Curriculum Vitae

James C. Schnable

Nebraska Corn Checkoff Presidential Chair
Center for Plant Science Innovation
Department of Agronomy & Horticulture
University of Nebraska-Lincoln

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[a]Clickable 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

(Interim) Technology Lead (L7), Visiting Position During Sabbatical	2022

Danforth Plant Science Center & Chinese Academy of Agricultural Sciences

NSF PGRP Fellowship Supported Visiting Scholar	2013-2014

Education

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

Selected Honors and Awards

Outstanding Original Research Article The Plant Journal	2024
Outstanding Postdoc Mentor University of Nebraska-Lincoln	2024
Fellow Nebraska Center for Entrepreneurship	2023
Fellow PhenoRob Cluster of Excellence	2022
Paper of the Year The Plant Phenome Journal	2020

Early Career Award 2019
American Society of Plant Biologists

Plant Phenotyping Early Career Award 2019
North American Plant Phenotyping Network

Outstanding Scientific Article 2018
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)

Marcus Rhoades Early Career Award 2018
Maize Genetics Community

Junior Faculty Excellence in Research Award 2016
University of Nebraska-Lincoln

Research Support

$30.4M in total federal funding as PI/co-PI 2015-Present
(Excludes $40M in awards as part of two NSF Centers.)

Federal (Current)

USDA-NIFA "Sorghum grain: a domestic source of high-value natural waxes to increase harvest value and supply chain security." (co-PI) 2025-2028 $650k

NSF "TRTech-PGR: Digital Ideotype for Optimal Canopy Architecture" (co-PI) 2024-2027 $2.0M

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

NSF "AI Institute for Resilient Agriculture" (Investigator) 2021-2026 $20M

Non-Federal (Current)

Nebraska Corn Board "Nebraska Nitrogen Initiative." (PI) 2025-2026 $209k

Nebraska Corn Board "Genomes to Fields (G2F) - Predicting Final Yield Performance in Variable Environments." (PI) 2016-2026 $500k *(to date)*

Completed Projects

USDA-NIFA "High Intensity Phenotyping Sites: Transitioning To A Nationwide Plant Phenotyping Network." (co-PI) 2020-2025 $3M

ARPA-E "CORN (Crop Optimization Realized through Neuralnets) Demonstration" (PI) 2024-2025 $649k

NSF "RII Track-2 FEC: Functional analysis of nitrogen responsive networks in Sorghum." (co-PI) 2018-2024 $4M

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

FFAR "Crops in silico: Increasing crop production by connecting models from the microscale to the macroscale." (co-PI) 2019-2024 $5M

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

University of Nebraska "SPACE2: Space, Policy, Agriculture, Climate, and Extreme Environment." (co-PI) 2022-2024 $150k.

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 throughput 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

Founder, Dryland Genetics LLC 2014-Present
Uses 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 in arid regions where conventional agriculture fails in the absence of irrigation.

Co-Founder, Data2Bio LLC 2010-Present
Provides patented tGBS genotyping and genomic selection services to public and private sector plant and animal breeders in the USA and China.

Co-Founder, EnGeniousAg LLC 2017-2024
Designed, field tested, and deployed a low-cost in-field nutrient sensor to optimize nitrogen fertilizer applications. Acquired by CropX in 2024.

Entrepreneurship-Related Funding

NSF (to EnGeniousAg) "SBIR Phase II: Low-cost in-planta nitrate sensor" 2023-2024 $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

Industry Cooperation

Scientific Advisory Council, GeneSeek, Inc 2017-Present

Advisory Board, Afflo Sensors 2023-Present

Advisory Board, Heritable Agriculture 2025-Present

External Advisor to the Scientific Advisory Board, Indigo Agriculture 2017

External Advisor to the Scientific Advisory Board, Syngenta AG 2016

Intellectual Property

US Utility Patent 12,016,285 "Higher yielding proso (DLG240)" issued 25 June 2024 (Assignee: Dryland Genetics)

US Utility Patent 12,336,472 "Higher yielding proso (DLG40)" issued 11 June 2025 (Assignee: Dryland Genetics)

US Plant Variety Protection (PVP) Certificate 202100200 "DLG-024256 (DLG240)" issued 11 Feb 2025 (Assignee: Dryland Genetics)

US Plant Variety Protection (PVP) Certificate 202100185 "DLG-024888 (DLG40)" issued 10 Dec 2024 (Assignee: Dryland Genetics)

International Patent Application WO2025184161A1 "Higher-yielding proso varieties DLG197 and DLG317" (PCT/US2025/017324) 2025, status pending (Assignee: Dryland Genetics Inc)

US Patent Application 19/096,148 "Residuals Method to Decouple Correlated Phenotypes" 2025 (Assignee: Google)

US Patent Application 19/226,059 "Systems and Methods for Identifying DNA Sequences Regulating Pattern of Expression for Genes of Interest" 2025 (Assignee: NuTech Ventures)

US Provisional Patent Filing "A computational method for identifying specific DNA sequences that regulate the level and pattern of RNA expression for genes of interest" (Assignee: Heritable Agriculture)

Mentoring

Current Postdoctoral Mentees: Zhongjie Ji

Current Graduate Advisees: Nikee Shrestha (PhD, Complex Biosystems, FFAR Career Development Fellow), Waqar Ali (PhD, Complex Biosystems, US-Pakistan Knowledge Corridor Scholar), Jensina Davis (PhD, Complex Biosystems, NSF Grad Fellow), Harshita Mangal (PhD, Plant Breeding and Genetics), Karla Cuellar (PhD, Complex Biosystems), Ozgur Altundas (PhD, Agronomy), Sofiya Arora (MS, Agronomy), Hadiya Kounsar (MS, Agronomy)

Undergraduate Researchers: 8 NSF supported REU (Research Experience for Undergraduates) students; 3 USDA supported REEU (Research and Extension Experience for Undergraduates) students; 3 UCARE (Undergraduate Creative Activities and Research Experience) students; and 56 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.

Trainee Outcomes

12 former trainees are now faculty members across 4 countries: 5 in USA, 4 in China, 2 in Turkey, 1 in Poland.

Former Postdoctoral Mentees: Marcin Grzybowski (Assistant Professor, University of Warsaw), Guangchao Sun (Professor, Sichuan Agricultural University), Xiaoxi "Peggy" Meng (Assistant Professor, University of South Florida), Ranjita Thapa (Research Scientist, Inari Agriculture), Sunil KK Raju (Assistant Professor, University of California, Riverside), Ravi Mural (Assistant Professor, South Dakota State University), Jinliang Yang (Associate Professor, University of Nebraska–Lincoln), Yang Zhang (Research Scientist, St. Jude Children's Research Hospital)

Former Visiting Scientists and Scholars: Caner Yavuz (Assistant Professor, Nigde Omer Halisdemir University, Turkey), Khang Hoang (Genetic Data Analyst, PlantEdits), Deniz Istipliler (Assistant Professor, Ege University), Lang Yan (Professor, XiChang University)

Graduated Advisees: Daniel Carvalho, PhD (Postdoc, Federal University of Minas Gerais), Zhikai Liang, PhD (Assistant Professor, NDSU), Chenyong Miao, PhD (Phenomics Data Scientist, Bayer Crop Science), Nate Korth, PhD (Postdoc, North Carolina State University), Michael Tross, PhD (AI Developer, Corteva), Henrique Moura Dias, PhD (Postdoctoral Researcher, South Dakota State University), Hongyu Jin, PhD (Postdoc, South China Agricultural University), Fangyi Li, PhD (Postdoc, Kunming Institute of Botany), Xianjun Lai, PhD (Associate Professor, XiChang University), Xiuru Dai, PhD (Assistant Professor, Shandong Agricultural University), Santos Yenandy Barrera Lemus, PhD (Research Scientist, World Coffee Research), Preston Hurst, MS (Research Scientist, Syngenta), Mackenzie Zwiener, MS (Statistician, US Dept. of Homeland Security), Kyle Linders, MS (Research Agronomist, PivotBio), Ramesh Kanna Mathivanan, MS (PhD Student, Texas A&M), Kahheetah Barnoskie, MS, Bhushit Agarwal, MS (Software Engineer, MyVest), Srinidhi Bashyam, MS (Systems Software Developer, University of Nebraska)

Publications

H-Index: 54

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

Preprints

Shrestha N, **Ji Zhongjie**, **Dai X**, Li P, **Schnable JC**§ (2025) A sequence-based classifier distinguishes phenotype-associated genes from other gene models in plants. bioRxiv doi: 10.64898/2025.11.30.691407

Ji Z, Ge Y, **Schnable JC**§ (2025) Scalable methods for quantifying the stay green ability of corn for yield prediction by using satellite image. agriRxiv doi: 10.31220/agriRxiv.2025.00339

Zaremehrjerdi H, Coffey L, Jubery TZ, Liu H, **Turkus J**, **Linders K**, **Schnable JC**, Schnable PS, Ganapathysubramanian B§ (2025) MaizeEar-SAM: Zero-shot maize ear phenotyping. arXiv arXiv:2502.13399

Creach M, Webster B, Newton L, **Turkus J**, **Schnable JC**, Thompson A, VanBuren R§ (2025) Predicting complex phenotypes using multi-omics data in maize. bioRxiv doi: 10.1101/2025.09.30.679283

Tross MC, Duggan G, **Shrestha N**, **Schnable JC**§ (2024) Models trained to predict differential expression across plant organs identify distal and proximal regulatory regions. bioRxiv doi: 10.1101/2024.06.04.597477

Faculty Publications

175. Engelhorn J, Snodgrass S, Kok A, Seetharam A, Schneider M, Kiwit T, Singh A, Banf M, Khaipho-Burch 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§ (2025) Phenotypic variation in maize can be largely explained by genetic variation at transcription factor binding sites. Nature Genetics doi: 10.1038/s41588-025-02246-7 bioRxiv doi: 10.1101/2023.08.08.551183
Selected as an Editor's Choice by MaizeGDB Editorial Board August 2025

174. **Mangal H**, **Linders K**, **Turkus J**, **Shrestha N**, Long B, Kuang X, Cebert E, **Torres-Rodriguez JV**, **Schnable JC**§ (2025) Genes and pathways determining flowering time variation in temperate adapted sorghum. The Plant Journal doi: 10.1111/tpj.70250

173. **Shrestha N***, Powadi A*, **Davis J**, Ayanlade TT, Liu H, **Tross MC**, **Mathivanan RK**, Bares J, **Lopez-Corona L**, **Turkus J**, Coffey L, Jubery TZ, Ge Y, Sarkar S, **Schnable JC**§, Ganapathysubramanian B§, Schnable PS§ (2025) Plot-level satellite imagery can substitute for UAVs in assessing maize phenotypes across multistate field trials. Plants, People, Planet doi: 10.1002/ppp3.10613 agriRxiv doi: 10.31220/agriRxiv.2024.00251
Cover Article, June 2025 doi: 10.1002/ppp3.10528

172. Van Haute MJ, Yang Q, **Korth N**, Happ M, Kok CR, **Miao C**, Clarke J, Karnik K, Eskridge K, Urrea CA, Hyten DL, **Schnable JC**, Rose D, Benson A§ (2025) Genetic variation and historical breeding patterns in common bean (*Phaseolus vulgaris* L.) affect fermentation patterns by the human gut microbiome. Communications Biology doi: 10.1038/s42003-025-09089-2

171. Powadi A, Jubery TZ, **Tross MC**, **Shrestha N**, Coffey L, **Schnable JC**, Schnable PS, Ganapathysubramanian B§ (2025) Enhancing yield prediction from plot-level satellite imagery through genotype and environment feature disentanglement. Frontiers in Plant Science doi: 10.3389/fpls.2025.1617831

170. **Jin H**, Park A, Sreedasyam A, Li G, Ge Y, Swaminathan K, Schmutz J, Clemente TE, **Schnable JC**, Yang J§ (2025) Nitrogen response and growth trajectory of sorghum CRISPR-Cas9 mutants using high-throughput phenotyping. Genomics Communications doi: 10.48130/gcomm-0025-0011

169. **Ali W**, **Grzybowski M**, **Torres-Rodriguez JV**, **Li F**, **Shrestha N**, **Mathivanan RK**, de Bernardeaux G, Hoang K, **Mural R**, Roston RL, **Schnable JC**§, Sahay S§ (2025) Quantitative genetics of photosynthetic trait variation in maize. Journal of Experimental Botany doi: 10.1093/jxb/eraf198

168. **Istipliler D**, **Tross MC**, **Bouwens B**, **Jin H**, Yufeng Ge, Yang J, **Mural RV**, **Schnable JC**§ (2025) Heritability, heterosis, and hybrid/inbred classification ability of maize leaf hyperspectral signals under changing soil nitrogen. Crop Science doi: 10.1002/csc2.70073
"Leaf Spectra Reveal Maize Hybrid Vigor" feature in CSA News CSA News October 2025

167. **Davis JM**, Coffey LM, **Turkus J**, **López-Corona L**, **Linders K**, **Ullagaddi C**, Santra DK, Schnable PS, **Schnable JC**§ (2025) Assessing the impact of yield plasticity on hybrid performance in maize. Physiologia Plantarum doi: 10.1111/ppl.70278

166. **Davis JM**, Gaillard M, **Tross MC**, **Shrestha N**, Ostermann I, **Grove RJ**, Li B, Benes B, **Schnable JC**§ (2025) 3D reconstruction enables high-throughput phenotyping and quantitative genetic analysis of phyllotaxy. Plant Phenomics doi: 10.1016/j.plaphe.2025.100023

165. Ojeda-Rivera JO, Barnes AC, Ainsworth EA ... **Schnable JC** (48th of 56 authors) ... Zambrano MA, Zhai J, Zou J, Buckler ES§ (2025) Designing a nitrogen-efficient cold-tolerant maize for modern agricultural systems. The Plant Cell doi: 10.1093/plcell/koaf139

164. Ozair F, Adak A, Murray SC§, Alpers RT, Aviles AC, Lima DC, Edwards J, Ertl D, Gore MA, Hirsch CN, Knoll JE, **Schnable JC**, Singh MP, Sparks EE, Thompson A, Weldekidan T, Xu W (2025) Phenotypic plasticity in maize grain yield: Genetic and environmental insights of response to environmental gradients. The Plant Genome doi: 10.1002/tpg2.70078

163. Izere P, Zhao B, **Schnable JC**, Ge Y, Shi Y§ (2025) Positioning accuracy of RTK-GNSS-enabled drones and their performance in agricultural crop sensing. Journal of the ASABE doi: 10.13031/ja.16306

162. Quach TN, Guo M, Nazarenus T, Sato SJ, Wang M, Zhang T, Nersesian N, Ge Z, **Ullagaddi C**, Yu B, **Schnable JC**, and Clemente TE§ (2025) In context promoter bashing of the *Sorghum bicolor* gene models functionally annotated as bundle sheath cell preferred expressing phosphoenolpyruvate carboxykinase and alanine aminotransferase. Crop Science doi: 10.1002/csc2.70039

161. **Shrestha N**, **Mangal H**, **Torres-Rodriguez JV**, **Tross MC**, **Lopez-Corona L**, **Linders K**, **Sun G**, **Mural RV**, **Schnable JC**§ (2025) Off-the-shelf image analysis models outperform human visual assessment in identifying genes controlling seed color variation in sorghum. The Plant Phenome Journal doi: 10.1002/ppj2.70013 bioRxiv doi: 10.1101/2024.07.22.604683

160. Shrestha K, Thapa K, Kaler E, Taniguchi M, Sattler SE, **Schnable JC**, Louis J§ (2025) Employing spectral features to accelerate sorghum phenotyping against sap-feeding aphids. Plant Direct doi: 10.1002/pld3.70092

159. **Li F**, **Grzybowski M**, Roston RL, **Schnable JC**§ (2025) Nighttime fluorescence phenotyping reduces environmental variability for photosynthetic traits and enables the identification of candidate loci in maize. Frontiers in Plant Science doi: 10.3389/fpls.2025.1595339

158. **Mathivanan RK**, **Pedersen C**, **Turkus J**, **Shrestha N**, **Ali W**, **Torres-Rodriguez JV**, **Mural RV**, Obata T, **Schnable JC**§ (2025) Transcripts and genomic intervals associated with variation in metabolite abundance in maize leaves under field conditions. BMC Genomics doi: 10.1186/s12864-025-11580-3

157. **Torres-Rodriguez JV**, Li D, **Schnable JC**§ (2025) Evolving best practices for transcriptome-wide association studies accelerate discovery of gene-phenotype links. Current Opinion in Plant Biology doi: 10.1016/j.pbi.2024.102670

156. Singh A, Newton L, **Schnable JC**, Thompson AM§ (2025) Unveiling shared genetic regulators for plant architectural and biomass yield traits in sorghum. Journal of Experimental Botany doi: 10.1093/jxb/eraf012 bioRxiv doi: 10.1101/2024.03.13.584802

155. Boatwright L, Thudi M, Sangiredday MKR, Coffin AW, Tadesse HK, Vutla S, Harris-Shultz K, Knoll JE, Cuevas H, Kumar N, Soman C, **Schnable JC**, Punnuri SM[§] (2024) GWAS analysis for plant height and stem diameter in sorghum using multiple phenotyping approaches. The Plant Phenome Journal doi: 10.1002/ppj2.70008

154. Powadi A, Jubery TZ, **Tross M**, **Schnable JC**, Ganapathysubramanian B[§] (2024) Disentangling genotype and environment specific latent features for improved trait prediction using a compositional autoencoder. Frontiers in Plant Science doi: 10.3389/fpls.2024.1476070

153. Wei J, Guo T, Mu Q, Alladassi M, **Mural RV**, Boyles RE, Hoffman L, Hayes CM, **Sigmon B**, Thompson AM, Salas-Fernandez M, Rooney WL, Kresovich S, **Schnable JC**, Li X, Yu J[§] (2024) Genetic and environmental patterns underlying phenotypic plasticity in flowering time and plant height in sorghum. Plant, Cell and Environment doi: 10.1111/pce.15213

152. Delen Y, **Mural RV**, Xu G, Delen SP, **Schnable JC**, Dweikat I, Yang J[§] (2024) Dissecting the genetic architecture of sunflower disc diameter using genome-wide association study. Plant Direct doi: 10.1002/pld3.70010

151. Ostermann I, Benes B[§], Gaillard M, Li B, **Davis J**, **Grove RJ**, **Shrestha N**, **Tross MC**, **Schnable JC** (2024) Sorghum segmentation and leaf counting using an *in silico* trained deep neural model. The Plant Phenome Journal doi: 10.1002/ppj2.70002

150. **Moura Dias H**, de Teledo NA, **Mural RV**, **Schnable JC**, Van Sluys MA[§] (2024) THI1 gene evolutionary trends: A comprehensive plant-focused Assessment via data Mining and large-scale analysis. Genome Biology and Evolution doi: 10.1093/gbe/evae212

149. Sahay S[*], **Shrestha N**[*], **Moura Dias H**, **Mural RV**, **Grzybowski M**, **Schnable JC**[§], Glowacka K[§] (2024) Nonphotochemical quenching kinetics GWAS in sorghum identifies genes that may play conserved roles in maize and Arabidopsis thaliana photoprotection. The Plant Journal doi: 10.1111/tpj.16967

148. Bai G, Barker B, Scoby D, Irmak S, Luck JD, Neale CMU, **Schnable JC**, Awada T, Ge Y[§] (2024) High-throughput physiological phenotyping of crop evapotranspiration at the plot scale. Field Crop Research doi: 10.1016/j.fcr.2024.109507

147. **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[§] (2024) TWAS facilitates gene-scale trait genetic dissection through gene expression, structural variations, and alternative splicing in soybean. Plant Communications doi: 10.1016/j.xplc.2024.101010

146. **Korth N**, Yang Q, Van Haute MJ, **Tross MC**, Peng B, **Shrestha N**, **Zwiener M**, **Mural RV**, **Schnable JC**, Benson AK[§] (2024) Genomic co-localization of variation affecting agronomic and human gut microbiome traits in a meta-analysis of diverse sorghum G3 doi: 10.1093/g3journal/jkae145 bioRxiv doi: 10.1101/2023.09.20.558616

145. Khound R, Rajput SG, **Schnable JC**, Mani V, Dipak SK[§] (2024) Genome-wide association study reveals marker-trait associations for major agronomic traits in proso millet (*Panicum miliaceum* L.). Planta 10.1007/s00425-024-04465-4

144. Jia Y, **Ullagaddi C**, Allen C, Rausch K, Singh V, **Schnable JC**, Kamruzzaman M[§] (2024) Optimizing feature selection with gradient boosting machines in PLS regression for predicting moisture and protein in multi-Country corn kernels via NIR spectroscopy. Food Chemistry doi: 10.1016/j.foodchem.2024.140062

143. **Raju SKK**, **Zhang Y**, Mahboub S, **Ngu DW**, Qiu Y, Harmon FG, **Schnable JC**[§], Roston RL[§] (2024) Rhythmic lipid and gene expression responses to chilling in panicoid grasses. Journal of Experimental Botany doi: 10.1093/jxb/erae247 bioRxiv doi: 10.1101/2023.09.29.560160

142. **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 doi: 10.1002/ppj2.20106 bioRxiv doi: 10.1101/2023.12.15.571950

141. **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 doi: 10.1111/tpj.16801 bioRxiv doi: 10.1101/2023.10.31.565032
SEB-Wiley-TPJ Outstanding Original Article Award, 2024

140. **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
"Computers Learn to Predict Yield the Same Way Plant Breeders Do" feature in CSA News CSA News August 2024

139. 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

138. 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

137. 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

136. **Linders KM**, Santra D, **Schnable JC**, **Sigmon B**[§] (2024) Variation in leaf chlorophyll concentration in response to nitrogen application across maize hybrids in contrasting environments. microPublication Biology doi: 10.17912/micropub.biology.001115

135. **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
Selected as an Editor's Choice by MaizeGDB Editorial Board August 2023

134. **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
Cover Article, March 2023 "Research Highlight" doi: 10.1111/tpj.16163
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46. Ott A,[*] Liu S,[*] **Schnable JC**, Yeh CT, Wang C, Schnable PS[§] (2017) Tunable Genotyping-By-Sequencing (tGBS®) enables reliable genotyping of heterozygous loci. Nucleic Acids Research doi: 10.1093/nar/gkx853

45. **Lai X**, **Schnable JC**, Liao Z, Xu J, Zhang G, Li C, Hu E, Rong T, Xu Y, Lu Y[§] (2017) Genome-wide characterization of non-reference transposable elements insertion polymorphisms reveals genetic diversity in tropical and temperate maize. BMC Genomics doi: 10.1186/s12864-017-4103-x

44. Mei W, Boatwright L, Feng G, **Schnable JC**, Barbazuk WB[§] (2017) Evolutionarily conserved alternative splicing across monocots. Genetics doi: 10.1534/genetics.117.300189
Cover Article October 2017 Issue

43. Pandey P, Ge Y[§], Stoerger V, **Schnable JC** (2017) High throughput in vivo analysis of plant leaf chemical properties using hyperspectral imaging. Frontiers in Plant Science doi: 10.3389/fpls.2017.01348

42. **Zhang Y**, **Ngu DW**,[‡] **Carvalho D**, **Liang Z**, Qiu Y, Roston RL, **Schnable JC**[§] (2017) Differentially regulated orthologs in sorghum and the subgenomes of maize. The Plant Cell doi: 10.1105/tpc.17.00354
Selected as an Editor's Choice by MaizeGDB Editorial Board August 2017

41. **Lai X**,[*] Behera S,[*] **Liang Z**, Lu Y, Deogun JS, **Schnable JC**[§] (2017) STAG-CNS: An order-aware conserved noncoding sequence discovery tool for arbitrary numbers of species. Molecular Plant. doi: 10.1016/j.molp.2017.05.010

40. **Lai X**, **Schnable JC**[§] (2017) Harnessing the potential of the tea tree genome. Molecular Plant. doi: 10.1016/j.molp.2017.05.009

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

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

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
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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

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

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

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

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

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

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

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

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

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 C_4 grasses. Genome Biology and Evolution doi: 10.1093/gbe/evaa251 bioRxiv doi: 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

25. Studer AJ*, **Schnable JC***, Weissmann S, Kolbe AR, McKain MR, Shao Y, Cousins AB, Kellogg EA, Brutnell TP[§] (2016) The draft genome of *Dichanthelium oligosanthes*: A C3 panicoid grass species. Genome Biology doi: 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
"Insight" highlighting this article by PA Christin also published in JXB doi: 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

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

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

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

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

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

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

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
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

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

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

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

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

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
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, Jiang J§ (2012) High-resolution mapping of open chromatin in the rice genome. Genome Research doi: 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
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

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
Commentary by Birchlier and Veitia also published in Frontiers in Plant Science doi: 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

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
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
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

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

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

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 Online Only, California, USA doi: 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 Online Only, California, USA doi: 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

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

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

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, Amsterdam

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, Amsterdam

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

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 2018-2020

MaizeGDB Advisory Committee 2018-2020

Host Committee for International Plant Phenotyping Network 2024 Conference 2023-2024

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

Public Engagement

Video

Big Ten Network "B1G Impact Research" Feature on corn genetics research (2024 football season) 2024

Farm Journal: Mapping the Corn Genome 2023

RFD-TV Interview on telomere-to-telomere maize genome assembly 2023

Psomagen: A Look into Plant DNA Analysis at the Schnable Lab in Nebraska 2021

Market Journal: Sorghum as Biofuel 2019

10/11 News: Researchers aim to use FitBit technology to test water supply in corn fields 2019

Audio and Podcast

GVENCK Interview at 9th International Meeting on Plant Breeding 2025

Brownfield Ag News: University of Nebraska researcher helping develop virtual replica corn field 2024

Genome Insider Podcast: Crops as Tough as World Cup Turf 2023

Brownfield Ag News: New sensors can measure nitrates in water and growing plants 2023

KRVN Radio Interview on corn genetics 2023

1010 KSIR Farm Radio: Proso millet for the high plains 2022

Brownfield Ag News: Researchers develop Fitbit-like sensor to measure corn water use 2019

Peggy Smedley Show: IoT measures and manages plants 2018

Print and Online Stories

The Hindu: Clustering maize plants together can improve their insect resistance 2025

Lincoln Journal Star: Nebraska researchers help further understanding of how genetics affect corn development 2025

Ethanol Producer Magazine: Corn's Next Step Change 2024

Midwest Messenger: In his DNA: New Nebraska Corn Checkoff presidential chairman is leader in groundbreaking corn genetic fieldwork 2023

Nebraska Public Media: Millets — ancient drought-resistant grains — could help the Midwest survive climate change 2023

Illinois Farmer Today: Scientist develops new crop genetics for food and profit 2023

High Plains Journal: Genetic mapping offers new promise for proso millet 2019

Omaha World Herald: Nebraska, Iowa researchers developing "Fitbit for corn" to make water use more efficient 2019

Lincoln Journal Star: Robots in the cornfield? UNL team believes it's the next big thing 2019

Plantae: Faculty Job: Myths & Realities — an interview with James Schnable 2019

Invited Talks

At External Institutions

University of California-Berkeley, Berkeley, CA, USA 2025

Texas Tech, Lubbock, TX, USA 2025

The Traits Company, Durham, NC, USA 2025

North Carolina State University, Raleigh, NC, USA 2025

Bayer, St. Louis, MO USA 2025

South Dakota State University, Brookings, SD, USA 2024

University of Toronto, Toronto, Canada 2024

University of Georgia-Athens, Athens, GA, 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 *(Remote)*
CIRAD, Montpellier, France	2022
California State East Bay, Hayward, CA, USA	2021 *(Remote, COVID)*
University of Missouri, Columbia, MO, USA	2020 *(Remote, COVID)*
Rutgers University, New Brunswick, NJ, USA	2020 *(Remote, COVID)*
Bayer Crop Science, St. Louis, MO, USA	2020 *(Remote, COVID)*
University of Bonn, Bonn, Germany	2020 *(Remote, COVID)*
King Abdullah University of Science and Technology, Jeddah, Saudi Arabia	2020 *(Remote, COVID)*
University of Hawaii, Manoa, HI, USA *(Brewbaker Lecture)*	2019
Miami University, Oxford, OH, USA	2019
University of Massachusetts Amherst, Amherst, MA, 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.

Pan-Regulatory Genomics, Plant and Animal Genome, San Diego, CA, USA 2026

Molecular Plant Science, Genomics, and AI for Research and Breeding, Plant and Animal Genome, San Diego, CA, USA 2026

Plant Cistromics, Plant and Animal Genome, San Diego, CA, USA 2026

KWS Vegetable Breeding and Research, Wageningen, Netherlands 2025 *(Remote)*

9th International Meeting on Plant Breeding (Student Organized), Piracicaba, Sao Paulo, Brazil 2025

Corteva New Frontiers Conference, Johnston, IA, USA 2025

Baker Plant Breeding Symposium (Student Organized), Ames, IA, USA 2025

Scaling Trait Discovery Session, Plant and Animal Genome, San Diego, CA, USA 2025

CSU Crop Adaptation Symposium (Student Organized), Fort Collins, CO, USA 2024

West African Plant Science Symposium (Student Organized) 2024 *(Remote)*

CROPS, Huntsville, AL, USA 2024

Freeling Symposium, Berkeley, CA, USA 2024

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 *(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 *(Remote, COVID)*
National Association of Plant Breeders Annual Meeting, Lincoln, NE, USA	2020 *(Remote, COVID)*
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^2IRC 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

American Society for Plant Biology Midwest, Lincoln, NE	2025
Nebraska Sorghum Symposium, Grand Island, NE	2025
Great Plains Network Annual Meeting, Lincoln, NE	2024
Nebraska Agribusiness Club, Lincoln, NE	2024
Animal Science Departmental Seminar Series, UNL	2023
CROPS Entrepreneurship/Industry Career Panel (Student Organized), UNL	2023
Complex Biosystems Seminar Series, UNL	2021 *(In Person, COVID)*
Agronomy & Horticulture Departmental Seminar Series, UNL	2020 *(Remote, COVID)*
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