# Matheus D. Krause

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# **EDUCATION**

# **Doctoral Degree in Plant Breeding with Statistics Minor**

IOWA STATE UNIVERSITY, USA (05/2018 - 06/2023) | ADVISOR: DR. WILLIAM D. BEAVIS

Title: Untangling genetic and non-genetic factors for soybean breeding optimization.

# Master's Degree in Plant Breeding and Genetics

UNIVERSITY OF SÃO PAULO, BRAZIL (03/2016 - 04/2018) | ADVISOR: DR. ANTONIO A. F. GARCIA

**Title:** Boosting predictive ability of maize hybrids via genotype by environment interaction under multivariate GBLUP models.

#### Bachelor's Degree in Agronomy

Londrina State University, Brazil (03/2010 - 12/2015) | Advisor: Dr. Josué M. Ferreira

Title: Combining ability of maize inbred lines S<sub>9</sub> derived from ST15 and S709 synthetics.

## Exchange Student in Plant Breeding & Engineering for Mediterranean and Tropical Areas

L'Institut Agro Montpellier, France (08/2013 - 05/2014) | Supervisors: Dr. Jean-Luc Regnard

Title: Productibilité semencière de nouveaux géniteurs maïs : faisabilité de l'utilisation de données de production.

# **EXPERIENCE**

### Plant Breeding Scientist | CORTEVA AGRISCIENCE, JOHNSTON - IOWA (07/2023 - PRESENT)

- Support for several late maturity corn breeding programs in the USA.
- Discovery breeding across crops for North America.

# Graduate Research Assistant | DEPARTMENT OF AGRONOMY, IOWA STATE UNIVERSITY (05/2018 - 06/2023)

- Development of a metric to estimate realized rate of genetic gain on an annual basis using soybean routine field trials.
- Unraveling genotype by environment variation to identify mega-environments with genetic and non-genetic factors.
- Development of software to correct partially informative markers from backcross one derived double-haploid lines.
- Genome-wide association for complex binary (case-control) and continuous traits.
- Mentored several graduate students (20+) with plant breeding data analysis and R programming.

#### Graduate Research Assistant | DEPARTMENT OF GENETICS, UNIVERSITY OF SÃO PAULO (03/2016 - 04/2018)

- Applying multivariate linear mixed models to predict yield performance of single-cross maize hybrids based on information from genomics and genotype by environment interaction.

# Intern | Tropical Breeding & Genetics, Soybean Breeding (08/2015 - 11/2015)

- Plant phenotyping for soybean cyst nematode, *Phytophthora sojae* and *Sclerotinia sclerotiorum*, generation advancement in greenhouses, crossing blocks, seed packing, and general activities in the biotechnology laboratory.

#### Undergraduate Research Assistant | DEPARTMENT OF BIOLOGY, LONDRINA STATE UNIVERSITY (06/2010 - 07/2015)

- Development and evaluation of inbred lines for common and sweet corn via classical and double-haploid techniques.
- Evaluation and development of single-cross hybrids and synthetic populations for both common and sweet corn.
- Participation in an extension project to teach farmers how to produce their seeds of synthetic populations.

#### Intern | LIMAGRAIN EUROPE, DEPARTMENT OF SEED PRODUCTION TO RESEARCH (03/2014 - 06/2014)

- Data mining to support early decision-making on the profitability of female maize inbred lines (seed production).
- Stability analysis to identify stable check cultivars to be used in seed production.

#### SELECTED JOURNAL PUBLICATIONS

Araújo, MS; Chaves, SFS; Dias, LAS; Ferreira, FM; Pereira, GR; Bezerra, ARG; Alves, RS; Heinemann, AB; Breseghello, F; Carneiro, P; **Krause, MD**; Costa-Neto, G; Dias KOG. GIS-FA: an approach to integrating thematic maps, factor-analytic, and envirotyping for cultivar targeting. Theoretical and Applied Genetics, 2024. DOI: 10.1007/s00122-024-04579-z. 🗗

Chaves, SFS; **Krause**, **MD**; Dias, LAS; Garcia, AFG; Dias, KOG. ProbBreed: a novel tool for calculating the risk of cultivar recommendation in multienvironment trials. G3: Genes, Genomes, Genetics, 2024. DOI: 10.1093/g3journal/jkae013. C3

Krause, MD; Piepho, HP; Dias, KOG; Singh, AK; Beavis, WD. Models to estimate genetic gain of soybean seed yield from annual multi-environment field trials. Theoretical and Applied Genetics, 2023. DOI: 10.1007/s00122-023-04470-3. ☑

Krause, MD; Dias, KOG; Singh, AK; Beavis, WD. Using soybean historical field trial data to study genotype by environment variation and identify mega-environments with the integration of genetic and non-genetic factors. bioRxiv, 2022. DOI: 10.1101/2022.04.11.487885. ௴

Trentin, HU; **Krause**, **MD**; Zunjare, RU; Almeida, VC; Peterlini, E; Rotarenco, V; Frei, UK; Beavis, WD; Lübberstedt, T. Genetic basis of maize maternal haploid induction beyond MATRILINEAL and ZmDMP. Frontiers in Plant Science, 2023. DOI: 10.3389/fpls.2023.1218042. \(\mathbf{Z}\)

Dias, KOG; dos Santos, JPR; **Krause, MD**; Piepho, HP; Guimarães, LJM; Pastina, MM; Garcia, AAF. Leveraging probability concepts for cultivar recommendation in multi-environment trials. Theoretical and Applied Genetics, 2022. DOI: 10.1007/s00122-022-04041-y. C3

Montes, CR; Fox, C; Sanz-Sáez, A; Serbin, SP; Kumagai, E; **Krause**, **MD**; Xavier, A; Specht, J; Beavis, WD; Bernacchi, CJ; Diers, BW; Ainsworth, EA. High-throughput characterization, correlation, and mapping of leaf photosynthetic and functional traits in the soybean (*Glycine max*) nested association mapping population. Genetics, 2022. DOI: 10.1093/genetics/iyac065. ©

Verzegnazzi, AL; Santos, I; **Krause, MD**; Hufford, M; Frei, UK; Campbell, J; Almeida, VC; Zuffo, LT; Boerman, N; Lübberstedt, T. Major locus for spontaneous haploid genome doubling detected by a case–control GWAS in exotic maize germplasm. Theoretical and Applied Genetics, 2021. DOI: 10.1002/csc2.20253. <sup>12</sup>

Krause, MD; Dias, KOG; dos Santos, JPR; Oliveira, AAO; Guimarães, LJM; Pastina, MM; Margarido, GRA; Garcia, AAF. Boosting predictive ability of tropical maize hybrids via genotype by environment interaction under multivariate GBLUP models. Crop Science, 2020. DOI: 10.1002/csc2.20253. ♂

## PEER REVIEW

Crop Science • Journal of Agronomy and Crop Science • Plant Breeding • Frontiers in Genetics • SoftwareX

## SKILL SET

#### SPECIFIC SKIILS

- Data science: Linear and generalized mixed models, bayesian inference, stochastic simulations, probability theory. Data mining, curation, and acquisition for statistical inference. Cloud / high performance computing.
- Plant breeding: Genomic prediction, QTL mapping, GWAS, GxE analysis, experimental designs.
- I am a constant learner eager to collaborate across diverse groups.

#### PROGRAMMING EXPERIENCE

- Advanced R programming language, basic Python and Julia, Linux, and MEX.
- Developer of the R package SoyURT. [2]

#### **LEADERSHIP**

- 2020-2021 Committee member in the 7th and 8th annual R. F. Baker Plant Breeding Symposium at Iowa State University.
- 2011-2013 Student representative of Agronomy in the Regional Council of Engineering and Agronomy in Brazil.

#### LANGUAGE

English, Portuguese (native), basic French.

# TFACHING, SEMINAR & AWARDS

#### **TEACHING & SEMINAR**

- 2023 Talk on "From PDF Files to Biological Insights into Soybean Breeding: An Example of How Recovered Historical Yield Data Can be Valuable", in the "Big data: manage your data before your data kills you" workshop at the Plant & Animal Genome Conference, in San Diego, California USA.
- 2020 and 2022 Lecture on "Simulations in Plant Breeding An emphasis on *AlphaSimR*" in Agron 523, Molecular Plant Breeding, graduate-level course under Dr. Thomas Lübberstedt at Iowa State University.
- 2017 Instructor of R programming at the University of São Paulo.

#### **AWARDS**

- 2022 C. R. Weber for Excellence in Plant Breeding from the Department of Agronomy at Iowa State University.
- 2020 and 2022 Bayer Travel Scholarship & Mentoring Program for Graduate Students and Postdoctoral Researchers.

#### FOR MORE INFORMATION, PLEASE ACCESS





