

# Marnin D. Wolfe

**Quantitative Genetics • Plant Breeding • Ecology and Evolution • Genomics  
Sustainable Cropping Systems • Reproducible Research Methods**

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## ACADEMIC APPOINTMENTS

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- 2022 -**            **Assistant Professor of Quantitative Genetics**  
**Auburn University, Auburn, AL**  
Department of Crop Soil and Environmental Sciences  
College of Agriculture
- 2016 - 2022**    **Research Associate**  
**Cornell University, Ithaca, NY**  
Section on Plant Breeding and Genetics  
Supervisor: Dr. Jean-luc Jannink
- 2013 - 2016**    **Post-doctoral Associate**  
**Cornell University, Ithaca, NY**  
Section on Plant Breeding and Genetics  
Supervisor: Dr. Jean-luc Jannink

## EDUCATION

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- 2007 - 2013**    **University of Pittsburgh, Pittsburgh, PA**  
Department of Biological Sciences  
Ph.D. Ecology and Evolution  
Advisor: Dr. Stephen J. Tonsor
- 2002 - 2006**    **Eckerd College, St. Petersburg, FL**  
B.S. Biology, Advisor: Dr. Peter Meylan

## PUBLICATION HIGHLIGHTS

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**Wolfe, M. D.**, Bauchet, G. J., Chan, A. W., Lozano, R., Ramu, P., Egesi, C., Kawuki, R., Kulakow, P., Rabbi, I., Jannink, J.-L. 2019. **Historical Introgressions from a Wild Relative of Modern Cassava Improved Important Traits and May Be Under Balancing Selection.** *Genetics*. <https://doi.org/10.1534/genetics.119.302757/>

This article reveals that large megabase scale historical (1940's) introgressions from a wild relative (*M. glaziovii*) are segregating in modern cultivated cassava (*M. esculenta*) germplasm. We used a combination of association mapping, genomic variance partitioning and prediction to quantify the phenotypic consequences of introgressions. Introgressions accounted for a significant (mean 20%, max 56%) portion of the heritability of tested traits. Our results enable future work to track and target recombination of introgressions, which will increase the efficiency of cassava breeding by allowing simultaneous fixation of beneficial alleles and purging of genetic load.

**Wolfe, M.D.**, D. Pino Del Carpio, O. Alabi, C. Egesi, L.C. Ezenwaka, U.N. Ikeogu, R.S. Kawuki, I.S. Kayondo, P. Kulakow, R. Lozano, I.Y. Rabbi, E. Williams, A.A. Ozimati, and J.-L. Jannink. 2017. **Prospects for genomic selection in cassava breeding.** *The Plant Genome*. <https://doi.org/10.3835/plantgenome2017.03.0015>

This study represents an extensive evaluation genomic prediction in cassava. I selected it as it was the culmination of quite a lot of analysis done to support applied breeding efforts. We thoroughly investigated and compared methods and scenarios of prediction in three breeding program's training populations. We also test training population optimization using a genetic algorithm to select lines for phenotyping. We present a schematic for proceeding with genomic selection in cassava. We conclude that prediction accuracies are acceptable and are improving with training population size, justifying continued investment in GS for cassava breeding.

**Wolfe, M.D.**, P. Kulakow, I.Y. Rabbi, and J.-L. Jannink. 2016. **Marker-Based Estimates Reveal Significant Non-additive Effects in Clonally Propagated Cassava (*Manihot esculenta*): Implications for the Prediction of Total Genetic Value and the Selection of Varieties.** *G3: Genes|Genomes|Genetics*. <https://doi.org/10.1534/g3.116.033332>

I selected this study because it has had a lasting impact on how we think about selection in clonal crop breeding, at least for cassava. We used genomic mixed-models with dominance and epistasis covariance matrices to quantify the genetic variation for three key traits in a breeding population of cassava. We confirmed previous findings based on diallel crosses that non-additive variation is significant for esp. root yields. We showed that including dominance and epistasis improved prediction accuracies for root yields, but not for dry matter content. The implication of this work has been that we now consider the inclusion of dominance and epistasis (non-additive effects) in genomic predictions, especially for root yields. Selection of a clone for advancement as a variety should be made based on predictions of *total* genetic merit (additive plus non-additive effects). Selection of parents, in contrast, relies on an additive-only prediction of the breeding value.

**Wolfe, M.D.**, I.Y. Rabbi, C. Egesi, M. Hamblin, R. Kawuki, P. Kulakow, R. Lozano, D.P. del Carpio, P. Ramu, and J.-L. Jannink. 2016. **Genome-wide association and prediction reveals the genetic architecture of cassava mosaic disease resistance and prospects for rapid genetic improvement.** *Plant Genome*. <https://doi.org/10.3835/plantgenome2015.11.0118>

I selected to highlight this study as it represents the first genome-wide association study conducted in cassava and also my first contribution to the cassava breeding and genetics literature. We studied the genetic architecture and prediction of cassava mosaic disease resistance. We found that cassava mosaic disease resistance has a narrow genetic basis in breeding germplasm. We also found evidence that two possibly epistatic loci and/or multiple resistance alleles segregate at a single major QTL. This study led to the development of locus-targeted (KASP-based) markers which are currently in use for marker-assisted selection. Cassava mosaic disease is increasingly rare among advanced breeding lines.

Iragaba, P., Kawuki, R.S., Bauchet, G., Ramu, P., Tufan, H. A., Earle, E.D., Gore, M.A. and **Wolfe, M.** 2020. **Genomic characterization of Ugandan smallholder farmer-preferred cassava (*Manihot esculenta* Crantz) varieties.** *Crop Science*. <https://doi.org/10.1002/csc2.20152>.

I selected this work as it represents my first senior author article. The first author was a graduate student with whom I worked as a mentor extensively, including supervising the planning, implementation, analysis and writing of this study. The work itself is quite interesting with regards to the landscape in Uganda of cassava landraces. We conducted an genetic analysis of 547 samples of cassava grown by 192 smallholder farmers in Uganda. Among our discoveries, a landrace that appears to be an interspecific hybrid with introgressions from *M. glaziovii*. We conclude that available breeding germplasm are genetically representative of the genotypes currently grown by farmers.



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**UPCOMING PUBLICATIONS**

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1. Morales, N., .... **Wolfe, M.**, ... Mueller, L. 2022. Breedbase: a digital ecosystem for modern plant breeding. *In Review*.
2. Moore, V., **Wolfe, M.**, Chopra, R., Lorenz, A., Moore, K., Roberts, L., Ryan, M.R., Schlautman, B. 2022. Plant breeding for intercropping in temperate field crop systems: a review. *In Review*.

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**PEER-REVIEWED PUBLICATIONS ([Google Scholar](#))**

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3. Chalermopol, P., Aiemnaka, P., Nathaisong, P., Hunsawattanakul, S., Fungfoo, P., Rojanaridpiched, C., Vichukit, V., Kongsil, P., Kittipadakul, P., Wannarat, W., Chunwongse, J., Tongyoo, P., Kijkhunasatian, C., Chotineeranat, S., Piyachomkwan, K., **Wolfe, M.**, Jannink, J-L., Sorrels, M. 2022. Genome Wide Association Mapping and Genomic Prediction of Yield-related Traits and Starch Pasting Properties in Cassava. *Theoretical and Applied Genetics*. Volume 135, pages 145–171. <https://doi.org/10.1007/s00122-021-03956-2>
4. **Wolfe, M.**, Chan, A.W., Kulakow, P., Rabbi, I.Y. and J-L. Jannink. 2021. Genomic mating in outbred species: predicting cross usefulness with additive and total genetic covariance matrices. *Genetics*, Volume 219 (3), <https://doi.org/10.1093/genetics/iyab122>
5. Esuma, W., Ozimati, A., Kulakow, P., Gore, M., **Wolfe, M.**, Nuwamanya, E., Egesi, C., and Kawuki, R.. 2021. Effectiveness of genomic selection for improving provitamin A carotenoid content and associated traits in cassava. *G3 Genes|Genomes|Genetics*, Volume 11, Issue 9, September 2021, jkab160, <https://doi.org/10.1093/g3journal/jkab160>
6. **Wolfe, M.**, Kantar, M., Jannink, J-L., N. Santantonio. 2021. Multi-species genomics-enabled selection for improving agroecosystems across space and time. *Front. Plant Sci.* <https://doi.org/10.3389/fpls.2021.665349>
7. Rabbi, I.Y., Kayondo, S.J., Bauchet, G., Muyideen, Y., Aghogho, C.I., Ogunpaimo, K., Uwugiaren, R., Ipan, A.S., Peteti, P., Agbona, A., Parkes, E., Ezenwaka, L., **Wolfe, M.**, Jannink, J-L., Egesi, C., Kulakow, P. Genome-wide association analysis reveals new insights into the genetic architecture of defensive, agro-morphological and quality-related traits in cassava. *Plant Molecular Biology*. <https://doi.org/10.1007/s11103-020-01038-3>.
8. Omar Yonis, B., Pino del Carpio, D., **Wolfe, M.**, Jannink, J.-L., & Rabbi, I. 2020. Improving root characterisation for genomic prediction in cassava. *Scientific Reports*. <https://doi.org/10.1038/s41598-020-64963-9>.
9. Iragaba, P., Kawuki, R.S., Bauchet, G., Ramu, P., Tufan, H. A., Earle, E.D., Gore, M.A. and **Wolfe, M.** 2020. Genomic characterization of Ugandan smallholder farmer-preferred cassava (*Manihot esculenta* Crantz) varieties. *Crop Science*. <https://doi.org/10.1002/csc2.20152>.
10. Ibrahim, M.S., Kulembeka, H., Mtunda, K., Mrema, E.O., Salum, K; **Wolfe, M.**; Rabbi, I.Y., Egesi, C., Kawuki, R., Ozimati, A., Lozano, R., Jannink, J-L. 2020. Genomic prediction and

- quantitative trait locus discovery in a cassava training population constructed from multiple breeding stages. *Crop Science*. <https://doi.org/10.1002/csc2.20003>
11. Ikeogu, U.N., Akdemir, D., **Wolfe, M.**, Okeke, U.G., Amaefula, C., Jannink, J.-L. and Egesi, C.N. 2019. Genetic Correlation, Genome-Wide Association and Genomic Prediction of Portable NIRS Predicted Carotenoids in Cassava Roots. *Frontiers in Plant Science*. <https://doi.org/10.3389/fpls.2019.01570>
  12. **Wolfe, M. D.**, Bauchet, G. J., Chan, A. W., Lozano, R., Ramu, P., Egesi, C., Kawuki, R., Kulakow, P., Rabbi, I., Jannink, J.-L. 2019. Historical Introgressions from a Wild Relative of Modern Cassava Improved Important Traits and May Be Under Balancing Selection. *Genetics*. <https://doi.org/10.1534/genetics.119.302757>.
  13. Kawuki, R.S., Williams E., Ozimati, A., Kayondo, I.S., Nandudu, L., **Wolfe, M.D.** 2019. Alternative Approaches For Assessing Cassava Brown Streak Root Necrosis To Guide Resistance Breeding And Selection. *Frontiers In Plant Science*. <https://doi.org/10.3389/fpls.2019.01461>
  14. Ozimati, A., Kawuki, R., Esuma, W., Kayondo, S. I., Pariyo, A., **Wolfe, M.**, & Jannink, J.-L. 2019. Genetic Variation and Trait Correlations in an East African Cassava Breeding Population for Genomic Selection. *Crop Science*, 59(2), 460. <https://doi.org/10.2135/cropsci2018.01.0060>
  15. Ozimati, A., Kawuki, R., Esuma, W., Kayondo, I. S., **Wolfe, M.**, Lozano, R., ... Jannink, J.-L. (2018). Training Population Optimization for Prediction of Cassava Brown Streak Disease Resistance in West African Clones. *G3: Genes|Genomes|Genetics*, 8, g3.200710.2018. <https://doi.org/10.1534/g3.118.200710>
  16. Ismail, K., D.P. del Carpio, R. Lozano, A. Ozimati, **M.D. Wolfe**, Y. Baguma, V.E. Gracen, O. Samuel, M. Ferguson, R.S. Kawuki, and J. Jean-Luc. 2017. Genome-wide association mapping and genomic prediction unravels CBSD resistance in a Manihot esculenta breeding population. *Sci. Rep.* 8(1): 1549. <https://doi.org/10.1038/s41598-018-19696-1>
  17. Del Carpio, D.P., R. Lozano, **M.D. Wolfe**, J.-L. Jannink. Genome-Wide Association Studies and Heritability Estimation in the Functional Genomics Era. 2018. In: Population Genomics, pp 351-425. Springer.
  18. **Wolfe, M.D.**, D. Pino Del Carpio, O. Alabi, C. Egesi, L.C. Ezenwaka, U.N. Ikeogu, R.S. Kawuki, I.S. Kayondo, P. Kulakow, R. Lozano, I.Y. Rabbi, E. Williams, A.A. Ozimati, and J.-L. Jannink. 2017. Prospects for genomic selection in cassava breeding. *Plant Genome*, 10(3): 1–19. <https://doi.org/10.3835/plantgenome2017.03.0015>
  19. Hickey, J.M., T. Chiurugwi, I. Mackay, W. Powell and **Implementing Genomic Selection in CGIAR Breeding Programs Workshop Participants**. 2017. Genomic prediction unifies animal and plant breeding programs to form platforms for biological discovery. *Nature Genet.* 49(9): 1297–1303. <https://doi.org/10.1038/ng.3920>
  20. Charvet, C.J., G. Šimić, I. Kostović, V. Knezović, M. Vukšić, M.B. Leko, E. Takahashi, C.C. Sherwood, **M.D. Wolfe**, and B.L. Finlay. 2017. Coevolution in the timing of GABAergic and pyramidal neuron maturation in primates. *Proc. R. Soc. B Biol. Sci.* 284(1861).
  21. Rabbi, I.Y., L.I. Udoh, **M.D. Wolfe**, E.Y. Parkes, M.A. Gedil, D. Alfred, R. Punna, J. Jean-Luc, and K. Peter. 2017. Genome-wide association mapping of correlated traits in cassava: dry matter and total carotenoid content. *Plant Genome*, 10(3): 1–14. <https://doi.org/10.3835/plantgenome2016.09.0094>
  22. **Wolfe, M.D.**, P. Kulakow, I.Y. Rabbi, and J.-L. Jannink. 2016. Marker-Based Estimates Reveal

- Significant Non-additive Effects in Clonally Propagated Cassava (*Manihot esculenta*): Implications for the Prediction of Total Genetic Value and the Selection of Varieties. *Genes|Genomes|Genetics*, 6(November): 3497-3506. <https://doi.org/10.1534/g3.116.033332>
23. **Wolfe, M.D.**, I.Y. Rabbi, C. Egesi, M. Hamblin, R. Kawuki, P. Kulakow, R. Lozano, D.P. del Carpio, P. Ramu, and J.-L. Jannink. 2016. Genome-wide association and prediction reveals the genetic architecture of cassava mosaic disease resistance and prospects for rapid genetic improvement. *Plant Genome* 9(2): 1–13. <https://doi.org/10.3835/plantgenome2015.11.0118>
24. **Wolfe, M.D.** & S.J. Tonsor. 2014. Adaptation to spring heat and drought in northeastern Spanish *Arabidopsis thaliana*. *New Phytol.*, 201, 323–34. <https://doi.org/10.1111/nph.12485>
25. **Wolfe, M.D.** 2013. Life history and carbon economic trade-offs adapting an annual plant across a climate gradient. *University of Pittsburgh*. [Dissertation Link](#).
26. **Wolfe, M.D.**, E.M. Monroe, and D.J. Berg. 2007. Population Genetic Structure of the Freshwater Mussel *Lampsilis siliquoidea* (Bivalvia: Unionidae) In the Darby Creek Watershed, Central Ohio. *Journal of Young Investigators* 16(3), <https://www.jyi.org/2007-march/2017/11/11/population-genetic-structure-of-the-freshwater-mussel-lampsilis-siliquoidea-bivalvia-unionidae-in-the-darby-creek-watershed-central-ohio>

## TEACHING EXPERIENCE

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### Short Courses and Workshops

- Breeding Data Science Working Group*. Lead a periodic workshop and working group supporting graduate students and post-docs, esp. to re: genomic selection.  
March 2020 - Ongoing
- [Statistical methods for genomic prediction](#). GOBII/NGC Workshop. Co-taught with Dr. Guillaume Bauchet at the Boyce Thompson Institute. Oct. 11th, 2018.
- [Genomic selection in theory and practice](#). Co-taught with Dr. Jean-luc Jannink. Excellence in Breeding (EiB) project. Amsterdam, Netherlands. Sept. 24-27, 2018.
- [Breeding Data Analysis in R](#). National Root Crops Resources Research Institute (NaCRRI), Namulonge, Uganda. August 2017
- [Data analysis, including genomic selection in R](#). International Institute for Tropical Agriculture (IITA), Ibadan, Nigeria. October 2016
- [Data analysis, including genomic selection and GWAS in R](#). National Root Crops Research Institute, Umudike, Nigeria. May 2015
- [Statistical methods for genomic prediction](#). Texas A&M University, College Station, Texas. September 4th, 2015.
- Why plants rule the world (and how they do it)*. Phipps Conservatory High

School Internship Program: Learning for a Greener Future. Pittsburgh, PA.  
July, 2013; June 2012.

<b>Graduate Teaching</b>	Ecology Laboratory Fall 2008
	Genetics Recitation Spring 2009, Summer 2009, Spring 2010, Fall 2010, Spring 2011
	Field Botany Summer 2011
	Intro Biology Lab Summer 2011
<b>Undergraduate Teaching</b>	Biodiversity I & II Fall 2004, Spring 2005

## LEADERSHIP, MENTORSHIP, MANAGEMENT

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<b>Quality Champions leadership</b>	<b>Quality Champions</b> , a NextGen Cassava Project-wide cross-functional team dedicated to improving the quality of data- and field-related practices in plant breeding. I led the creation and organization of this group starting in late 2017.
<b>Genomic selection and bioinformatics coordinator</b>	Since 2013, I have led the application of bioinformatics and genomics-enabled prediction that supports cassava breeding project-wide (5 breeding programs, 4 countries). In this integral role, I ensure communication and time-sensitive coordination between stakeholders and team members distributed across continents and time zones, and provide decision support to breeding programs.
<b>Mentorship</b>	I have been honored to mentor and participate in the supervision of graduate and undergraduate students since my own PhD work. Since 2013 in particular, I have had an important role in advising from start-to-PhD many students, including: Drs. Alfred Ozimati, Paula Iragaba, Ugochukwu Ikeogu, Ariel Chan, Roberto Lozano, Olumide Alabi.

## PROFESSIONAL EXPERIENCE

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- Peer Reviewer** Genetics, Frontiers in Plant Science, The Plant Genome Journal, Heredity, Scientia Agricola, American Journal of Botany, Crop Science\*, BMC Plant Biology, Ecology Letters, Journal of Environmental and Experimental Botany, Journal of the Linnaean Society, Plant Molecular Biology, Crop Breeding, Genetics and Genomics  
\***2017 Outstanding Reviewer Award**
- Professional Training** **Optimization of Plant Breeding Systems.** Training in operations research methods by Bill Beavis, Lizhi Wang, Guiping Hu, Sotirios Archontoulis and Deniz Akdemir. May 20-24th, 2019.
- HFP Leadership Training,** sponsored by the Bill and Melinda Gates Foundation. Oct. 13-15, 2018.
- Two intensive courses: **(1) Statistical Genetics of Quantitative Traits and Complex Disease** with Dr. Matthew Robinson, **(2) Genomic Selection in the Era of Genome Sequencing** with Dr. Ben Hayes. 5th International Conference on Quantitative Genetics. June 2016.
- Plant and Animal Association Mapping.** 15th Annual Summer Institute in Statistical Genetics. University of Washington, Seattle, WA. 2010
- Affiliations** Genetics Society of America, 2019-
- Other** Graduate Recruiting Coordinator, 2011
- Category Judge in Biology, Pittsburgh Regional Science Fair, 2010
- Seminar Coordinator, Ecology & Evolution Seminar Series, 2008-2009
- Grants** Sigma Xi Grant-in-Aid Award, 2009
- Contributor, Next Generation Cassava Breeding Phase II, Bill & Melinda Gates Foundation + DFID (~\$35M USD total).

## PRESENTATIONS

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- Talks** Wolfe, M. and Jannink, J-L. **Genomic mate selection for clonally propagated crops: improving the chance of breeding top ranking clones by predicted variance in total genetic merit.** 6th International Conference on Quantitative Genetics. *Selected oral presentation, Nov. 3rd, 2020. [Video via Google Drive.](#)*
- Wolfe, M. and Jannink, J-L Update on Genotyping, Imputation, Genomic Prediction and Mate Selection Research. NextGen Cassava Virtual Annual Meeting. September 29th, 2020. [Video via Google Drive.](#)



Wolfe, M. and Jannink, J-L. **Mate selection criteria for (outbred) clonal crops based on multi-trait prediction of the additive and total genetic (co)variance of untested cassava crosses.** University of Edinburgh Computational Biology Discussion Group, June 9, 2020. <https://vimeo.com/427452738>

Wolfe, M.D., et al. 2018. **Introgressions from *Manihot glaziovii* play important roles in modern cassava breeding.** Presented at the Cassava Genomics session, PAG XXVI on January 16<sup>th</sup>, 2018.

Wolfe, M. D. **Genomic Selection: Prediction Methodology & Practical Application.** Video Lecture Presentation to the Regional Southeast Asian Cassava Breeder's Network Training on November 22<sup>nd</sup>, 2016.

Wolfe, M. D., Jean-Luc Jannink, *et al.*, **Next Generation Cassava Breeding: Progress Implementing Genomic Selection.** *Plenary seminar presented to the World Congress on Root and Tuber Crops in Nanning, China on January 21<sup>st</sup>, 2016.*

Wolfe, M. D. and I.Y. Rabbi. **Genomic Selection in RTB Crops.** *Presented to the Implementing GS in CGIAR Breeding meeting in Montpellier, France on December 7<sup>th</sup>, 2015.*

Wolfe, M. D., Jannink, J-L *et al.* **Next Generation Cassava Breeding: First attempts at Genomic Selection.** *Presented to the Plant Breeding Symposium at Texas A&M University, College Station, Texas on September 3<sup>rd</sup>, 2015*

**Talks,  
cont.**

Wolfe, M. D., Jannink, J-L *et al.* **Next Generation Cassava Breeding: First attempts at Genomic Selection.** *Presented to the Cassava Forum at Kasetsart University, Bangkok Thailand on June 15<sup>th</sup>, 2015*

Wolfe, M.D. & Jannink, J-L. **GWAS and GS: First attempts in Cassava.** *Presented to the Department of Plant Breeding and Genetics, Cornell University on March 10<sup>th</sup>, 2015*

Wolfe, M.D., Rabbi, I.Y., Jannink, J-L. *et al.* **The Genomic Architecture of Cassava Mosaic Disease Resistance.** *Presented at Plant and Animal Genome Conference XXIII on January 13<sup>th</sup>, 2015.*

Wolfe, M.D. The role of rosette economic variation in adaptation across a climate gradient in *Arabidopsis thaliana*. *Presented at the 2013 Conference of the Society for the Study of Evolution in Snowbird, UT, on June 23<sup>rd</sup>, 2013.*

Wolfe, M.D. The Tortoise and the Hare: Mediterranean vs. Montane Adaptation in *Arabidopsis thaliana*. *Presented at the First Joint Congress on Evolutionary Biology in Ottawa, ON, CA on July 7<sup>th</sup>, 2012.*

- Posters** Wolfe, M. and Jannink, J-L. **Genomic mate selection for outbred clonal crops: predicting offspring variance in additive and total merit.** *The (virtual) Allied Genetics Conferences (TAGC)*, April 17, 2020. [View poster via FigShare](#).
- Wolfe, M.D., Guillaume Bauchet, Dunia Pino Del Carpio, Chiedozi Egesi, Robert S. Kawuki, Peter Kulakow, Ramu Punna, Ismail Y. Rabbi, Jean-Luc Jannink. **Introgressed Manihot glaziovii alleles segregate in cassava germplasm and influence key traits.** Presented at the first annual Three Rivers Evolution Event (TREE) in Pittsburgh, PA on September 9<sup>th</sup>, 2017.
- Wolfe, M.D., Guillaume Bauchet, Dunia Pino Del Carpio, Chiedozi Egesi, Robert S. Kawuki, Peter Kulakow, Ramu Punna, Ismail Y. Rabbi, Jean-Luc Jannink. **Introgressed genome segments from Manihot glaziovii impact key phenotypes in cassava (M. esculenta) germplasm.** Presented at the Gordon Conference on Quantitative Genetics in Galveston, TX on March 1<sup>st</sup> and 2<sup>nd</sup>, 2017.
- Wolfe, M.D., P. Kulakow, I.Y. Rabbi and J-L Jannink. 2016. **Significant non-additive variance in clonally propagated cassava detected with genome-wide markers.** Presented at the 5<sup>th</sup> International World Congress on Quantitative Genetics in Madison, WI on June 15<sup>th</sup>, 2016.
- Wolfe, M.D., P. Kulakow, I.Y. Rabbi and J-L Jannink. 2016. **Non-additive effects in clonally propagated cassava revealed by genome-wide markers: implications for prediction of total genetic value and selection of varieties.** Presented at the Plant and Animal Genome Conference on January 5<sup>th</sup>, 2016.
- Posters, cont.** Wolfe, M.D. & S.J. Tonsor. 2013. **Adaptive shifts in time and resources from vegetative to reproductive structures across a climate gradient in Arabidopsis thaliana.** Presented at the 2013 Conference of the Society for the Study of Evolution on June 24<sup>th</sup>, 2013.
- Wolfe, M.D. & S.J. Tonsor. 2013. **Heat and drought avoidance is traded-off for winter weather tolerance leading to local adaptation along an elevation gradient in N.E. Spanish Arabidopsis thaliana.** Presented at the 2013 Graduate Student Research Expo on March 21<sup>st</sup>, 2013.
- Wolfe, M.D. & S.J. Tonsor. 2009. **Differentiation across the climatic niche of Arabidopsis thaliana.** Presented at the 2009 Conference of the Society for the Study of Evolution on June 14<sup>th</sup>, 2009.
- Wolfe, M.D. & S.J. Tonsor. 2008. **Responses to heat and drought in two species of Collinsia from contrasting environments.** Presented at the 2008 Graduate Student Research Expo on March 4<sup>th</sup>, 2008.

## REFERENCES

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