

# Jason G. Wallace

Associate Professor

## Curriculum Vitae

March 2022

Department of Crop & Soil Sciences, University of Georgia  
wallacelab.uga.edu  
+1-706-542-9696  
jason.wallace@uga.edu  
jgwall  
jason-wallace-a874b845

## Academic History

<b>Present Rank</b>	Associate Professor
<b>Recommended Rank</b>	Full Professor
<b>Proportion Time Assignment</b>	80% research, 20% teaching
<b>Tenure Status</b>	Tenured
<b>Graduate Faculty</b>	2015-Present

## Education

2011	<b>Ph. D. – Yale University</b>	Molecular, Cellular and Developmental Biology
2008	<b>M. S. – Yale University</b>	Molecular, Cellular and Developmental Biology
2006	<b>B. S. – Brigham Young University</b>	Integrative Biology

## Professional Experience

2020–Present	<b>Associate Professor</b>	University of Georgia – Crop & Soil Sciences (Athens, GA)
2015–2020	<b>Assistant Professor</b>	University of Georgia – Crop & Soil Sciences (Athens, GA)
2012–2015	<b>Postdoctoral associate</b>	Cornell University (Ithaca, NY)
2006–2011	<b>Graduate research assistant</b>	Yale University (New Haven, CT)
2007–2007	<b>Graduate research intern</b>	Bristol-Myers Squibb Pharmaceuticals (Wallingford, CT)
2005–2006	<b>Undergraduate research assistant</b>	Brigham Young University (Provo, UT)

## Awards

March 2019	<b>Nomination - 40 under 40</b>	Georgia Trend Magazine
November 2018	<b>New Innovator in Food and Agriculture Research Award</b>	Foundation for Food and Agriculture Research
July 2015	<b>Travel Awards for Early Career Professionals</b>	Phytobiomes Conference 2015
2010–2011	<b>Annie Le Memorial Fellowship</b>	Yale University
September 2010	<b>Poster award for “Most Creative Project”</b>	Yale University MCDB Departmental Retreat
2000–2001, 2003–2006	<b>Gordon B. Hinckley Presidential Scholarship</b>	Brigham Young University

## Instruction

### Instructor of Record

CRSS 8010	<b>Research Methods and Design in Crop Science</b>	3 credits
	<ul style="list-style-type: none"><li>Fall 2022</li><li>Fall 2020</li><li>Fall 2018</li><li>Fall 2016</li></ul>	
PBGG 8860	<b>PBGG Student Communication Seminar</b>	1 credit
	<ul style="list-style-type: none"><li>Spring 2022</li></ul>	
PBGG 8861	<b>PBGG Student Research Seminar</b>	1 credit
	<ul style="list-style-type: none"><li>Spring 2022</li></ul>	
PBGG 8874	<b>Genomic selection</b>	1 credit
	<ul style="list-style-type: none"><li>Spring 2021</li><li>Spring 2019</li><li>Spring 2017</li></ul>	
PBGG 8875	<b>Genome-wide association in plants</b>	1 credit
	<ul style="list-style-type: none"><li>Spring 2021</li><li>Spring 2019</li><li>Spring 2017</li></ul>	

## Guest Lectures

Spring 2021	<b>PBGG Student Communication Seminar</b> (PBGG 8860)
Spring 2021	<b>PBGG Student Research Seminar</b> (PBGG 8861)
17 Sept 2020	<b>Genome-wide Association</b> (CRSS 8872)
24 May 2019	<b>Plant Breeding Practicum – Maize</b> (PBGG 6000)
20 & 27 Mar 2019	<b>Reproducibility in Research</b> (CTEGD Lunch & Learn)
13 Feb 2019	<b>Maize Domestication</b> (FYOS 1001)
6 Mar 2018	<b>Genome-wide Association</b> (CRSS 8820)

## Student Mentorship

### Chair (Current)

PhD 2020-present	<b>Talamantes, Darrian “Roy”</b>	UGA Institute of Bioinformatics
PhD 2019-present	<b>Corut, Kivanc</b>	UGA Institute of Bioinformatics
PhD 2019-present	<b>Li, Hanxia “Roy”</b>	UGA Institute of Bioinformatics
PhD 2019-present	<b>Schultz, Corey</b>	UGA Institute of Bioinformatics

### Chair (Prior)

MS 2022	<b>Griffis, Holly</b>	UGA Department of Genetics
MS 2021	<b>Rodman, Naomi</b>	UGA Department of Crop & Soil Sciences (incomplete)
PhD 2020	<b>Johnson, Matthew</b>	UGA Institute of Plant Breeding, Genetics, and Genomics
MS 2020	<b>Kovar, Lynsey</b>	UGA Institute of Bioinformatics

### Co-Chair (Prior)

PhD 2021	<b>Voghoei, Sahar</b>	UGA Department of Computer Science
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### Committee Member (Current)

PhD 2020-present	<b>Kwon, Kheeman</b>	UGA Department of Plant Pathology (Melissa Mitchum lab)
MS 2020-present	<b>Wang, Li</b>	UGA Department of Plant Pathology (Pingsheng Ji lab)
PhD 2019-present	<b>Bhattarai, Guarab</b>	UGA Institute of Plant Breeding, Genetics, and Genomics (Patrick Connor lab)
PhD 2019-present	<b>Fernandez-Canela, Josue</b>	UGA Department of Plant Biology (Jeff Bennetzen Lab)
MS 2019-present	<b>Meinecke, Colton</b>	UGA Warnell School of Forestry (Caterina Villari lab)
PhD 2019-present	<b>Miller, Mark</b>	UGA Institute of Plant Breeding, Genetics, and Genomics (Zenglu Li lab)
MS 2019-present	<b>Pathania, Sakshi</b>	UGA Department of Horticulture (Dario Chavez lab)
PhD 2019-present	<b>Piri, Rebecca</b>	UGA Institute of Bioinformatics (Kelly Dawe lab)
PhD 2019-present	<b>Singh, Lovepreet</b>	UGA Department of Crop & Soil Sciences (Andy Paterson lab)
PhD 2018-present	<b>Choi, Soyeon</b>	UGA Department of Genetics (Katrien Devos lab)
PhD 2018-present	<b>Liu, Jianing</b>	UGA Department of Genetics (Kelly Dawe lab)
PhD 2018-present	<b>Sapkota, Manoj</b>	UGA Institute of Plant Breeding, Genetics, and Genomics (Esther van der Knap lab)
PhD 2018-present	<b>Tran, Dung (“Ivy”)</b>	UGA Institute of Plant Breeding, Genetics, and Genomics (Zenglu Li lab)
PhD 2018-present	<b>Wright, Hallie</b>	UGA Institute of Plant Breeding, Genetics, and Genomics (Katrien Devos lab)
PhD 2017-present	<b>Adhikari, Jeevan</b>	UGA Plant Genome Mapping Laboratory (Andy Paterson lab)

### Committee Member (Prior)

MS 2020	<b>Conway, Tara</b>	UGA Plant Genome Mapping Laboratory (Andrew Paterson lab)
MS 2020	<b>Moore, Bryshal (“Bri”)</b>	Fort Valley State University Department of Plant Biotechnology (Som Punnuri lab)
PhD 2020	<b>Taitano, Nathan</b>	UGA Institute of Plant Breeding, Genetics, and Genomics (Esther van der Knaap lab)
PhD 2019	<b>Gimode, Davis</b>	UGA Institute of Plant Breeding, Genetics, and Genomics (Peggy Ozias-Akins lab)
PhD 2019	<b>Taborda, Carolina</b>	UGA Institute of Plant Breeding, Genetics, and Genomics (Scott Jackson lab)
PhD 2018	<b>Steketee, Clint</b>	UGA Institute of Plant Breeding, Genetics, and Genomics (Zenglu Li lab)
PhD 2018	<b>Sumabat, Leilani</b>	UGA Department of Plant Pathology (Marin Brewer lab)

## Visiting Scientists

Spring 2016	<b>Yuan, Yibing</b>	Graduate student	Sichuan Agricultural University, China
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## Undergraduate Mentoring

Summer 2016	<b>Sanford, Tierra</b>	Undergraduate field technician (UGA)
2016-2017	<b>Bagwell, John</b>	Undergraduate field technician (UGA)
Summer 2016;	<b>Rodriguez, David</b>	REU student (New Mexico State University)
2016-2019	<b>Giangacomo, Cecelia</b>	Undergraduate researcher (UGA)
2017	<b>Forester, Ethan</b>	Undergraduate field technician (UGA)
Summer 2017	<b>Mcdonald, Miles</b>	Undergraduate field technician (UGA)
Summer 2017	<b>Randolf, Hayden</b>	Undergraduate field technician (UGA)
Summer 2017	<b>Bejdic, Haris</b>	Undergraduate field technician (UGA)
Spring 2018	<b>Daftarian, Melody</b>	Undergraduate intern (Athens Technical College)
Summer 2018	<b>Morris, Samuel</b>	Undergraduate field technician (UGA)
Summer 2018	<b>Sangoyomi, Bamidele</b>	Undergraduate field technician (UGA)
Summer 2018	<b>Caro, Spencer</b>	Undergraduate field technician (UGA)
Summer 2018	<b>Andrews, Amaja</b>	REEU student & McNair scholar (UGA)
Fall 2018	<b>Leake, Jackson</b>	Undergraduate technician (UGA)
Fall 2018-present	<b>Fox, Laurel</b>	Undergraduate researcher (UGA)
Summer 2019	<b>Brantley, Kamaya</b>	REEU student (UGA)
Summer 2019	<b>Grindle, Coleman</b>	Undergraduate field technician (UGA)
Summer 2019	<b>McCabe, Allison</b>	Undergraduate field technician (UGA)
Summer 2020	<b>### TODO: Summer 2020 undergrads ###</b>	TODO HERE (UGA)
2019-present	<b>Wideman, Kya</b>	Undergraduate researcher (UGA)
2020-present	<b>Kirkpatrick, Caitlin</b>	Undergraduate researcher (UGA)

## High School Students

Spring 2018 **Weinmeister, Nathan** Clarke Central High School

## Scholarly Activities

### Publications

	Research Article	Review	Book Chapter
Associate Professor	5	0	0
Assistant Professor	16	2	1
Postdoc	1	1	0
PhD	3	0	0
<i>Total</i>	25	3	1

## Associate Professor (5)

- Wang, X., Chen, S., Ma, X., Yssel, A. E. J., Chaluvadi, S. R., Johnson, M. S., Gangashetty, P., Hamidou, F., Sanogo, M. D., Zwaenepoel, A., Wallace, J., Peer, Y. V. de, Bennetzen, J. L., & Deynze, A. V. (2021). Genome sequence and genetic diversity analysis of an under-domesticated orphan crop, white fonio (*digitaria exilis*). In *GigaScience* (Vol. 10, Issue 3). Oxford University Press (OUP). <https://doi.org/10.1093/gigascience/giab013>
- Giangacomo, C., Mohseni, M., Kovar, L., & Wallace, J. G. (2021). Comparing DNA extraction and 16S rRNA gene amplification methods for plant-associated bacterial communities. In *Phytobiomes Journal* (Vol. 5, Issue 2, pp. 190–201). Scientific Societies. <https://doi.org/10.1094/pbiomes-07-20-0055-r>
- Diepenbrock, C. H., Ilut, D. C., Magallanes-Lundback, M., Kandianis, C. B., Lipka, A. E., Bradbury, P. J., Holland, J. B., Hamilton, J. P., Wooldridge, E., Vaillancourt, B., Góngora-Castillo, E., Wallace, J. G., Cepela, J., Mateos-Hernandez, M., Owens, B. F., Tiede, T., Buckler, E. S., Rocheford, T., Buell, C. R., ... DellaPenna, D. (2020). Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. In *The Plant Cell* (Vol. 33, Issue 4, pp. 882–900). Oxford University Press (OUP). <https://doi.org/10.1093/plcell/koab032>
- McFarland, B. A., AlKhalifah, N., Bohn, M., Bubert, J., Buckler, E. S., Ciampitti, I., Edwards, J., Ertl, D., Gage, J. L., Falcon, C. M., Flint-Garcia, S., Gore, M. A., Graham, C., Hirsch, C. N., Holland, J. B., Hood, E., Hooker, D., Jarquin, D., Kaeppler, S. M., ... Leon, N. de. (2020). Maize genomes to fields (G2F): 2014/2017 field seasons: Genotype, phenotype, climatic, soil, and inbred ear image datasets. In *BMC Research Notes* (Vol. 13, Issue 1). Springer Science; Business Media LLC. <https://doi.org/10.1186/s13104-020-4922-8>

5. Kusmec, A., Yeh, C.-T. "Eddy", Fields Initiative, T. G. to, & Schnable, P. S. (2020). Data-driven identification of environmental variables influencing phenotypic plasticity to facilitate breeding for future climates: A case study involving grain yield of hybrid maize. In *SSRN Electronic Journal*. Elsevier BV. <https://doi.org/10.2139/ssrn.3684755>

#### Assistant Professor (19)

1. Johnson, M., Deshpande, S., Vetriventhan, M., Upadhyaya, H. D., & Wallace, J. G. (2019). Genome-wide population structure analyses of three minor millets: Kodo millet, little millet, and proso millet. In *The Plant Genome* (Vol. 12, Issue 3, p. 190021). Wiley. <https://doi.org/10.3835/plantgenome2019.03.0021>
2. Harris-Shultz, K. R., Davis, R. F., Wallace, J., Knoll, J. E., & Wang, H. (2019). A novel QTL for root-knot nematode resistance is identified from a south african sweet sorghum line. In *Phytopathology* (Vol. 109, Issue 6, pp. 1011–1017). Scientific Societies. <https://doi.org/10.1094/phyto-11-18-0433-r>
3. Wallace, J. G., & May, G. (2018). Endophytes: The other maize genome. In *Compendium of plant genomes* (pp. 213–246). Springer International Publishing. [https://doi.org/10.1007/978-3-319-97427-9\\_14](https://doi.org/10.1007/978-3-319-97427-9_14)
4. Walters, W. A., Jin, Z., Youngblut, N., Wallace, J. G., Sutter, J., Zhang, W., González-Peña, A., Peiffer, J., Koren, O., Shi, Q., Knight, R., Rio, T. G. del, Tringe, S. G., Buckler, E. S., Dangl, J. L., & Ley, R. E. (2018). Large-scale replicated field study of maize rhizosphere identifies heritable microbes. In *Proceedings of the National Academy of Sciences* (Vol. 115, Issue 28, pp. 7368–7373). Proceedings of the National Academy of Sciences. <https://doi.org/10.1073/pnas.1800918115>
5. Dawe, R. K., Lowry, E. G., Gent, J. I., Stitzer, M. C., Swentowsky, K. W., Higgins, D. M., Ross-Ibarra, J., Wallace, J. G., Kanizay, L. B., Alabady, M., Qiu, W., Tseng, K.-F., Wang, N., Gao, Z., Birchler, J. A., Harkess, A. E., Hodges, A. L., & Hiatt, E. N. (2018). A kinesin-14 motor activates neocentromeres to promote meiotic drive in maize. In *Cell* (Vol. 173, Issue 4, pp. 839–850.e18). Elsevier BV. <https://doi.org/10.1016/j.cell.2018.03.009>
6. Pucher, A., Hash, C. T., Wallace, J. G., Han, S., Leiser, W. L., & Haussmann, B. I. G. (2018). Mapping a male-fertility restoration locus for the A4 cytoplasmic-genic male-sterility system in pearl millet using a genotyping-by-sequencing-based linkage map. In *BMC Plant Biology* (Vol. 18, Issue 1). Springer Science; Business Media LLC. <https://doi.org/10.1186/s12870-018-1267-8>
7. Chandnani, R., Kim, C., Guo, H., Shehzad, T., Wallace, J. G., He, D., Zhang, Z., Patel, J. D., Adhikari, J., Khanal, S., & Paterson, A. H. (2018). Genetic analysis of gossypium fiber quality traits in reciprocal advanced backcross populations. In *The Plant Genome* (Vol. 11, Issue 1, p. 170057). Wiley. <https://doi.org/10.3835/plantgenome2017.06.0057>
8. Diepenbrock, C. H., Kandianis, C. B., Lipka, A. E., Magallanes-Lundback, M., Vaillancourt, B., Góngora-Castillo, E., Wallace, J. G., Cepela, J., Mesberg, A., Bradbury, P. J., Ilut, D. C., Mateos-Hernandez, M., Hamilton, J., Owens, B. F., Tiede, T., Buckler, E. S., Rocheford, T., Buell, C. R., Gore, M. A., & DellaPenna, D. (2017). Novel loci underlie natural variation in vitamin e levels in maize grain. In *The Plant Cell* (Vol. 29, Issue 10, pp. 2374–2392). Oxford University Press (OUP). <https://doi.org/10.1105/tpc.17.00475>
9. Varshney, R. K., Shi, C., Thudi, M., Mariac, C., Wallace, J., Qi, P., Zhang, H., Zhao, Y., Wang, X., Rathore, A., Srivastava, R. K., Chitikineni, A., Fan, G., Bajaj, P., Pununuri, S., Gupta, S. K., Wang, H., Jiang, Y., Couderc, M., ... Xu, X. (2017). Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. In *Nature Biotechnology* (Vol. 35, Issue 10, pp. 969–976). Springer Science; Business Media LLC. <https://doi.org/10.1038/nbt.3943>
10. Strable, J., Wallace, J. G., Unger-Wallace, E., Briggs, S., Bradbury, P. J., Buckler, E. S., & Vollbrecht, E. (2017). Maize YABBY genes drooping leaf1 and drooping leaf2 regulate plant architecture. In *The Plant Cell* (Vol. 29, Issue 7, pp. 1622–1641). Oxford University Press (OUP). <https://doi.org/10.1105/tpc.16.00477>
11. Wallace, J. G., & Mitchell, S. E. (2017). Genotyping-by-sequencing [Review of *Genotyping-by-sequencing*]. *Current Protocols in Plant Biology*, 2(1), 64–77. Wiley. <https://doi.org/10.1002/cppb.20042>
12. McCaw, M. E., Wallace, J. G., Albert, P. S., Buckler, E. S., & Birchler, J. A. (2016). Fast-flowering mini-maize: Seed to seed in 60 days. In *Genetics* (Vol. 204, Issue 1, pp. 35–42). Oxford University Press (OUP). <https://doi.org/10.1534/genetics.116.191726>
13. Wallace, J. G., Zhang, X., Beyene, Y., Semagn, K., Olsen, M., Prasanna, B. M., & Buckler, E. S. (2016). Genome-wide association for plant height and flowering time across 15 tropical maize populations under managed drought stress and well-watered conditions in sub-saharan africa. In *Crop Science* (Vol. 56, Issue 5, pp. 2365–2378). Wiley. <https://doi.org/10.2135/cropsci2015.10.0632>
14. Pununuri, S. M., Wallace, J. G., Knoll, J. E., Hyma, K. E., Mitchell, S. E., Buckler, E. S., Varshney, R. K., & Singh, B. P. (2016). Development of a high-density linkage map and tagging leaf spot resistance in pearl millet using genotyping-by-sequencing markers. In *The Plant Genome* (Vol. 9, Issue 2). Wiley. <https://doi.org/10.3835/plantgenome2015.10.0106>

15. Upadhyaya, H. D., Vetriventhan, M., Deshpande, S. P., Sivasubramani, S., Wallace, J. G., Buckler, E. S., Hash, C. T., & Ramu, P. (2015). Population genetics and structure of a global foxtail millet germplasm collection. In *The Plant Genome* (Vol. 8, Issue 3). Wiley. <https://doi.org/10.3835/plantgenome2015.07.0054>
16. Zhang, N., Gibon, Y., Wallace, J. G., Lepak, N., Li, P., Dedow, L., Chen, C., So, Y.-S., Kremling, K., Bradbury, P. J., Brutnell, T., Stitt, M., & Buckler, E. S. (2015). Genome-wide association of carbon and nitrogen metabolism in the maize nested association mapping population. In *Plant Physiology* (Vol. 168, Issue 2, pp. 575–583). Oxford University Press (OUP). <https://doi.org/10.1104/pp.15.00025>
17. Wallace, J. G., Upadhyaya, H. D., Vetriventhan, M., Buckler, E. S., Hash, C. T., & Ramu, P. (2015). The genetic makeup of a global barnyard millet germplasm collection. In *The Plant Genome* (Vol. 8, Issue 1). Wiley. <https://doi.org/10.3835/plantgenome2014.10.0067>

### Postdoc (2)

1. Wallace, J. G., Bradbury, P. J., Zhang, N., Gibon, Y., Stitt, M., & Buckler, E. S. (2014). Association mapping across numerous traits reveals patterns of functional variation in maize. In J. O. Borevitz (Ed.), *PLoS Genetics* (Vol. 10, Issue 12, p. e1004845). Public Library of Science (PLOS). <https://doi.org/10.1371/journal.pgen.1004845>
2. Wallace, J. G., Larsson, S. J., & Buckler, E. S. (2013). Entering the second century of maize quantitative genetics [Review of *Entering the second century of maize quantitative genetics*]. *Heredity*, 112(1), 30–38. Springer Science; Business Media LLC. <https://doi.org/10.1038/hdy.2013.6>

### PhD (3)

1. Wallace, J. G., Zhou, Z., & Breaker, R. R. (2012). OLE RNA protects extremophilic bacteria from alcohol toxicity. In *Nucleic Acids Research* (Vol. 40, Issue 14, pp. 6898–6907). Oxford University Press (OUP). <https://doi.org/10.1093/nar/gks352>
2. Wallace, J. G., & Breaker, R. R. (2011). Improved genetic transformation methods for the model alkaliphile *Bacillus halodurans* c-125. In *Letters in Applied Microbiology* (Vol. 52, Issue 4, pp. 430–432). Wiley. <https://doi.org/10.1111/j.1472-765x.2011.03017.x>
3. Block, K. F., Puerta-Fernandez, E., Wallace, J. G., & Breaker, R. R. (2010). Association of OLE RNA with bacterial membranes via an RNA-protein interaction. In *Molecular Microbiology* (Vol. 79, Issue 1, pp. 21–34). Wiley. <https://doi.org/10.1111/j.1365-2958.2010.07439.x>

### Invited Presentations (\* = international)

- |             |                                                                                                                                                                                  |
|-------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 11 Nov 2019 | <b>Unraveling the Mechanisms of Microbe-Induced Abiotic Stress tolerance in Plants.</b> Crop Science Society of America annual meeting (San Antonio, Texas).                     |
| 22 Jul 2019 | <b>Harnessing microbes to improve agriculture.</b> Noble Research Institute seminar (Ardmore, Oklahoma).                                                                         |
| 16 Jan 2019 | <b>Genomics of Crop-Microbiome interactions.</b> Plant & Animal Genome XXVII (San Diego, California).                                                                            |
| 06 Nov 2018 | <b>*La Microbiome del Maíz.</b> UNITEC Universidad Tecnológica de México – Campus León Seminar Series (Guanajuato, Mexico (via webinar)).                                        |
| 12 Oct 2018 | <b>Harnessing Plant Microbiomes for Agriculture.</b> University of Kentucky Department of Plant & Soil Sciences Seminar Series (Lexington, Kentucky).                            |
| 23 Jul 2018 | <b>*Quantitative Genetics of the Maize Microbiome.</b> Chinese Agriculture University – University of Georgia collaboration conference (Beijing, China).                         |
| 22 Mar 2018 | <b>*The Maize Microbiome.</b> MaizeGDB workshop in conjunction with the 60th Annual Maize Genetics Conference (Saint Malo, France).                                              |
| 04 Dec 2017 | <b>The Maize Microbiome as a Target for Breeding and Management.</b> Annual Corn Breeder's Research Meeting (Chicago, Illinois).                                                 |
| 23 Oct 2017 | <b>The effect of host genetics on maize-microbiome interaction.</b> ASA-CSSA-SSSA Annual Meeting (Tampa, Florida).                                                               |
| 18 Jul 2017 | <b>Harnessing Fungi to Improve Agriculture.</b> Mycological Society of America (Athens, Georgia).                                                                                |
| 09 Mar 2017 | <b>Unraveling the Genetics of Maize-Microbiome Interactions.</b> NewLeaf Symbiotics invited presentation (Saint Louis, Missouri).                                                |
| 14 Jan 2017 | <b>Exploring the other maize genome: Quantitative analysis of how maize plants interact with their microbial communities.</b> Plant & Animal Genome XXV (San Diego, California). |
| 16 Aug 2016 | <b>*Nested Association Mapping for QTL Discovery and Genome-Wide Association.</b> 7th International Crop Science Congress (Beijing, China).                                      |
| 26 Apr 2016 | <b>*Genotyping by Sequencing (GBS) Method Overview.</b> West African Center for Crop Improvement seminar series (Accra, Ghana).                                                  |
| 25 Apr 2016 | <b>*Leveraging Genomics to Improve Staple Crops.</b> West African Center for Crop Improvement seminar series (Accra, Ghana).                                                     |
| 22 Apr 2016 | <b>*Genotyping by Sequencing (GBS) Method Overview.</b> BMZ Heterosis Project Meeting & Training (Niamey, Niger).                                                                |

- 22 Apr 2016 **\*TASSEL/GBS Practical Examples.** BMZ Heterosis Project Meeting & Training (Niamey, Niger).
- 20 Mar 2016 **The effect of host genetics on the maize leaf microbiome across 270 diverse inbred lines.** 58th Annual Maize Genetics Conference (Jacksonville, Florida).
- 13 Jan 2016 **Analyzing the Leaf Microbiome across 270 Diverse Maize Lines.** Plant & Animal Genome XXIV (San Diego, California).
- 30 Oct 2015 **Leveraging Genomics to Improve Staple Crops.** UGA Plant Center Retreat (Helen, Georgia).
- 30 Jun 2015 **Analyzing the Leaf Microbiome across 270 Diverse Maize Lines.** Phytobiomes 2015 (Washington, D.C.).
- 19 Feb 2015 **\*Applying High-Throughput Genomics to Crops for the Developing World.** Next Generation Genomics and Integrated Breeding for Crop Improvement (Hyderabad, India).
- 13 Feb 2015 **\*Leveraging Genomics to Improve Staple Crops.** International Crops Research Institute for the Semi-Arid Tropics invited speaker (Hyderabad, India).

**TODO Posters & Abstracts****TODO: Other Creative Contributions****Research Grants****TODO: Grants (inc. summary table)****TODO: Professional Development****TODO: Academic Service****TODO: University Service****TODO: Service to the wider field (rename)****TODO: Public Outreach and Service****Other****TODO: Meetings attended****TODO: Society memberships****TODO: Major Accomplishments**