

CURRICULUM VITAE

JAMES C. SCHNABLE

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Employment

University of Nebraska-Lincoln	
Professor, Department of Agronomy and Horticulture	2022-Present
Charles O. Gardner Professor of Maize Quantitative Genetics	2019-Present
Associate Professor, Department of Agronomy and Horticulture	2019-2022
Assistant Professor, Department of Agronomy and Horticulture	2014-2019
Chinese Academy of Agricultural Sciences	
NSF PGRP Fellowship Supported Visiting Scholar	2014
Donald Danforth Plant Science Center	
NSF PGRP Fellowship Supported Postdoctoral Researcher	2013

Education

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

Selected Honors and Awards

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	2018
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	
Marcus Rhoades Early Career Award	2018
Maize Genetics Community	
Tansley Medal Finalist	2018
New Phytologist Trust	

Junior Faculty Excellence in Research Award
University of Nebraska-Lincoln

2016

Research Support

\$25.6M 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)

DOE “TGCM: (T)rait, (G)ene, and (C)rop Growth (M)odel directed targeted gene characterization in sorghum.” (PI) 2019-2022. \$2.7M

NSF “RoL: FELS: EAGER: Genetic constraints on the increase of organismal complexity over time.” (PI) 2018-2021. \$300k

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) 2019-2021. \$300k

USDA-NIFA “High Intensity Phenotyping Sites: Transitioning To A Nationwide Plant Phenotyping Network.” (co-PI) 2020-2023. \$3M

USDA-NIFA “High Intensity Phenotyping Sites: A multi-scale, multi-modal sensing and sense-making cyber-ecosystem for Genomes to Fields.” (co-PI) 2020-2023. \$2.7M

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

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

NSF “RII Track-2 FEC: Functional analysis of nitrogen responsive networks in Sorghum.” (co-PI) 2018-2022. \$4M

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

FFAR “Crops in silico: Increasing crop production by connecting models from the microscale to the macroscale.” (co-PI) 2019-2023. \$5M

NSF “AI Institute for Resilient Agriculture” (Investigator) 2021-2026 \$20M

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

Non-Federal (Current)

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

Nebraska Corn Board “Genomes to Fields (G2F) - Predicting Final Yield Performance in Variable Environments.” (PI) 2016-2022. \$300k (to date)

Wheat Innovation Foundation “A Low-Cost, High-Throughput Cold Stress Perception Assay for Sorghum Breeding.” (co-PI) 2019-2021. \$205k

Completed Projects

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](#) (USA) & DATA生物科技（北京）有限公司 (China) 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 I: Low-cost in-planta nitrate sensor” 2019-2020 \$225k

USDA (to EnGeniousAg) “SBIR Phase I: Low-cost field-deployable sensors to monitor nitrate in soil and water.” 2019-2020 \$100k

Industry Cooperation

Scientific Advisory Council, GeneSeek, Inc	2017-Present
External Advisor to the Scientific Advisory Board, Indigo Agriculture	2017
External Advisor to the Scientific Advisory Board, Syngenta AG	2016

Advising

Current Graduate Advisees: Hongyu Jin (PhD, Complex Biosystems), Michael Tross (PhD, Complex Biosystems), Nate Korth (co-advised, PhD, Food Science), Fangyi Li (co-advised, PhD, Complex Biosystems), Kahheetah Barnoskie (co-advised MS, Agronomy & Horticulture), Kyle Linders (co-advised MS, Agronomy & Horticulture)

Thesis Committees: Yen Ning Chai (PhD, Agronomy & Horticulture), Qinnan Yang (PhD, Food Science), J. Preston Hurst (PhD, Agronomy & Horticulture), Rituj Khound (PhD, Agronomy & Horticulture), Sergio Manuel Gabriel Peralta (PhD, Plant Pathology), Shimin Chen (PhD, Food Science), Zachery Shomo (PhD, Biochemistry), Jared Haupt (PhD, Biochemistry), Sarah Johnson (PhD, Agronomy & Horticulture), Semra Palali (PhD, Agronomy & Horticulture)

Graduated Advisees: Daniel Carvalho (PhD, Agronomy & Horticulture), Zhikai Liang (PhD, Agronomy & Horticulture), Chenyong Miao (PhD, Agronomy & Horticulture), Preston Hurst (MS, Agronomy & Horticulture), Xianjun 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), Bhushit Agarwal (co-advised, MS, Computer Science & Engineering), Srinidhi Bashyam (co-advised, MS, Computer Science & Engineering)

Undergraduate Researchers: 7 NSF supported REU (Research Experience for Undergraduates) students; 3 UCARE (Undergraduate Creative Activities and Research Experience) students; and 36 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: 36

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

Preprints

Mural RV, Sun G, Grzybowski M, Tross MC, Jin H, Smith C, Newton L, Andorf CM, Woodhouse MR, Thompson AM, **Sigmon B, Schnable JC**[§] Association mapping across a multitude of traits collected in diverse environments identifies pleiotropic loci in maize. *bioRxiv* doi: [10.1101/2022.02.25.480753](https://doi.org/10.1101/2022.02.25.480753)

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**[§] Genome sequence of *Paspalum vaginatum* indicates trehalose may act as a conserved trigger for increased nitrogen use efficiency in grasses. *bioRxiv* doi: [10.1101/2021.08.18.456832](https://doi.org/10.1101/2021.08.18.456832)

Yang Q, Van Haute M, **Korth N**, Sattler S, Toy J, Rose D, **Schnable JC**, Benson A[§] Complex trait analysis of human gut microbiome-active traits in *Sorghum bicolor*: a new category of human health traits in food crops. *RESEARCH SQUARE* doi: [10.21203/rs.3.rs-1490527/v1](https://doi.org/10.21203/rs.3.rs-1490527/v1)

Xu G, Lyu J, Obata T, Liu S, Ge Y, **Schnable JC**, Yang J^S A historically balanced locus under recent directional selection in responding to changed nitrogen conditions during modern maize breeding. *BioRxiv* doi: [10.1101/2022.02.09.479784](https://doi.org/10.1101/2022.02.09.479784)

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**^S A role for heritable transcriptomic variation in maize adaptation to temperate environments. *BioRxiv* doi: [10.1101/2022.01.28.478212](https://doi.org/10.1101/2022.01.28.478212)

Meier MA, Xu G, Lopez-Guerrero MG, Li G, **Smith C**, **Sigmon B**, Herr JR, Alfano J, Ge Y, **Schnable JC**, Yang J^S Maize root-associated microbes likely under adaptive selection by the host to enhance phenotypic performance. *BioRxiv* doi: [10.1101/2021.11.01.466815](https://doi.org/10.1101/2021.11.01.466815)

Miao C, **Hoban TP**[‡], **Pages A**[‡], Xu Z, Rodene E, Ubbens J, Stavness I, Yang J, **Schnable JC**^S Simulated plant images improve maize leaf counting accuracy. *BioRxiv* doi: [10.1101/706994](https://doi.org/10.1101/706994)

Zhang Z^S, Chen C, Rutkoski J, **Schnable JC**, Murray S, Wang L, Jin X, Stich B, Crossa J, Hayes B. Harnessing Agronomics Through Genomics and Phenomics in Plant Breeding: A Review. *PREPRINTS.ORG* doi: [10.20944/preprints202103.0519.v1](https://doi.org/10.20944/preprints202103.0519.v1)

Faculty Publications

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 (Accepted)* *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)

107. **Sun G^S, Mural RV, Turkus JD, Schnable JC** (2021) Quantitative resistance loci to southern rust mapped in a temperate maize diversity panel. *PHYTOPATHOLOGY* doi: [10.1094/PHYTO-04-21-0160-R](https://doi.org/10.1094/PHYTO-04-21-0160-R) *BIORxIV* doi: [10.1101/2021.04.02.438220](https://doi.org/10.1101/2021.04.02.438220)
106. **Mural RV, Grzybowski M, Miao C, Damke A[†], Sapkota S, Boyles RE, Salas Fernandez MG, Schnable PS, Sigmon B, Kresovich S, Schnable JC^S** (2021) Meta-analysis identifies pleiotropic loci controlling phenotypic trade-offs in sorghum. *GENETICS* doi: [10.1093/genetics/iyabo87](https://doi.org/10.1093/genetics/iyabo87) *BIORxIV* doi: [10.1101/2020.10.27.355495](https://doi.org/10.1101/2020.10.27.355495)
105. **Grzybowski M, Wijewardane NK, Atefi A, Ge Y, Schnable JC^S** (2021) The potential of hyperspectral reflectance as a tool for quantitative genetics in crops. *PLANT COMMUNICATIONS* doi: [10.1016/j.xplc.2021.100209](https://doi.org/10.1016/j.xplc.2021.100209)
104. Zhou Y, Kusmec A, Mirnezami SV, Srinivasan L, Jubery TZ, **Schnable JC**, Salas-Fernandez MG, Nettleton D, Ganapathysubramanian B, Schnable PS^S (2021) Identification and utilization of genetic determinants of trait measurement errors in image-based, high-throughput phenotyping. *THE PLANT CELL* doi: [10.1093/plcell/koab134](https://doi.org/10.1093/plcell/koab134)
103. Atefi A, Ge Y^S, Pitla S, **Schnable JC** (2021) Robotic Technologies for High-Throughput Plant Phenotyping: Reviews and Perspectives. *FRONTIERS IN PLANT SCIENCE* doi: [10.3389/fpls.2021.611940](https://doi.org/10.3389/fpls.2021.611940)
102. Alzadjali A, Veeranampalayam-Sivakumar A, Alali MH, Deogun JS, Scott S, **Schnable JC**, Shi Y^S (2021) Maize tassel detection from UAV imagery using deep learning. *FRONTIERS IN ROBOTICS AND AI* [10.3389/frobt.2021.600410](https://doi.org/10.3389/frobt.2021.600410)
101. Meier MA, Lopenz-Guerrero MG, Guo M, Schmer MR, Herr JR, **Schnable JC**, Alfano JR, Yang J^S (2021) Rhizosphere microbiomes in a historical maize/soybean rotation system respond to host species and nitrogen fertilization at genus and sub-genus levels. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY* doi: [10.1128/AEM.03132-20](https://doi.org/10.1128/AEM.03132-20) *BIORxIV* doi: [10.1101/2020.08.10.244384](https://doi.org/10.1101/2020.08.10.244384)
100. Serb DD, **Meng X, Schnable JC**, Bashir E, Michaud JP, Vara Prasad PV, Perumal R (2021) Comparative transcriptome analysis reveals genetic mechanisms of sugarcane aphid resistance in grain sorghum. *INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES* doi: [10.3390/ijms22137129](https://doi.org/10.3390/ijms22137129)
99. Hurst JP, **Schnable JC**, Holding DR^S (2021) Tandem duplicate expression patterns are conserved between maize haplotypes of the α -zeingene family. *PLANT DIRECT* doi: [10.1002/pld3.346](https://doi.org/10.1002/pld3.346)
98. Busta L, Schmitz E, Kosma D, **Schnable JC**, Cahoon EB^S (2021) A co-opted steroid synthesis gene, maintained in sorghum but not maize, is associated with a divergence in leaf wax chemistry. *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA* doi: [10.1073/pnas.2022982118](https://doi.org/10.1073/pnas.2022982118)
97. **Meng X, Liang Z, Dai X, Zhang Y, Mahboub S, Ngu DW[†], Roston RL, Schnable JC^S** (2021) Predicting transcriptional responses to cold stress across plant species. *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*. doi: [10.1073/pnas.2026330118](https://doi.org/10.1073/pnas.2026330118) *BIORxIV* doi: [10.1101/2020.08.25.266635](https://doi.org/10.1101/2020.08.25.266635)
96. Sankaran S^S, Marzougui A, **Hurst JP**, Zhang C, **Schnable JC**, Shi Y (2021) Can high resolution satellite imagery be used in high-throughput field phenotyping? *TRANSACTIONS OF THE ASABE* doi: [10.13031/trans.14197](https://doi.org/10.13031/trans.14197)
95. Zhu Y, Chen Y, Ali Md. A, Dong L, Wang X, Archontoulis SV, **Schnable JC**, Castellano MJ^S (2021) Continuous in situ soil nitrate sensors: a comparison with conventional measurements and the value of high temporal resolution measurements. *SOIL SCIENCE SOCIETY OF AMERICA JOURNAL* doi: [10.1002/saj2.20226](https://doi.org/10.1002/saj2.20226)
94. **Lai X, Bendix C, Zhang Y, Schnable JC**, Harmon FG^S (2021) 72-hour diurnal RNA-seq analysis of fully expanded third leaves from maize, sorghum, and foxtail millet at 3-hour resolution. *BMC RESEARCH NOTES* doi: [10.1186/s13104-020-05431-5](https://doi.org/10.1186/s13104-020-05431-5)

93. Rogers AR, Dunne JC, Romay C ... **Schnable JC** (24th of 39 authors) ... Kaeppler S, De Leon N, Holland JB[§] (2021) The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. G3:GENES | GENOMES | GENETICS doi: [10.1093/g3journal/jkaa050](https://doi.org/10.1093/g3journal/jkaa050)
Selected as an Editor's Choice by MaizeGDB Editorial Board February 2021
92. Jarquin D, de Leon N, Romay C ... **Schnable JC** (24th of 33 authors) ... Wisser RJ, Xu W, Lorenz A (2021) Utility of climatic information via combining ability models to improve genomic prediction for yield within the Genomes to Fields maize project. FRONTIERS IN GENETICS doi: [10.3389/fgene.2020.592769](https://doi.org/10.3389/fgene.2020.592769)
91. DiMario RJ, Kophs AN, Pathare VS, **Schnable JC**, Cousins AB[§] (2021) Phosphoenolpyruvate carboxylase kinetic variation provides opportunity to enhance C₄ photosynthetic efficiency. THE PLANT JOURNAL doi: [10.1111/tpj.15141](https://doi.org/10.1111/tpj.15141)
90. Thudi M, Palakurthi R, **Schnable JC**, Chitikineni A, Dreisigacker S, Mace E, Srivastava RK, Satyavathi CT, Odeny D, Tiwari VK, Lam HM, Hong YB, Singh VK, Li G, Xu Y, Chen X, Nguyen H, Sivasankar S, Close TJ, Stein N, Jackson SA, Shubo W, Varshney RK[§] (2021) Genomic resources in plant breeding for sustainable agriculture. JOURNAL OF PLANT PHYSIOLOGY doi: [10.1016/j.jplph.2020.153351](https://doi.org/10.1016/j.jplph.2020.153351)
89. **Raju SKK**, Atkins M[†], **Enerson A[†]**, **Carvalho DS**, Studer AJ, Ganapathysubramanian B, Schnable PS, **Schnable JC[§]** (2020) Leaf Angle eXtractor - A high throughput image processing framework for leaf angle measurement in maize and sorghum. APPLICATIONS IN PLANT SCIENCES doi: [10.1002/aps3.11385](https://doi.org/10.1002/aps3.11385)
88. Gaillard M*, **Miao C***, **Schnable JC[§]**, Benes B[§] (2020) Voxel carving based 3D reconstruction of sorghum identifies genetic determinants of radiation interception efficiency. PLANT DIRECT doi: [10.1002/pld3.255](https://doi.org/10.1002/pld3.255) BIORxIV doi: [10.1101/2020.04.06.028605v1](https://doi.org/10.1101/2020.04.06.028605v1)
87. **Raju SKK[§]**, Thompson AM, **Schnable JC** (2020) Advances in plant phenomics: From data and algorithms to biological insights. APPLICATIONS IN PLANT SCIENCES doi: [10.1002/aps3.11386](https://doi.org/10.1002/aps3.11386)
86. Atefi A, Ge Y[§], Pitla S, **Schnable JC** (2020) Robotic detection and grasp of maize and sorghum: stem measurement with contact. ROBOTICS doi: [10.3390/robotics9030058](https://doi.org/10.3390/robotics9030058)
85. Wang R, Qiu Y,[§] Zhou Y, **Liang Z**, **Schnable JC** (2020) A high-throughput phenotyping pipeline for image processing and functional growth curve analysis. PLANT PHENOMICS doi: [10.34133/2020/7481687](https://doi.org/10.34133/2020/7481687)
84. **Lai X**, Bendix C, **Yan L**, **Zhang Y**, **Schnable JC**, Harmon F[§] (2020) Interspecific analysis of diurnal gene regulation in panicoid grasses identifies known and novel regulatory motifs. BMC GENOMICS doi: [10.1186/s12864-020-06824-3](https://doi.org/10.1186/s12864-020-06824-3)
Selected as an Editor's Choice by MaizeGDB Editorial Board October 2020
83. Han J, Wang P, Wang Q, Lin Q, Yu G, **Miao C**, Dao Y, Wu R, **Schnable JC**, Tang H, Wang K[§] (2020) Genome-wide characterization of DNase I-hypersensitive sites and cold response regulatory landscapes in grasses. THE PLANT CELL doi: [10.1105/tpc.19.00716](https://doi.org/10.1105/tpc.19.00716)
"In Brief" highlighting this article by SKK Raju doi: [10.1105/tpc.20.00471](https://doi.org/10.1105/tpc.20.00471)
82. Moiseyev G, Park K, Cui X, Freitas D, Rajagopa D, Konda A, Martin-Olenski M, Mcham M, Liu K, Du Q, **Schnable JC**, Moriyama E, Cahoon E, Chi Z[§] (2020) RGPDB: Database of root-associated genes and promoters in maize, soybean, and sorghum. DATABASE doi: [10.1093/database/baaa038](https://doi.org/10.1093/database/baaa038)
81. **Miao C**, Xu Y, Liu S, Schnable PS, **Schnable JC[§]** (2020) Increased power and accuracy of causal locus identification in time-series genome-wide association in sorghum. PLANT PHYSIOLOGY doi: [10.1104/pp.20.00277](https://doi.org/10.1104/pp.20.00277) BIORxIV doi: [10.1101/2020.02.16.951467](https://doi.org/10.1101/2020.02.16.951467)
"News and Views" highlighting this article by Y Yu doi: [10.1104/pp.20.00797](https://doi.org/10.1104/pp.20.00797)
80. **Dai X**, Xu Z, **Liang Z**, Tu X, Zhong S, **Schnable JC[§]**, Li P[§] (2020) Non-homology based prediction of gene functions. THE PLANT GENOME doi: [10.1002/tpg2.20015](https://doi.org/10.1002/tpg2.20015) BIORxIV doi: [10.1101/730473](https://doi.org/10.1101/730473)

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5. **Schnable JC**, Pedersen BS, Subramaniam S, Freeling M^S (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^S**, 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^S (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^S (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

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, Dalapati 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

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
UNL Faculty Greenhouse Committee	2015-Present
Nebraska Food for Health Center Faculty Advisory Committee	2017-Present
Department of Agronomy and Horticulture Awards Committee	2019-Present
Department of Agronomy and Horticulture Graduate Admissions Committee	2019-Present
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
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

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, Jeddah, 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.

IPPN-CEPPG Workshop on Environment Simulation and Phenotyping, Gatersleben, Germany	2022
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 (Remote, COVID)
Plant Science Symposium West Africa (Student Organized)	2021 (Remote, COVID)
Soybean Breeders Workshop	2021 (Remote, COVID)
NAPPN 2021	2021 (Remote, COVID)

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 Diego, CA, USA	2012
CSSA Translational Genomics Session, Plant and Animal Genome, San Diego, CA, USA	2012

Internal

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