

CURRICULUM VITAE

JAMES C. SCHNABLE

Quantitative Life Sciences Initiative
Center for Plant Science Innovation
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^aClickable hyperlinks are in red throughout

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

NAPPN Plant Phenotyping Early Career Award	2019
Marcus Rhoades Early Career Award	2018
Tansley Medal Finalist	2018
Junior Faculty Excellence in Research Award, University of Nebraska-Lincoln	2016
Faculty Fellow, Robert B. Dougherty Water for Food Institute	2016-Present

Research Support

Federal (Current)

NSF "RoL: FELS: EAGER: Genetic Constraints on the Increase of Organismal Complexity Over Time"
(PI)

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

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)

NSF “RII Track-2 FEC: Functional analysis of nitrogen responsive networks in Sorghum.” (co-PI)

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

ARPA-E “Low cost wireless chemical sensor networks.” (co-PI)

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

NSF “Center for Root and Rhizobiome Innovation.” (Investigator & Management Team Member)

Non-Federal (Current)

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

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

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

Midwest Big Data Hub “Automatic feature extraction pipeline development for high-throughput plant phenotyping” (co-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)

Completed Projects

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

Iowa Corn Board “Field Deployable Cameras to Quantify Dynamic Whole Plant Phenotypes in the Field.” (PI)

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

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)

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

Economic Development

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
<i>Providing patented tGBS genotyping and genomic selection services to public and private sector plant and animal breeders in the USA and China.</i>	
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 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), Nate Korth (co-advised, PhD, Food Science)

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), Ronghao Wang (PhD, Statistics), 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: 24 **Google Scholar**

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

Preprints

Liang Z, Qiu Y, **Schnable JC**.[§] Distinct characteristics of genes associated with phenome-wide variation in maize (*Zea mays*). *BioRxiv* doi: [10.1101/534503](https://doi.org/10.1101/534503)

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)

Hurst P, **Liang Z**, **Smith C**, Yerka M, **Sigmon B**, Rodriguez O, **Schnable JC**.[§] Genome wide analysis of Ga1-s modifiers in maize. *BioRxiv* doi: [10.1101/543264](https://doi.org/10.1101/543264)

Other Manuscripts in Review

Bai G, Ge Y.[§] Scoby D, Leavit B, Irmak S, Graef G, **Schnable JC**, Awada T. NU-Spidercam: A large-scale, cable-driven, integrated sensing and robotic system for precision phenotyping, remote sensing, and agronomic research. (*In Review*)

Qi P, Eudy D, **Schnable JC**, Schmutz J, Raymer P, Devos KM.[§] High density genetic maps of seashore paspalum using genotyping-by-sequencing and their relationship to the *Sorghum bicolor* genome. (*In Review*)

Zheng Z, Hey S, Jubery T, Liu T, Yang Y, Coffey L, **Miao C, Sigmon B, Schnable JC**, Hochholdinger F, Ganapathysubramanian B, Schnable PS.[§] Shared genetic control of root system architecture between *Zea mays* and *Sorghum bicolor*. (In Review)

Schnable JC[§] Genes and Gene Models: an Important Distinction (In Review)

Faculty Publications

59. 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[§] (2019) The genome of broomcorn millet (2018) NATURE COMMUNICATIONS doi: [10.1038/s41467-019-08409-5](https://doi.org/10.1038/s41467-019-08409-5)
58. **Miao C, Yang, J, Schnable JC**[§] (2018) Optimizing the identification of causal variants across varying genetic architectures in crops. PLANT BIOTECHNOLOGY JOURNAL doi: [10.1111/pbi.13023](https://doi.org/10.1111/pbi.13023) BIORxIV doi: [10.1101/310391](https://doi.org/10.1101/310391)
57. Ott A, **Schnable JC**, Yeh CT, Wu L, Liu C, Hu HC, Dolgard CL, Sarkar S, Schnable PS[§] (2018) Linked read technology for assembling large complex and polyploid genomes. BMC GENOMICS doi: [10.1186/s12864-018-5040-z](https://doi.org/10.1186/s12864-018-5040-z)
56. Liu S,* **Schnable JC**,* Ott A,* Yeh CT, Springer NM, Yu J, Meuhbauer G, Timmermans MCP, Scanlon MJ, Schnable PS[§] (2018) Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. MOLECULAR BIOLOGY AND EVOLUTION doi: [10.1093/molbev/msy174](https://doi.org/10.1093/molbev/msy174)
55. **Raju SKK**, Barnes A, **Schnable JC**, Roston RL[§] (2018) Low-temperature tolerance in land plants: Are transcript and membrane responses conserved? PLANT SCIENCE doi: [10.1016/j.plantsci.2018.08.002](https://doi.org/10.1016/j.plantsci.2018.08.002)
54. **Miao C**, Fang J, Li D, Liang P, Zhang X, **Yang J, Schnable JC**, Tang H[§] (2018) Genotype-Corrector: improved genotype calls for genetic mapping. SCIENTIFIC REPORTS doi: [10.1038/s41598-018-28294-0](https://doi.org/10.1038/s41598-018-28294-0)
53. Alkhalifah N, Campbell DA, Falcon CM, ... **Schnable JC** (31 of 44 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 doi: [10.1186/s13104-018-3508-1](https://doi.org/10.1186/s13104-018-3508-1)
52. **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**[§] (2018) Phenotypic data from inbred parents can improve genomic prediction in pearl millet hybrids. G3: GENES GENOMES GENETICS doi: [10.1534/g3.118.200242](https://doi.org/10.1534/g3.118.200242)
Selected as the outstanding scientific article of 2018 by ICRISAT's research program in Asia.
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 doi: [10.1177/1176934318764683](https://doi.org/10.1177/1176934318764683) 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/tbj.13806](https://doi.org/10.1111/tbj.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^S (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^S (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^S (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^S (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^S (2018). Location of low copy genes in chromosomes of *Brachiaria* spp. *MOLECULAR BIOLOGY REPORTS* doi: [10.1007/s11033-018-4144-5](https://doi.org/10.1007/s11033-018-4144-5)
24. Studer AJ*, **Schnable JC***, Weissmann S, Kolbe AR, McKain MR, Shao Y, Cousins AB, Kellogg EA, Brutnell TP^S (2016) The draft genome of *Dichanthelium oligosanthos*: 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^S (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^S (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^S (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^S (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^S, **Schnable JC**, Bennetzen JL, Li J^S (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,^S Wang X^S (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^S (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^S (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,^S Freeling M^S (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^S (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^S (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^S, 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^S, 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^S (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^S (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^S (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^S (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^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

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
Biotech Seminar Series Committee	2017-Present
Agronomy and Horticulture Faculty Advisory Committee	2017-Present
Nebraska Food for Health Center Faculty Advisory Committee	2017-Present
Department of Agronomy and Horticulture Awards Committee	2019-Present
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
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

Invited Talks:

External at Institutions

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

External at Conferences

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

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

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