

CURRICULUM VITAE

JAMES C. SCHNABLE

Quantitative Life Sciences Initiative
Center for Plant Science Innovation
Department of Agronomy & Horticulture
University of Nebraska-Lincoln

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^aClickable hyperlinks are in blue throughout

Employment

University of Nebraska-Lincoln	
Professor, Department of Agronomy and Horticulture	2022-Present
Nebraska Corn Checkoff Presidential Chair	2023-Present
Charles O. Gardner Professor of Agronomy	2019-2023
Associate Professor, Department of Agronomy and Horticulture	2019-2022
Assistant Professor, Department of Agronomy and Horticulture	2014-2019
X, Google, Alphabet	
(<i>Interim</i>) Technology Lead (L7)	2022
Danforth Plant Science Center & Chinese Academy of Agricultural Sciences	
NSF PGRP Fellowship Supported Visiting Scholar	2013-2014

Education

PhD Plant Biology	2008-2012
University of California-Berkeley	
BA Biology	2004-2008
Cornell University	

Selected Honors and Awards

Outstanding Postdoc Mentor	2024
University of Nebraska-Lincoln	
Fellow	2023
Nebraska Center for Entrepreneurship	
Fellow	2022
PhenoRob	
Outstanding Paper of the Year	2020
The Plant Phenome Journal	
Early Career Award	2019
American Society of Plant Biologists	
Plant Phenotyping Early Career Award	2019
North American Plant Phenotyping Network	

Outstanding Scientific Article Award International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	2018
Marcus Rhoades Early Career Award Maize Genetics Community	2018
Tansley Medal Finalist New Phytologist Trust	2018
Junior Faculty Excellence in Research Award University of Nebraska-Lincoln	2016

Research Support

\$29.6M in total federal funding as PI/co-PI 2015-Present
(Excludes \$20M NSF Center for Root and Rhizobiome Innovation award (2016) and \$20M NSF AI Institute for Resilient Agriculture award (2021).)

Federal (Current)

- NSF "RESEARCH-PGR: Cycling to low-temperature tolerance." (co-PI) 2024-2027 \$1.8M
- USDA-NIFA "Improving Causal Gene Detection across Crop and Livestock Species." (co-PI) 2023-2026. \$1.3M
- DOE "Phenotypic and Molecular Characterization of Nitrogen Responsive Genes in Sorghum." (co-PI) 2022-2025. \$2.7M
- DOE "TGCM: (T)rait, (G)ene, and (C)rop Growth (M)odel directed targeted gene characterization in sorghum." (PI) 2019-2024. \$2.7M
- NSF "BTT EAGER: A wearable plant sensor for real-time monitoring of sap flow and stem diameter to accelerate breeding for water use efficiency." (PI) 2019-2024. \$300k
- USDA-NIFA "High Intensity Phenotyping Sites: Transitioning To A Nationwide Plant Phenotyping Network." (co-PI) 2020-2024. \$3M
- USDA-NIFA "High Intensity Phenotyping Sites: A multi-scale, multi-modal sensing and sense-making cyber-ecosystem for Genomes to Fields." (co-PI) 2020-2024. \$2.7M
- NSF "RII Track-2 FEC: Functional analysis of nitrogen responsive networks in Sorghum." (co-PI) 2018-2024. \$4M
- FFAR "Crops in silico: Increasing crop production by connecting models from the microscale to the macroscale." (co-PI) 2019-2024. \$5M
- NSF "AI Institute for Resilient Agriculture" (Investigator) 2021-2026 \$20M

Non-Federal (Current)

- University of Nebraska "SPACE2: Space, Policy, Agriculture, Climate, and Extreme Environment." (co-PI) 2022-2024 \$150k.
- Nebraska Corn Board "Genomes to Fields (G2F) - Predicting Final Yield Performance in Variable Environments." (PI) 2016-2024. \$350k (to date)

Completed Projects

USDA-NIFA "CPS: Medium: Field-scale, single plant-resolution agricultural management using coupled molecular and macro sensing and multi-scale data fusion and modeling" (co-PI) (2020-2023) \$1.05M

ARPA-E "Soil Organic Carbon Networked Measurement System (SOCNET)" (co-PI) 2020-2023 \$1.9M

Wheat Innovation Foundation "A Low-Cost, High-Throughput Cold Stress Perception Assay for Sorghum Breeding." (co-PI) 2019-2023. \$205k

ICRISAT "Identifying Novel Loci Controlling Priority Traits in Pearl Millet and Sorghum using Supervised Classification Algorithms." (PI) 2020-2021 \$50k

ARPA-E "CORN- Crop Optimization Realized through Neuralnets" (co-PI) 2020-2022 \$620k

ARPA-E "Low cost wireless chemical sensor networks." (co-PI) 2019-2022. \$2.2M

NSF "Center for Root and Rhizobiome Innovation." (Investigator & Management Team Member) 2016-2021. \$20M

NSF "RoL: FELS: EAGER: Genetic constraints on the increase of organismal complexity over time." (PI) 2018-2022. \$300k

USDA-NIFA "Identifying mechanisms conferring low temperature tolerance in maize, sorghum, and frost tolerant relatives." (PI) 2015-2020. \$455k

ARPA-E "In-plant and in-soil microsensors enabled high-throughput phenotyping of root nitrogen uptake and nitrogen use efficiency." (co-PI) 2017-2019. \$1.1M

USDA/NSF Joint Program "PAPM EAGER: Transitioning to the next generation plant phenotyping robots." (co-PI) 2016-2018. \$285k

North Central Sun Grants "High through put phenotyping to accelerate biomass sorghum improvement." (co-PI) 2017-2019. \$193k

Daugherty Water for Food Global Institute "Optimizing the Water Use Efficiency of C₄ Grain Crops Using Comparative Phenomics and Crop Models to Guide Breeding Targets." (PI) 2017-2019. \$27k

Agricultural Research Division "A High Throughput Phenotyping Reference Dataset for GWAS in Sorghum" (PI) 2016-2018. \$100k

ICRISAT "Application of tGBS And Genomic Selection to a Hybrid Pearl Millet Breeding Program." 2015-2017. \$45k

ConAgra "Marker Discovery & Genetic Diversity." (replacement PI) 2014-2017. \$162k

Iowa Corn Board "Field Deployable Cameras to Quantify Dynamic Whole Plant Phenotypes in the Field." (PI) 2014-2016. \$43k

Midwest Big Data Hub "Automatic feature extraction pipeline development for high-throughput plant phenotyping" (co-PI) 2017-2018. \$5k

Layman Award "Developing genomic tools in proso millet and comparing water use efficiency among panicoid grass crops (proso millet, corn, sorghum, foxtail millet)" (co-PI) 2014-2015. \$10k

Economic Development

Entrepreneurship

Co-Founder, [EnGeniousAg LLC](#) 2017-Present
Designs, manufactures, and deploys low-cost, instant readout, high-performance, field-based nutrient sensors for crops, soil, and water, improving agronomic management practices, increasing grower profitability and reducing the environmental footprint of agriculture.

Founder, [Dryland Genetics LLC](#) 2014-Present
Using high throughput quantitative genetics and field phenotyping technologies to develop and commercialize higher yielding cultivars of crops already naturally adapted to using little water and growing arid regions where conventional agriculture fails in the absence of irrigation.

Co-Founder, [Data2Bio LLC](#) 2010-Present
Providing patented tGBS genotyping and genomic selection services to public and private sector plant and animal breeders in the USA and China.

Entrepreneurship-Related Funding

NSF (to EnGeniousAg) "SBIR Phase II: Low-cost in-planta nitrate sensor" 2023-2025 \$1M

NSF (to EnGeniousAg) "SBIR Phase I: Low-cost in-planta nitrate sensor" 2019-2022 \$225k

USDA (to EnGeniousAg) "SBIR Phase I: Low-cost field-deployable sensors to monitor nitrate in soil and water." 2019-2021 \$100k

Raised more than \$7M in private sector equity funding.

Industry Cooperation

Scientific Advisory Council, GeneSeek, Inc 2017-Present

Advisor, DeepCropVision (UNL student lead-startup) 2022-Present

Advisory Board, Afflo Sensors 2023-Present

External Advisor to the Scientific Advisory Board, Indigo Agriculture 2017

External Advisor to the Scientific Advisory Board, Syngenta AG 2016

Mentoring

Current Postdoctoral Mentees: Vladimir Torres-Rodriguez

Former Postdoctoral Mentees: Ravi Mural (Assistant Professor, SDSU), Marcin Grzybowski (Assistant Professor, University of Warsaw), Deniz Istipliler (Assistant Professor, Ege University), Guangchao Sun (Professor, Sichuan Agricultural University), Xiaoxi "Peggy" Meng (Bioinformatics Scientist, St. Jude Children's Hospital), Ranjita Thapa (Computational Biologist, Inari), Sunil KK Raju (Postdoctoral Scholar, NYU), Lang Yan (Professor, XiChang College), Yang Zhang (Bioinformatics Scientist, St. Jude Children's Research Hospital)

Current Graduate Advisees: Michael Tross (PhD, Complex Biosystems, UNL Life Sciences Fellow), Nikee Shrestha (PhD, Complex Biosystems, FFAR Career Development Fellow), Waqar Ali (PhD, Complex Biosystems, US-Pakistan Knowledge Corridor Scholar), Jensina Davis (PhD, Complex Biostems, NSF Grad Fellow) Hongyu Jin (co-advised, PhD, Complex Biosystems), Fangyi Li (co-advised, PhD, Complex Biosystems), Ramesh Kanna Mathivanan (MS, Plant Breeding and Genetics), Harshita Man-gal (MS, Plant Breeding and Genetics)

Graduated Advisees: Daniel Carvalho (PhD, Agronomy & Horticulture), Zhikai Liang (PhD, Agronomy & Horticulture), Chenyong Miao (PhD, Agronomy & Horticulture, Widaman Fellow), Nate Korth (co-advised, PhD, Food Science, FFAR Fellow), Preston Hurst (MS, Agronomy & Horticulture), Xi-anjun Lai (PhD, Sichuan Agriculture University), Xiuru Dai (PhD, Shandong Agriculture University), Santos Yenandy Barrera Lemus (co-advised, PhD, Agronomy & Horticulture) Mackenzie Zweiner (MS, Agronomy & Horticulture), Kyle Linders (co-advised MS, Agronomy & Horticulture) Bhushit Agarwal (co-advised, MS, Computer Science & Engineering), Srinidhi Bashyam (co-advised, MS, Computer Science & Engineering)

Undergraduate Researchers: 8 NSF supported REU (Research Experience for Undergraduates) students; 2 USDA supported REEU (Research and Extension Experience for Undergraduates) students; 3 UCARE (Undergraduate Creative Activities and Research Experience) students; and 51 undergraduate students supported by regular research funding.

High School Researchers: 2 students supported through the Young Nebraska Scientist program; 1 supported by regular research funding.

Publications

H-Index: 48

Lab members in **bold**, *authors contributed equally, †undergraduate author, §corresponding author

Preprints

Sahay S, **Shrestha N**, **Moura Dias H**, **Mural RV**, **Grzybowski M**, **Schnable JC**[§], Glowacka K[§] Comparative GWAS identifies a role for Mendel's green pea gene in the nonphotochemical quenching kinetics of sorghum, maize, and arabidopsis. *BIORxiv* doi: [10.1101/2023.08.29.555201](https://doi.org/10.1101/2023.08.29.555201)

Wang X, Hatasaka B, Liu Z, Tope S, Mohit K, Noh S, Sium F, **Mural RV**, Kim H, Mastrangelo C, Zang L, **Schnable JC**, Ji M. SPARC-LoRa: A scalable, power-efficient, affordable, reliable, and cloud service-enabled LoRa networking system for agriculture applications. *ARXIV* doi: [10.48550/arXiv.2401.13569](https://doi.org/10.48550/arXiv.2401.13569)

Engelhorn J, Snodgrass S, Kok A, Seetharam A, Schneider M, Kiwit T, Singh A, Banf M, Khaiphoburch M, Runcie D, Camargo V, **Torres-Rodriguez JV**, **Sun G**, Stam M, Fiorani F, **Schnable JC**, Bass H, Hufford M, Stich B, Frommer W, Ross-Ibarra J, Hartwig T[§] Phenotypic variation in maize can be largely explained by genetic variation at transcription factor binding sites. *BIORxiv* doi: [10.1101/2023.08.08.551183](https://doi.org/10.1101/2023.08.08.551183)

Li D, Wang Q, Tian Y, Lyu X, Zhang H, Sun Y, Hong H, Gao H, Li Y, Zhao C, Wang J, Wang R, Yang J, Liu B, Schnable PS, **Schnable JC**[§], Li Y[§], Qiu L[§] Transcriptome brings variations of gene expression, alternative splicing, and structural variations into gene-scale trait dissection in soybean. *BIORxiv* doi: [10.1101/2023.07.03.545230](https://doi.org/10.1101/2023.07.03.545230)

Faculty Publications

140. **Tross MC**, **Grzybowski M**, Jubery TZ, **Grove RJ**[†], **Nishimwe AV**[†], **Torres-Rodriguez JV**, **Sun G**, Ganapathysubramanian B, Ge Y, **Schnable JC**[§] (2024) Data driven discovery and quantification of hyperspectral leaf reflectance phenotypes across a maize diversity panel. *THE PLANT PHENOME JOURNAL* (Accepted) *BIORxiv* doi: [10.1101/2023.12.15.571950](https://doi.org/10.1101/2023.12.15.571950)
139. **Torres-Rodriguez JV**, Li D, **Turkus J**, Newton L, **Davis J**, **Lopez-Corona L**, **Ali W**, **Sun G**, **Mural RV**, **Grzybowski M**, Zamft B, Thompson AM, **Schnable JC**[§] (2024) Population level gene expression can repeatedly link genes to functions in maize. *THE PLANT JOURNAL* Accepted *BIORxiv* doi: [10.1101/2023.10.31.565032](https://doi.org/10.1101/2023.10.31.565032)

138. **Jin H, Tross MC, Tan R, Newton L, Mural RV, Yang J, Thompson AM, Schnable JC[§]** (2024) Imitating the “breeder’s eye”: predicting grain yield from measurements of non-yield traits. *THE PLANT PHENOME JOURNAL* doi: [10.1002/ppj2.20102](https://doi.org/10.1002/ppj2.20102)
137. Sahay S, **Grzybowski M, Schnable JC**, Glowacka K[§] (2024) Genotype-specific nonphotochemical quenching responses to nitrogen deficit are linked to chlorophyll a to b ratios. *JOURNAL OF PLANT PHYSIOLOGY* doi: [10.1016/j.jplph.2024.154261](https://doi.org/10.1016/j.jplph.2024.154261)
136. Zarei A[§], Li B, **Schnable JC**, Lyons E, Pauli D, Benes B, Barnard K (2024) PlantSegNet: 3D point cloud instance segmentation of nearby plant organs with identical semantics. *COMPUTERS AND ELECTRONICS IN AGRICULTURE* doi: [10.1016/j.compag.2024.108922](https://doi.org/10.1016/j.compag.2024.108922)
135. Rodene E, Fernando GD, Piyush V, Ge Y, **Schnable JC**, Ghosh S, Yang J[§] (2024) Image filtering to improve maize tassel detection accuracy using machine learning algorithms. *SENSORS* doi: [10.3390/s24072172](https://doi.org/10.3390/s24072172)
134. **Sun G, Yu H, Wang P, Lopez-Guerrero MG, Mural RV, Mizero ON[†], Grzybowski M, Song B, van Dijk K, Schachtman DP, Zhang C, Schnable JC[§]** (2023) A role for heritable transcriptomic variation in maize adaptation to temperate environments. *GENOME BIOLOGY* doi: [10.1186/s13059-023-02891-3](https://doi.org/10.1186/s13059-023-02891-3) *Selected as an Editor’s Choice by MaizeGDB Editorial Board* August 2023
133. **Grzybowski M[§], Mural RV, Xu G, Turkus, J, Yang Jinliang, Schnable JC** (2023) A common resequencing-based genetic marker dataset for global maize diversity. *THE PLANT JOURNAL* doi: [10.1111/tpj.16123](https://doi.org/10.1111/tpj.16123) *Cover Article, March 2023 “Research Highlight”* doi: [10.1111/tpj.16123](https://doi.org/10.1111/tpj.16123) *Selected as an Editor’s Choice by MaizeGDB Editorial Board* December 2023
132. Sahay S*, **Grzybowski M*, Schnable JC**, Glowacka K[§] (2023) Genetic control of photoprotection and photosystem II operating efficiency in plants. *NEW PHYTOLOGIST* doi: [10.1111/nph.18980](https://doi.org/10.1111/nph.18980)
131. **Sun G, Wase N, Shu S, Jenkins J, Zhou B, Chen C, Sandor L, Plott C, Yoshinga Y, Daum C, Qi P, Barry K, Lipzen A, Berry L, Gottilla T, Foltz A[†], Yu H, O’Malley R, Zhang C, Devos KM, Sigmon B, Yu B, Obata T, Schmutz J[§], Schnable JC[§]** (2023) Genome of *Paspalum vaginatum* and the role of trehalose mediated autophagy in increasing maize biomass. *NATURE COMMUNICATIONS* doi: [10.1038/s41467-022-35507-8](https://doi.org/10.1038/s41467-022-35507-8) *BIORxIV* doi: [10.1101/2021.08.18.456832](https://doi.org/10.1101/2021.08.18.456832) *“Research Highlight” in Nature Plants* doi: [10.1038/s41477-023-01343-x](https://doi.org/10.1038/s41477-023-01343-x)
130. DiMario R, Kophs A, Apalla A, **Schnable JS**, Cousins A[§] (2023) Multiple highly expressed phosphoenolpyruvate carboxylase genes have divergent enzyme kinetic properties in two C₄ grasses. *ANNALS OF BOTANY* doi: [10.1093/aob/mcad116](https://doi.org/10.1093/aob/mcad116)
129. Barnes AC, Myers JL, Surber SM, **Liang Z**, Mower JP, **Schnable JC**, Roston RL[§] (2023) Oligogalactolipid production during cold challenge is conserved in early diverging lineages. *JOURNAL OF EXPERIMENTAL BOTANY* doi: [10.1093/jxb/erad241](https://doi.org/10.1093/jxb/erad241)
128. Chen J, Wang Z, Tan K, Huang W, Shi J, Li T, Hu J, Wang K, Xin B, Zhao H, Song W, Hufford MB, **Schnable JC**, Ware DH, Jin W, Lai J[§] (2023) A complete telomere-to-telomere assembly of the maize genome. *NATURE GENETICS* doi: [10.1038/s41588-023-01419-6](https://doi.org/10.1038/s41588-023-01419-6) *Selected as an Editor’s Choice by MaizeGDB Editorial Board* August 2023
127. Kick D, Wallace J, **Schnable JC**, Kolkman JM, Alaca B, Beissinger TM, Ertl D, Flint-Garcia S, Gage JL, Hirsch CN, Knoll JE, de Leon N, Lima DC, Moreta D, Singh MP, Weldekidan T, Washburn JD[§] Yield prediction through integration of genetic, environment, and management data through deep learning. *G3* doi: [10.1093/g3journal/jkad006](https://doi.org/10.1093/g3journal/jkad006) *BIORxIV* doi: [10.1101/2022.07.29.502051](https://doi.org/10.1101/2022.07.29.502051)
126. Lima DC[§], Aviles AC, Alpers RT ... **Schnable JC** (26th of 37 authors) ... Wisser RJ, Xu W, de Leon N (2023) 2018–2019 field seasons of the Maize Genomes to Fields (G2F) G x E project. *BMC GENOMIC DATA* doi: [10.1186/s12863-023-01129-2](https://doi.org/10.1186/s12863-023-01129-2)

125. Wijewardane NK, Zhang H, Yang J, **Schnable JC**, Schachtman DP, Ge Y^S (2023) A leaf-level spectral library to support high throughput plant phenotyping: Predictive accuracy and model transfer. *JOURNAL OF EXPERIMENTAL BOTANY* doi: [10.1093/jxb/erad129](https://doi.org/10.1093/jxb/erad129)
124. Lima DC, Aviles AC, Alpers RT ... **Schnable JC** (24th of 35 authors) ... Weldekidan T, Xu W, de Leon N^S (2023) 2020-2021 field seasons of Maize GxE project within the Genomes to Fields Initiative. *BMC RESEARCH NOTES* doi: [10.1186/s13104-023-06430-y](https://doi.org/10.1186/s13104-023-06430-y)
123. Gaillard M, Benes B, **Tross MC**, **Schnable JC** (2023) Multi-view triangulation without correspondences. *COMPUTERS AND ELECTRONICS IN AGRICULTURE* doi: [10.1016/j.compag.2023.107688](https://doi.org/10.1016/j.compag.2023.107688)
122. **Grzybowski M^S**, **Zweiner M**, **Jin H**, Wijewardane NK, Atefi A, Naldrett MJ, Alvarez S, Ge Y, **Schnable JC** (2022) Variation in morpho-physiological and metabolic responses to low nitrogen stress across the sorghum association panel. *BMC PLANT BIOLOGY* doi: [10.1186/s12870-022-03823-2](https://doi.org/10.1186/s12870-022-03823-2) *BIORxIV* doi: [10.1101/2022.06.08.495271](https://doi.org/10.1101/2022.06.08.495271)
121. Yang Q, Van Haute M, **Korth N**, Sattler S, Toy J, Rose D, **Schnable JC**, Benson A (2022) Genetic analysis of seed traits in Sorghum bicolor that affect the human gut microbiome. *NATURE COMMUNICATIONS* doi: [10.1038/s41467-022-33419-1](https://doi.org/10.1038/s41467-022-33419-1)
"In Brief" in *Nature Reviews Genetics* doi: [10.1038/s41576-022-00543-z](https://doi.org/10.1038/s41576-022-00543-z)
"Genome Watch" in *Nature Reviews Microbiology* doi: [10.1038/s41579-022-00850-6](https://doi.org/10.1038/s41579-022-00850-6)
120. Li D, Bai D, Tian Y, Li Y, Zhao C, Wang Q, Gou S, Gu Y, Luan X, Wang R, Yang J, Hawkesford MJ, **Schnable JC**, Jin X, Qiu L (2022) Time series canopy phenotyping enables the identification of genetic variants controlling dynamic phenotypes in soybean. *JOURNAL OF INTEGRATIVE PLANT BIOLOGY* doi: [10.1111/jipb.13380](https://doi.org/10.1111/jipb.13380)
119. Khound R, **Sun G**, **Mural RV**, **Schnable JC**, Santra D^S (2022) SNP Discovery in Proso millet (*Panicum miliaceum* L.) using low-pass genome sequencing. *PLANT DIRECT* doi: [10.1002/pld3.447](https://doi.org/10.1002/pld3.447)
118. Zhang K, Yang Y, Zhang X, Zhang L, Fu Y, Guo Z, Chen S, Wu J, **Schnable JC**, Yi K, Wang X, Cheng F^S (2022) The genome of *Orychophragmus violaceus* provides genomic insights into the evolution of Brassicaceae polyploidization and its distinct traits. *PLANT COMMUNICATIONS* doi: [10.1016/j.xplc.2022.100431](https://doi.org/10.1016/j.xplc.2022.100431)
117. **Mural RV**, **Sun G**, **Grzybowski M**, **Tross MC**, **Jin H**, **Smith C**, Newton L, Andorf CM, Woodhouse MR, Thompson AM, **Sigmon B**, **Schnable JC^S** (2022) Association mapping across a multitude of traits collected in diverse environments identifies pleiotropic loci in maize. *GIGASCIENCE* doi: [10.1093/gigascience/giac080](https://doi.org/10.1093/gigascience/giac080) *BIORxIV* doi: [10.1101/2022.02.25.480753](https://doi.org/10.1101/2022.02.25.480753)
116. Meier M, Xu G, Lopez-Guerrero, Li G, **Smith C**, **Sigmon B**, Herr J, Alfano J, Ge Y, **Schnable JC**, Yang J^S (2022) Maize root-associated microbes likely under adaptive selection by the host to enhance phenotypic performance. *eLIFE* doi: [10.7554/eLife.75790](https://doi.org/10.7554/eLife.75790)
115. **Korth N**, Parsons L, Van Haute M, Yang Q, Hurst JP, **Schnable JC**, Holding DR, Benson AK^S The unique seed protein composition of quality protein popcorn promotes growth of beneficial bacteria from the human gut microbiome. *FRONTIERS IN MICROBIOLOGY* doi: [10.3389/fmicb.2022.921456](https://doi.org/10.3389/fmicb.2022.921456)
114. **Mural RV**, **Schnable JC^S** (2022) Can the grains offer each other helping hands? Convergent molecular mechanisms associated with domestication and crop improvement in rice and maize. *MOLECULAR PLANT* doi: [10.1016/j.molp.2022.04.003](https://doi.org/10.1016/j.molp.2022.04.003)
Peer Reviewed Invited Perspective
113. Boatwright JL, Sapkota S, **Jin H**, **Schnable JC**, Brenton Z, Boyles R, Kresovich S^S (2022) Sorghum Association Panel whole-genome sequencing establishes pivotal resource for dissecting genomic diversity. *THE PLANT JOURNAL* doi: [10.1111/tpj.15853](https://doi.org/10.1111/tpj.15853) *BIORxIV* doi: [10.1101/2021.12.22.473950](https://doi.org/10.1101/2021.12.22.473950)

112. Rodene E, Xu G, Delen SP, **Smith C**, Ge Y, **Schnable JC**, Yang J^S (2022) A UAV-based high-throughput phenotyping approach to assess time-series nitrogen responses and identify traits associated genetic components in maize. *THE PLANT PHENOME JOURNAL* doi: [10.1002/ppj2.20030](https://doi.org/10.1002/ppj2.20030) *BIORxIV* doi: [10.1101/2021.05.24.445447](https://doi.org/10.1101/2021.05.24.445447)
111. Yu H, Sandhu J, **Sun G**, Nguyen H, Clemente T, **Schnable JC**, Walia H, Xie W, Yu B, Mower JP, Zhang C^S (2022) Pervasive misannotation of the smallest microexons that are evolutionarily conserved and crucial for gene function in plants. *NATURE COMMUNICATIONS* doi: [10.1038/s41467-022-28449-8](https://doi.org/10.1038/s41467-022-28449-8)
110. **Tross MC**†, Gaillard M, **Zweiner M**†, **Miao C**, **Grove RJ**, Li B, Benes B, **Schnable JC**^S (2021) 3D reconstruction identifies loci linked to variation in angle of individual sorghum leaves. *PEERJ* doi: [10.7717/peerj.12628](https://doi.org/10.7717/peerj.12628) *BIORxIV* doi: [10.1101/2021.06.15.448566](https://doi.org/10.1101/2021.06.15.448566)
109. Diao X^S, Zhang H, Tang S, **Schnable JC**, He Q, Gao Y, Luo M, Jia G, Feng B, Zhi H (2021) Genome-Wide DNA polymorphism analysis and molecular marker development of *Setaria italica* variety ‘SSR41’ and application in positional cloning of *Setaria* white leaf sheath gene SiWLS1. *FRONTIERS IN PLANT SCIENCE* doi: [/10.3389/fpls.2021.743782](https://doi.org/10.3389/fpls.2021.743782)
108. **Miao C**, **Guo A**†, Thompson AM, Yang J, Ge Y, **Schnable JC**^S (2021) Automation of leaf counting in maize and sorghum using deep learning. *THE PLANT PHENOME JOURNAL* doi: [10.1002/ppj2.20022](https://doi.org/10.1002/ppj2.20022) *BIORxIV* doi: [10.1101/2020.12.19.423626](https://doi.org/10.1101/2020.12.19.423626)
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39. Mei W, Liu S, **Schnable JC**, Yeh C, Springer NM, Schnable PS, Barbazuk WB[§] (2017) A comprehensive analysis of alternative splicing in paleopolyploid maize. *FRONTIERS IN PLANT SCIENCE* doi: [10.3389/fpls.2017.00694](https://doi.org/10.3389/fpls.2017.00694)
38. Joyce BL, Huag-Baltzell A, Davey S, Bomhoff M, **Schnable JC**, Lyons E[§] (2016) FractBias: a graphical tool for assessing fractionation bias after whole genome duplications. *BIOINFORMATICS* doi: [10.1093/bioinformatics/btw666](https://doi.org/10.1093/bioinformatics/btw666)
37. Walley JW,* Sartor RC,* Shen Z, Schmitz RJ, Wu KJ, Urich MA, Nery JR, Smith LG, **Schnable JC**, Ecker JR, Briggs SP[§] (2016) Integration of omic networks in a developmental atlas of maize. *SCIENCE* doi: [10.1126/science.aag1125](https://doi.org/10.1126/science.aag1125)
Selected as an Editor's Choice by MaizeGDB Editorial Board September 2016
36. Ge Y[§], Bai G, Stoerger V, **Schnable JC** (2016) Temporal dynamics of maize plant growth, water use, and plant water content using automated high throughput RGB and hyperspectral imaging. *COMPUTERS AND ELECTRONICS IN AGRICULTURE* doi: [10.1016/j.compag.2016.07.028](https://doi.org/10.1016/j.compag.2016.07.028)
35. **Liang Z**, **Schnable JC**[§] (2016) RNA-seq based analysis of population structure within the maize inbred B73. *PLOS ONE* doi: [10.1371/journal.pone.0157942](https://doi.org/10.1371/journal.pone.0157942)
34. Rajput SG, Santra DK[§], **Schnable JC** (2016) Mapping QTLs for morpho-agronomic traits in proso millet (*Panicum miliaceum* L.). *MOLECULAR BREEDING* doi: [10.1007/s11032-016-0460-4](https://doi.org/10.1007/s11032-016-0460-4)
33. Chao S, Wu J, Liang J, **Schnable JC**, Yang W, Cheng F, Wang X[§] (2016) Impacts of whole genome triplication on MIRNA evolution in *Brassica rapa*. *GENOME BIOLOGY AND EVOLUTION* doi: [10.1093/gbe/evv206](https://doi.org/10.1093/gbe/evv206)
32. Tang H, Bomhoff MD, Briones E, **Schnable JC**, Lyons E[§] (2015) SynFind: compiling syntenic regions across any set of genomes on demand. *GENOME BIOLOGY AND EVOLUTION* doi: [10.1093/gbe/evv219](https://doi.org/10.1093/gbe/evv219)
31. Washburn JD, **Schnable JC**, Davidse G, Pires JC[§] (2015) Phylogeny and photosynthesis of the grass tribe Paniceae. *AMERICAN JOURNAL OF BOTANY* doi: [10.3732/ajb.1500222](https://doi.org/10.3732/ajb.1500222)
30. Tang H, Zhang X, **Miao C**, Zhang J, Ming R, **Schnable JC**, Schnable PS, Lyons E, Lu J[§] (2015) ALLMAPS: robust scaffold ordering based on multiple maps. *GENOME BIOLOGY* doi: [10.1186/s13059-014-0573-1](https://doi.org/10.1186/s13059-014-0573-1)
29. **Schnable JC**[§] (2015) Genome evolution in maize: from genomes back to genes. *ANNUAL REVIEW OF PLANT BIOLOGY* doi: [10.1146/annurev-arplant-043014-115604](https://doi.org/10.1146/annurev-arplant-043014-115604)
28. Paschold A, Larson NB, Marcon C, **Schnable JC**, Yeh C, Lanz C, Nettleton D, Piepho H, Schnable PS, Hochholdinger F[§] (2014) Nonsyntenic genes drive highly dynamic complementation of gene expression in maize hybrids. *PLANT CELL* doi: [10.1105/tpc.114.130948](https://doi.org/10.1105/tpc.114.130948)

Postdoctoral Publications

27. Weissmann S, Huang P, Wiechert M, Furoyama K, Brutnell TP, Taniguchi M, **Schnable JC**,[§] Mockler TC[§] (2021) DCT4 - a new member of the dicarboxylate transporter family in C₄ grasses. *GENOME BIOLOGY AND EVOLUTION* doi: [10.1093/gbe/evaa251](https://doi.org/10.1093/gbe/evaa251) *BIORxIV* doi: [10.1101/762724](https://doi.org/10.1101/762724)

26. Nani TF, **Schnable JC**, Washburn JD, Albert P, Pereira WA, Sobrinho FS, Birchler JA, Techia VH[§] (2018). Location of low copy genes in chromosomes of *Brachiaria* spp. MOLECULAR BIOLOGY REPORTS doi: [10.1007/s11033-018-4144-5](https://doi.org/10.1007/s11033-018-4144-5)
25. Studer AJ*, **Schnable JC***, Weissmann S, Kolbe AR, McKain MR, Shao Y, Cousins AB, Kellogg EA, Brutnell TP[§] (2016) The draft genome of *Dichantheium oligosanthes*: A C₃ panicoid grass species. GENOME BIOLOGY doi: [10.1186/s13059-016-1080-3](https://doi.org/10.1186/s13059-016-1080-3)
24. Huang P, Studer AJ, **Schnable JC**, Kellogg EA, Brutnell TP[§] (2016) Cross species selection scans identify components of C₄ photosynthesis in the grasses. JOURNAL OF EXPERIMENTAL BOTANY doi: [10.1093/jxb/erw256](https://doi.org/10.1093/jxb/erw256)
"Insight" highlighting this article by PA Christin also published in JXB doi: [10.1093/jxb/erw390](https://doi.org/10.1093/jxb/erw390)
23. Liu X, Tang S, Jia G, **Schnable JC**, Su X, Tang C, Zhi H, Diao X[§] (2016) The C-terminal motif of SiAGO1b is required for the regulation of growth, development and stress responses in foxtail millet [*Setaria italica* (L.) P. Beauv.]. JOURNAL OF EXPERIMENTAL BOTANY doi: [10.1093/jxb/erw135](https://doi.org/10.1093/jxb/erw135)
22. Jia G, Liu X, **Schnable JC**, Niu Z, Wang C, Li Y, Wang Sh, Wang Su, Liu J, Gou E, Diao X[§] (2015) Microsatellite variations of elite *Setaria* varieties released during last six decades in China. PLOS ONE doi: [10.1371/journal.pone.0125688](https://doi.org/10.1371/journal.pone.0125688)
21. Qie L, Jia G, Zhang W, **Schnable JC**, Shang Z, Li W, Liu B, Li M, Chai, Y, Zhi H, Diao X[§] (2014) Mapping of quantitative trait loci (QTLs) that contribute to germination and early seedling drought tolerance in the interspecific cross *Setaria italica* x *Setaria viridis*. PLOS ONE doi: [10.1371/journal.pone.0101868](https://doi.org/10.1371/journal.pone.0101868)
20. Diao X[§], **Schnable JC**, Bennetzen JL, Li J[§] (2014) Initiation of *Setaria* as a model plant. FRONTIERS OF AGRICULTURAL SCIENCE AND ENGINEERING doi: [10.15302/J-FASE-2014011](https://doi.org/10.15302/J-FASE-2014011)

Graduate Publications

19. Woodhouse MR[§], Sen S, Schott D, Portwood JL, Walley JL, Andorf CM, **Schnable JC** (2021) qTeller: A tool for comparative multi-genomic gene expression analysis. BIOINFORMATICS doi: [10.1093/bioinformatics/btab604](https://doi.org/10.1093/bioinformatics/btab604)
18. Cheng F, Sun C, Wu J, **Schnable JC**, Woodhouse MR, Liang J, Cai C, Freeling M,[§] Wang X[§] (2016) Epigenetic regulation of subgenome dominance following whole genome triplication in *Brassica rapa*. NEW PHYTOLOGIST doi: [10.1111/nph.13884](https://doi.org/10.1111/nph.13884)
17. Almeida AMR, Yockteng R, **Schnable JC**, Alvarez-Buylla ER, Freeling M, Specht CD[§] (2014) Co-option of the polarity gene network shapes filament morphology in angiosperms. SCIENTIFIC REPORTS doi: [10.1038/srep06194](https://doi.org/10.1038/srep06194)
16. Martin JA, Johnson NV, Gross SM, **Schnable JC**, Meng X, Wang M, Coleman-Derr D, Lindquist E, Wei C, Kaeppler S, Chen F, Wang Z[§] (2014) A near complete snapshot of the *Zea mays* seedling transcriptome revealed from ultra-deep sequencing. SCIENTIFIC REPORTS doi: [10.1038/srep04519](https://doi.org/10.1038/srep04519)
Selected as an Editor's Choice by MaizeGDB Editorial Board May 2014
15. Garsmeur O,* **Schnable JC,*** Almeida A, Jourda C, D'Hont A,[§] Freeling M[§] (2014) Two evolutionarily distinct classes of paleopolyploidy. MOLECULAR BIOLOGY AND EVOLUTION doi: [10.1093/molbev/mst230](https://doi.org/10.1093/molbev/mst230)
14. Turco G, **Schnable JC**, Pedersen B, Freeling M[§] (2013) Automated conserved noncoding sequence (CNS) discovery reveals differences in gene content and promoter evolution among the grasses. FRONTIERS IN PLANT SCIENCES doi: [10.3389/fpls.2013.00170](https://doi.org/10.3389/fpls.2013.00170)
13. **Schnable JC**, Wang X, Pires JC, Freeling M[§] (2012) Escape from preferential retention following repeated whole genome duplication in plants. FRONTIERS IN PLANT SCIENCE doi: [10.3389/fpls.2012.00094](https://doi.org/10.3389/fpls.2012.00094)

12. Freeling M[§], Woodhouse MR, Subramaniam S, Turco G, Lisch D, **Schnable JC** (2012) Fractionation mutagenesis and similar consequences of mechanisms removing dispensable or less-expressed DNA in plants. *CURRENT OPINION IN PLANT BIOLOGY* doi: [10.1016/j.pbi.2012.01.015](https://doi.org/10.1016/j.pbi.2012.01.015)
11. Tang H[§], Woodhouse MR, Cheng F, **Schnable JC**, Pedersen BS, Conant GC, Wang X, Freeling M, Pires JC (2012) Altered patterns of fractionation and exon deletions in *Brassica rapa* support a two-step model of paleohexaploidy. *GENETICS* doi: [10.1534/genetics.111.137349](https://doi.org/10.1534/genetics.111.137349)
10. **Schnable JC**, Freeling M, Lyons E[§] (2012) Genome-wide analysis of syntenic gene deletion in the grasses. *GENOME BIOLOGY AND EVOLUTION* doi: [10.1093/gbe/evs009](https://doi.org/10.1093/gbe/evs009)
Selected as an Editor's Choice by MaizeGDB Editorial Board Dec 2012
9. Zhang W, Wu Y, **Schnable JC**, Zeng Z, Freeling M, Crawford GE, and Jiang J[§] (2012) High-resolution mapping of open chromatin in the rice genome. *GENOME RESEARCH* doi: [10.1101/gr.131342.111](https://doi.org/10.1101/gr.131342.111)
8. Eichten SR,* Swanson-Wagner RA,* **Schnable JC**, Waters AJ, Hermanson PJ, Liu S, Yeh C, Jia Y, Gendler K, Freeling M, Schnable PS, Vaughn MW, Springer NM[§] (2011) Heritable epigenetic variation among maize inbreds. *PLoS GENETICS* doi: [10.1371/journal.pgen.1002372](https://doi.org/10.1371/journal.pgen.1002372)
Selected as an Editor's Choice by MaizeGDB Editorial Board Jan 2012
Recommended by Faculty of 1000
7. **Schnable JC**, Lyons E[§] (2011) Comparative genomics with maize and other grasses: from genes to genomes. *MAYDICA* 56(1763) 77-93 [Link directly to PDF](#)
6. Tang H, Lyons E, Pedersen B, **Schnable JC**, Paterson AH, Freeling M. (2011) Screening synteny blocks in pairwise genome comparisons through integer programming. *BMC BIOINFORMATICS* doi: [10.1186/1471-2105-12-102](https://doi.org/10.1186/1471-2105-12-102)
5. **Schnable JC**, Pedersen BS, Subramaniam S, Freeling M[§] (2011) Dose-sensitivity, conserved noncoding sequences and duplicate gene retention through multiple tetraploidies in the grasses. *FRONTIERS IN PLANT SCIENCE* doi: [10.3389/fpls.2011.00002](https://doi.org/10.3389/fpls.2011.00002)
Commentary by Birchler and Veitia also published in Frontiers in Plant Science doi: [10.3389/fpls.2011.00064](https://doi.org/10.3389/fpls.2011.00064)
4. **Schnable JC**[§], Freeling M (2011) Genes identified by visible mutant phenotypes show increased bias towards one of two maize subgenomes. *PLoS ONE* doi: [10.1371/journal.pone.0017855](https://doi.org/10.1371/journal.pone.0017855)
3. **Schnable JC**, Springer NM, Freeling M[§] (2011) Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss. *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES* doi: [10.1073/pnas.1101368108](https://doi.org/10.1073/pnas.1101368108)
Selected as an Editor's Choice by MaizeGDB Editorial Board May 2011
2. Woodhouse MR,* **Schnable JC**,* Pedersen BS, Lyons E, Lisch D, Subramaniam S, Freeling M[§] (2010) Following tetraploidy in maize, a short deletion mechanism removed genes preferentially from one of the two homeologs. *PLoS BIOLOGY* doi: [10.1371/journal.pbio.1000409](https://doi.org/10.1371/journal.pbio.1000409)
Selected as an Editor's Choice by MaizeGDB Editorial Board August 2010
PLoS Biology Cover Article Recommended by Faculty of 1000
1. The International Brachypodium Initiative (2010) Genome sequencing and analysis of the model grass *Brachypodium distachyon*. *NATURE* doi: [10.1038/nature08747](https://doi.org/10.1038/nature08747)

Peer Reviewed Conference Papers

12. Noh M, Sium F, Tope S, Khan S, Karkhanis M, Wang L, Deshpande A, Dalapati R, **Mural RV**, Mastrangelo C, Zang L, Ji M, **Schnable JC**, Kim H (2023) Localization of crop damage utilizing a wake up gas sensor network. *TRANSDUCERS 2023* Kyoto, Japan

11. Khan SH, Karkhanis M, Hatasaka B, Tope S, Noh S, Bulbul A, Banerjee A, Ji M, Mastrangelo CH, Kim H, Dalapati R, Zang L, **Mural RV, Schnable JC**, Kim K (2022) Field deployment of a nanogap gas sensor for crop damage detection. 35TH INTERNATIONAL CONFERENCE ON MICRO ELECTRO MECHANICAL SYSTEMS CONFERENCE (MEMS) Berlin, Germany doi: [10.1109/MEMS51670.2022.9699614](https://doi.org/10.1109/MEMS51670.2022.9699614)
10. Khan SH, Tope S, Dalpati R, Kim KH, Noh M, Bulbul A, **Mural RV**, Banerjee A, **Schnable JC**, Ji M, Mastrango C, Zang L, Kim H (2021) Development of a gas sensor for green leaf volatile detection. TRANSDUCERS 2021 doi: [10.1109/Transducers50396.2021.9495597](https://doi.org/10.1109/Transducers50396.2021.9495597)
9. Gaillard M, **Miao C, Schnable JC**, Benes B (2020) Sorghum Segmentation by Skeleton Extraction. COMPUTER VISION PROBLEMS IN PLANT PHENOTYPING (CVPPP 2020) Glasgow, UK
8. Sankaran S, Zhang C, **Hurst JP**, Marzougui A, Sivakumar ANV, Li J, **Schnable JC**, Shi Y (2020) Investigating the potential of satellite imagery for high-throughput field phenotyping applications. SPIE DEFENSE + COMMERCIAL SENSING California, USA doi: [10.1117/12.2558729](https://doi.org/10.1117/12.2558729)
7. Al-Zadjali A, Shi Y, Scott S, Deogun JS, and **Schnable JC** (2020) Faster-R-CNN based deep learning for locating corn tassels in UAV imagery. SPIE DEFENSE + COMMERCIAL SENSING California, USA doi: [10.1117/12.2560596](https://doi.org/10.1117/12.2560596)
6. **Miao C, Pages A,† Xu Z, Schnable JC** (2019) Sorghum organ classification in hyperspectral images using supervised machine learning classification methods. SECOND INTERNATIONAL WORKSHOP ON MACHINE LEARNING FOR CYBER-AGRICULTURAL SYSTEMS (MLCAS 2019) Ames, IA, USA
5. **Askey B,† Yang Q, Benson AK, Schnable JC** (2019) Computer vision phenotyping of 371 Sorghum bicolor BTx623 x ISC3620C recombinant inbred lines for QTL detection. SECOND INTERNATIONAL WORKSHOP ON MACHINE LEARNING FOR CYBER-AGRICULTURAL SYSTEMS (MLCAS 2019) Ames, IA, USA
4. Jiao Y, Wang X, Chen Y, Castellano MJ, **Schnable JC**, Schnable PS, Dong L (2019) In-planta nitrate detection using insertable plant microsensor. 20TH INTERNATIONAL CONFERENCE ON SOLID-STATE SENSORS, ACTUATORS AND MICROSYSTEMS Berlin, Germany doi: [10.1109/TRANSDUCERS.2019.8808527](https://doi.org/10.1109/TRANSDUCERS.2019.8808527)
3. Ali MA, Wang X, Chen Y, Jiao Y, Castellano MJ, **Schnable JC**, Schnable PS, Dong L (2019) Novel all-solid-state soil nutrient sensor using nanocomposite of poly(3-octyl-thiophene) and molybdenum sulfate. 20TH INTERNATIONAL CONFERENCE ON SOLID-STATE SENSORS, ACTUATORS AND MICROSYSTEMS Berlin, Germany doi: [10.1109/TRANSDUCERS.2019.8808341](https://doi.org/10.1109/TRANSDUCERS.2019.8808341)
2. Behera S, Deogun JS, **Lai X, Schnable JC** (2017) B529 DiCE: Discovery of Conserved Noncoding Sequences Efficiently. IEEE BIBM 2017 Kansas City, MO, USA doi: [10.1109/BIBM.2017.8217628](https://doi.org/10.1109/BIBM.2017.8217628)
1. Chaudhury SD, Steorger V, Samal A, **Schnable JC, Liang Z**, Yu J (2016) [Automated vegetative stage phenotyping analysis of maize plants using visible light images](#). KDD: DATA SCIENCE FOR FOOD, ENERGY AND WATER San Francisco, CA, USA

Selected Other Publications

5. **Liang Z, Meng X, Schnable JC** (2023) A transferable machine learning framework for predicting transcriptional responses of genes across species. Plant Gene Regulatory Networks: Methods and Protocols. Editors: Kerstin Kaufmann and Klaas Vandepoele Publisher: Springer, New York, NY.
4. Clark J, Qiu Y, **Schnable JC**. (2019) Experimental design for controlled environment high throughput plant phenotyping. High Throughput Plant Phenotyping: Methods and Protocols. Editor: Argelia Lorence Publisher: Springer, New York, NY.
3. Tang H, Lyons E, **Schnable JC** (2013) Early history of the angiosperms. Genomes of Herbaceous Land Plants. Editor: Andrew Paterson Publisher: Academic Press

2. Goff SA, **Schnable JC**, Feldmann KA (2013) The evolution of plant gene and genome sequencing. Genomes of Herbaceous Land Plants Editor: Andrew Paterson Publisher: Academic Press
1. **Schnable JC** and Freeling M (2012) Maize (*Zea mays*) as a model for studying the impact of gene and regulatory sequence loss following whole genome duplication. Polyploidy and Genome Evolution. Editors: Soltis PS & Soltis DE Publisher: Springer New York, NY

Selected Recent Service

University

Consortium for Integrated Translational Biology (CITB)	2014-Present
Nebraska Food for Health Center Faculty Advisory Committee	2017-Present
Department of Agronomy and Horticulture Promotion and Tenure Committee	2023-Present
UNL Faculty Greenhouse Committee	2015-2021
Department of Agronomy and Horticulture Awards Committee	2019-2021
Department of Agronomy and Horticulture Graduate Admissions Committee	2019-2022
Biotech Seminar Series Committee	2017-2019
Agronomy and Horticulture Faculty Advisory Committee	2017-2019
Agronomy and Horticulture Strategic Planning Committee	2018-2019
Department of Agronomy and Horticulture Peer Evaluation Committee	2016-2018
Search Committee, Nebraska EPSCoR/IDeA Director	2018
Organizing Committee " International Millet Symposium 2018 "	2018
Organizing Committee " Predictive Crop Design, Genome to Phenome "	2017
Search Committee, Director of Phenomic Sciences	2017
Search Committee, Agricultural Research Division	2016
Search Committee, Quantitative Life Sciences Initiative	2016
Search Committee, Department of Agronomy and Horticulture	2016
Organizing Committee " Plant Phenomics: from pixels to traits "	2015

Professional

Associate Editor: Molecular Plant	2014-Present
Guest Editor: The Plant Cell	2019-Present
Data Management Subcommittee, Maize Genetics Research Collaboration Network	2018-Present
MaizeGDB Advisory Committee	2018-Present
Host Committee for International Plant Phenotyping Network 2024 Conference	2023-Present
Grant Reviewer: NSF (panel & ad hoc), USDA (panel), JGI (panel), Genome British Columbia (ad hoc).	

Peer Reviewer (selected, recent): Bioinformatics, BMC Genomics, BMC Plant Biology, G3: Genes | Genomes | Genetics, Genome Biology, Genome Biology & Evolution, Heredity, Journal of Experimental Botany, JoVE, Molecular Biology and Evolution, Molecular Plant, Nature Communications, Nature Plants, New Phytologist, Nucleic Acids Research, PeerJ, Photosynthesis Research, Physiologia Plantarum, Plant Cell, Plant Cell & Environment, Plant Direct, The Plant Genome, The Plant Journal, Plant Methods, Plant Physiology, PLoS Genetics, Proceedings of the National Academy of Sciences, Science Science Advances

Invited Talks:

At External Institutions

University of Georgia-Athens, Athens, Georgia, USA	2023
University of Arizona, Tucson, AZ, USA	2023
Oregon State University, Corvallis, OR, USA	2023
Carnegie Institution for Science, Stanford, CA, USA	2022
Center for Sorghum Improvement, Manhattan, KS, USA	2022 (<i>Remote</i>)
CIRAD, Montpellier, France	2022
California State East Bay, Hayward, CA, USA	2021 (<i>Remote, COVID</i>)
University of Missouri, Columbia, MO, USA	2020 (<i>Remote, COVID</i>)
Rutgers University, New Brunswick, NJ, USA	2020 (<i>Remote, COVID</i>)
Bayer Crop Science, St. Louis, MO, USA	2020 (<i>Remote, COVID</i>)
University of Bonn, Bonn, Germany	2020 (<i>Remote, COVID</i>)
King Abdullah University of Science and Technology, Jeddeh, Saudi Arabia	2020 (<i>Remote, COVID</i>)
University of Hawaii, Manoa, HI, USA (<i>Brewbaker Lecture</i>)	2019
Miami University, Oxford, OH, USA	2019
University of Massachusetts Amherst, Oxford, OH, USA	2019
Cornell University, Ithaca, NY, USA	2019
Research Triangle Park, NC, USA	2018
Washington State University, Pullman, WA, USA	2018
University of Delaware, Newark, DE, USA	2018
Chinese Academy of Agricultural Sciences, Beijing, China	2017
Beijing Academy of Agricultural and Forestry Sciences, Beijing, China	2017
University of Minnesota, St. Paul, MN, USA	2017
Iowa State University, Ames, IA, USA	2017
University of Missouri-Columbia, Columbia, MO, USA	2017
Kansas State University, Manhattan, KS, USA	2016

University of Georgia-Athens, Athens, GA, USA	2016
University of California-San Diego, San Diego, CA, USA	2016
Chinese Academy of Agricultural Sciences, Beijing, China	2015
Beijing Academy of Agricultural and Forestry Sciences, Beijing, China	2015
Sichuan Agricultural University, Chengdu, China	2015
Huazhong Agricultural University, Wuhan, China	2015
Shandong Agricultural University, Tai'an, China	2015
Monsanto, St. Louis, MO, USA	2015
Henan Agricultural University, Zhengzhou, China	2014
Chinese Academy of Tropical Agriculture, Haikou, China	2014
Cornell University, Ithaca, NY, USA	2014
Interdisciplinary Plant Group Seminar Series, University of Missouri, Columbia, MO, USA	2012
Donald Danforth Plant Science Center, St. Louis, MO, USA	2012
China Agricultural University, Beijing, China	2012
Chinese Academy of Agricultural Sciences, Beijing, China	2012
MaizeGDB, Ames, IA, USA	2012
University of Arizona, Tucson, AZ, USA	2011

At External Conferences

Invited presentations only. Excludes presentations selected based on abstracts or applications.

Purdue Plant Science Symposium (Student Organized), West Lafayette, IN USA	2023
IROS (Intelligent Robots and Systems), Detroit, MI USA	2023
Sorghum in the 21st Century, Montpellier, France	2023
Corteva Symposium Series, North of Rio de Janeiro State University (Student Organized), Campos dos Goytacazes, Brazil	2023(Remote)
Iowa Biotech Showcase, Ankeny, IA USA	2023
SFBV (French Society of Plant Biology), Montpellier, France	2022
Plant Response to Stresses and Environmental Signals, Beijing, China	2022 (Remote)
IPPN-CEPPG Workshop on Environment Simulation and Phenotyping, Gatersleben, Germany	2022 (Remote)
Michigan State Genome Sciences Symposium (Student Organized), East Lansing, MI, USA	2022
Nexus Informatics, Kansas City, MO, USA	2022
Molecular Plant Virtual Seminar Series	2022 (Remote, COVID)
DIGICROP 2022	2022 (Remote, COVID)

Machine Learning for Cyber-Agricultural Systems (Keynote)	2021 (<i>Remote, COVID</i>)
Plant Science Symposium West Africa (Student Organized)	2021 (<i>Remote, COVID</i>)
Soybean Breeders Workshop	2021 (<i>Remote, COVID</i>)
NAPPN 2021	2021 (<i>Remote, COVID</i>)
DIGICROP 2020	2020 (<i>Remote, COVID</i>)
National Association of Plant Breeders Annual Meeting, Lincoln, NE, USA	2020 (<i>Remote, COVID</i>)
iGenomX Session, Plant and Animal Genome, San Diego, CA, USA	2020
Systems Biology and Ontologies Session, Plant and Animal Genome, San Diego, CA, USA	2020
Guelph Plant Sciences Symposium (Student Organized), Guelph, Ontario, Canada	2019
Future of Machine Learning for Cyber-Agricultural Systems Panel, Ames, IA, USA	2019
Gene Mapping Session, Plant and Animal Genome, San Diego, CA, USA	2019
Plant Energy Biology Forum, Perth, Australia	2018
The Plant Phenome Journal Webinar Series	2018
Entrepreneurship Panel, USDA FACT: Genomes to Fields, Ames, IA, USA	2018
Plant Phenotype Session, Plant and Animal Genome, San Diego, CA, USA	2018
Plant Genome Evolution, Sitges, Spain	2017
Purdue Plant Science Symposium (Student Organized), West Lafayette, IN, USA	2017
P ² IRC Annual Symposium, Saskatoon, Saskatchewan, Canada	2017
Maize Tools and Resources (Maize Genetics Conference pre-meeting), St. Louis, MO, USA	2017
Phenome, Tucson, AZ, USA	2017
Corn Breeding Research Meeting, Jacksonville, FL, USA	2016
Molecular Plant Symposium: From Model Species to Crops, Shanghai, China	2015
Corn Breeding Research Meeting, St. Charles, IL, USA	2015
Life Technologies Session, Plant and Animal Genome, San Diego, CA, USA	2015
Maize Session, Plant and Animal Genome, San Diego, CA, USA	2015
Millet as Crop: Past and Future, Aohan, Inner Mongolia, China	2014
Plant Genomes in China Meeting, Tai'an, China	2012
American Society of Plant Biology, Austin, TX, USA	2012
Polyploidy Session, Plant and Animal Genome, San Deigo, CA, USA	2012
CSSA Translational Genomics Session, Plant and Animal Genome, San Diego, CA, USA	2012

Internal

Animal Science Departmental Seminar Series, UNL,	2023
CROPS Entrepreneurship/Industry Career Panel (Student Organized), UNL	2023
Complex Biosystems Seminar Series, UNL	2021 (<i>In Person, COVID</i>)
Agronomy & Horticulture Departmental Seminar Series, UNL	2020 (<i>Remote, COVID</i>)
Nebraska Plant Science Symposium (Student Organized)	2019
UNL Plant Phenomics Symposium	2018
NeDA 2017: 2nd Nebraska Data Analytics Workshop, UNL	2017
Water for Food Global Conference, UNL	2017
Complex Biosystems Seminar Series, UNL	2017
Food Science Departmental Seminar Series, UNL	2016
Animal Science Departmental Seminar Series, UNL	2016
Agronomy & Horticulture Departmental Seminar Series, UNL	2015
Plant Science Retreat, UNL	2014

Professional Memberships

American Society of Plant Biology
 Crop Science Society of America
 North American Plant Phenotyping Network
 American Association for the Advancement of Science