

Jason G. Wallace

Associate Professor

Curriculum Vitae

March 2022

Department of Crop & Soil Sciences, University of Georgia
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Academic History

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

Education

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

Professional Experience

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

Awards

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

Instruction

Instructor of Record

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

Guest Lectures

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

Student Mentorship

Chair (Current)

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

Chair (Prior)

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

Co-Chair (Prior)

PhD 2021	Voghoei, Sahar	UGA Department of Computer Science
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Committee Member (Current)

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

Committee Member (Prior)

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

Visiting Scientists

Spring 2016	Yuan, Yibing	Graduate student	Sichuan Agricultural University, China
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Undergraduate Mentoring

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

Assistant Professor (23)

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

- 22 Apr 2016 ***Genotyping by Sequencing (GBS) Method Overview.** 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).

Posters & Abstracts

Assistant Professor (14)

- 05 Sep 2019 Wallace, J. G. and Young, C. A **We are using Tall Fescue to understand how plants work with beneficial microbes.** Plant Genome Research Program 22nd Annual Awardee Meeting (Washington, D.C.).
- 05 Sep 2019 Parrott, W. A. and Wallace, J. G. **The small Bladderwort genome is a promising source of regulatory elements for genetic engineering.** Plant Genome Research Program 22nd Annual Awardee Meeting (Washington, D.C.).
- 13 May 2019 Johnson, M., Coolong, T., & Wallace, J. G. **Bringing Hemp to Georgia: A project to Develop Hemp Varieties for Georgia.** UGA Institute of Plant Breeding, Genetics & Genomics annual retreat (Amicalola Falls, Georgia).
- 26 Sep 2018 Kovar, L., & Wallace, J. G. **Leaf microbiome community structure, co-abundance analysis, and correlation with phenotype across 270 diverse maize lines.** UGA Plant Center Retreat (Helen, Georgia).
- 06 Sep 2018 Wallace, J. G. and Young, C. A. **ECA-PGR: Identifying Host Factors that Influence the Association of Tall Fescue (*Festuca arundinacea*) with beneficial *Epichloë* endophytes.** Plant Genome Research Program 21st Annual Awardee Meeting (Washington, D.C.).
- 06 Sep 2018 Parrott, W. A. and Wallace, J. G. **TRANSFORM-PGR: Mining the compact *Utricularia* genome as source of novel regulatory elements for crop biotechnology.** Plant Genome Research Program 21st Annual Awardee Meeting (Washington, D.C.).
- 20 Jun 2018 Wallace, J. G., Kremling, KA, Chen, SY, Su, MH, Pardo, J, Lepak, NK, Budka, JS, Buckler, ES. **The Effect of Host and Environment on the Maize microbiome.** 21st Annual Penn State Plant Biology Symposium: Wild and Tame Phytobiomes (State College, PA).
- 10 May 2018 Kovar, L., & Wallace, J. G. (2018). **Untangling bacterial interactions in the maize leaf microbiome - A co-abundance network approach.** UGA Institute of Plant Breeding, Genetics & Genomics annual retreat (Pine Mountain, Georgia).
- 22 Mar 2018 *Wallace, J. G., Kremling, KA, Chen, SY, Su, MH, Pardo, J, Lepak, NK, Budka, JS, Buckler, ES. **The Effect of Host and Environment on the Maize microbiome.** 60th Annual Maize Genetics Conference (Saint-Malo, France).
- 26 Oct 2017 Johnson, M., Rodriguez, D., Upadhyaya, H., Wallace, J.G. **First Population Genetic Analysis of Three Minor Millets.** UGA Plant Center Retreat (Helen, Georgia).
- 10 Mar 2017 Wallace, J. G., Kremling, KA, Chen, SY, Su, MH, Pardo, J, Lepak, NK, Budka, JS, Buckler, ES. **Quantitative Analysis of the Maize Leaf Microbiome.** 59th Annual Maize Genetics Conference (St. Louis, Missouri).
- 10 Jan 2017 Wallace, J. G., Kremling, K. A., Chen, S. -Y., Su, M. -H., Pardo, J. D., Lepak, N. K., ... Buckler, E. S. **Analyzing the Leaf Microbiome across 270 Diverse Maize Lines.** Plant and Animal Genome XXIV (San Diego, California).
- 01 Nov 2016 Wallace, J. G., Kremling, KA, Chen, SY, Su, MH, Pardo, J, Lepak, NK, Budka, JS, Buckler, ES. **The Effect of Host Genetics on the Maize Leaf Microbiome across 270 Diverse Inbred Lines.** Phytobiomes: From Microbes to Plant Ecosystems (Santa Fe, New Mexico).
- 01 Mar 2015 Wallace, J. G., Beyene, Y., Semagn, K., Zhang, X., & Buckler, E. S. **Combined mapping of height and flowering time across 15 biparental populations using both traditional and Bayesian association mapping.** 57th Annual Maize Genetics Conference (St. Charles, Illinois).

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