IVAN ROBIN BAXTER, Ph.D.

Principal Investigator and Member
Donald Danforth Plant Sciences Center
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PROFESSIONAL EXPERIENCE

CURRENT POSITIONS

Metablify **May 2024-present**
Chief Scientific Officer
St. Louis, Missouri

Donald Danforth Plant Science Center **2020-present**
Member
St. Louis, Missouri

Washington University **2012-present**
Adjunct Assistant Professor
St. Louis, Missouri

University of Missouri **2012-present**
Adjunct Assistant Professor
Columbia, Missouri

PREVIOUS EXPERIENCE

USDA-ARS Plant Genetics Research Unit **2009-2018**
Research Computational Biologist
St. Louis, Missouri

Donald Danforth Plant Science Center **2015-2020**
Associate Member
St. Louis, Missouri

Donald Danforth Plant Science Center **2009-2015**
Assistant Member
St. Louis, Missouri

Purdue University Bindley Bioscience Center **2006-2009**
Senior Research Associate
West Lafayette, Indiana

EDUCATION

POST-GRADUATE

Postdoctoral Researcher **2004-2006**
Purdue University
Center for Phytoremediation Research and Development Bindley Bioscience Center
West Lafayette, Indiana

GRADUATE & UNDERGRADUATE

DOCTOR of PHILOSOPHY **May 2004**

Graduate Student, Cell Biology Department **2000-2004**
Laboratory of Jeffrey F. Harper
The Scripps Research Institute (TSRI)
La Jolla, California

Graduate Student, Molecular Biology Department **1998-2000**
Laboratory of James R. Williamson
The Scripps Research Institute (TSRI)
La Jolla, California

Graduate Student, Department of Chemistry **1996-1997**
Laboratory of James R. Williamson
Massachusetts Institute of Technology
Cambridge, Massachusetts

Bachelor of Arts in Chemistry General Honors, Honors in Chemistry **1992-1996**
Goucher College
Towson, Maryland

PUBLICATIONS

Cited by:	All	Since 2020
Citations	15030	6254
h-index	49	40
i10-index	82	73

Google Scholar page can be viewed here

PREPRINTS

(6) Geoffrey P. Morris, Avril M. Harder, Adam L. Healey, Chloee M. McLaughlin, Brian R. Rice,Clara Cruet-Burgos, Jerry W. Jenkins, Joanna L. Rifkin, Shengqiang Shu, John J. Spiekerman, Carl J. VanGessel, Erica Agnew, Alain Audebert, Kerrie Barry, **Ivan Baxter**, Gregory Beurier, Lori Beth Boston, Richard E. Boyles, Siobhan M. Brady, Victoria Bunting, Jacqueline M. Chaparro, Chaney Courtney, Joseph Sékou B. Dembele, Santosh Deshpande, Cyril Diatta, Nathaniel Eck, Andrea L. Eveland, Jacques M. Faye, Daniel Fonceka, Boubacar Gano, Marie de Gracia Coquerel, David Goodstein, Jane Grimwood, Matthew E. Hudson, Jana Kholova, Katherine Johnson, Kristen K. Johnson, Dorota Kawa, Mamoutou Kouressy, Stephen Kresovich, Scott Lee, Peggy Lemaux, Robert Lowery, Delphine Luquet, Fanna Maina, Todd P. Michael, Taye T. Mindaye, John Mullet, Philip Ozersky, Christopher Plott, Jessica E. Prenni, Gael Pressoir, Jean-François Rami, Trevor W, Rife, Jocelyn Saxton, Bassirou Sine, Avinash Sreedasyam, Jayson Talag, Niaba Teme, Mitchell R. Tuinstra, Vincent Vadez, John P. Vogel, Rachel Walstead, Jianan Wang, Jenell Webber, Melissa Williams, Todd C. Mockler, Jesse R. Lasky, Jeremy Schmutz, Nadia Shakoor, John T. Lovell (2025) Developing future resilience from signatures of adaptation across the sorghum pangenome. doi: https://doi.org/10.1101/2025.08.01.667986

(5) Hui Jiang, Erik A Myers, Britney Millman, Dong-Yeon Lee, Dmitri A. Nusinow, Daniel F Voytas, **Ivan Baxter** (2025) Development of male-sterile lines of *Setaria viridis* to accelerate C4 model plant genetics. In bioRxiv, doi**:** https://doi.org/10.1101/2025.07.14.664229

(4) Renee Dale, Darshi Banan, Britney Millman, Andrew D.B. Leakey, Shanka Mukherji, **Ivan Baxter** (2023) Competition for resources during development drives allometric patterns in the grass Setaria. In bioRxiv, doi: https://doi.org/10.1101/2023.12.28.573563

(3) Whitt, L., Mahood, E. H., Ziegler, G., Luebbert, C., Gillman, J. D., Norton, G. J., Price, A. H., Salt, D.E., Dilkes, B., **Baxter, I.** (2023) A comparative approach for selecting orthologous candidate genes underlying signal in genome-wide association studies across multiple species. In bioRxiv. doi: https://doi.org/10.1101/2023.10.05.561051

(2) Hubbard A, Connelly L, Kambhampati S, Evans B, **Baxter I.** (2021) A novel paradigm for optimal mass feature peak picking in large scale LC-MS datasets using the ‘isopair’: isoLock, autoCredential and anovAlign. In bioRxiv. doi: https://doi.org/10.1101/2021.12.05.471237

(1) Ziegler, G., Kear, P, Wu, Dr., Ziyomo, C., Lipka, A., Gore, M., Hoekenga, O., **Baxter, I.** (2017) Elemental accumulation in kernels of the maize nested association mapping panel reveals signals of gene by environment interactions. In bioRxiv (p. 164962). doi: https://doi.org/10.1101/164962

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2025

(77) Ravneet Kaur, Mary Durstock, Stephen A. Prior, G. Brett Runion, Elizabeth A. Ainsworth, **Ivan Baxter**, Alvaro Sanz-Sáez, Courtney P. Leisner (2025) Investigating the Impact of Elevated CO_2 on Biomass Accumulation and Mineral Concentration in Foliar and Edible Tissues in Soybeans. Plant, Cell & Environment, https://doi.org/10.1111/pce.70141.

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2024

(74) Anna M O'Brien, Ruairidh J H Sawers, Jaime Gasca-Pineda, **Ivan Baxter**, Luis E Eguiarte, Jeffrey Ross-Ibarra, Sharon Y Strauss (2024) Teosinte populations exhibit weak local adaptation to their rhizosphere biota despite strong effects of biota source on teosinte fitness and traits. Evolution, https://doi.org/10.1093/evolut/qpae130.

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2023

(70) Avinash Sreedasyam, Christopher Plott, Md Shakhawat Hossain, John T Lovell, Jane Grimwood, Jerry W Jenkins, Christopher Daum, Kerrie Barry, Joseph Carlson, Shengqiang Shu, Jeremy Phillips, Mojgan Amirebrahimi, Matthew Zane, Mei Wang, David Goodstein, Fabian B Haas, Manuel Hiss, Pierre-François Perroud, Sara S Jawdy, Yongil Yang, Rongbin Hu, Jenifer Johnson, Janette Kropat, Sean D Gallaher, Anna Lipzen, Eugene V Shakirov, Xiaoyu Weng, Ivone Torres-Jerez, Brock Weers, Daniel Conde, Marilia R Pappas, Lifeng Liu, Andrew Muchlinski, Hui Jiang, Christine Shyu, Pu Huang, Jose Sebastian, Carol Laiben, Alyssa Medlin, Sankalpi Carey, Alyssa A Carrell, Jin-Gui Chen, Mariano Perales, Kankshita Swaminathan, Isabel Allona, Dario Grattapaglia, Elizabeth A Cooper, Dorothea Tholl, John P Vogel, David J Weston, Xiaohan Yang, Thomas P Brutnell, Elizabeth A Kellogg, **Ivan Baxter**, Michael Udvardi, Yuhong Tang, Todd C Mockler, Thomas E Juenger, John Mullet, Stefan A Rensing, Gerald A Tuskan, Sabeeha S Merchant, Gary Stacey, Jeremy Schmutz. (2023) JGI Plant Gene Atlas: an updateable transcriptome resource to improve functional gene descriptions across the plant kingdom. NAR, https://doi.org/10.1093/nar/gkad616

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(67) Lucker, B., Panchy, N., Temple, J., Benning, U., Bibik, J., Neofotis, P., Weissman, J., **Baxter, I.**, Shui, S., Kramer, D. (2022) Selection-Enriched Genomic Loci (SEGL) Reveals Genetic Loci for Environmental Adaptation and Photosynthetic Productivity in Chlamydomonas reinhardtii. Algal Research, https://doi.org/10.1016/j.algal.2022.102709

2021

(66) Goad, D., Kellogg, E., **Baxter, I.**, Olsen, K. (2021) Intraspecific variation in elemental accumulation and its association with salt tolerance in Paspalum vaginatum. G3, doi: https://doi.org/10.1101/2021.03.04.433795

(65) Baseggio, M., Murray, M., Wu, D., Ziegler, G., Kaczmar, N., Chamness, J., Hamilton, J., Buell, R., Vatamaniuk, O., Buckler, E., Smith, M., **Baxter, I.**, Tracy, W., Gore, M. (2021) Genome-wide association study suggests an independent genetic basis of zinc and cadmium concentrations in fresh sweet corn kernels. G3, https://doi.org/10.1093/g3journal/jkab186

(64) Sorgini, C., Roberts, L., Cousins, AB., **Baxter, I.**, Studer, A., (2021) The Genetic Architecture of Leaf Stable Carbon Isotope Composition in Zea mays and the Effect of Transpiration Efficiency on Elemental Accumulation. G3, https://doi.org/10.1093/g3journal/jkab222

(63) Prakash, P., Banan, D., Paul, R., Feldman, M., Xie, D., Freyfogle, L., **Baxter, I.**, Leakey, A. (2021) Correlation and co-localization of QTL for stomatal density and canopy temperature under drought stress in Setaria. Journal of Experimental Botany, Volume 72, Issue 13, 22 June 2021, https://doi.org/10.1093/jxb/erab166

2020

(62) Whitt, L., Ricachenevsky, F. K., Ziegler, G., Clemens, S., Walker, E., Maathuis, F., Kear, P., & **Baxter, I.** (2020) A curated list of genes that control elemental accumulation in plants. Plant Direct, https://doi.org/10.1002/pld3.272

(61) Mamidi, S., Healey, A., Huang, P., **Baxter, I.**, et al. (2020) A genome resource for green millet Setaria viridis enables discovery of agronomically valuable loci. Nature Biotechnology, 38, 1203-1210. https://doi.org/10.1038/s41587-020-0681-2

(60) Goad, D., **Baxter, I.**, Kellogg, E., Olsen, K. (2020) Hybridization, polyploidy and clonality influence geographic patterns of diversity and salt tolerance in the model halophyte seashore paspalum (Paspalum vaginatum). Molecular Ecology, https://doi.org/10.1111/mec.15715

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2019

(57) Taliercio, E., Scaboo, A., **Baxter, I.** and Locke, A.M. (2019) The Ionome of a Genetically Diverse Set of Wild Soybean Accessions. Crop Science, 59: 1983- 1991. https://doi.org/10.2135/cropsci2019.02.0079

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2018

(55) Köhler, I. H., Huber, S. C., Bernacchi, C. J., & **Baxter, I. R.** (2019) Increased temperatures may safeguard the nutritional quality of crops under future elevated CO2 concentrations. The Plant Journal: For Cell and Molecular Biology, 97(5), 872– 886.

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(52) Feldman, M. J., Ellsworth, P. Z., Fahlgren, N., Gehan, M. A., Cousins, A. B., & **Baxter, I.** (2018) Components of Water Use Efficiency Have Unique Genetic Signatures in the Model C4 Grass Setaria. Plant Physiology, 178(2), 699–715.

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(50) Ziegler, G., Nelson, R., Granada, S., Krishnan, H. B., Gillman, J. D., & **Baxter, I.** (2018) Genomewide association study of ionomic traits on diverse soybean populations from germplasm collections. Plant Direct, 2(1), e00033.

(49) Schaefer, R. J., Michno, J.-M., Jeffers, J., Hoekenga, O., Dilkes, B., **Baxter, I.**, & Myers, C. (2018) Integrating Coexpression Networks with GWAS to Prioritize Causal Genes in Maize. The Plant Cell, Volume 30, Issue 12, https://doi.org/10.1105/tpc.18.00299

2017

(48) Flores-Ramirez MR, Rellan-Alvarez R, Wozniak B, Gebreselassie M-N, Jakobsen I, Olalde-Portugal V, **Baxter I**, Paszkowski U, Sawers R. Coordinated changes in the accumulation of metal ions in maize (Zea mays ssp. may L.) in response to inoculation with the arbuscular mycorrhizal fungus Funneliformis mosseae. Plant and Cell Physiology. Published October 2017. doi: 10.1093/pcp/pcx100.

(47) Sawers, R., **Baxter, I.**, et al. Phosphorus acquisition efficiency in arbuscular mycorrhizal maize is correlated with the abundance of root-external hyphae and the accumulation of transcripts encoding PHT1 phosphate transporters.
https://pdfs.semanticscholar.org/dc92/d299afc9ea706e4b36820eb34bef8a799ee6.p df

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(45) Veley, K. M., Berry, J. C., Fentress, S. J., & Schachtman, D. P., **Baxter, I.**, Bart, R. (2017) High-throughput profiling and analysis of plant responses over time to abiotic stress. Plant Direct, Volume 1, Issue 4, https://doi.org/10.1002/pld3.23

(44) Hindt, M. N., Akmakjian, G. Z., Pivarski, K. L., Punshon, T., **Baxter, I.**, Salt. D.E, Guerinot, M.L. (2017) BRUTUS and its paralogs, BTS LIKE1 and BTS LIKE2, encode important negative regulators of the iron deficiency response in Arabidopsis thaliana. Metallomics, https://doi.org/10.1039/c7mt00152e

2016

(43) Asaro, A., Ziegler, G., Ziyomo, C., Hoekenga, O. A., Dilkes, B. P., & **Baxter, I.** (2016) The Interaction of Genotype and Environment Determines Variation in the Maize Kernel Ionome. G3, 6(12), 4175–4183.

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<u>2015</u>

(39) Fahlgren, N., Feldman, M., Gehan, M. A., Wilson, M. S., Shyu, C., Bryant, D. W., Hill, S. T., McEntee, C. J., Warnasooriya, S. N., Kumar, I., Ficor, T., Turnipseed, S., Gilbert, K. B., Brutnell, T. P., Carrington, J. C., Mockler, T. C., & **Baxter, I.** (2015) A Versatile Phenotyping System and Analytics Platform Reveals Diverse Temporal Responses to Water Availability in Setaria. Molecular Plant, 8(10), 1520–1535.

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(37) Kusano, M., **Baxter, I.**, Fukushima, A., Oikawa, A., Okazaki, Y., Nakabayashi, R., Bouvrette, D. J., Achard, F., Jakubowski, A. R., Ballam, J. M., Phillips, J. R., Culler, A. H., Saito, K., & Harrigan, G. G. (2015) Assessing metabolomic and chemical diversity of a soybean lineage representing 35 years of breeding. Metabolomics, 11(2), 261–270.

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<u>2014</u>

(35) **Baxter, I. R.**, Ziegler, G., Lahner, B., Mickelbart, M. V., Foley, R., Danku, J., Armstrong, P., Salt, D. E., & Hoekenga, O. A. (2014) Single-kernel ionomic profiles are highly heritable indicators of genetic and environmental influences on elemental accumulation in maize grain (Zea mays). PloS One, 9(1), e87628.

(34) Huang, P., Feldman, M., Schroder, S., Bahri, B. A., Diao, X., Zhi, H., Estep, M., **Baxter, I.**, Devos, K. M., & Kellogg, E. A. (2014). Population genetics of Setaria viridis, a new model system. Molecular Ecology, 23(20), 4912–4925.

(33) Zhang, M., Pinson, S. R. M., Tarpley, L., Huang, X.-Y., Lahner, B., Yakubova, E., **Baxter, I.**, Guerinot, M. L., & Salt, D. E. (2014) Mapping and validation of quantitative trait loci associated with concentrations of 16 elements in unmilled rice grain. TAG. Theoretical and Applied Genetics. Theoretische Und Angewandte Genetik, 127(1), 137–165.

<u>2013</u>

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(31) Gillman, J. D., **Baxter, I.**, & Bilyeu, K. (2013). Phosphorus Partitioning of Soybean Lines Containing Different Mutant Alleles of Two Soybean Seed-Specific Adenosine Triphosphate-Binding Cassette Phytic Acid Transporter Paralogs. The Plant Genome, 6. https://doi.org/10.3835/plantgenome2012.06.0010

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__2012__

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2010

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1998

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REVIEWS AND WHITE PAPERS

(14) Robert M. Stupar, Anna M. Locke, Doug K. Allen, Minviluz G. Stacey, Jianxin Ma, Jackie Weiss, Rex T. Nelson, Matthew E. Hudson, Trupti Joshi, Zenglu Li, Qijian Song, Joseph R. Jedlicka, Gustavo C. MacIntosh, David Grant, Wayne A. Parrott, Tom E. Clemente, Gary Stacey, Yong-qiang Charles An, Jose Aponte-Rivera, Madan K. Bhattacharyya, **Ivan Baxter**, Kristin D. Bilyeu, Jacqueline D. Campbell, Steven B. Cannon, Steven J. Clough, Shaun J. Curtin, Brian W. Diers, Anne E. Dorrance, Jason D. Gillman, George L. Graef, C. Nathan Hancock, Karen A. Hudson, David L. Hyten, Aardra Kachroo, Jenny Koebernick, Marc Libault, Aaron J. Lorenz, Adam L. Mahan, Jon M. Massman, Michaela McGinn, Khalid Meksem, Jack K. Okamuro, Kerry F. Pedley, Katy Martin Rainey, Andrew M. Scaboo, Jeremy Schmutz, Bao-Hua Song, Adam D. Steinbrenner, Benjamin B. Stewart-Brown, Katalin Toth, Dechun Wang, Lisa Weaver, Bo Zhang, Michelle A. Graham, Jamie A. O'Rourke (2024) Soybean genomics research community strategic plan: A vision for 2024-2028. The Plant Genome, http://dx.doi.org/10.1002/tpg2.20516

(13) Rocío Deanna, Bethann Garramon Merkle, Kwok Pan Chun, Deborah Navarro-Rosenblatt, **Ivan Baxter**, Nora Oleas, Alejandro Bortolus, Patricia Geesink, Luisa Diele-Viegas, Valeria Aschero, Maria Jose de Leone, Sonia Oliferuk, Rui Zuo, Andrea Cosacov, Mariana Grossi, Sandra Knapp, Alicia Lopez-Mendez, Elina Welchen, Pamela Ribone, Gabriela Auge. (2022) Community voices: the importance of diverse networks in academic mentoring. Nature Communications, https://www.nature.com/articles/s41467-022-28667-0

(12) Interdisciplinary Plant Science Consortium (**Baxter, Ivan, corresponding author**). (2023) Inclusive collaboration across plant physiology and genomics: Now is the time! Plant Direct, https://doi.org/10.1002/pld3.493

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(10) **Baxter, I.** (2020). We aren’t good at picking candidate genes, and it's slowing us down. Current Opinion in Plant Biology, 54, 57–60.

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(5) Guerinot, M. L., **Baxter, I.**, & Salt, D. E. (2009). From the Ionome to the Genome:
Identifying the Gene Networks that Control the Mineral Content Of Plants. In J. A. Roberts (Ed.), Annual Plant Reviews online (Vol. 141, pp. 290–303). John Wiley & Sons, Ltd.

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(1) Peer, W. A., **Baxter, I. R.**, Richards, E. L., Freeman, J. L., & Murphy, A. S. (2006). Phytoremediation and hyperaccumulator plants. In M. J. Tamas & E. Martinoia (Eds.), Molecular Biology of Metal Homeostasis and Detoxification: From Microbes to Man (pp. 299–340). Springer Berlin Heidelberg.

INTELLECTUAL PROPERTY

DDPSC0138: CORRECTING DRIFT EFFECTS IN LC-MS DATA BASED ON RETENTION TIME: Allen Hubbard, Brad Evans, Louis Connolly, and Ivan Baxter. Application number 63/505, 952

DDPSC0139: BATCH EFFECT DETECTION AND ADJUSTMENTS OF LC-MS DATA: Allen Hubbard, Louis Connelly, and Ivan Baxter. Application number 63/505, 935

DDPSC0140: SIGNAL AMPLIFICATION FOR MASS DETECTION: Allen Hubbard, Louis Connelly, and Ivan Baxter. Application number 63/505, 941

DDPSC0160: Harnessing the Law of Large Numbers to Overcome Drift. Serial number 63/561.

DDPSC0130: Annotation and Identification of Metabolite Derivatives. Serial number PCT/US2024/015206.

EXTERNALLY FUNDED RESEARCH

CURRENT AWARDED FUNDING

Rooting for Sustainability: Unearthing Maize Genes for Enhanced Nitrogen Use Efficiency and AMFSynergy. Chris Topp, Lead PI. FFAR. 1/1/2025 – 12/31/2027. Total Amount Requested: $2,196,825 ($999,996 requested from FFAR; $1,196,829 in matching funds).

SINC PoC - Maize performance in cover crops. Ivan Baxter, Lead PI. 06/01/2025-05/31/2026. Proof of Concept, Internal Funding. Total Award Amount: $50,000. Baxter Lab Amount: $50,000

SINC. 02/01/2021-08/31/2025. Baxter Lab Amount: $570,726

RESEARCH-PGR: Atomic Numbers: Identifying the conserved genes driving element accumulation in plants. Ivan Baxter, Lead PI. NSF PGRP. Planned Submission. Total Amount Requested: $2,390,017.; Baxter Lab Amount: $1,155,879.

Integrated engineering of whole plant water use efficiency in Sorghum and Setaria. Ivan Baxter, Lead PI. DOE. 09/2022 – 08/2027. $16,639,189.

Dissecting the physiological mechanisms of plant nutrient responses to rising atmospheric carbon dioxide levels. Courtney Leisner (Virginia Tech), Lead PI. USDA NIFA. 1/1/2022 – 12/31/2025 (NICE). Total Award Amount: $635,169. Baxter Lab Amount: $109,372.

BII: New Roots for Restoration: integrating plant traits, communities, and the soil ecosphere to advance restoration of natural and agricultural systems. Allison Miller, Lead PI. NSF Biology Integration Institute. 9/1/2021 – 8/31/2026. Total Award Amount: $12,499,623. Baxter Lab Amount: $876,121.

Metablify. Ivan Baxter, Lead PI. 5/1/2024 – 4/30/2026. Total Award Amount: $692,754.

PENDING PROPOSALS

N-SYNC: Engineering synchronized nitrogen efficiency traits in corn agriculture. Chris Topp, Lead PI. ARPA-E. 4/2025-3/2029. Total Requested Amount: $6,080,464.

Metabolic gene function discovery in Sorghum bicolor by pathway-metabolite regulatory analysis. Ivan Baxter, Lead PI. DOE BER. 06/2025-05/2028. Total Requested Amount: $2,999,959.

PRIOR FUNDING

Further Development of the IAA Suite of Software. Ivan Baxter, Lead PI. 7/1/22 – 4/30/24. Proof of Concept, Internal Funding. Total Award Amount: $200,000.

Using systems approaches to improve photosynthesis and water use efficiency in sorghum. Ivan Baxter, Lead PI. DOE Biological and Environmental Research. 9/15/2017 – 9/14/2023. Total Award Amount: $16,067,707; DDPSC Amount: $6,519,127. (Baxter and Mockler)

IN2 Atlas. Ivan Baxter, Lead PI. Wells Fargo. 9/1/2021 – 7/31/2023. Total Award Amount: $170,000.

Physiological genomics workshop in St. Louis, MO, April 2020: Finding and mending the knowledge gaps between plant physiology and plant functional genetics/genomics. Ivan Baxter, Lead PI. NSF Workshop. 8/1/2019 – 7/31/2022. Total Award Amount: $93,617.

NIFA: Proposal for supplemental funds for NSF Workshop: Finding and mending the knowledge gaps between plant physiology and plant functional genetics/genomics. USDA NIFA. 4/1/2020 – 7/31/2022. Total Award Amount: $10,000.

IN2 Intrinsyx. Ivan Baxter, Lead PI. Wells Fargo. 6/26/2019 – 7/31/2021. Total Award Amount: $200,000. Baxter Lab Amount: $117,151.

An integrated phenomics approach to identifying the genetic basis for Maize root structure and control of plant nutrient relations. Christopher Topp, Lead PI. NSF Plant Genome Research Program. 6/1/2016 – 5/31/2021 (NCE). Total Award Amount: $3,914,246; Baxter Lab Amount: $560,366.

Predicting drought adaptation In C4 plants with high throughput quantitative phenotyping. Brian Dilkes, Lead PI (Purdue University). NSF EAGER. 9/1/2014 - 8/31/2016. Total Award Amount: $299,587. Baxter Lab Amount: $8,000.

A systems-level analysis of drought and density response in the model C4 grass Setaria viridis. Tom Brutnell, Lead PI. Department of Energy. 10/1/2012 – 9/30/2017. Total Award Amount: $12,140,437. Baxter Lab Amount: $997,692.

GEPR: Mineral nutrient gene discovery and gene X environment interactions using the nested association mapping population in Maize. Ivan Baxter, Lead PI. NSF Plant Genome Research Program. 1/1/2012 – 12/31/2015 Total Award Amount: $1,387,118. Baxter Lab Amount: $655,458.

High throughput phenotyping for elemental accumulation QTL mapping of traits under supra-optimal temperatures and water-limited conditions. Cotton Inc. 1/1/2013 – 12/31/2013. Total Award Amount: $15,840.

Ionomics: Investigation of Algal Nutrient Requirements. Jose Olivares, Lead PI The National Association of Advanced Biofuels and Bioproducts (NAABB). Department of Energy. 4/1/2010-3/31/2013. Total Award Amount: $44,036,473. Baxter Award Amount: $402,000.

High throughput phenotyping for elemental accumulation QTL mapping of traits under supra-optimal temperatures and water-limited conditions. Cotton Inc. 1/1/2014 – 12/31/2014. Baxter Award Amount: $9,000.

LECTURES

INVITED SEMINARS AND CONFERENCE PRESENTATIONS (2005 to present)

2025

(104) ASPB Webinar (2025) Plantae Presents-More Money, More Data: Data-driven Versus Hypothesis-driven Research.

(103) 67th Annual Maize Genetics Meeting Keynote (2025) You need a real maize geneticist.

2024

(102) Raymond F. Baker Plant Breeding Symposium (2024) Integrating Metabolomics and High Throughput Phenotyping to Understand the Response of C4 Crops to Water Deficit.

(101) Plant and Animal Genome Conference (2024) A Comparative Approach for Selecting Orthologous Candidate Genes Underlying Signal in Genome-Wide Association across Multiple Species.

2023

(100) Genomic Science Program Annual Principal Investigator (PI) Meeting (2023)

Integrated Engineering of Whole Plant Water Use Efficiency in Sorghum and Setaria.

2022

(99) Genomic Science Program Annual Principal Investigator (PI) Meeting (2022) Integrated understanding and engineering of whole plant water use efficiency in Sorghum and Setaria.

2021

(98) Radcliff Exploratory Seminar (2021) Cross-Cutting Studies on Elemental Dynamics and Interactions in Living Systems.

2020

(97) Plant Biology (2020) Leveraging high-throughput and tightly controlled environments to understand the physiological and genetic mechanisms underlying water-use efficiency in C4 grasses.

(96) Donald Danforth Plant Science Center, Weekly Seminar Series (2020)

Mind the G×E=P; Elemental Content in Plants.

(95) Genomic Science Program Annual Principal Investigator (PI) Meeting (2020) Leveraging high-throughput and tightly controlled environments to understand the physiological and genetic mechanisms underlying water-use efficiency in C4 grasses.

2019

(94) Corn Breeding Research Annual Meeting, St Louis, (2019) Integrating systems biology approaches to understand gene by environment interactions underlying elemental accumulation.

(93) Biochemistry and Plant Molecular Physiology, University of Montpellier, France (2019) Mind the GxE=P; elemental content in plants.

(92) Laboratory of genetics, Wageningen University & Research, Netherlands (2019), Mind the GxE=P; elemental content in plants.

(91) University of Nottingham, Nottingham, England (2019), Mind the GxE=P; elemental content in plants.

(90) Bayer Crop Sciences, St, Louis (2019), Mind the GxE=P; elemental content in plants.

(89) Interdisciplinary Plant Group, University of Missouri, Columbia, MO (2019)

(88) Corn Breeding Research Meeting (March 2019), St. Louis, MO. Integrating systems biology approaches to understand gene by environment interactions underlying elemental accumulation.

2018

(87) John Innes Centre (2018) Mapping the Ionome.

(86) Institute of Integrative Biology of the Cell (2018) Can We Use Elemental Profiles to Understand How Plants Adapt to Their Environments?

(85) South Dakota State University (2018) Public Lecture: It's Element-ary: soil composition and genetic effects on plant growth.

(84) South Dakota State University (2018) The complex interaction between plant genetics and the environment determines the elemental content of our food.

(83) Saint Louis University (2018) Can We Use Elemental Profiles to Understand How Plants Adapt to Their Environments?

(82) Genomic Science Principal Investigator Annual Meeting, Arlington, VA. (2018) High-throughput phenotyping and quantitative genetics to understand productivity and drought traits in the model C4 grass Setaria.

(81) Phenome (2018). Tucson, AZ. Bioinformatics Approaches to Identifying Candidate Genes for Elemental Accumulation.

(80) Plant and Animal Genomics Conference. (2018). San Diego, CA. Bioinformatics Approaches to Identifying Candidate Genes for Elemental Accumulation.

(79) Maize Genetics Conference. St. Malo, France. (2018) Gene by environment interactions of the Maize ionome: analysis of the G2F project.

(78) Society for In Vitro Biology conference (2018) Using High Throughput Controlled Environmental Phenotyping to Understand Water Use Efficiency.

(77) ASPB. Montreal, Canada. (2018) Using High Throughput Controlled Environmental Phenotyping to Understand Water Use Efficiency.

2017

(76) Michigan State University (2017) Can We Use Elemental Profiles to Understand How Plants Adapt to Their Environments?

(75) Genomic Science Principal Investigator Annual Meeting, Arlington, VA. (2017)

(74) Phenome (2017). Tucson, AZ.

(73) ICAR (2017). St. Louis, MO. Using preprints to accelerate your career.

(72) ASPB (2017). Honolulu, HI. Systems Biology tools to interpret ionomic GWAS results across plant species.

2016

(71) Southern Illinois University at Edwardsville (2016) What can the ionome tell us about how plants adapt to the environment?

(70) Iowa State University (2016) Using elemental profiles to understand plant adaptation to the environment.

(69) American Society of Agronomy, Crop Science Society of America, and Soil Science Society of America Annual Meeting, Phoenix, AZ (2016) Ionomics of Micronutrients in Staple Crops; High-Throughput Phenotyping Approaches for Understanding Gene By Environment Interactions: Lessons Learned from Ionomics and Imaging.

(68) 5th International Controlled Environment Conference / AusPheno 2016, Canberra, Australia (2016)

(67) Maize Genetics Conference, Jacksonville, FL (2016) Elemental profiles are inherently the product of gene by environment interactions.

(66) Plant and Animal Genome XXIV, San Diego, CA (2016) Using Elemental Profiling and Systems Biology to Identify Genes Underlying Toxic Element Uptake in Plants.

(65) Corn Breeding Research Meeting, Jacksonville, FL (2016)

(64) Rank Prize Fund Mini-Symposium on The Role of Crops in Providing Micronutrients (Fe, Zn, Se) for Human Health. Grasmere, England (2016) Ionomics of Micronutrients in Staple Crops.

(63) Danforth Plant Science Center, St. Louis, MO (2016) Collaborator Symposium.

What elemental profiles tell us about how and where plants grow?

<u>2015</u>

(62) Chinese Academy of Science, Shanghai, China (2015) Location, location, location, and genetics! The ionome is a sensitive indicator of a plant’s interaction with its environment.

(61) University of Missouri, Columbia, MO (2015) Using the Ionome to understand Gene by Environment interactions in Soybean.

(60) Florida International University, Miami, Florida (2015) Ionomics and Genome-wide Association Studies.

(59) Department of Energy Genomic Sciences Grantees Meeting, Washington DC (2015) High-throughput phenomic approaches to understanding drought adaptation in the C4 model Setaria.

(58) International Workshop on Plant Ionomics and Nutrient Use Efficiency, Nanjing Agricultural University, China (2015) Moving from ionomics GWAS to ionomics genes: comparative and network approaches.

(57) American Society of Plant Biologists, Minneapolis MN (2015) Canopy Position Has a Profound Effect on Soybean Seed Composition.

(56) Joint Danforth Center/Missouri Botanical Garden Symposium: From Darwin to Borlaug, Danforth Center, St. Louis, Mo (2015). Location, Location, Location, and Genetics! Elemental profiles reveal insights into how crop plants adapt to their environment.

<u>2014</u>

(55) University of Illinois, Urbana-Champaign, IL (2014) Location, location, location, and genetics! The ionome is a sensitive indicator of a plant’s interaction with its environment.

(54) University of Nottingham, Nottingham, England (2014) Location, Location, Location, and Genetics! The Ionome is a Sensitive Indicator of a Plant’s Interaction with Its Environment.

(53) Purdue Plant Sciences Lecture Series (2014) Using High-Throughput Ionomics and Phenotyping to Study Gene by Environment Interactions.

(52) Washington University Science on Tap (2014) It’s Elementary: Soil Composition and Genetic Effects on Plant Growth.

(51) American Chemical Society and Royal Society of Chemistry, Reno, NV (2014) How integrating genetics with high throughput elemental profiling leads to knowledge about plant adaptation to the environment.

(50) Society for Experimental Biology, Manchester, England (2014) Location, Location, Location, and Genetics! The Ionome is a Sensitive Indicator of a Plant’s Interaction with Its Environment.

(49) Plant and Animal Genome XXII, San Diego, CA (2014) Drought Studies in Setaria using the Bellwether Foundation Phenotyping Facility at the Danforth Center.

2013

(48) UC Davis, Genetics Graduate Group seminar series on Genomics and Epigenetics (2013) Location, Location, Location, and Genetics! The Ionome is a Sensitive Indicator of a Plant's Interaction with Its Environment.

(47) Washington State University Molecular Plant Sciences Graduate Program (2013) Location, Location, Location, and Genetics! The Ionome is a Sensitive Indicator of a Plant's Interaction with Its Environment.

(46) Plant and Animal Genome XXI, San Diego, CA (2013) Maize Ionomics Identifies Gene by Environment Interactions Affecting Elemental Accumulation.

2012

(45) University of Missouri, Columbia, Mo (2012) G2Ionome: Linking the Genome with the Social Network of Elements.

(44) San Diego Center for Algal Biotechnology, San Diego, Ca (2012) Surfing algal growth hyperspace: Exploring growth media space and optimizing genetics for biofuels applications.

(43) ASA, CSSA, and SSA International Annual Meeting, Cincinnati, OH (2012) Ionomics of Corn and Soybeans: Using High Throughput Elemental Profiling to Study How Plants Accumulate Minerals.

(42) IPG Symposium, Columbia, Mo (2012) Using the Seed Ionome as an Indicator of Plant Physiological Properties.

(41) Maize Genetics Meeting, Portland, Oregon (2012) Ionomics of the Maize Nested Association Mapping Population.

(40) Plant and Animal Genome XX, San Diego, Ca (2012) Soybean Ionomics.

2011

(39) USDA-ARS Arid Land Agricultural Research Center, Maricopa AZ (2011) G2Ionome: Linking the Genome with the Social Network of Elements.

(38) Saint Louis University, St. Louis, Mo (2011) G2Ionome: Linking the Genome with the Social Network of Elements.

(37) Monsanto, St. Louis, Mo (2011) What can the ionome tell us about how plants adapt to the environment? Lessons from Arabidopsis, Maize and Soybean.

(36) University of Missouri-St. Louis, St. Louis, Mo (2011) What can the ionome tell us about how plants adapt to the environment? Lessons from Maize and Arabidopsis.

(35) Banbury Conference: Genomes to Phenomes, Cold Spring Harbor, NY (2011)
Ionomics.

(34) Danforth Symposium: Genomes to Phenomes, Danforth Center, St. Louis, MO (2011) G2Ionome: Linking the Genome with the Social Network of Elements.

2010

(33) Cornell University, Ithaca NY, (2010) What can the ionome tell us about how plants adapt to the environment? Lessons from Maize and Arabidopsis.

(32) University of Arizona, Tucson, AZ (2010) What can the ionome tell us about how plants adapt to the environment? Lessons from Maize, Arabidopsis and Yeast.

(31) American Society of Plant Biologists, Montreal, Quebec (2010) Ionomics of the Maize Nested Association Mapping Panel.

(30) 12th International Association for Plant Biotechnology Congress, St. Louis, MO (2010) Ionomics of the Maize Nested Association Mapping Panel.

2009

(29) Washington University, Saint Louis MO (2009) How Plants Alter their Elemental Composition to Adapt to Different Soil Environments.

(28) University of Minnesota, St. Paul, MN (2009) How Plants Alter their Elemental Composition to Adapt to Different Soil Environments.

(27) The Ohio State University, Columbus, OH (2009) How Plants Alter their Elemental Composition to Adapt to Different Soil Environments.

(26) Danforth Plant Science Center, St. Louis, MO (2009) How Plants Alter their Elemental Composition to Adapt to Different Soil Environments.

(25) USDA-ARS/ University of Missouri, Columbia, MO (2009) How Plants Alter their Elemental Composition to Adapt to Different Soil Environments.

(24) University of Nebraska-Lincoln, Lincoln, NE (2009) How Plants Alter their Elemental Composition to Adapt to Different Soil Environments.

(23) Iowa State University, Ames, IA (2009) How Plants Alter their Elemental Composition to Adapt to Different Soil Environments.

(22) International Plant Molecular Biology Conference, St. Louis, MO (2009) Combining Association Mapping with Ionomics to Identify Genes Important for Stress Tolerance.

(21) Danforth Symposium, St. Louis, MO (2009) Yeast Ionomics: probing the effects of sub-cellular processes on elemental accumulation in a single celled organism.

2008

(20) Dow AgroSciences, Indianapolis, IN (2008) Mapping and Modeling the Arabidopsis Ionome.

(19) University of Massachusetts, Amherst, MA (2008) Mapping and Modeling the Arabidopsis Ionome.

(18) Baylor College of Medicine, Houston, TX (2008) Mapping and Modeling the Ionome in Yeast and Arabidopsis.

(17) Danforth Plant Science Center, St. Louis, MO (2008) Mapping and Modeling the Arabidopss Ionome.

(16) Michigan State University, East Lansing, MI (2008) Mapping and Modeling the Arabidopsis Ionome.

2007

(15) Seminis Woodland, CA (2007) Mapping and Modeling the Arabidopsis Ionome.

(14) Michigan State University, East Lansing, MI (2007) Mapping and Modeling the Arabidopsis Ionome.

(13) Institute for Systems Biology, Seattle, WA (2007) Mapping the Arabidopsis Ionome.

(12) Pioneer Hi-Bred, Johnston, IA (2007) Mapping the Arabidopsis Ionome.

(11) Purdue University, Plant Biology Lecture Series, West Lafayette, IN (2007) Linking Genetic Variation to Environmental Variation in the Arabidopsis Ionome.

(10) International Symposium on Metalomics, Nagoya, Japan (2007) Mapping the Arabidopsis Ionome. Keynote lecture.

(9) ASPB Plant Biology 2007, Chicago, IL (2007) Deletion and Duplication Detection in Arabidopsis Using Tiling Arrays.

(8) Plant Biology Symposium and Plant Proteomics Mini-Symposium, Columbia, MO (2007) Ab initio Prediction of Protein Kinase Target Sites.

(7) Midwest Developmental Biology Meeting, Chicago, IL (2007) Linking Genetic Variation to Environmental Variation in the Arabidopsis Ionome. Runner-up, Best Post-Doc Talk.

2006

(6) Purdue University, Bioinformatics Seminar Series, West Lafayette, IN (2006) From Genome to Gene: Using an “-omic” Approach to Identify Causal Loci.

(5) University of Nevada, Reno, NV (2006) Array-Based Mapping, a Novel, Rapid Technique for Gene Identification: An Ionomics Case Study.

(4) Pan American Plant Membrane Biology Workshop, South Padre Island, TX (2006) DNA Microarray-Based Mapping, a Novel, Rapid Technique for Gene Identification: An Ionomics Case Study.

(3) ASPB Plant Biology 2006, Boston, MA (2006) Natural Ionomic variation in Arabidopsis Identifies an E3 Ubiquitin Ligase Involved in Regulating Shoot Mo.

2005

(2) ASPB Plant Biology 2005, Seattle, WA (2005) A Plasma Membrane H+-ATPase is Required for the Formation of Proanthocyanidins in the Seed Coat Endothelium of Arabidopsis thaliana.

(1) International Conference on Arabidopsis Research, Madison, WI (2005) Mapping the Arabidopsis Ionome.

SERVICE

SERVICE TO THE SCIENTIFIC COMMUNITY

Editorial Roles and Journal Review Activity

Manuscript Reviews

BMC Plant Biology, Crop Science, G3, Genetics, Journal of Experimental Botany, Journal of Plant Nutrition and Soil Science, Metallomics, Molecular Genetics and Genomics, New Phytologist, Physiologia Planarium, Plant Cell, The Plant Genome, The Plant Journal, Plant Physiology, Plant Physiology and Biochemistry, PloS Genetics, Plos One, PNAS, Rice, Theoretical and Applied Genetics, Scientific Reports, Communication Biology, Journal of the Royal Society Interface, Plant, Cell & Environment

Editor

Plant Direct, Founding Editor in Chief	2017-2022
PLoS ONE, Academic Editor	2006-2016
PLoS ONE Plant Biology, Section Editor	2008-2016

Chair and Member of Workshops and Meetings

American Society of Plant Biologists Publications Committee	2025-2030
DOE JGI: Establishing a Vision for a DOE Plant Transformation Capability Workshop	2025
Committee Member-Scientific Advisory Board for the 5th Annual MANA Conference, University of Missouri-Columbia	2023
Chair: Finding and Mending the Knowledge Gaps between Plant Physiology and Plant Functional Genetics/Genomics.	2021
Program Chair, Phenome 2020	2020
Program Chair, Phenome 2019	2019
Organizer and presenter, When to Preprint/When to Publish	2019
Phenome Steering Committee	2018-2020
Broadening the Impact of Plant Science Through Community-Based Innovation, "Evaluation and Sharing of Outreach Programs"	2018
Organizer and presenter, How to Review, Plant Biology	2018
Organizer and presenter, Common Author Errors and How to Avoid Them	2017
Organizer and presenter, Plant Direct: New Journal, New Ideas, Plant Biology	2017
Presenter, Careers Beyond the Academy. Panel Presentation and Discussion, ICAR	2017
Co- Organizer and Presenter, Communicating your science to peers and beyond, ICAR	2017
Scientific Co-Organizer, Danforth Center Symposium: Macro-Influence of Microorganisms: Host-Microbe Interactions and Inspired Technologies	2014
Scientific Co-Organizer, Danforth Center Symposium: PhenoDays: Imaging and Robotics for 21st Century Science	2013
Scientific Co-Organizer, Danforth Center Symposium: Genomes to Phenomes	2011
Co-Chair: iPlant Mineral Nutrition Working Group	2010-2012
Session Chair: ASPB Plant Biology	2007

American Society of Plant Biologist Lab Leadership Workshop	2006

Grant Panelist and Reviewer

Grant Panelist – NSF panels 2013 and 2015 (2), 2022, 2024 DOE panels 2019, 2022, 2023, 2024
Grant Reviewer, 20+ NSF grants since 2010
Grant Reviewer, 2 USDA grants since 2015
Panelist, Triennial Review of Joint Genome Institute Program 2024

Service on Doctoral Advising & Defense Committees

Washington University

Saint Louis, Missouri

Brian Early	Graduated 2021
David Goad	Graduated 2021
Alex Liu	Graduated 2025
Anastassia Onyshchenko (Chair)	Graduated 2025
Michell Cho (Chair)	Graduated 2025
Antonio Brazelton (Chair)	Active
Sherri Ji	Active

University of Nottingham, UK

Sebastian Garcia-Gaga	Graduated 2025
Konrad Neugebauer	Graduated 2019

University of Missouri-Columbia

Prema Mutyala	Active

Other

Fellow of ASPB Award	2025
Joint Genome Institute User Executive Committee	2025-present

Co-host of the ASPB podcast 'The Taproot', exploring the stories behind scientific publications. Downloaded >95,000, the podcast won a gold medal in the podcast category of the EXCEL awards from the Association Media and Publishing organization.

Graduate and Undergraduate Awards and Honors

Deep Gene Travel Award (ASPB Plant Biology 2003)	2003
American Society of Plant Biologists Travel Award Recipient	2002
Biochemistry Lab Teaching Assistant, MIT	1997
Freshman Chemistry, Head Teaching Assistant, MIT	1996
Phi Beta Kappa	1996
President, Student Government Association, Goucher College	1995-1996
Claasen Chemistry Scholar, Goucher College	1993-1996
Dean's List, Goucher College	1993-1996
Dean's Scholarship Recipient, Goucher College	1992-1996

SERVICE TO THE USDA-ARS

Organizer: USDA-ARS Big Data Genetics of Populations Workshop	2015
Writing team: Big Data and Computing Building a Vision for ARS Information	2013

Management	
Writing team: USDA-ARS National Program 301 Action Plan	2012

SERVICE TO THE DONALD DANFORTH PLANT SCIENCE CENTER

Oversight or Regular Committee Member

Chair, Grant Support/Admin Assistant Advisory Committee	2025-present
Danforth Center Bioanalytical Chemistry Core Oversight Committee	2024-present
Member, Presidents Faculty Advisory Council	2022-present
Danforth Center Data Science Core Oversight Committee	2012-present
Administrative Assistant Management	2023-2025
Grant Specialist Management	2023-2025
Acting Director: Phenotyping Core	2021-2022
Member: Danforth Center Diversity, Equity, and Inclusion Advisory Council	2020-2022
Chair: Danforth Center Responsible Conduct of Research Training Committee	2013-2018
Danforth Center eLab Notebook Committee	2012-2018
Chair: Phenotyping Core Oversight Committee	2011-2025
Danforth Center Proteomics and Mass-Spec Core Oversight Committee	2010-2012
Danforth Center Institutional Equipment Fund Committee	2009-2018
Co-Chair: Danforth Center Responsible Conduct of Research Training Committee	2009-2018
Advisor: Danforth Center Future PIs peer mentoring group	2018

MENTORING AND OUTREACH ACTIVITIES

Lecturer, Courses and Workshops

Washington University

Saint Louis, Missouri

DBBS Ethics Course, Instructor	Spring 2014 6 sessions
Bio 4028, Lecturer, 2 lectures	2010, 2011
Bio527 Journal Club	2011, 2012
Bio527 Journal Club Organizer	Fall 2013
Bio5702, Lecturer	Spring 2018-2025
Bio5491, Lecturer	Spring 2024-2025

University of Missouri

Columbia, Missouri

Guest Lecturer, PS8010 – Professionalism and Ethics	Fall 2025
Guest Lecturer, PS8530	2011-2025
Instructor PS8010- Professionalism and Ethics	2020-2021

Lab Outreach Activities

Plant Tech Jam table	2024- present
Jackie Joyner-Kersee Food, Agriculture, and Nutrition Innovation Center (JJK FAN), 6-week after school program for middle schoolers	2024-present
La Salle Middle School, 6-week after school program for middle schoolers	2017-2019

St. Louis County Science Fair Judge	2015, 2016, 2017
Bioinformatics High School teacher workshop St. Louis, Missouri	January 2013
Bioinformatics High School teacher workshop St. Paul, Minnesota	November 2013

Mentoring, Postdoctoral Scientists, Graduate, Undergraduate and Other

Current Lab Personnel (14):

Greg Ziegler, Staff Scientist II	
PhD in 4/2014; thesis was written exclusively on work done in Baxter lab.	11/22/10-present
Jennifer Barrett, Administrative Lab Manager	1 2/6/10-present
Allen Hubbard, Research Scientist III	7/1/18-present
Collin Luebbert, Data Scientist II	2/3/19-present
Louis Connelly, Data Scientist II	5/24/21-present
Hui Jiang, Research Associate II	6/1/18-present
Philip Ozersky, Data Scientist II	2/5/16-present
Britney Millman, Research Technician II	3/8/21-present
Micah Kelleher, Data Science Associate	7/19/21-present
Magdalena Janik, Graduate Student (WUSTL)	2/15/23-present
Prashant Bhandari, Postdoctoral Associate	5/16/23-present
Stella Woeltjen, Postdoctoral Associate	7/17/23-present
Kyle Koch, Graduate Student (WUSTL)	3/10/25-present
Anastasiia Onyshchenko, Graduate Student (WUSTL)	9/1/25-present

Past/Current Lab Personnel:

Postdoctoral Associates (9)

Prashant Bhandari, Postdoctoral Associate	5/16/23-present
Stella Woeltjen, Postdoctoral Associate	7/17/23-present
Renee Dale	5/15/19-12/24
Jessica Wedow	6/20-10/21
Charles Pignon	5/19-1/20
Megan Khangura	5/19-10/19
Max Feldman	01/13-9/2018
Catherine Ziyomo	10/12-1/14
Aimee Terauchi	10/10-2/13

PhD Graduate Students (5)

Kyle Koch, Washington University, Saint Louis	5/1/25-present
Magdalena Janik, Washington University, Saint Louis	2/15/23-present
Anastasiia Onyshchenko, Washington University, Saint Louis	9/1/25-present
Alexandra (Asaro) Fikas, Washington University, Saint Louis	1/14-1/20
Lauren Whitt, University of Missouri-Columbia	10/30/17-4/25/24

Rotation Students (6)

Kyle Koch, Washington University, Saint Louis	3/10/25-4/30/25
Antonio Brazelton, Washington University, Saint Louis	11/21-2/22
Emmily Moses, Washington University, Saint Louis	8/23-11/23

Haina Jin, Washington University, Saint Louis	2/24-6/24
Erin Mattoon, Washington University, Saint Louis	1/18-3/18
Maria Sorkin, Washington University, Saint Louis	9/16-11/16

Visiting Scientists (2)

Marcio Ferreira	12/1/21-7/11/23
Xuecheng Sun	9/1/11-8/30/12

Staff Scientist II (1)

Greg Ziegler, Research Manager	
PhD in 4/2014; thesis was written exclusively on work done in Baxter lab.	11/22/10-present

Administrative Lab Manager (1)

Jennifer Barrett, Administrative Lab Manager	1 2/6/10-present

Research Scientist III & Research Associate II (2)

Allen Hubbard, Research Scientist III	7/1/18-present
Hui Jiang, Research Associate II	6/1/18-present

Data Scientists, Data Science Associate & Programmers (7)

Collin Luebbert, Data Scientist II	2/3/19-present
Louis Connelly, Data Scientist II	5/24/21-present
Philip Ozersky, Data Scientist II	2/5/16-present
Micah Kelleher, Data Science Associate	7/19/21-present
Molly Wohl, Programmer	11/14-9/2018
Ryan Hartwig, Programmer	11/14-12/2015
Tim Parker, Programmer	10/2018-10/2021

Bioinformation Laboratory Assistant (1)

Rijan Dhakal, Bioinformatics Laboratory Assistant	5/22/23-7/31/25

Research Technicians & Research Assistants (10)

Britney Millman, Research Technician II	3/8/21-present
Tuany Volz, Research Assistant	1/3/24-8/1/2025
Jennifer Jaros	10/7/19-12/2020
Kim Green	9/12-1/2018
Walter Iverson	3/10-8/11
Janna Hutchinson	11/11-12/2016
Xiaoping Li	6/18-11/22
Spencer Navrude	2/14/23-4/25/23
Zhonghui Wang	2/14/23-2/1/2024
Tim Kosfeld	10/13/21-6/2/24

Lab Assistants (7)

Sravani Valligari	5/22/23-2024
Melissa Jurkowski	11/25/13-2024
Amisha Poojari	1/30/24-7/31/24
Henry Frees	5/23-7/24
Henry Bloch	5/23-8/23

Amber Wolf	1/18-6/18
Maddie Schuler	Summer 2016

REU Interns (18)

Anyia Thomas	Summer 2024
Juliana Shields	Summer 2023
Melanie Cabrera	Summer 2022
Raymond Castillo	Summer 2021
Alexander Liu	Summer 2019
Brandon Vestal	Summer 2018
Preston Bruce	Summer 2017
Jacob Roth	Summer 2016
Elizabeth Mahood	Summer 2015
Rebecca Valle	Summer 2015
Evan Kesinger	Summer 2014
Joe (Nathan) Lindsey	Summer 2014
Elise Viox	6/10-7/10, 5/13-8/13, 12/13-1/14
Derrick Smith	Summer 2013
Stephanie Grenada	Summer 2013
Anthony Becker	5/10-8/11, 5/12–7/12
Bruce Green	Summer 2012
Anne Kearney	Summer 2011

Undergraduate Interns (5)

Emma Harding	January 2023
Louis Connelly	Spring 2021
Stewart Craig	Spring 2021
Elizabeth Mahood	6/15-6/17
Paul Smelcer	2011

High School Student Interns (11)

E'sabel Merriweather	1/9/25-04/22/2025
Finn Reeves	12/23-1/24; 6/24-12/24
Amisha Poojari	7/23-8/23
Aric Wang	6/23-8/23
Henry Bloch	1/23-4/23
Zoraya Piedra	6/22-8/22
Shinoy Mammen	2/22-4/22
Omkar Venkatesh	Summer 2016
Rebecca Rodell	6/13–9/15
Jailin Ding	5/13–9/13, 6/14-9/14
Adaisia Stevens	6/12-7/12

Fellowships

Renee Dale	NSF PGRP Fellow (2021-24)
Stella Woeltjen	USDA Postdoctoral Fellowship (2025-)

Trainee Accomplishments

Allen Hubbard

(2) Kambhampati, S., **Hubbard, A.H.,** Koley, S., Gomez, J.D., Marsolais, F., Evans, B., Young, J.D., Allen, D.K. (2024) SIMPEL: using stable isotopes to elucidate dynamics of context specific metabolism. Communications Biology 7, 172. https://doi.org/10.1038 /s42003-024-05844-z

(1) Invention Disclosure. Isolock and autoCredential: A pair of algorithms to identify metabolite masses among high resolution mass spectrometry data. Isolock corrects for instrument mass drift while autoCredential validates metabolite masses through the presence of C13 isotopologues after pooling drift corrected files into a merged mass spectra to increase the signal-to-noise ratio. Inventors: Allen Hubbard, Brad Evans and Shrikaar Kambhampati. Application No. 63/185,674, filed May 2, 2021.

Max Feldman

(1) Gehan MA, Fahlgren N, Abbasi A, Berry JC, Callen ST, Chavez L, Doust AN, **Feldman MJ**, Gilbert KB, Hodge JG, Hoyer JS, Lin A, Liu S, Lizárraga C, Lorence A, Miller M, Platon E, Tessman M, Sax T. (2017). PlantCV v2: Image analysis software for high-throughput plant phenotyping. PeerJ 5:e4088 https://doi.org/10.7717/peerj.4088

Presentations/Posters

Renee Dale

(9) Competition for resources during semi-sequential growth of developmental units drive allometric patterns in grasses. Physics & Biology of Plant Growth Workshop, Ein Gedi, Israel [Talk]. 2023.

(8) Competition for resources during semi-sequential growth of developmental units drives allometric patterns in the grass Setaria. Society for Mathematical Biology Annual Meeting, The Ohio State University. [Talk] 2023.

(7) Competition for resources during semi-sequential growth of developmental units drive allometric patterns in Setaria. International Conference for Arabidopsis Research Meeting, Chiba, Japan. [Poster] 2023.

(6) Competition for resources during semi-sequential growth of developmental units drive allometric patterns in Setaria. North American Plant Phenotyping Network Annual Meeting, St. Louis, Missouri. [Poster] 2023.

(5) Competition for resources during semi-sequential growth of developmental units drive allometric patterns in grasses. GRC and GRS on Stochastic Physics in Biology, Ventura, California. [Poster] 2023.

(4) Understanding factors affecting internode length variability in Setaria using mathematical modeling. PlantBiology 2022, Portland, Oregon. [Poster] 2022.

(3) Mathematical modeling to deepen our understanding of complex biological systems.

(2) Plant Science Department, University of Arizona. [Talk] 2022.

CS-1-5 - Using a Trait-based Dynamic Mathematical Framework to Investigate the Relationship Between Phenotypic Dynamical Parameters and the Genome in Setaria.

(1) Plant Biology Worldwide Summit, ASPB. [Talk] 2020.

Lauren Whitt

(13) Computational methods to identify ionome genes [Poster Lightning Talk]. 65th Annual Maize Genetics Meeting, Saint Louis, MO. 2023.

(12) Computational methods to identify plant ionome genes. 7th Annual MU Corteva Plant Research Symposium. University of Missouri, Columbia, MO. 2023.

(11) Computational methods to identify elemental accumulation genes [Poster]. North American Plant Phenotyping Network. 2023.

(10) Filtering ionomics candidate genes using comparative genetics [Updated data & analysis] [Poster]. 7th Annual MU Corteva Plant Research Symposium. 2023.

(9) A comparative approach to selecting candidate genes in GWAS. Plant Genome Online (virtual). 2022.

(8) Filtering ionomics candidate genes using comparative genetics. DDPSC CSTM BioBash. 2022.

(7) Exploring the Unknown: How to expand the genetic toolboxes for next-gen crops.

FFAR Fellows Lighting Talk 2021 competition (virtual). NC State University. 2021.

(6) Improved candidate gene selection methods using comparative genomics.

Comprehensive exam (virtual). University of Missouri, Columbia, MO. June 2021.

(5) FiReMAGE: a tool for candidate gene selection. Danforth Mentoring Seminar (virtual). Saint Louis, MO, 2020.

(4) Computational methods to identify elemental accumulation genes. Plant Sciences Graduate Seminar. University of Missouri, Columbia, MO, 2020.

(3) FiReMAGE: Turning GWAS into candidate genes. Danforth Center Fall Symposium Lightning Talks. Saint Louis, MO, 2019.

(2) Rooted in Missouri. Conversations: Big Ideas 2.0. Donald Danforth Plant Science Center, Saint Louis, MO, 2019.

(1) CGAS: Turning GWAS results into candidate genes. Bioinformatics & Beers. Donald Danforth Plant Science Center, Saint Louis, MO, 2019.

Louis Connelly

(1) From Leaf to Locus: Associating Plant Metabolites with Genomic Regions. Danforth Retreat at Missouri Botanical Garden. Saint Louis, MO. 2023.

Charles Pignon

(1) Accelerating stomatal movement under fluctuating light. Phenome. Tucson, AZ. 2019.

Alexandra Asaro

(3) A Combinatorial Approach of Ionomics, Quantitative Trait Locus Mapping, and Transcriptome Analysis to Characterize Element Homeostasis in Maize. Thesis Defense, May 2019.

(2) Using two parent genome mapping to identify expression level quantitative loci in Maize roots. Maize Genetics Conference. St. Malo, France. 2018.

(1) Gene by Environment Interaction in the Maize Ionome. American Society of Plant Biologists. Minneapolis, MN. 2015.

Max Feldman

(12) Trait components of whole plant water use efficiency are defined by unique, environmentally responsive genetic signatures in the model C4 grass Setaria. Phenome 2018 Research Conference. Tucson, AZ. 2018.

(11) My NSF I-Corps Journey: Evaluating the Commercialization Potential of an Inexpensive, Modular, Robotic Plant Phenotyping Platform. Donald Danforth Plant Science Center. St. Louis, MO. 2018.

(10) Facilitating discovery from whole plant measurements. University of Minnesota – Twin Cities. Minneapolis, MN. 2018.

(9) Components of water use efficiency have unique genetic signatures in the model C4 grass Setaria. Salt and Water Stress in Plants Gordon Research Conference. Waterville Valley, NH. 2018.

(8) Time dependent genetic analysis links field and controlled environmental phenotypes in the model C4 grass Setaria. Phenome 2017 Research Conference. Tucson, AZ. 2017.

(7) Computational tools for high-throughput quantitative genetics. Bioinformatics & Beers, St. Louis, MO. 2017.

(6) Stable isotopes, ratios & linear models: Disentangling the correlation between plant size and water use to map the genetic components of transpiration efficiency. Donald Danforth Plant Science Center Scientific Retreat, Potosi, MO. 2017.

(5) The trait components which constitute water use efficiency are defined by unique, environmentally responsive genetic signatures in the model C4 grass Setaria. Signat Workshop on Environmental Regulation of Plant Development, Santiago, Chile. 2017.

(4) Time Dependent Genetic Analysis Links Field and Controlled Environment Phenotypes in the Model C4 Grass Setaria. Multiscale Plant Vascular Biology - Gordon Research Conference, Sunday River, ME. 2016.

(3) Setaria Travels into the 4th Dimension: The Genetic Architecture of Plant Height. Washington University Plant and Microbial Biosciences Annual Retreat, Tyson Research Center at Washington University, St. Louis, MO. 2015.

(2) High-throughput Phenomics Approaches to Understanding Drought Adaptation in the C4 model grass Setaria. ASPB Midwest Sectional Meeting, Donald Danforth Plant Science Center, St. Louis, MO. 2015.

(1) Aggregating Quantitative Phenotypes to Delineate the Genetic Architecture of Drought Tolerance in Setaria. Donald Danforth Plant Science Center Annual Retreat, Pere Marquette Lodge & Conference Center, Grafton, IL. 2014.

Collin Luebbert

(4) Genome Wide Association Study of Multiple High-Throughput Phenotyping Experiments to Identify Genetic Loci Controlling Water Use Efficiency in C4 Grass Setaria viridis. 15-minute talk, NAPPN Conference, St. Louis, MO, 2023.

(3) Multi-year, Intensive Phenotyping Reveals Genetic Diversity in Nitrogen Related Traits. Poster, Maize Genetics Conference, St. Louis, MO, 2023.

(2) Genome Wide Association of Many Diverse Phenotypes in Nitrogen Limited Field Conditions. Lightning talk, NAPPN Conference, Athens, GA, 2022.

(1) Investigating Sources of Phenotypic Variation in Nitrogen Limited Field Conditions. Danforth Center Scientific Retreat, St. Louis, MO. 2022.

Micah Kelleher

(2) A practical haplotype graph map of the ZeaSynthetic population enables integration of teosinte alleles into breeding efforts. Maize Genetics Meeting Talks, Raleigh, NC, 2024.

(1) A practical haplotype graph of the ZeaSynthetic population. Bioinformatics & Beers, Lightning Talks. Saint Louis, MO, 2024.

Prashant Bhandari

(9) Integrating Metabolomics and Phenomics to Understand the Response of C4 Crops to Water Deficit. Predictive Phenomics Conference, 2025. [Talk]

(8) Multiple evolutionary conserved loci underlie plant water use efficiency in Sorghum and Setaria. 67th Annual Maize Genetics Meeting, 2025. [Poster]

(7) A Systems Biology Approach to Water Deficit Response in C4 Crops. 2025 Bioinformatics and Beers, Donald Danforth Plant Science Center, 2025. [Lightning Talk]

(6) Multiple Conserved Loci Underlie Plant Water Use Efficiency in Sorghum and Setaria, PMB Retreat Washington University-St. Louis, 2024. [Talk]

(5) Multiple Conserved Loci Underlie Plant Water Use Efficiency in Sorghum and Setaria. H_20-C meeting, 2024. [Talk]

(4) Multiple evolutionary conserved loci underlie plant water use efficiency in Sorghum and Setaria. Salt and Water Stress in Plants, Gordon Research Conference, 2024. [Poster]

(3) Genetic architecture of water-use efficiency in Sorghum and Setaria. New Phytologist next generation scientists, Duke University, 2024. [Poster]

(2) Genetic mapping of plant water use efficiency in Sorghum & Setaria. Mentoring Seminar, Donald Danforth Plant Science Center, 2024. [Talk]

(1) Mapping plant-water use efficiency genes in C4 Crops. 2024 Bioinformatics and Beers, Donald Danforth Plant Science Center, 2024. [Lightning Talk]

Hui Jiang
(4) Harnessing Male Sterility to Accelerate Genetic Research in the C4 Model *Setaria viridis.* Maize Genetics Conference, St. Louis, 2025. [Poster]
(3) Forward Genetic Screen to Identify PEPC Suppressor Mutants, H_2O-C project meeting, September 2024. [Poster]
(2) Male Sterile Setaria, H_2O-C project meeting, September 2024. [Talk]
(1) Sequencing-Driven Accelerated Discovery of Genes Regulating Water Use Efficiency and Stomatal Patterning in C4 Crops with High-throughput Phenotyping, DOE BSD PI Meeting, March 2024. [Poster]