

# CURRICULUM VITAE

## JAMES C. SCHNABLE

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

Office: E207 Beadle Center  
Phone: (402) 472-3192  
Email: [schnable@unl.edu](mailto:schnable@unl.edu)  
Web: [schnablelab.org](http://schnablelab.org)

### 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

Junior Faculty Excellence in Research Award	2016
UNL Nominee, New Innovator in Food and Agriculture Research	2017
Faculty Fellow, Robert B. Dougherty Water for Food Institute	2016,2017

### Current Support

#### *Federal*

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

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

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

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)

**Economic Development**

Founder, Dryland Genetics LLC 2014-Present

Co-Founder, **Data2Bio LLC** 2010-Present

**Current Advising**

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

PhD Committee: Abbas Atefi (Biological Systems Engineering), Waseen Huassain (Agronomy & Horticulture), Ying Ren (Agronomy & Horticulture), Mallory Suhr (Food Science)

Masters Committee: Piyush Pandey (Biological Systems Engineering), Thao Yu (Statistics)

**Publications**

H-Index: 16 **Google Scholar**

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

*Preprints*

**Zhang Y, Ngu DW,† Carvalho D, Liang Z, Qiu Y, Roston RL, Schnable JC.**§ Differentially regulated orthologs in sorghum and the subgenomes of maize. **bioRxiv** doi: **10.1101/120303**

Ott A,\* Liu S,\* **Schnable JC**, Yeh CT, Wang C, Schnable PS.§ Tunable Genotyping-By-Sequencing (tGBS®) enables reliable genotyping of heterozygous loci. **bioRxiv** doi: **10.1101/100461**

Mei W, Boatwright L, Feng G, **Schnable JC**, Barbazuk WB.§ Evolutionarily conserved alternative splicing across monocots. **bioRxiv** doi: **10.1101/120469**

*Other Manuscripts in Review*

**Miao C**, Fang J, Liang P, Zhang X, **Schnable JC**, Tang H.<sup>§</sup> Genotype-Corrector: improved genotype calls for genetic mapping. (*In Review*)

Pandey P, Ge Y<sup>§</sup>, Stoerger V, **Schnable JC**. High throughput in vivo analysis of plant leaf chemical properties using hyperspectral imaging. (*In Review*)

Washburn JD, **Schnable JC**, Brutnell TP, Shao Y, **Zhang Y**, Ludwig M, Davidse G, Pires JC.<sup>§</sup> Genome-Guided Phylo-Transcriptomics. (*In Review*)

*Faculty Publications*

38. **Lai X**,\* **Behera S**,\* **Liang Z**, Lu Y, Deogun JS, **Schnable JC**<sup>§</sup> (2017) STAG-CNS: An order-aware conserved noncoding sequence discovery tool for arbitrary numbers of species. *MOLECULAR PLANT*. (*In Press*) [BIORxiv preprint doi: 10.1101/120428](https://doi.org/10.1101/120428)
37. **Lai X**, **Schnable JC**<sup>§</sup> (2017) Harnessing the potential of the tea tree genome. *MOLECULAR PLANT*. (*In Press*)
36. Mei W, Liu S, **Schnable JC**, Yeh C, Springer NM, Schnable PS, Barbazuk WB<sup>§</sup> (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)
35. Joyce BL, Huag-Baltzell A, Davey S, Bomhoff M, **Schnable JC**, Lyons E<sup>§</sup> (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)
34. Walley JW,\* Sartor RC,\* Shen Z, Schmitz RJ, Wu KJ, Urich MA, Nery JR, Smith LG, **Schnable JC**, Ecker JR, Briggs SP<sup>§</sup> (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*
33. Ge Y<sup>§</sup>, 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)
32. **Liang Z**, **Schnable JC**<sup>§</sup> (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) [BIORxiv preprint doi: 10.1101/043513](https://doi.org/10.1101/043513)
31. Rajput SG, Santra DK<sup>§</sup>, **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)
30. Chao S, Wu J, Liang J, **Schnable JC**, Yang W, Cheng F, Wang X<sup>§</sup> (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)
29. Tang H, Bomhoff MD, Briones E, **Schnable JC**, Lyons E<sup>§</sup> (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)
28. Washburn JD, **Schnable JC**, Davidse G, Pires JC<sup>§</sup> (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)
27. Tang H, Zhang X, **Miao C**, Zhang J, Ming R, **Schnable JC**, Schnable PS, Lyons E, Lu J<sup>§</sup> (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)
26. **Schnable JC**<sup>§</sup> (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)

25. Paschold A, Larson NB, Marcon C, **Schnable JC**, Yeh C, Lanz C, Nettleton D, Piepho H, Schnable PS, Hochholdinger F<sup>S</sup> (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

24. Studer AJ\*, **Schnable JC\***, Weissmann S, Kolbe AR, McKain MR, Shao Y, Cousins AB, Kellogg EA, Brutnell TP<sup>S</sup> (2016) The draft genome of *Dichanthelium oligosanthes*: A C<sub>3</sub> 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<sup>S</sup> (2016) Cross species selection scans identify components of C<sub>4</sub> 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<sup>S</sup> (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<sup>S</sup> (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<sup>S</sup> (2014) Mapping of Quantitative Trait Locus (QTLs) that Contribute to Germination and Early Seedling Drought Tolerance in the Interspecific Cross *Setaria italica* x *Setaria viridis*. *PLoS ONE* doi: [10.1371/journal.pone.0101868](https://doi.org/10.1371/journal.pone.0101868)
19. Diao X<sup>S</sup>, **Schnable JC**, Bennetzen JL, Li J<sup>S</sup> (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,<sup>S</sup> Wang X<sup>S</sup> (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<sup>S</sup> (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<sup>S</sup> (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,<sup>S</sup> Freeling M<sup>S</sup> (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<sup>S</sup> (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<sup>S</sup> (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<sup>§</sup>, 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<sup>§</sup>, 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<sup>§</sup> (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<sup>§</sup> (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<sup>§</sup> (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<sup>§</sup> (2011) Comparative genomics with maize and other grasses: from genes to genomes. *MAYDICA* [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<sup>§</sup> (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**<sup>§</sup>, 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<sup>§</sup> (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. <sup>†</sup>Woodhouse MR,\* **Schnable JC**,\* Pedersen BS, Lyons E, Lisch D, Subramaniam S, Freeling M<sup>§</sup> (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*

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

*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 from last 2 years

*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 Committee	2017-Present
Organizing Committee “ <b>Predictive Crop Design, Genome to Phenome</b> ”	2017
Agricultural Research Division Faculty Search Committee	2016
Quantitative Life Sciences Initiative Faculty Search Committee	2016
Department of Agronomy and Horticulture Faculty Search Committee	2016
Organizing Committee “ <b>Plant Phenomics: from pixels to traits</b> ”	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, Plant Cell, Plant Cell & Environment, The Plant Genome, The Plant Journal, Plant Methods, Plant Physiology, PLoS Genetics

## Invited Talks:

*External at Institutions*

Iowa State University, Ames, IA	2017
University of Missouri-Columbia, Columbia, MO	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.*

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*

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