

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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Employment

Assistant Professor Department of Agronomy and Horticulture, University of Nebraska-Lincoln	2014-present
NSF PGRP Fellowship Supported Visiting Scholar Chinese Academy of Agricultural Sciences	2014
NSF PGRP Fellowship Supported Postdoctoral Researcher Donald Danforth Plant Science Center	2013

Education

PhD Plant Biology (with Michael Freeling) University of California-Berkeley	2008-2012
BA Biology Cornell University	2004-2008

Honors and Awards

Marcus Rhoades Early Career Award	2018
Junior Faculty Excellence in Research Award, University of Nebraska-Lincoln	2016
Faculty Fellow, Robert B. Dougherty Water for Food Institute	2016-Present

Current Support

Federal

USDA-NIFA "Identifying mechanisms conferring low temperature tolerance in maize, sorghum, and frost tolerant relatives." (PI)

USDA/NSF Joint Program "PAPM EAGER: Transitioning to the next generation plant phenotyping robots." (co-PI)

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

NSF-EPSCoR "Center for Root and Rhizobiome Innovation." (Investigator & Management Team Member)

DOE-JGI Community Sequencing Program "Expanding grass genome comparators."

Non-Federal

ICRISAT “Application of tGBS And Genomic Selection to a Hybrid Pearl Millet Breeding Program.”

North Central Sun Grants “High through put phenotyping to accelerate biomass sorghum improvement.” (co-PI)

ConAgra “Marker Discovery & Genetic Diversity.” (in popcorn)

Nebraska Corn Board “Genomes to Fields (G2F) - Predicting Final Yield Performance in Variable Environments.” (PI)

Agricultural Research Division “A High Throughput Phenotyping Reference Dataset for GWAS in Sorghum” (PI)

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)

Economic Development

Co-Founder, EnGeniousAg LLC	2017-Present
Founder, Dryland Genetics LLC	2014-Present
Co-Founder, Data2Bio LLC	2010-Present
Scientific Advisory Council, GeneSeek, Inc	2017,2018
External Advisor to the Scientific Advisory Board, Indigo Agriculture	2017
External Advisor to the Scientific Advisory Board, Syngenta AG	2016

Advising

Current Advisees: Daniel Carvalho (PhD, Agronomy & Horticulture), Zhikai Liang (PhD, Agronomy & Horticulture), Chenyong Miao (PhD, Agronomy & Horticulture), Xiuru Dai (PhD, Shandong Agriculture University), Preston Hurst (MS, Agronomy & Horticulture),

Thesis Committee: Abbas Atefi (PhD, Biological Systems Engineering), Yen Ning Chai (PhD, Agronomy & Horticulture), Waseen Huassain (PhD, Agronomy & Horticulture), Ying Ren (PhD, Agronomy & Horticulture), Mallory Suhr (PhD, Food Science), Qinnan Yang (PhD, Food Science), Piyush Pandey (MS, Biological Systems Engineering), Thao Yu (MS, Statistics)

Graduated Advisees: Xianjun Lai (PhD, Sichuan Agriculture University), Bhushit Agarwal (co-advised, MS, Computer Science & Engineering), Srinidhi Bashyam (co-advised, MS, Computer Science & Engineering)

Publications

H-Index: 20 **Google Scholar**

*Lab members in bold, *equal contribution, †undergraduate, §corresponding*

Preprints

Yan L, Lai X, Rodriguez O, Mahboub S, Roston RL, **Schnable JC**.[§] Parallels between artificial selection in temperate maize and natural selection in the cold-adapted crop-wild relative *Tripsacum*. bioRxiv doi: [10.1101/187575](https://doi.org/10.1101/187575)

Other Manuscripts in Review

Zou C, Miki D, Li D, Tang Q, Xiao L, Rajput S, Deng P, Peng L, Huang R, Zhang M, Sun Y, Hu J, Fu X, Schnable P, Li F, Zhang H, Feng B, Zhu X, Liu R, **Schnable JC**, Zhu JK, Zhang H.[§] The genome of broomcorn millet (*Panicum miliaceum* L.) (*In Review*)

Ott A, **Schnable JC**, Yeh CT, Wu L, Liu C, Hu HC, Dolgard CL, Sarkar S, Schnable PS.[§] Linked read technology for assembling large complex and polyploid genomes. (*In Review*)

Liang Z, Gupta SK, Yeh CT, **Zhang Y**, Ngu DW,[‡] Kumar R, Patil HT, Mungra KD, Yadav DV, Rathore A, Srivastava RK, Gupkta R, **Yang J**, Varshney RK, Schnable PS, **Schnable JC**.[§] Phenotypic data from inbred parents can improve genomic prediction in pearl millet hybrids. (*In Review*)

Faculty Publications

53. **Miao C**, Fang J, Liang P, Zhang X, **Schnable JC**, Tang H.[§] (2018) Genotype-Corrector: improved genotype calls for genetic mapping. SCIENTIFIC REPORTS (*Accepted pending revision*)
52. Alkhalifah N, Campbell DA, Falcon CM, ... **Schnable JC** (31 of 42 authors) ... Spalding EP, Edwards J, Lawrence-Dill CJ[§] (2018) Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. BMC RESEARCH NOTES (*Accepted pending minor revisions*)
51. Xu Y, Qiu Y, **Schnable JC**.[§] (2018) Functional modeling of plant growth dynamics. THE PLANT PHENOME doi: [10.2135/tppj2017.09.0007](https://doi.org/10.2135/tppj2017.09.0007) BIORxIV doi: [10.1101/190967](https://doi.org/10.1101/190967)
50. **Carvalho DS**, **Schnable JC**, Almeida AMR[§] (2018) Integrating phylogenetic and network approaches to study gene family evolution: the case of the AGAMOUS family of floral genes. EVOLUTIONARY BIOINFORMATICS (*In Press*) BIORxIV doi: [10.1101/195669](https://doi.org/10.1101/195669)
49. **Lai X**, **Yan L**, Lu Y, **Schnable JC**[§] (2018) Largely unlinked gene sets targeted by selection for domestication syndrome phenotypes in maize and sorghum. THE PLANT JOURNAL doi: [10.1111/tpj.13806](https://doi.org/10.1111/tpj.13806) BIORxIV doi: [10.1101/184424](https://doi.org/10.1101/184424)
48. **Liang Z**, **Schnable JC**[§] (2017) Functional divergence between subgenomes and gene pairs after whole genome duplications. MOLECULAR PLANT doi: [10.1016/j.molp.2017.12.010](https://doi.org/10.1016/j.molp.2017.12.010)
47. **Liang Z**, Pandey P, Stoerger V, Xu Y, Qiu Y, Ge Y, **Schnable JC**[§] (2017) Conventional and hyperspectral time-series imaging of maize lines widely used in field trials. GIGASCIENCE doi: [10.1093/giga-science/gix117](https://doi.org/10.1093/giga-science/gix117) BIORxIV doi: [10.1101/169045](https://doi.org/10.1101/169045)
46. Gage J, Jarquin D, Romay M, ... **Schnable JC** (29th of 40 authors) .. Yu J, de Leon N[§] (2017) The effect of artificial selection on phenotypic plasticity in maize. NATURE COMMUNICATIONS doi: [10.1038/s41467-017-01450-2](https://doi.org/10.1038/s41467-017-01450-2)
Selected as an Editor's Choice by MaizeGDB Editorial Board December 2017
45. Washburn JD, **Schnable JC**, Brutnell TP, Shao Y, **Zhang Y**, Ludwig M, Davidse G, Pires JC[§] (2017) Genome-guided phylo-transcriptomic methods and the nuclear phylogenetic tree of the paniceae grasses. SCIENTIFIC REPORTS doi: [10.1038/s41598-017-13236-z](https://doi.org/10.1038/s41598-017-13236-z)
44. 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](https://doi.org/10.1093/nar/gkx853)
43. **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](https://doi.org/10.1186/s12864-017-4103-x)

42. Mei W, Boatwright L, Feng G, **Schnable JC**, Barbazuk WB^S (2017) Evolutionarily conserved alternative splicing across monocots. *GENETICS* doi: [10.1534/genetics.117.300189](https://doi.org/10.1534/genetics.117.300189)
Cover Article October 2017 Issue
41. Pandey P, Ge Y^S, 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](https://doi.org/10.3389/fpls.2017.01348)
40. **Zhang Y**, Ngu DW,[‡] **Carvalho D**, **Liang Z**, Qiu Y, Roston RL, **Schnable JC**^S (2017) Differentially regulated orthologs in sorghum and the subgenomes of maize. *THE PLANT CELL* doi: [10.1105/tpc.17.00354](https://doi.org/10.1105/tpc.17.00354)
Selected as an Editor's Choice by MaizeGDB Editorial Board August 2017
39. **Lai X**,* **Behera S**,* **Liang Z**, Lu Y, Deogun JS, **Schnable JC**^S (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](https://doi.org/10.1016/j.molp.2017.05.010)
38. **Lai X**, **Schnable JC**^S (2017) Harnessing the potential of the tea tree genome. *MOLECULAR PLANT*. doi: [10.1016/j.molp.2017.05.009](https://doi.org/10.1016/j.molp.2017.05.009)
37. Mei W, Liu S, **Schnable JC**, Yeh C, Springer NM, Schnable PS, Barbazuk WB^S (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)
36. Joyce BL, Huag-Baltzell A, Davey S, Bomhoff M, **Schnable JC**, Lyons E^S (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)
35. Walley JW,* Sartor RC,* Shen Z, Schmitz RJ, Wu KJ, Urich MA, Nery JR, Smith LG, **Schnable JC**, Ecker JR, Briggs SP^S (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
34. Ge Y^S, 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)
33. **Liang Z**, **Schnable JC**^S (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)
32. Rajput SG, Santra DK^S, **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)
31. Chao S, Wu J, Liang J, **Schnable JC**, Yang W, Cheng F, Wang X^S (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)
30. Tang H, Bomhoff MD, Briones E, **Schnable JC**, Lyons E^S (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)
29. Washburn JD, **Schnable JC**, Davidse G, Pires JC^S (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)
28. Tang H, Zhang X, **Miao C**, Zhang J, Ming R, **Schnable JC**, Schnable PS, Lyons E, Lu J^S (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)
27. **Schnable JC**^S (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)
26. Paschold A, Larson NB, Marcon C, **Schnable JC**, Yeh C, Lanz C, Nettleton D, Piepho H, Schnable PS, Hochholdinger F^S (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

25. 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. MOLEUCLEAR BIOLOGY REPORTS doi: [10.1007/s11033-018-4144-5](https://doi.org/10.1007/s11033-018-4144-5)
24. 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](https://doi.org/10.1186/s13059-016-1080-3)
23. 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)
22. 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)
21. 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)
20. 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* × *Setaria viridis*. PLOS ONE doi: [10.1371/journal.pone.0101868](https://doi.org/10.1371/journal.pone.0101868)
19. 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

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
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
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 Proceedings

3. 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)
2. Nani T, **Schnable JC**, Washburn J, Albert P, Pereira W, Birchler J, Souza Sobrinho F, Technio V. (2017) Construction of physical maps of chromosomes in brachiaria spp. beginning a journey. *11TH EUROPEAN CYTOGENETICS CONFERENCE Florence, Italy*

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

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

Service: selected, 2014-Present

University

Consortium for Integrated Translational Biology (CITB)	2014-Present
UNL Faculty Greenhouse Committee	2015-Present
Department of Agronomy and Horticulture Peer Evaluation Committee	2016-Present
Biotech Seminar Series Committe	2017-Present
Agronomy and Horticulture Faculty Advisory Committee	2017-Present
Nebraska Food for Health Center Faculty Advisory Committee	2017-Present
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

Peer Reviewer (selected, recent): Bioinformatics, G3: Genes | Genomes | Genetics, Genome Biology & Evolution, Heredity, Molecular Biology and Evolution, Molecular Plant, Nature Communications, Nature Plants, New Phytologist, PeerJ, Photosynthesis Research, Plant Cell, Plant Cell & Environment, The Plant Genome, The Plant Journal, Plant Methods, Plant Physiology, PLoS Genetics

Invited Talks:

External at Institutions

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	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

External at Conferences

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

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 Deigo, 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

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