Dr. James Chen - Assistant Professor of Animal Data Sciences at Virginia Tech – [niche@vt.edu](mailto:niche@vt.edu)