

FIVE YEAR PUBLICATION LIST

JAMES C. SCHNABLE

H-Index: 30

Lab members in **bold**.

Postdoc/visiting scholar† in Schnable Lab.

Graduate student‡ in Schnable Lab.

Undergraduate authors in Schnable Lab.

Authors contributed equally*

Journal Publications 2020-2016

2020 Journal Publications (N=18)

71. **Liang Z‡**, Qiu Y, **Schnable JC** (2020) Distinct characteristics of genes associated with phenome-wide variation in maize (*Zea mays*). MOLECULAR PLANT doi: [10.1016/j.molp.2020.03.003](https://doi.org/10.1016/j.molp.2020.03.003) bioRxiv doi: [10.1101/534503](https://doi.org/10.1101/534503)
Selected as an Editor's Choice by MaizeGDB Editorial Board May 2020
JOURNAL IMPACT FACTOR (2020 REPORT): 12.1
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 52 (96th)
SCHNABLE LAB PERCENT CONTRIBUTION: 80%
CONTRIBUTION STATEMENT: All aspects of the paper with the exception of generating the original statistical method (Y. Qiu).
70. **Miao C‡**, Xu Y, Liu S, Schnable PS, **Schnable JC** (2020) Increased power and accuracy of causal locus identification in time-series genome-wide association in sorghum. PLANT PHYSIOLOGY doi: [10.1104/pp.20.00277](https://doi.org/10.1104/pp.20.00277) bioRxiv doi: [10.1101/2020.02.16.951467](https://doi.org/10.1101/2020.02.16.951467)
"News and Views" highlighting this article by Y Yu doi: [10.1104/pp.20.00797](https://doi.org/10.1104/pp.20.00797)
JOURNAL IMPACT FACTOR (2020 REPORT): 6.9
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 29 (91st)
SCHNABLE LAB PERCENT CONTRIBUTION: 80%
CONTRIBUTION STATEMENT: Y. Xu ran a new type of statistical analysis he had generated at Iowa State, S. Liu and PS Schnable contributed genotyping data for the sorghum population, all other aspects of the paper carried out by Schnable lab members.
69. **Dai X‡**, Xu Z, **Liang Z‡**, Tu X, Zhong S, **Schnable JC**, Li P (2020) Non-homology based prediction of gene functions. THE PLANT GENOME doi: [10.1002/tpg2.20015](https://doi.org/10.1002/tpg2.20015) bioRxiv doi: [10.1101/730473](https://doi.org/10.1101/730473)
JOURNAL IMPACT FACTOR (2020 REPORT): 3.8
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 16 (96th)
SCHNABLE LAB PERCENT CONTRIBUTION: 90%
CONTRIBUTION STATEMENT: Z Xu, X Tu, and S Song contributed data. P Li co-mentored X Dai with Prof. Schnable. All other aspects of the paper carried out by Schnable lab members.
68. **Miao C‡**, **Pages A**, Xu Z, Rodene E, Yang J, **Schnable JC** (2020) Semantic segmentation of sorghum using hyperspectral data identifies genetic associations. PLANT PHENOMICS doi: [10.34133/2020/4216373](https://doi.org/10.34133/2020/4216373)
JOURNAL IMPACT FACTOR (2020 REPORT): New Journal
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 32 (93rd)
SCHNABLE LAB PERCENT CONTRIBUTION: 80%
CONTRIBUTION STATEMENT: R Rodene and J Yang contributed data. Z Xu advised on statistical analysis methods. All other aspects of the paper carried out by Schnable lab members.

67. **Carvalho DS†, Nishimwe AV, Schnable JC** (2020) IsoSeq transcriptome assembly of C₃ panicoid grasses provides tools to study evolutionary change in the Panicoideae. *PLANT DIRECT* [10.1002/pld3.203](https://doi.org/10.1002/pld3.203) *BioRxiv* doi: [10.1101/689356](https://doi.org/10.1101/689356)
 JOURNAL IMPACT FACTOR (2020 REPORT): 1.7
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 26 (92nd)
 SCHNABLE LAB PERCENT CONTRIBUTION: 100%
 CONTRIBUTION STATEMENT: N/A

66. **Lai X†, Bendix C, Yan L†, Zhang Y†, Schnable JC, Harmon F** (2020) Interspecific analysis of diurnal gene regulation in panicoid grasses identifies known and novel regulatory motifs. *BMC GENOMICS* doi: [10.1186/s12864-020-06824-3](https://doi.org/10.1186/s12864-020-06824-3)
Selected as an Editor's Choice by MaizeGDB Editorial Board October 2020
 JOURNAL IMPACT FACTOR (2020 REPORT): 3.6
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 11 (91st)
 SCHNABLE LAB PERCENT CONTRIBUTION: 75%
 CONTRIBUTION STATEMENT: Plants were grown and RNA samples were collected in the Harmon lab. RNA-seq libraries were build and sequenced in the Schnable lab. Expression, comparative genomics, and promoter motif analysis conducted in the Schnable lab. Phylogenetic analysis of clock genes conducted in the Harmon lab.

65. Adams J, Qiu Y, Xu Y, **Schnable JC** (2020) Plant segmentation by supervised machine learning methods. *THE PLANT PHENOME JOURNAL* doi: [10.1002/ppj2.20001](https://doi.org/10.1002/ppj2.20001)
 JOURNAL IMPACT FACTOR (2020 REPORT): New Journal
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 9 (71st)
 SCHNABLE LAB PERCENT CONTRIBUTION: 25%
 CONTRIBUTION STATEMENT: Provided the datasets employed in the paper. Originated idea for including neighborhood information for pixel classification. Drafted portions of the paper and revised the remainder.

64. **Raju SKK†, Atkins M, Enerson A, Carvalho DS†, Studer AJ, Ganapathysubramanian B, Schnable PS, Schnable JC** (2020) Leaf Angle eXtractor - A high throughput image processing framework for leaf angle measurement in maize and sorghum. *APPLICATIONS IN PLANT SCIENCES* doi: [10.1002/aps3.11385](https://doi.org/10.1002/aps3.11385)
 JOURNAL IMPACT FACTOR (2020 REPORT): 1.6
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 25 (73rd)
 SCHNABLE LAB PERCENT CONTRIBUTION: 75%
 CONTRIBUTION STATEMENT: AJ Studer collaborated with JC Schnable in generating one of the several time lapse datasets analyzed. M Atkins, B Ganapathysubramanian and PS Schnable developed a new algorithm to track leaf angles in images. All other aspects of the paper conducted in the Schnable lab.

63. Han J, Wang P, Wang Q, Lin Q, Yu G, **Miao C†, Dao Y, Wu R, Schnable JC, Tang H, Wang K** (2020) Genome-wide characterization of DNase I-hypersensitive sites and cold response regulatory landscapes in grasses. *THE PLANT CELL* doi: [10.1105/tpc.19.00716](https://doi.org/10.1105/tpc.19.00716)
"In Brief" highlighting this article by SKK Raju doi: [10.1105/tpc.20.00471](https://doi.org/10.1105/tpc.20.00471)
 JOURNAL IMPACT FACTOR (2020 REPORT): 9.6
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 20 (65th)
 SCHNABLE LAB PERCENT CONTRIBUTION: 20%
 CONTRIBUTION STATEMENT: Generating conserved noncoding sequence data, coming up with an implementing a method to compare patterns of change open chromatin data for equivalent regions of gene promoters across species.

62. Zheng Z, Hey S, Jubery T, Liu T, Yang Y, Coffey L, **Miao C†, Sigmon B, Schnable JC, Hochholdinger F, Ganapathysubramanian B, Schnable PS** (2020) Shared genetic control of root system architecture between *Zea mays* and *Sorghum bicolor*. *PLANT PHYSIOLOGY* doi: [10.1104/pp.19.00752](https://doi.org/10.1104/pp.19.00752)
 JOURNAL IMPACT FACTOR (2020 REPORT): 6.9

ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 41 (95th)

SCHNABLE LAB PERCENT CONTRIBUTION: 25%

CONTRIBUTION STATEMENT: Sorghum portion of paired maize and sorghum field trials. Developing and implementing a method to compare the outcomes of GWAS analyses between maize and sorghum.

61. Gaillard M*, Miao C†*, Schnable JC, Benes B (2020) Voxel carving based 3D reconstruction of sorghum identifies genetic determinants of radiation interception efficiency. PLANT DIRECT doi: [10.1002/pld3.255](https://doi.org/10.1002/pld3.255) bioRxiv doi: [10.1101/2020.04.06.028605v1](https://doi.org/10.1101/2020.04.06.028605v1)
JOURNAL IMPACT FACTOR (2020 REPORT): 1.7
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 23 (88th)
SCHNABLE LAB PERCENT CONTRIBUTION: 50%
CONTRIBUTION STATEMENT: Schnable lab generated data. Benes lab analyzed data to construct 3D models. Schnable lab conducted the GWAS and analyzed the results. Writing was shared equally between the two groups.
60. Wang R, Qiu Y, Zhou Y, Liang Z†, Schnable JC (2020) A high-throughput phenotyping pipeline for image processing and functional growth curve analysis. PLANT PHENOMICS doi: [10.34133/2020/7481687](https://doi.org/10.34133/2020/7481687)
JOURNAL IMPACT FACTOR (2020 REPORT): New Journal
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 18 (74th)
SCHNABLE LAB PERCENT CONTRIBUTION: 20%
CONTRIBUTION STATEMENT: Contributed the image data used in this paper. Evaluated the outcomes of multiple iterations of the new code being developed. Drafted portions of the paper and edited the remainder.
59. Jarquin D, Howard R, Liang Z†, Gupta SK, Schnable JC, Crossa J (2020) Enhancing hybrid prediction in pearl millet using genomic and/or multi-environment phenotypic information of inbreds. FRONTIERS IN GENETICS doi: [10.3389/fgene.2019.01294](https://doi.org/10.3389/fgene.2019.01294)
JOURNAL IMPACT FACTOR (2020 REPORT):
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 8 (73rd)
SCHNABLE LAB PERCENT CONTRIBUTION: 10%
CONTRIBUTION STATEMENT: Diego, from our own department, should get the lion's share of credit for this paper. We had a cool dataset we were able to share with him and Reka (from Statistics). If he's claimed anything less than 70% credit on his own report, please bump him up.
58. Raju SKK†, Thompson AM, Schnable JC (2020) Advances in plant phenomics: From data and algorithms to biological insights. APPLICATIONS IN PLANT SCIENCES doi: [10.1002/aps3.11386](https://doi.org/10.1002/aps3.11386)
JOURNAL IMPACT FACTOR (2020 REPORT): 1.6
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 17 (66th)
SCHNABLE LAB PERCENT CONTRIBUTION: 67%
CONTRIBUTION STATEMENT: Drafted 2/3rds of the paper, edited the remaining 1/3.
57. Peng B, Guan K, Ainsworth EA, Asseng S, Bernacchi CJ, Cooper M, Delucia EH, Elliot JW, Ewert F, Grant RF, Gustafson DI, Hammer GL, Jin Z, Jones JW, Kimm H, Lawrence DM, Li Y, Lombardozzi DL, Marshall-Colon A, Messina CD, Ort DR, Schnable JC, Tang J, Vallejos CE, Wu A, Yin X, Zhou W (2020) Advancing multi-scale crop modeling for agricultural climate change adaptation assessment. NATURE PLANTS doi: [10.1038/s41477-020-0625-3](https://doi.org/10.1038/s41477-020-0625-3)
JOURNAL IMPACT FACTOR (2020 REPORT): 13.2
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 97 (76th)
SCHNABLE LAB PERCENT CONTRIBUTION: 4%
CONTRIBUTION STATEMENT: Drafted one section of the manuscript and edited and provided feedback for the remainder.
56. Benes B, Guan K, Lang M, Long S, Lynch J, Marshall-Colon A, Peng B, Schnable JC, Sweetlove L, Turk M (2020) Multiscale computational models can guide experimentation and targeted measurements for crop improvement. THE PLANT JOURNAL doi: [10.1111/tpj.14722](https://doi.org/10.1111/tpj.14722)

JOURNAL IMPACT FACTOR (2020 REPORT): 6.1

ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 17 (86th)

SCHNABLE LAB PERCENT CONTRIBUTION: 10%

CONTRIBUTION STATEMENT: Drafted one section of the manuscript and edited and provided feedback for the remainder.

55. Moissejev G, Park K, Cui X, Freitas D, Rajagopa D, Konda A, Martin-Olenski M, Mcham M, Liu K, Du Q, **Schnable JC**, Moriyama E, Cahoon E, Chi Z (2020) RGPDB: Database of root-associated genes and promoters in maize, soybean, and sorghum. DATABASE doi: [10.1093/database/baaa038](https://doi.org/10.1093/database/baaa038)
JOURNAL IMPACT FACTOR (2020 REPORT): 2.6
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 7
SCHNABLE LAB PERCENT CONTRIBUTION: 7%
CONTRIBUTION STATEMENT: Provided a purality of data. Contributed to database design decisions. Edited the manuscript.
54. McFarland BA, AlKhalifah N, Bohn ... **Schnable JC** (34 of 54 authors) ... Xu W, Yeh CT, de Leon N (2020) Maize Genomes to Fields (G2F): 2014 –2017 field seasons' genotype, phenotype, climatic, soil and inbred ear image datasets. BMC RESEARCH NOTES doi: [10.1186/s13104-020-4922-8](https://doi.org/10.1186/s13104-020-4922-8)
JOURNAL IMPACT FACTOR (2020 REPORT): 1.3
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 25 (97th)
SCHNABLE LAB PERCENT CONTRIBUTION: 11%
CONTRIBUTION STATEMENT: Secured funding for and conducted yield trials and phenotyping for hundreds of ex-PVP hybrids in eight of sixty-eight total unique environments (eastern and western nebraska with and without irrigation in 2016 and 2017) covered in this data release paper.

2019 Journal Publications (N=10)

53. Qi P, Eudy D, **Schnable JC**, Schmutz J, Raymer P, Devos KM (2019) High density genetic maps of seashore paspalum using genotyping-by-sequencing and their relationship to the *Sorghum bicolor* genome. SCIENTIFIC REPORTS doi: [10.1038/s41598-019-48257-3](https://doi.org/10.1038/s41598-019-48257-3)
JOURNAL IMPACT FACTOR (2020 REPORT): 4.0
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 8 (67th percentile)
SCHNABLE LAB PERCENT CONTRIBUTION: 15%
CONTRIBUTION STATEMENT: Draft genome sequence used to generate one of the two sets of genetic maps used in this paper.
52. **Schnable JC** (2019) Genes and gene models, an important distinction. NEW PHYTOLOGIST doi: [10.1111/nph.16011](https://doi.org/10.1111/nph.16011)
JOURNAL IMPACT FACTOR (2020 REPORT): 8.5
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 45 (90th)
SCHNABLE LAB PERCENT CONTRIBUTION: 100%
CONTRIBUTION STATEMENT: N/A
51. Ge Y, Atefi A, Zhang H, **Miao C†**, Ramamurthy RK, **Sigmon B**, Yang J, **Schnable JC** (2019) High-throughput analysis of leaf physiological and chemical traits with VIS-NIR-SWIR spectroscopy: A case study with a maize diversity panel. PLANT METHODS doi: [10.1186/s13007-019-0450-8](https://doi.org/10.1186/s13007-019-0450-8)
JOURNAL IMPACT FACTOR (2020 REPORT): 3.6
ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 25 (95th)
SCHNABLE LAB PERCENT CONTRIBUTION: 35%
CONTRIBUTION STATEMENT: Conducted field component of the research. J Yang & RK Ramamurthy conducted greenhouse component. Y Ge, A Atefi and H Zhang analyzed the data.
50. Ali MA, Wang X, Chen Y, Jiao Y, Mahal NK, Satyanarayana M, Castellano MJ, **Schnable JC**, Schnable PS, Dong L (2019) Continuous Monitoring of Nitrate Variation Using Miniature Soil Sensor with

- Poly(3-octyl-thiophene) and Molybdenum Disulfide Nanocomposite. ACS APPLIED MATERIALS & INTERFACES doi: [10.1021/acsami.9b07120](https://doi.org/10.1021/acsami.9b07120)
 JOURNAL IMPACT FACTOR (2020 REPORT): 8.8
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 2
 SCHNABLE LAB PERCENT CONTRIBUTION: 10%
 CONTRIBUTION STATEMENT: Conducted field experiments to validate the sensor described in the manuscript.
49. Li Y, **Li D**, Jiao Y, **Schnable JC**, Li Y, Li H, Chen H, Hong H, Zhang T, Liu B, Liu Z, You Q, Tian Y, Gou Y, Guan R, Zhang L, Chang R, Zhang Z, Reif J, Zhou X, Schnable PS, Qiu L. (2019) Identification of Loci Controlling Adaptation in Chinese Soybean Landraces via a Combination of Conventional and Bioclimatic GWAS. PLANT BIOTECHNOLOGY JOURNAL doi: [10.1111/pbi.13206](https://doi.org/10.1111/pbi.13206)
 JOURNAL IMPACT FACTOR (2020 REPORT): 8.1
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL):
 SCHNABLE LAB PERCENT CONTRIBUTION: 15%
 CONTRIBUTION STATEMENT: Designed concept and implementation strategy for bioclimactic GWAS using data on original GPS tagged collection locations of soybean lines. Outlined manuscript and edited draft written by collaborators.
 48. Atefi A, Ge Y, Pitla S, **Schnable JC** (2019) *In vivo* human-like robotic phenotyping of leaf traits in maize and sorghum. COMPUTERS AND ELECTRONICS IN AGRICULTURE doi: [10.1016/j.compag.2019.104854](https://doi.org/10.1016/j.compag.2019.104854)
 JOURNAL IMPACT FACTOR (2020 REPORT): 3.9
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 142 (99th)
 SCHNABLE LAB PERCENT CONTRIBUTION: 25%
 CONTRIBUTION STATEMENT: Co-originated concept and approaches for validation and visualization. Drafted sections of manuscript and edited others.
 47. Li L, Li X, Li L, **Schnable JC**, Gu R, J Wang (2019) QTL identification and epistatic effect analysis of seed size- and weight-related traits in *Zea mays* L. MOLECULAR BREEDING doi: [10.1007/s11032-019-0981-8](https://doi.org/10.1007/s11032-019-0981-8)
 JOURNAL IMPACT FACTOR (2020 REPORT): 2.1
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 6 (87th)
 SCHNABLE LAB PERCENT CONTRIBUTION: 15%
 CONTRIBUTION STATEMENT: Proposed additional analyses/visualizations. Drafted portions of the manuscript and edited others.
 46. **Yan Lt**, **Kumar SKK†**, **Lai Xt**, **Zhang Y†**, **Dai Xt**, Rodriguez O, Mahboub S, Roston RL, **Schnable JC** (2019) Parallels between artificial selection in temperate maize and natural selection in the cold-adapted crop-wild relative *Tripsacum*. THE PLANT JOURNAL doi: [10.1111/tpj.14376](https://doi.org/10.1111/tpj.14376) [10.1101/187575](https://doi.org/10.1101/187575) [BIORxiv doi: 10.1101/187575](https://doi.org/10.1101/187575)
 JOURNAL IMPACT FACTOR (2020 REPORT): 6.1
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 20 (84th)
 SCHNABLE LAB PERCENT CONTRIBUTION: 90%
 CONTRIBUTION STATEMENT: O Rodriguez collected *tripsacum* accessions. RL Roston and S Mahboub generated lipid data. All other aspects of the paper conducted in the Schnable lab.
 45. Bai G, Ge Y, Scoby D, Leavit B, Irmak S, Graef G, **Schnable JC**, Awada T. (2019) NU-Spidercam: A large-scale, cable-driven, integrated sensing and robotic system for precision phenotyping, remote sensing, and agronomic research. COMPUTERS AND ELECTRONICS IN AGRICULTURE doi: [10.1016/j.compag.2019.03.009](https://doi.org/10.1016/j.compag.2019.03.009)
 JOURNAL IMPACT FACTOR (2020 REPORT): 3.9
 ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 9 (76th)
 SCHNABLE LAB PERCENT CONTRIBUTION: 15%
 CONTRIBUTION STATEMENT: Conducted 1/2 of the field experiments described in this study.
 44. 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. NATURE COMMUNICATIONS doi: [10.1038/s41467-019-08409-5](https://doi.org/10.1038/s41467-019-08409-5)

JOURNAL IMPACT FACTOR (2020 REPORT): 12.1

ALTMETRIC SCORE (PERCENTILE AT JOURNAL): 89 (85th)

SCHNABLE LAB PERCENT CONTRIBUTION: 14%

CONTRIBUTION STATEMENT: Generated a genetic map using an asian/north american cross of *Panicum miliaceum* which was used to order and orient the scaffolds of the genome into pseudo-molecules.

2018 Journal Publications (N=11)

43. **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)
JOURNAL IMPACT FACTOR (2020 REPORT): 8.1
TIMES CITED TO DATE: 13
CONTRIBUTION STATEMENT: All analyses and writing conducted by lab members.
42. 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)
JOURNAL IMPACT FACTOR (2020 REPORT): 3.6
TIMES CITED TO DATE: 15
CONTRIBUTION STATEMENT: Conducted an analysis of a linked read genome assembly of proso millet, a previously unsequenced allotetraploid grass to assess the accuracy with which separate subgenomes were assembled and resolved using this new linked-reads technique.
41. 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)
JOURNAL IMPACT FACTOR (2020 REPORT): 11.1
TIMES CITED TO DATE: 2
CONTRIBUTION STATEMENT: Analysis of relative correlation between recombination frequency per megabase and the relative density of either syntenic or nonsyntenic genes separately was conducted in the Schnable Lab@UNL.
40. **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)
JOURNAL IMPACT FACTOR (2020 REPORT): 3.6
TIMES CITED TO DATE: 17
CONTRIBUTION STATEMENT: Sunil and I wrote the portions of this review focused on conserved patterns transcriptional responses to cold stress across diverse plants, and worked collaboratively with the Roston lab on the combined transcript/lipid analyses.
39. **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)
JOURNAL IMPACT FACTOR (2020 REPORT): 4.0
TIMES CITED TO DATE: 7
CONTRIBUTION STATEMENT: Improved and documented the core algorithm. Conducted tests of how much the core algorithm improved genotype call accuracy in a RIL and F2 population when using sub-optimal sequencing depth. Wrote the paper collaboratively with Haibao Tang.
38. 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)

JOURNAL IMPACT FACTOR (2020 REPORT): 1.3

TIMES CITED TO DATE: 13

CONTRIBUTION STATEMENT: Data collection from grow outs of Genomes to Fields hybrids at Nebraska field sites, assisted in writing the manuscript itself.

37. **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.

JOURNAL IMPACT FACTOR (2020 REPORT): 2.8

TIMES CITED TO DATE: 14

CONTRIBUTION STATEMENT: Built the libraries, analyzed the SNP data, conducted the GS tests, wrote the paper. Field data and extracted DNA contributed by ICRISAT collaborators. Sequencing and SNP calling contributed by ISU collaborators.

36. Xu Y, Qiu Y, **Schnable JC** (2018) Functional modeling of plant growth dynamics. *THE PLANT PHENOME JOURNAL* 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)

Received the "Outstanding Paper Award" from TPPJ editorial board in 2020.

JOURNAL IMPACT FACTOR (2020 REPORT): Not yet assigned.

TIMES CITED TO DATE: 7

CONTRIBUTION STATEMENT: Conceived of the experiment to test subsampling on different days. Wrote the paper

35. **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)

JOURNAL IMPACT FACTOR (2020 REPORT): 2.1

TIMES CITED TO DATE: 2

CONTRIBUTION STATEMENT: Conducted the majority of the analyses. Wrote the paper.

34. **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)

JOURNAL IMPACT FACTOR (2020 REPORT): 6.1

TIMES CITED TO DATE: 11

CONTRIBUTION STATEMENT: All experiments, analysis, and writing conducted by lab members.

33. 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](https://doi.org/10.1007/s11033-018-4144-5)

JOURNAL IMPACT FACTOR (2020 REPORT): 2.1

TIMES CITED TO DATE: 3

CONTRIBUTION STATEMENT: Identified candidate low copy genes which were used to design probes for hybridization.

2017 Journal Publications (N=12)

32. **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)

JOURNAL IMPACT FACTOR (2020 REPORT): 12.1

TIMES CITED TO DATE: 29

CONTRIBUTION STATEMENT: All experiments, analysis, and writing conducted by lab members.

31. **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)
JOURNAL IMPACT FACTOR (2020 REPORT): 6.95
TIMES CITED TO DATE: 25
CONTRIBUTION STATEMENT: All analyses and writing conducted by lab members. Ge, Qiu, and Xu labs each assisted in developing new analytical approaches. Vincent Stoerger assisted with data generation.
30. 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
JOURNAL IMPACT FACTOR (2020 REPORT): 12.1
TIMES CITED TO DATE: 42
CONTRIBUTION STATEMENT: Generated and contributed yield and field phenotyping data from Nebraska field sites of Genomes to Fields project.
29. 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)
JOURNAL IMPACT FACTOR (2020 REPORT): 4.0
TIMES CITED TO DATE: 11
CONTRIBUTION STATEMENT: Grew plants, extracted RNA, built and sequenced libraries and shared data. Consulted with the lead author on the syntenic gene analysis.
28. 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)
JOURNAL IMPACT FACTOR (2020 REPORT):
TIMES CITED TO DATE: 56
CONTRIBUTION STATEMENT: Wrote portions of the manuscript, designed additional analyses to validate datasets which were executed by Alina Ott.
27. **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)
JOURNAL IMPACT FACTOR (2020 REPORT): 3.6
TIMES CITED TO DATE: 10
CONTRIBUTION STATEMENT: The majority of this paper was written by Xianjun Lai during his time in the Schnable lab. I redesigned several analyses for him to carry out and helped to re-write the paper.
26. Mei W, Boatwright L, Feng G, **Schnable JC**, Barbazuk WB (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
JOURNAL IMPACT FACTOR (2020 REPORT):
TIMES CITED TO DATE: 20
CONTRIBUTION STATEMENT: Conceived and designed a new approach to identifying orthologous plant exons based on a directed acyclic graph which was robust to the insertion or deletion of entire introns.
25. 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](https://doi.org/10.3389/fpls.2017.01348)
JOURNAL IMPACT FACTOR (2020 REPORT): 4.4
TIMES CITED TO DATE: 91

CONTRIBUTION STATEMENT: Designed a different cross validation technique which was implemented by the first author. Drafted portions of the introduction and discussion and revised the manuscript.

24. **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](https://doi.org/10.1105/tpc.17.00354) *Selected as an Editor's Choice by MaizeGDB Editorial Board* August 2017
JOURNAL IMPACT FACTOR (2020 REPORT): 9.6
TIMES CITED TO DATE: 34
CONTRIBUTION STATEMENT: All analyses and writing conducted by lab members. Qiu lab assisted in developing new analytical approaches to comparing gene expression across species. Roston lab assisted in interpreting biological responses to plant cold stress.
23. **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](https://doi.org/10.1016/j.molp.2017.05.010)
JOURNAL IMPACT FACTOR (2020 REPORT): 12.1
TIMES CITED TO DATE: 8
CONTRIBUTION STATEMENT: I defined the problem, Sairam Behera created the algorithm, Zhikai Liang and Xianjun Lai, both from my group, conducted multiple rounds of biological validation and provided feedback to Sairam, improving the core algorithm in an iterative process. My lab wrote the paper.
22. **Lai X†, Schnable JC** (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)
JOURNAL IMPACT FACTOR (2020 REPORT): 12.1
TIMES CITED TO DATE: 2
CONTRIBUTION STATEMENT: All analyses and writing conducted by lab members.
21. 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](https://doi.org/10.3389/fpls.2017.00694)
JOURNAL IMPACT FACTOR (2020 REPORT): 4.4
TIMES CITED TO DATE: 43
CONTRIBUTION STATEMENT: Developed approach to identifying orthologous exons across both maize subgenomes and co-orthologous genes in sorghum (an earlier iteration of the algorithm later used for paper # 42). Consulted with the lead author on the best ways to make comparisons across subgenomes.

2016 Journal Publications (N=10)

20. 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](https://doi.org/10.1093/bioinformatics/btw666)
JOURNAL IMPACT FACTOR (2020 REPORT): 5.6
TIMES CITED TO DATE: 3
CONTRIBUTION STATEMENT: Generated semi-manual subgenome assignments which are used as the basis for evaluating the accuracy of the automated assignments made by FractBias. Consulted with the lead author on the best ways to make comparisons across subgenomes.
19. 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](https://doi.org/10.1126/science.aag1125) *Selected as an Editor's Choice by MaizeGDB Editorial Board* September 2016
JOURNAL IMPACT FACTOR (2020 REPORT): 41.8

TIMES CITED TO DATE: 192

CONTRIBUTION STATEMENT: Suggested and provided the data which enabled the separate analysis of maize syntenic and non-syntenic genes. This analysis led to the discovery that non-syntenic maize genes are much less likely to be translated enough protein, even when they are transcribed into mRNAs than genes conserved at syntenic locations across multiple grass species. See Figure 1 in the final paper.

18. 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](https://doi.org/10.1016/j.compag.2016.07.028)
JOURNAL IMPACT FACTOR (2020 REPORT): 3.9
TIMES CITED TO DATE: 124
CONTRIBUTION STATEMENT: Provided plant material. Interpreted a portion of the resulting trait datasets. Wrote portions of the manuscript particularly those focused on the biological relevance of the measured traits.
17. **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](https://doi.org/10.1371/journal.pone.0157942)
JOURNAL IMPACT FACTOR (2020 REPORT): 2.7
TIMES CITED TO DATE: 15
CONTRIBUTION STATEMENT: All analyses and writing conducted by lab members.
16. 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](https://doi.org/10.1007/s11032-016-0460-4)
JOURNAL IMPACT FACTOR (2020 REPORT):
TIMES CITED TO DATE: 24
CONTRIBUTION STATEMENT: Taught Santosh Rajput how to analyze GBS data. Conducted analyses to generate a filtered set of dominant markers from homeologous loci collapsed across subgenomes which were ultimately used to generate the genetic map created in this paper.
15. 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](https://doi.org/10.1093/gbe/evv206)
JOURNAL IMPACT FACTOR (2020 REPORT): 3.5
TIMES CITED TO DATE: 18
CONTRIBUTION STATEMENT: Designed analyses carried out by the lead author.
14. 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)
JOURNAL IMPACT FACTOR (2020 REPORT): 10.8
TIMES CITED TO DATE: 24
CONTRIBUTION STATEMENT: Grew plants, collected tissue, generated genome assembly and annotations, drafted 1/2 of final paper.
13. 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)
JOURNAL IMPACT FACTOR (2020 REPORT): 5.9
TIMES CITED TO DATE: 40
CONTRIBUTION STATEMENT: Grew plants, collected tissue, sequenced and assembled transcriptomes and identified orthologous groups between species.
12. 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)
JOURNAL IMPACT FACTOR (2020 REPORT): 5.9

TIMES CITED TO DATE: 21

CONTRIBUTION STATEMENT: Used resequencing data from multiple foxtail millet lines to design markers which were employed for fine mapping by other authors.

11. 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)
JOURNAL IMPACT FACTOR (2020 REPORT): 8.5
TIMES CITED TO DATE: 49
CONTRIBUTION STATEMENT: Conducted a subset of analyses related to identifying gene deletions across subgenomes.
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Conference Articles & Book Chapters 2020-2016

2020 Conference Articles & Book Chapters (N=3)

10. Gaillard M, **Miao C†**, **Schnable JC**, Benes B (2020) Sorghum Segmentation by Skeleton Extraction. COMPUTER VISION PROBLEMS IN PLANT PHENOTYPING (CVPPP 2020) Glasgow, UK
 9. Sankaran S, Zhang C, **Hurst JP†**, Marzougui A, Sivakumar ANV, Li J, **Schnable JC**, Shi Y (2020) Investigating the potential of satellite imagery for high-throughput field phenotyping applications. SPIE DEFENSE + COMMERCIAL SENSING California, USA doi: [10.1117/12.2558729](https://doi.org/10.1117/12.2558729)
 8. Al-Zadjali A, Shi Y, Scott S, Deogun JS, and **Schnable JC** (2020) Faster-R-CNN based deep learning for locating corn tassels in UAV imagery. SPIE DEFENSE + COMMERCIAL SENSING California, USA doi: [10.1117/12.2560596](https://doi.org/10.1117/12.2560596)
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2019 Conference Articles & Book Chapters (N=5)

7. **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
 6. **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
 5. Jiao Y, Wang X, Chen Y, Castellano MJ, **Schnable JC**, Schnable PS, Dong L (2019) In-planta nitrate detection using insertable plant microsensor. 20TH INTERNATIONAL CONFERENCE ON SOLID-STATE SENSORS, ACTUATORS AND MICROSYSTEMS Berlin, Germany doi: [10.1109/TRANSDUCERS.2019.8808527](https://doi.org/10.1109/TRANSDUCERS.2019.8808527)
 4. Ali MA, Wang X, Chen Y, Jiao Y, Castellano MJ, **Schnable JC**, Schnable PS, Dong L (2019) Novel all-solid-state soil nutrient sensor using nanocomposite of poly(3-octyl-thiophene) and molybdenum sulfate. 20TH INTERNATIONAL CONFERENCE ON SOLID-STATE SENSORS, ACTUATORS AND MICROSYSTEMS Berlin, Germany doi: [10.1109/TRANSDUCERS.2019.8808341](https://doi.org/10.1109/TRANSDUCERS.2019.8808341)
 3. 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.
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2017 Conference Articles & Book Chapters

2. Behera S, Deogun JS, **Lai X†**, **Schnable JC** (2017) B529 DiCE: Discovery of Conserved Noncoding Sequences Efficiently. IEEE BIBM 2017 Kansas City, MO, USA doi: [10.1109/BIBM.2017.8217628](https://doi.org/10.1109/BIBM.2017.8217628)
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2016 Conference Articles & Book Chapters

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