

Jianming Yu

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Professional Experience

2023-present Director of Raymond F. Baker Center for Plant Breeding, Iowa State Univ.
2017-present Professor, Dept. of Agronomy, Iowa State Univ.
2013-present Pioneer Distinguished Chair in Maize Breeding, Dept. of Agronomy, Iowa State Univ.
2013-2017 Associate Professor, Dept. of Agronomy, Iowa State Univ.
2010-2012 Associate Professor, Dept. of Agronomy, Kansas State Univ.
2006-2010 Assistant Professor, Dept. of Agronomy, Kansas State Univ.
2004-2006 Postdoctoral Res. Assoc., Institute for Genomic Diversity, Cornell Univ.
2003-2004 Postdoctoral Res. Assoc., Dept. of Agronomy & Plant Genetics, Univ. of Minnesota
2000-2003 Graduate Res. Assistant, Dept. of Agronomy & Plant Genetics, Univ. of Minnesota
1998-2000 Graduate Res. Assistant, Dept. of Agronomy, Kansas State Univ.
1994-1998 Res. Assistant, Res. & Dev. Dept., China Natl. Seed Group Corp.

Education

2000-2003 Ph.D. Plant Breeding and Genetics, Univ. of Minnesota
1998-2000 M.S. Plant Breeding and Genetics, Kansas State Univ.
1990-1994 B.S. Agronomy, Northwest Agriculture and Forestry Univ.

Honors and Awards

Year	Honors and Awards	Level
2024	Outstanding Achievement in Research Award, Iowa State Univ.	University
2024	Outstanding Achievement in Research Award, College of Agriculture and Life Sciences, Iowa State Univ.	College
2023	Class 19 of the Lead21 Program, Leadership for the 21 st Century	National
2018	Highly Cited Researcher, Clarivate Analytics	International
2018	Fellow, American Association for the Advancement of Science	Professional Society
2018	Fellow, Crop Science Society of America	Professional Society
2018	Editor's Citation for Excellence, <i>The Plant Genome</i>	Journal
2017	Raymond and Mary Baker Agronomic Excellence Award, Agronomy, Iowa State Univ.	Departmental
2017	Mid-Career Achievement in Research Award, Iowa State Univ.	University
2017	Mid-Career Achievement in Research Award, College of Agriculture and Life Sciences, Iowa State Univ.	College
2015 - present	Faculty Scholar of Plant Sciences Institute, Iowa State Univ.	University
2014	Emerging Leader in Plant Sciences, Univ. of Minnesota	Alumni
2010	Young Crop Scientist Award, Crop Science Society of America	Professional Society
2010	Early Career Professional Award, American Society of Agronomy - Crop Science Society of America - Soil Science Society of America	Professional Society
2004	Summer Institute in Statistical Genetics Scholarship, North	University

	Carolina State Univ.	
2003	Crop Science Graduate Student Scholarship, Crop Science Society of America	Professional Society
2003	H.K. Hayes Graduate Student Award, Dept. of Agronomy & Plant Genetics, Univ. of Minnesota	Departmental
2002-2003	Doctoral Dissertation Fellowship, Graduate School, Univ. of Minnesota	University
2000-2002	Troyer/Darwin Fellowship, Dept. of Agronomy & Plant Genetics, Univ. of Minnesota	Departmental
2001	Gamma Sigma Delta, the Honor Society of Agriculture	Professional Society
1999	Dan M. Rodger's Graduate Scholarship, Dept. of Agronomy, Kansas State Univ.	Departmental
1991-1994	Outstanding Undergraduate Scholarship, Dept. of Agronomy, Northwest Agriculture and Forestry Univ.	Departmental

Research Summary

Jianming Yu is Professor, Pioneer Distinguished Chair in Maize Breeding, and Director of [Raymond F. Baker Center for Plant Breeding](#), in the Department of Agronomy, Iowa State University. The focus of Yu's program is to address significant questions in quantitative genetics by combining cutting-edge genomic technologies and plant breeding. Maize and sorghum are two major crops with annual nurseries with thousands of research plots, but the group has been working on many other crops through collaboration and open data. Yu's research integrates knowledge in quantitative genetics, genomics, plant breeding, molecular genetics, and statistics, and has the ultimate goal of developing and implementing new strategies and methods in complex trait dissection and crop improvement. Yu is a Faculty Scholar of [Plant Sciences Institute](#) and a member of [Crop Bioengineering Center](#).

(Note: All significant contributions listed below were only possible because of the collaboration with many intelligent and dedicated scientists.)

Complex Trait Dissection

- Developed an integrated framework for gene discovery underlying phenotypic plasticity and performance prediction across environments ([PNAS 115:6679-6683](#), [Genome Research 30:673-683](#), [Molecular Plant 14:874-887](#), [New Phytologist 233:1768-1779](#), [Journal of Experimental Botany 75:1004-1015](#)). This general framework facilitates biologically informed dissection of complex traits, enhanced performance prediction in breeding for future climates, and coordinated efforts to enrich our understanding of mechanisms underlying phenotypic variation.
- Uncovered a complete case of heterosis due to pseudo-overdominance ([PNAS 112:11823-11828](#)). While the pseudo-overdominance hypothesis (dominance with repulsion linkage) for heterosis has been proposed for a long time, clearly delineated cases are scarce in the literature.
- Quantified genic and nongenic contributions to quantitative trait variation in maize ([Genome Research 22:2436-2444](#)). This paper was the first attempt to answer the fundamental question about contributions of different genomic regions to quantitative traits in plants.

- Outlined the nested association mapping (NAM) strategy ([Genetics 138:539-551](#)), the approach that has been replicated in multiple crops to combine the strengths of linkage mapping using populations derived from bi-parental crosses and linkage disequilibrium mapping using diverse accessions. NAM strategy, combining the advantages of linkage analysis and association mapping, provided a high-resolution and cost-effective approach to dissecting the genetic architecture of complex traits.
- Developed the unified mixed model framework for genome-wide association studies (GWAS) ([Nature Genetics 38:203-208](#)), the standard method framework for complex trait dissection that is widely adopted in plant and human genetics. This research solved a long-standing scientific problem in genome-wide association analysis – too many false positive signals than expected from the analysis with simple methods due to the complex genetic relationship among individuals used in GWAS.

Breeding Methodology

- Developed several optimal training set design methods for genomic selection in hybrid crops ([Molecular Plant 12:390-401](#)). Identifying the superior hybrids among the immense number of possible combinations of parental inbreds is a long-standing challenge. By viewing plant breeding as a process of genetic space exploration, data mining and design thinking would help reshape the next generation breeding programs.
- Prototyped a comprehensive strategy based on genomic selection and other relevant technologies to mine the natural heritage stored in numerous gene banks ([Nature Plants 2:16150](#), [Plant Biotechnology Journal 18:2456-2465](#)). *Turbocharging genebanks through genomic prediction* repurposes the phenotyping process as training data collection so that data generated can be better used to generate prediction models to iteratively enhance the prediction power to guide the exploration of genetic space represented by the accessions in the genebanks.
- Pioneered genomic selection (GS) research in crops ([Crop Science 47:1082-1090](#)), the state-of-the-art breeding methodology that has been extensively implemented in plant breeding programs.

Crop Domestication

- Uncovered the first case of domestication triangle, in which human genetics interact with sorghum genetics and the environment to influence the proportion of tannin sorghums grown by farmers in different parts of Africa ([Nature Plants 5:1229-1236](#)). Cloned the pair of genes in sorghum underlying a trait (tannin in the sorghum grain) with incomplete domestication: *Tannin1* ([PNAS 109:10281-10286](#)) and *Tannin2* ([Nature Plants 5:1229-1236](#)). Crop domestication is a complex process of dynamically balancing two competing forces: artificial selection and natural selection. This discovery could help uncover future cases.
- Uncovered patterns of genome-wide nucleotide patterns in maize and soybean ([Genome Biology 20:74](#)). By examining how the process of domestication have affected the genomes of corn and soybean, the team found out that the [AT]-increase is more pronounced in genomic regions that are non-genic, pericentromeric, transposable elements; methylated; and with low recombination. These findings established the critical links among UV radiation, mutation, DNA repair, methylation, and genome evolution.
- Identified the *Shattering1* gene and its homologs underlying the parallel domestication of multiple cereal species: sorghum, maize, rice, and foxtail millet ([Nature Genetics 44:720-724](#)). Several follow-up studies further validated the findings in foxtail millet and an additional

subspecies of rice. In addition, this paper highlighted the challenge and solution to allelic heterogeneity in genetic mapping.

Genomes and Chromosomes

- Revealed the patterns in DNA base composition divergence in multiple species ([Nucleic Acids Research 43:3614-3625](#)). Base composition was found to follow the individual-strand base equality rule at the genome, chromosome, and polymorphic-site levels. Intriguingly, clear separation of base-composition values calculated across polymorphic sites was consistently observed between basal and derived groups across 8 population comparison sets.
- Revealed the patterns in chromosome size variation across diploid eukaryotic species with linear chromosomes ([Molecular Biology and Evolution 28:1901-1911](#)). Strikingly, variation in chromosome size for 886 chromosomes in 68 eukaryotic genomes can be viably captured by a single model.

Invited Talks (116 = 81 National + 35 International)

1. Apr. 24, 2024. Learning and leveraging artificial intelligence for crop improvement. AI in Plant Breeding Symposium, Genetics and Genomics, University of Georgia, Athens, GA.
2. Mar. 29, 2024. The path to discovery: technology, analytics, and design. Plant Sciences Symposium, Harvesting Synergies: Elevating Plant Sciences through Interdisciplinarity. University of Minnesota, St. Paul, MN.
3. Oct. 31, 2023. Realizing the potential of germplasm through turbocharging genebank. Symposium – Open Science Inspires Utilization of Genebank Collections through Genomics and Phenotyping. ASA-CSSA-SSSA International Annual Meeting, St. Louis, MO.
4. Sept. 1, 2023. Technology, analytics, and design in research and training. Department of Animal Science, Iowa State University, Ames, IA.
5. Jul. 14, 2023. Phenotypic plasticity to guide the exploration of gene-environment-development-phenotype process. China Academy of Agricultural Sciences, Beijing, **China**.
6. Jul. 13, 2023. Phenotypic plasticity to guide the exploration of gene-environment-development-phenotype process. Sinong Academic Forum, China Agricultural University, Beijing, **China**.
7. Jul. 11, 2023. Plant breeding innovations and artificial intelligence. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
8. May 10, 2023. Phenotypic plasticity: A framework to understand the gene-environment-development interplay. Interdepartmental Seminar Series (Cell, Molecular, and Developmental Biology; Genetic, Genomics & Bioinformatics; and Microbiology), University of California-Riverside, Riverside, CA.
9. Jan. 15, 2023. Dissection of phenotypic plasticity in flowering time and plant height in sorghum under natural field conditions. Sorghum and Millet Workshop, Plant and Animal Genome 30 Conference, Jan. 13-18, 2023, San Diego, CA.
10. Jan. 14, 2023. Advancing translational genomics through design thinking and systems thinking of phenotypic plasticity. CSSA Translation Genomics Workshop, Plant and Animal Genome 30 Conference, Jan. 13-18, 2023, San Diego, CA.
11. Nov. 3, 2022. Phenotypic plasticity connects gene, organism, environment, and development. GxExM Symposium, The University of Queensland, St Lucia, Brisbane and online, **Australia** (Virtual).
12. Sept. 13, 2022. Sorghum: Uncovering the relationships among gene, environment, crop, and

- human. Center for Sorghum Improvement Seminar Series, Kansas State University, Manhattan, KS (Virtual).
13. Jun. 27, 2022. Vision for the future germplasm use. NC-7 Hatch Multistate Project Regional Technical Advisory Committee. North Central Regional Plant Introduction Station, Ames, IA.
 14. Jun. 14, 2022. Phenotypic plasticity: Integrating genomics, phenomics, and enviromics for precision agriculture and sustainable agriculture. CROPS Conference, HudsonAlpha Institute for Biotechnology, Huntsville, AL.
 15. May 26, 2022. Quantitative genetics, plant breeding innovations, and omnigenic model. Quantitative Genetics Lecture Series, Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China** (Virtual).
 16. May 2, 2022. Plant breeding innovations: Technologies, analytics, and design. Sustainable Protein Production Supercluster Support Program Seminar Series, National Research Council Canada, Ottawa, ON, **Canada** (Virtual).
 17. Oct. 13, 2021. Coevolution among humans, plants, and environments linked by allelochemicals. Agriculture and Health Summit, University of Nebraska at Lincoln, Oct. 11-13, 2021 (Virtual).
 18. Sept. 13, 2021. Continuing the journey of excellence and innovation in plant breeding. Advanced Plant Breeding Symposium, Seed Science Foundation and National Association of Plant Breeders (Virtual).
 19. Aug. 5, 2021. An integrated framework reinstating the environmental dimension for GWAS and genomic selection. The 2021 International Conference on Molecular Plant Sciences: From Fundamental Research to Agricultural Applications, **China** (Virtual).
 20. May 13, 2021. Quantitative genetics: Current status and history. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China** (Virtual).
 21. Feb. 27, 2021. Genome-wide associate studies, genomic selection, and genome editing, but what about environment? Corn Breeding Research Meeting (Virtual).
 22. Nov. 10, 2020. Design thinking to enhance the synergy between genomic selection and genome editing. Genome Editing and Genomic Selection for Crop Improvement Session, ASA-CSSA-SSSA International Annual Meeting (Virtual).
 23. Apr. 1, 2020. Pattern finding for a better understanding of genes, organisms, and environments. Bayer Crop Science Zoom Seminar Series (Virtual).
 24. Nov. 29, 2019. Genome-wide association studies and discovery of tannins' role in agroecosystems. Shanghai Chenshan Plant Science Research Center, Shanghai, **China**.
 25. Nov. 29, 2019. An integrated understanding of genes, organisms, and environments. Shanghai Institute of Plant Physiology and Ecology, Chinese Academy of Sciences, Shanghai, **China**.
 26. Nov. 23, 2019. Design thinking for better agriculture: Genomic selection and genome editing. Nature Conference, Agricultural Genomics 2019 - Big Data for Better Agriculture, November 21-23, 2019, Shenzhen Marriott Hotel Golden Bay, Shenzhen, **China**.
 27. Sept. 13, 2019. ([YouTube](#)) Integrating design, analytics, and genomics in crop improvement. University of Nebraska - Lincoln, Lincoln, NE.
 28. Aug. 29, 2019. Design thinking, data mining, and the complex genotype-environment-phenotype relationship. Corteva, Johnston, IA.
 29. Jun. 20, 2019. Genomic selection, plant breeding design, and optimization. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
 30. May 31, 2019. ([YouTube](#)) Towards a better understanding of genes, organisms, and environments. Cornell University, Ithaca, NY.
 31. Apr. 3, 2019. Pattern discovery in genes, genomes, environments, and phenotypes. PIRS Mini-

- Symposium: Novel candidate gene discovery by computing on phenotypes. Iowa State University, Ames, IA.
32. Feb. 25, 2019. A unified synthesis framework of genes, organisms, and environments for gene discovery and performance forecasting. Purdue University, West Lafayette, IN.
 33. Jan. 12, 2019. Establishing a unified synthesis framework for genomic selection, genome-wide association studies, and genotype by environment interaction. Genomic Selection and Genome-Wide Association Studies workshop, Plant and Animal Genome XXVII Conference, Jan. 12-16, 2019, San Diego, CA.
 34. Dec. 13, 2018. Establishing a unified framework for genomic prediction of untested genotypes in untested environments. BASF, Morrisville, NC.
 35. Nov. 28, 2018. Uncovering patterns behind phenotypic plasticity for gene discovery and trait prediction. Colorado State University, Fort Collins, CO.
 36. Oct. 24, 2018. Probing the mechanisms of heterosis in defined genetic contexts in sorghum and maize. 5th International Symposium on Genomics and Crop Genetic Improvement-Heterosis, Huazhong Agricultural University, Wuhan, **China**.
 37. Sept. 5, 2018. Design and diversity for complex trait dissection and crop improvement. The 17th meeting of the EUCARPIA Section Biometrics in Plant Breeding, Ghent, **Belgium**.
 38. Jul. 22, 2018. Designing molecular breeding and green agriculture as space exploration. International Symposium on Molecular Breeding and Green Agriculture in 21 Century, Changchun, Jilin, **China**.
 39. Jul. 20, 2018. Genomic and environmental determinants and their interplay underlying phenotypic plasticity. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
 40. Apr. 20, 2018. ([YouTube](#)) Pattern discovery, predictive modeling, and design in plant breeding and genetics. Clemson Integrated Plant Sciences Symposium, Clemson, SC.
 41. Apr. 6, 2018. Genomic and environmental determinants underlying phenotypic plasticity. Texas A&M University, College Station, TX.
 42. Dec. 6, 2017. Exploring the genotype-phenotype relationship for germplasm enhancement. Germplasm Enhancement of Maize (GEM) Cooperator's Meeting, Chicago, IL.
 43. Nov. 15, 2017. Quantitative Genetics and Maize Breeding. ISU Plant Breeding Mini Retreat. Ames, IA
 44. Sept. 4, 2017. Design thinking and data mining in finding the optimal genetic combinations. The 4th International Symposium on Genomics of Plant Genetic Resources, Giessen, **Germany**. (**Opening Keynote**).
 45. Jul. 3, 2017. Design thinking and data mining in genetics and breeding. China Agricultural University, Beijing, **China**.
 46. Jun. 29, 2017. Design and application in genome-wide association studies and genomic selection. Henan University, Kaifeng, Henan, **China**.
 47. Jun. 6, 2017. Design and optimize genomic selection in the context of gene banks and practical breeding programs. CROPS 2017, HudsonAlpha Institute for Biotechnology, Huntsville, AL.
 48. Jan. 18, 2017. Thoughts and examples of turbocharging the gene banks with genomic prediction. DivSeek - Addressing the challenges and opportunities for information and data sharing associated with plant germplasm, Plant and Animal Genome XXV Conference, San Diego, CA.
 49. Nov. 29, 2016. Optimal design in complex trait dissection and genomic prediction. Design Optimal Genetics Improvement and Agronomic Systems. Ames, IA.
 50. Nov. 18, 2016. Breeding strategies with genomic selection. Hi Fidelity Genetics, Durham, NC.

51. Nov. 17, 2016. Genomic selection: Continuing the journey of excellence of plant breeding. Bayer CropScience, Morrisville, NC.
52. Nov. 9, 2016. Turbo-charging the genebanks through Genomic prediction. The Prominent Role of Plant Genetic Resources and Genebanks in the Post-Genomic Era, C8-Symposium, Phoenix, AZ, ASA-CSSA-SSSA meeting.
53. Aug. 30, 2016. Parallel evolution of alleles, genes, chromosomes, and taxa. Bioinformatics Seminar, Department of Statistics, Purdue University., West Lafayette, IN.
54. Jul. 14, 2016. Genetics of heterosis and plant breeding methods. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
55. Jul. 9, 2016. Genotype and phenotype relationship for different biological questions. Shandong Agricultural University, Tai'an, Shandong, **China**.
56. May 25, 2016. Defining a complex phenomenon and quantitative dissecting of heterosis. Heterosis: Working toward a genetic, molecular, developmental, and physiological basis. Interdepartmental Plant Group, University of Missouri, Columbia, MO.
57. Apr. 28, 2016. Genomic prediction contributes to a promising global strategy to evaluate plant germplasm in genebanks. Noble Foundation, Ardmore, OK.
58. Apr. 29, 2016. Genotype and phenotype relationship under different biological contexts for gene finding and trait selection. Plant Genotype-Phenotype (G2P) Association Discovery via Integrative Genome-scale Biological Network & Genome-wide Association Analysis, Noble Foundation, Ardmore, OK.
59. Jan. 9, 2016. Evolutionary patterns of chromosomes and genomes. Evolution of Genome Size workshop, Plant and Animal Genome XXIV Conference, San Diego, CA.
60. Sept. 2, 2015. Genetic dissection and genomic prediction of quantitative traits. Department of Bioagricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO.
61. Feb. 19, 2015. ([YouTube](#)) Genomic selection: Historical context, technical details, empirical findings, and perspectives. Texas A&M Plant Breeding Symposium, Texas A&M University, College Station, TX.
62. Jan. 13, 2015. Novel strategies in integrating genomic selection into the broad genomics-assisted breeding. Genomics-Assisted Breeding Workshop, Plant and Animal Genome XXIII Conference, San Diego, CA.
63. Nov. 10, 2014. Leveraging genomics and phenomics for a better understanding of genotype-phenotype relationship. Center for Sorghum Improvement, Kansas State University, Manhattan, KS.
64. Nov. 4, 2014. Challenges of G x E and how to overcome them. Integrating Genotypes and Phenotypes to Improve Crops for Challenging Environments, C1-Symposium, Long Beach, CA, ASA-CSSA-SSSA meeting.
65. Oct. 14, 2014. Emerging and long-standing questions in plant genetics and breeding. Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN.
66. Sept. 8, 2014. Quantitative perspectives in gene cloning, genotype by environment interaction, and germplasm enhancement. Interdepartmental Plant Group seminar series, Columbia, MO.
67. Jun. 30, 2014. Genomic selection and model prediction as an integrated breeding strategy. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
68. Apr. 28, 2014. Can we make a dent in genotype by environment interaction in this high throughput era? International Workshop on Engineered Crops, Iowa State University, Des Moines, IA.

69. Apr. 1, 2014. Significance of quantitative genetics in the era of high throughput genotyping and phenotyping. Plant Breeding and Genetics Symposium, University of Nebraska-Lincoln, Lincoln, NE.
70. Mar. 18, 2014. The significance of quantitative genetics in the high throughput era. Workshop at Center of Maize Improvement, China Agricultural University, Beijing, **China**.
71. Oct. 16, 2013. Parallel evolution of alleles, genes, chromosomes, and genomes. Genetic, Genomics, and Bioinformatics Program, University of California-Riverside, Riverside, CA.
72. Sept. 24, 2013. Genic and nongenic contributions to natural variation of maize quantitative traits in maize. Plant Genomics Congress USA, St. Louis, MO.
73. Aug. 9, 2013. The frequency issue in current genetics and genomics analysis. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
74. Jul. 31, 2013. Understanding the role of frequency in “complex” trait dissection in plants and humans. Huazhong Agricultural University, Wuhan, Hubei, **China**.
75. May 1, 2013. The critical role of frequency in genetics, genomics, and breeding. T-CAP spring 2013 webinar series, Ahead of the curve: Technologies for next-generation plant breeding.
76. Jan. 29, 2013. Interdisciplinary genetics analysis across plants, animals, and human. Department of Animal Sciences, Iowa State University, Ames, IA.
77. Jan. 12, 2013. Genome-wide landscape of genetic polymorphisms underlying quantitative trait variation. January 12, 2013. Maize Workshop, Plant and Animal Genome XXI Conference, San Diego, CA.
78. Jan. 13, 2013. Parallel domestication of the shattering1 genes in cereals. Sorghum and Millet Workshop, Plant and Animal Genome XXI Conference, Jan. 12-16, 2013, San Diego, CA.
79. Dec. 5, 2012. Genomic selection and application to grain, forage and bio-energy sorghum. Session of Genomic Selection in Corn, Sorghum and Wheat, 2012 American Seed Trait Association Meeting, Chicago, IL.
80. Sept. 20, 2012. Association mapping of genetic resources: achievement and future perspectives. Symposium "Genomics of Quantitative Traits: from QTL to genes", the 56th Annual Congress of Italian Society of Agricultural Genetics, Perugia, **Italy**.
81. Jun. 23, 2012. Opportunities and challenges of statistical genetics in genome-wide association studies. Session: Interactions Between Omics and Statistics: Analyzing High Dimensional Data, the 8th International Purdue Symposium on Statistics, West Lafayette, IN.
82. Apr. 23, 2012. Genome-wide association studies in crops and comparative genomics for gene cloning. Oklahoma State University, Stillwater, OK.
83. Jan. 17, 2012. Natural genetic variation at Tan1 defines tannin in sorghum grain and offers seedling cold tolerance. Genomics-Assisted Breeding Workshop, Plant and Animal Genome XX Conference, San Diego, CA.
84. Oct. 28, 2011. Opportunities and challenges of genome-wide association studies for plant breeding. Plant Breeding and Genetics Symposium, University of Wisconsin, Madison, WI.
85. Oct. 18, 2011. Enhancing gene discovery and plant breeding by combining genomic technology and genetic design. Chromatin, Lubbock, TX.
86. Sept. 29, 2011. Opportunities and challenges of going genome-wide. Donald Danforth Plant Science Center 2011 Fall Symposium: Plant Genomes to Phenomes, St. Louis, MO.
87. Sept. 8, 2011. Juggling between going genome-wide and nailing down the gene. Department of Plant Pathology, Kansas State University, Manhattan KS.
88. Jul. 4, 2011. Resequencing-based genome-wide association study and meta-genome analysis of chromosome evolution. Chinese Academy of Agricultural Sciences, Beijing, **China**.

89. Jul. 1, 2011. From meta-genome analyses to genome-wide signals to genes underlying complex traits. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
90. Jun. 22, 2011. What we can do with all these genome sequences and genomic technologies? China Agricultural University, Beijing, **China**.
91. Jun. 21, 2011. Genomics-assisted complex trait dissection and crop improvement. Institute of Crop Improvement, Tianjin Academy of Agricultural Research, Tianjin, **China**.
92. Jan. 16, 2011. Comparative analysis of genome and chromosome evolution across 128 species with sequenced genomes. Comparative Genomics Workshop, 2011 International Plant and Animal Genome Conference, San Diego, CA.
93. Jan. 16, 2011. Composite resequencing-based genome-wide association study (CR-GWAS) in Arabidopsis implicates both common and rare variants underlying flowering time. QTL Cloning Workshop, 2011 International Plant and Animal Genome Conference, San Diego, CA.
94. Aug. 11, 2010. AFRI National Cereal Germplasm Phenotyping - Future for public sorghum research. Great Plains Sorghum Conference, Mead, NE.
95. Apr. 5, 2010. Quantitative genetics in next generation genomics and plant breeding. Department of Agronomy, Purdue University, West Lafayette, IN.
96. Jan. 9, 2010. Statistical methods to control for population structure and relative kinship in association mapping with different sample types. Statistical Genomics Workshop, 2010 International Plant and Animal Genome Conference, San Diego, CA.
97. Dec. 11, 2009. Quantitative genetics in next generation genetics and plant breeding. Joint Graduate Program Symposium, Graduate Programs in Genetics and Plant Breeding, Genetics, and Biotechnology, Michigan State University, East Lansing, MI.
98. Sept. 1, 2009. Dissecting and selecting for complex traits. Monsanto, Ankeny, IA.
99. Aug. 18, 2009. Genomic mapping, genetic design, and genomewide selection in plants. Mendel Genetics, Lafayette, IN.
100. Jun. 23, 2009. Genomic mapping and next-generation genetics in plants. China Agriculture University, Beijing, **China**.
101. Jun. 25, 2009. Genomic mapping and next-generation genetics in plants. Chinese Academy of Agricultural Sciences, Beijing, **China**.
102. Jun. 25, 2009. Genomic mapping and next-generation genetics in plants. Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, **China**.
103. Jun. 29, 2009. Genomic mapping in plants. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
104. Mar. 3, 2009. Realizing the potential of genetic diversity and genomic technology in plant breeding. Montana State University, Bozeman, MT.
105. Feb. 25, 2009. Translational genomics in sorghum. Joint SICNA/NSP, Grapevine, TX.
106. Jan. 7, 2009. Assembling and scrambling the genomes for gene discovery. Exelixis Plant Sciences, Portland, OR.
107. Sept. 25, 2008. Methods and strategies for association mapping and genomewide selection. International Symposium on Approaches for Association Mapping and Genome-Wide Genotyping by Means of Chip Hybridization, University of Hohenheim, Stuttgart, **Germany**.
108. Sept. 3-4, 2008. Sweet sorghum improvement. Great Plains Sorghum Conference, Manhattan, KS.
109. Feb. 5, 2008. Strategies and methods for genome-wide association and genome-wide selection. Dow AgroSciences, Indianapolis, IN.

110. Jan. 16, 2008. Towards genome-wide association mapping and selection. Sorghum and Millet Workshop, Plant and Animal Genome XIV Conference, San Diego, CA.
111. Jul. 19-20, 2007. Association mapping in sorghum: progress and prospects. Great Plains Sorghum Conference, College Station, TX.
112. Oct. 25-26, 2006. Complex trait dissection through association mapping. Genomic Mapping Workshop, USDA-ARS, Lubbock, TX.
113. Jun. 2006. Association mapping in plants and animals. Summer Institute in Statistical Genetics, Washington State Univ. Seattle, WA.
114. Mar. 6, 2006. Association mapping in maize. The 42nd Illinois Corn Breeder's School, Urbana, IL.
115. Jan. 15, 2006. Association mapping accounting for multiple levels of relatedness. QTL Cloning Workshop, *Plant and Animal Genome XIV Conference*, San Diego, CA.
116. Nov. 9, 2005. Bridging molecular diversity with functional diversity: Complex trait dissection in maize. SNP Markers Symposium - Discovery, Development, Mapping, and Utilization, *ASA-CSSA-SSSA International Annual Meetings*, Salt Lake City, UT.

Other Presentations (6)

1. Nov. 3, 2021. Genome-wide associate studies, genomic selection, and genome editing, but what about environment? Interdepartmental Plant Biology Program, Iowa State University, (Virtual).
2. Apr. 4, 2018. Patter discovery and predictive modeling in biology research. Interdepartmental Plant Biology Program, Iowa State University, Ames, IA.
3. Oct. 4, 2017. Design thinking and data mining in genetics research. Interdepartmental Genetics and Genomics program, Iowa State University, Ames, IA
4. Aug. 31, 2015. Critical and creative thinking in genetics research. Interdepartmental Genetics and Genomics program, Iowa State University, Ames, IA.
5. Feb. 19, 2014. Parallel evolution of alleles, genes, chromosomes, and genomes. Interdepartmental Plant Biology Program, Iowa State University, Ames, IA.
6. November 14, 2006. Association mapping with diverse germplasm. Tuesday, *ASA-CSSA-SSSA International Annual Meetings*, Indianapolis, IN.

Teaching Experience

- 2014-present, Instructor, ISU Agron 621, Advanced Plant Breeding, Spring semester each year. Emphasis on quantitative genetics, breeding design, complex trait dissection, and relating statistics with biology and breeding.
- 2020-present, Instructor, ISU Agron 600A, Plant Breeding Seminar, Spring semester each year.
- Fall 2017, Instructor, ISU Genet 692, Conceptual Foundations of Genetics
- Fall 2013. Co-instructor, ISU Agron 621, Advanced Plant Breeding
- Fall 2007-2012. Instructor, KSU Agron 770, Plant Genetics
- Taught this class to a group of students with diverse backgrounds, including juniors, seniors, and graduate students (M.S. and Ph.D.) in Agronomy, Plant Pathology, Entomology, Biology, Grain Science, and the interdepartmental Genetics program. Average enrollment: 11. Average TEVAL score 4.4/5.0
- Fall 2010 and Fall 2012. Instructor, KSU Agron 980, Molecular Tools for Genetic Analysis
- Co-taught this class to Ph.D. students in Plant Breeding and Genetics. Enrollment: 5. Average

TEVAL score 4.9/5.0

June 2006. Instructor, Summer Institute in Statistical Genetics, Washington State Univ.

Co-taught the module with two other instructors, Association Mapping in Plants and Animals
2009. Teaching Retreat at K-State

Attended one-day workshop; On the road to teaching excellence: Our journey as teachers

Trainee (32)

Graduate Students (15), Postdoctoral Research Associates (11), and Visiting Students/Scholars (6).
*, co-advised with another faculty member, **, research done in this lab.

No.	Name	Degree/ Postdoc	Place	Duration	Research Area	Current Employment
15	Joseph DeTemple	Ph.D.	ISU	2022-	Genetics and Genomics	Iowa State University
14	Kiara Kappelmann*	Ph.D.	ISU	2022-	Plant Breeding & Genetics	Iowa State University
13	Karlene Negus	Ph.D.	ISU	2021-	Genetics and Genomics	Iowa State University
12	Mahule-Elyse-Boris Alladassi	Ph.D.	ISU	2018-	Plant Breeding & Genetics	Iowa State University
11	Jialu Wei	Ph.D.	ISU	2017-2022	Plant Breeding & Genetics	Quantitative Geneticist, Syngenta
10	Laura Tibbs Cortes	Ph.D.	ISU	2017-2022	Genetics & Genomics	ORISE Postdoc, USDA-ARS
9	James McNellie	Ph.D.	ISU	2016-2022	Genetics & Genomics	Research Scientist, USDA-ARS
8	Qi Mu	Ph.D.	ISU	2016-2021	Plant Breeding & Genetics	Postdoc Iowa State University
7	Jinyu Wang	Ph.D.	ISU	2014-2019	Plant Biology	Data Analyst, Guardant Health
6	Matt Dzievit	Ph.D.	ISU	2013-2019	Plant Breeding & Genetics	Research Scientist, Corteva
5	Brandon Hawkins	M.S. Online	ISU	2012-2016	Plant Breeding & Genetics	Research Associate, Corteva
4	Xin Li	Ph.D.	KSU-ISU	2010-2015	Plant Breeding & Genetics	Quantitative Geneticist, Damo Academy - Alibaba
3	Sivakumar Sukumaran	Ph.D.	KSU	2008-2012	Plant Breeding & Genetics	Geneticist, U. of Queensland
2	Guannan Sun**	M.S.	KSU	2009-2011	GRA, Statistics Major	Senior Statistician, Sanofi
1	Wenwen Xiang	M.S.	KSU	2007-2009	Plant Breeding & Genetics	Data Analyst, WaferGen
11	Dongdong Li	Postdoc	ISU	2022-	Quantitative Genetics	Postdoc, Iowa State University
10	Diana Escamilla Sanchez	Postdoc	ISU	2022-	Plant Breeding & Genetics	Postdoc, Iowa State University
9	Qi Mu	Postdoc	ISU	2021-	Plant Breeding & Genetics	Assistant Professor, University of Delaware
8	Hongwei Zhang	Postdoc	ISU	2016-2021	Plant Breeding & Genetics	Maze Breeder, Stine Seeds
7	Tingting Guo	Postdoc & Staff	ISU	2016-2019 2019-2022	Quantitative Genetics Quantitative Genetics	Huazhong Agricultural University
6	Adam Vanous	Postdoc	ISU	2018-2020	Plant Breeding & Genetics	Research Scientist, USDA-ARS
5	Xiaoqing Yu	Postdoc	ISU	2014-2018	Plant Breeding & Genetics	Entrepreneur

4	Xianran Li	Postdoc & Staff	KSU ISU	2008-2013 2013-2021	Genomics & Bioinformatics Genomics & Bioinformatics	Research Scientist, USDA-ARS
3	Chengsong Zhu	Postdoc	KSU-ISU	2007-2013	Quantitative Genetics	Biostatistician, UT Southwestern Medical Center
2	Yuye Wu	Postdoc	KSU	2008-2012	Plant Physiology	Professor, Shandong Agricultural University
1	Zhongwei Lin	Postdoc	KSU	2007-2012	Molecular Genetics	Professor, China Agricultural University
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6	Bingxin Wang	Visiting Scholar	ISU	2024-	Plant Breeding & Genetics	Northwest Agricultural and Forestry University
5	Danilo Hottis Lyra	Visiting Student	ISU	2015-2016 10 months	Quantitative Genetics	From University of São Paulo; BASF
4	Hewan Degu	Visiting Scholar	ISU	2014, 6 months	Plant Breeding & Genetics	African Women in Agricultural Research and Development Fellow; Hawassa University
3	Dindo Tabanao	Visiting Scholar	ISU	2013, 2 months	Plant Breeding & Genetics	Borlaug Fellow from Philippine Rice Institute; Corteva
2	Leonardo de Azevedo Peixoto	Visiting Student	ISU	2013-2014, 3 months	Plant Breeding & Genetics	From Universidade Federal de Viçosa; Universidade Federal de Viçosa
1	Chunlian Li	Visiting Scholar	KSU	2011-12, 12 months	Plant Breeding & Genetics	Northwest Agricultural and Forestry University; Professor

Graduate Student Committee (46)

Iowa State University (30 total = 29 Ph.D. + 1 M.S.)

Kansas State University (15 total = 10 Ph.D. + 5 M.S.)

Purdue University (1 total = 1 Ph.D.)

Leadership Activities and Professional Contributions

Associate Editor, *The Plant Genome* (2021-2026, 2012-2017)

Editorial Board, *Plant Communications* (2019-present)

Associate Editor, *Genetics* (2020-2022)

Associate Editor, *Molecular Breeding* (2018-2022)

Associate Editor, *Theoretical and Applied Genetics* (2007-2011)

Associate Editor, *Crop Science* (2008-2010)

Editorial Board, *Maize Genetic and Genomics Database (MaizeGDB)* (2006)

Maize Genetics Executive Committee (Chair 2018, Vice-Chair 2017; Member 2015-2020)

Maize Genetics Cooperation Awards and Nominations Committee (2023-2025)

Technical Steering Group, Germplasm Enhancement of Maize (2017-2023)

Scientific Organizing Committee: CROPS 2022, CROPS 2019, CROPS 2017, and CROPS 2015, HudsonAlpha Institute for Biotechnology (2014-present)

Chair of 2023 Corn Breeding Research Meeting, Union Station Hotel, St. Louis, MO.

Advisory Board, Genome to Phenome Bridge project funded by Foundation for Food and Agriculture

Research (2019-2020)

Scientific Organizing Committee: 5th International Symposium on Genomics and Crop Genetic Improvement-Heterosis, October 22-25, 2018, Huazhong Agricultural University, Wuhan, China
Advisory Panel, Plant Genomics Congress USA (2014-2016)

Scientific Advisor, Chromatin, Inc. (2012)

Scientific Advisory Board, Mendel Bioenergy Seeds (2009-2011)

Conference Organizing Committee: Sorghum Genomics Conference, November 15-16, 2012, Atlanta, GA

CSSA Board of Directors, C-7 Genomics, Molecular Genetics, Biotechnology Officers, 2022-01-01 - 2024-12-31

CSSA Science Policy Committee, 2022-01-01 - 2024-12-31

CSSA Crop Science Graduate Student Scholarship Committee, 2021-01-01 - 2023-12-31

ASA International Agronomy Award Committee, 2021-01-01 - 2022-12-31

CSSA Seed Science Award Committee, 2021-01-01 - 2022-12-31

CSSA Fellows Committee, 2019-01-01 - 2020-12-31

CSSA Div. C-8, Plant Genetic Resources Officers, Past Chair, Div. C-8, 2017-01-01 - 2017-12-31; Chair, Div. C-8, 2016-01-01 - 2016-12-31; Chair-Elect, Div. C-8, 2015-01-01 - 2015-12-31

CSSA Calvin Sperling Memorial Biodiversity Lectureship Committee, Chair, 2017-01-01 - 2017-12-31

CSSA Crop Science Research Award Committee, 2016-01-01 - 2017-12-31

CSSA Program Planning Committee, Chair, Div. C-8, 2016-01-01 - 2016-12-31

CSSA Nominations for President-Elect Committee, Chair, Div. C-8, 2016-01-01 - 2016-12-31

CSSA Nominations Committee for Div. C-8 Officers, Chair, 2016-01-01 - 2016-12-31

CSSA Frank N. Meyer Medal for Plant Genetic Resources Committee, Ex Officio, 2016-01-01 - 2016-12-31

CSSA Ron Phillips Plant Genetics Lectureship Committee, 2015-01-01 - 2015-12-31

ASA Tengtou Agricultural Science Award Committee, Chair, 2015-01-01 - 2015-12-31; Member, 2014-01-01 - 2014-12-31

CSSA Early Career Award Committee, Chair, 2013-01-01 - 2013-12-31; Member, 2011-01-01 - 2012-12-31

CSSA Crop Science Graduate Student Scholarship Committee, 2005-11-01 - 2007-10-31

Workshop Organizer for Plant & Animal Genome Conference, San Diego, CA: 1) Genomic Selection and Genome-Wide Association Studies (2013-present); 2) Hybridization, Heterosis and Balancing Selection (2017-present); 3) Phenotypic Plasticity and Genotype by Environment Interaction: Dissection and Prediction (2024-present); 4) Maize (2022)

Workshop Instructor and Organizer: Phenotypic Plasticity and Genotype by Environment Interaction: Dissection and Prediction, National Association of Plant Breeders Education Committee virtual, Feb 22, 2021; ASA-CSSA-SSSA meeting virtual, Nov. 10, 2020

Short-course Organizer: Genotype to phenotype models for traditional and new phenotyping data in plant breeding, Ames, IA, June 9-12, 2019

Workshop Instructor, Genomic Prediction in Plant Breeding, Advanced Topics in Plant Breeding Summer Institute 2015, Iowa State University, Ames, IA, June 29-30, 2015

Session Organizer & Moderator: Artificial Intelligence & Genomic Selection for Crop Improvement 2021 ASA-CSSA-SSSA Meeting (2021)

Symposium Moderator: Designs for Predictive Agriculture, 2021 ASA-CSSA-SSSA Meeting (2021)
Session Organizer: Big Data in Plant Science, the 9th International Purdue Symposium on Statistics, West Lafayette, IN (2018)
Symposium Organizer: The Prominent Role of Plant Genetic Resources and Genebanks in the Post-Genomic Era, C8-Symposium, Phoenix, AZ, 2016 ASA-CSSA-SSSA Meeting (2016)
Symposium Organizer: Using Genotypic Data to Strategically Develop Core Collections, Mini-Cores, and Trait-Specific Subsets, 2012 ASA-CSSA-SSSA Meeting (2012)
Session Organizer: Interactions Between Omics and Statistics: Analyzing High Dimensional Data, the 8th International Purdue Symposium on Statistics, West Lafayette, IN (2012)
Symposium Organizer: Translational Genomics for Plant Breeding, Sept. 23-24, 2009, Manhattan, KS
Symposium Organizer: Genomic Tools for Crop Improvement, 2007 ASA-CSSA-SSSA Meeting (2007)
Session Chair: Cultivar Development-II, C01 Crop Breeding & Genetics, 2006 Annual ASA-CSSA-SSSA Meeting (2006)

Review Panel: USDA-Agricultural Research Service (ARS), The NP 301 Grains Super Panel, Plant Genetic Resources, Genomics and Genetic Improvement National Program (2023) (virtual)
Review Panel: USDA-National Institute for Food and Agriculture (NIFA) Agriculture and Food Research Initiative (AFRI), Plant Breeding for Agricultural Production and Conventional Breeding for Cultivar Development (2021) (virtual)
Review Panel: Binational Agricultural Research & Development Fund (BARD) Crop Production (2017)
Review Panel: USDA-NIFA AFRI, Physiology of Agricultural Plants (2016)
Review Panel: NSF Plant Genome Research Program (2013)
Review Panel: NSF Molecular and Cellular Evolution (2011)
Review Panel: USDA NIFA AFRI, Plant Breeding and Education (2009)
Review Panel: USDA-Cooperative State Research, Education, and Extension Service (CSREES) National Research Initiative (NRI), Plant Genome Program and Coordinated Agriculture Project (CAP) (2007)

Grant reviewer: NSF Plant Genome Research Program (2019, 2022, 2023), NSF Molecular and Cellular Evolution (2015)
Grant Reviewer: Swiss National Science Foundation (2019, 2020, 2023)
Grant Reviewer: Czech Science Foundation (2022)
Grant Reviewer: European Research Council (2021)
Grant Reviewer: Deutsche Forschungsgemeinschaft (DFG) German Research Foundation (2019, 2020)
Grant reviewer: Plant Breeding Research for the Bioeconomy program by German Federal Ministry of Education and Research (2015)
Grant reviewer: University of Gent Industrial Research Fund (2014-2015)
Grant reviewer: BARD (2012)
Grant reviewer: National Science Foundation, Arabidopsis 2010, Cellular Systems (2010)
Grant reviewer: National Research Agency, Plant Genomics, France (2008, 2009, 2010)
Grant reviewer: SEEDS: Research Enhancement Competitive Grants, Ohio State University (2008)
Grant reviewer: South Central Sun Grant Initiative (2007)

Manuscript reviewer for *Cell*, *Nature*, *Science*, *Nature Genetics*, *Nature Biotechnology*, *Nature Review Genetics*, *PNAS*, *Genome Biology*, *Nature Communications*, *Nature Plants*, *Genome*

Research, Molecular Biology and Evolution, Molecular Plant, Plant Cell, Science Advances, eLife, Genetics, PLOS Genetics, Theoretical and Applied Genetics, Heredity, Crop Science, The Plant Genome, G3-(Genes, Genomes, Genetics), Genetics Research, Molecular Breeding, Bioinformatics, Briefings in Functional Genomics and Proteomics, Field Crops Research, Journal of Heredity, Bioenergy Research, Journal of Agricultural and Food Chemistry

Member of Crop Science Society of America (1999-present)

Member of American Society of Agronomy (2002-present)

Member of Genetic Society of America (2009-present)

Member of American Association for the Advancement of Science (2010-present)

Member of National Association of Plant Breeders (2014-2015, 2017-present)

Member of American Society of Plant Biology (2015-present)

On-Campus Service

ISU University: Panelist for Faculty Development Workshop: External Recognition for Your Career, Office of the Senior Vice President and Provost (2020, 2021); Judge for the Postdoctoral Research Excellence Award (2019, 2023); Admission Committee for the P3 specialty (2019); Curriculum Committee for the P3 specialty (2017-2019); Working group for Syngenta-ISU data sharing (2016); Advisory Council for Crop Bioengineering Consortium (2014-2015); Interim Director of Graduate Education for Plant Breeding program (2015-2016); Admission Committee of the Interdepartmental Genetics and Genomics (2016, 2014)

ISU Department of Agronomy: Promotion and Tenure Committee (Chair 2022, member 2024-2027; 2019-2022); Junior/Senior Curriculum Committee (2020-2022); Department Enhancement Program (DEP) Implementation Committee (Chair, 2019-2020); Research Committee for Departmental Review (2018-2019); Plant Breeding Awards Committee (Chair, 2016-present); Bayer Plant Graduate Student Travel Award (2017-present); Website Committee (2018-2019); Strategic Planning Committee (2016); Search Committee for Grant Coordinator (2016); Search Committee for USDA-ARS Maize GDB Computational Biologist (2015); Search Committee for Cropping Systems (2014); Uniform Written Prelim Committee (2014-2016).

Faculty Advisor, ISU Plant Breeding Symposium Organization Group (2013-present); ISU Iowa Corn Colligate Club (2021-present).

KSU University: Committee on Planning, Graduate Council (2009-2012); Review Committee for Faculty Development Award and University Small Research Grant (2010-2012); Sarachek Selection Committee for the Alvin and RosaLee Sarachek Predoctoral Fellowship and Travel Award (2009-2012), Federal Initiative for Integrated Life Sciences Genome Center (2010); NSF Science and Technology Center (2009); Kansas Bioscience Authority (KBA) Planning Grant Initiative (2008)

KSU College of Agriculture: Search Committee for Grant Support Lead (2011), Task Force for Proposal Support (2010)

KSU Department of Agronomy: Heyne Crop Science Lectureship Committee (2007-2012); Research Publication (2009-2012); Open House Committee (2007-2012); Graduate Scholarship Committee (2007-2012); Search Committee for Hays Sorghum Breeder Position (2009); Search Committee for Sorghum Breeder (2007)

Faculty Advisor, KSU Graduate Student Association in Plant Breeding and Genetics (2012)

Grants Funded (\$35.5 million total with \$7.8 million to Yu's program)

NSF PGRP, NSF-EPSCoR, USDA-NIFA AFRI, DOE ARPA-E, BARD, USDA-ARS, Iowa Corn Promotion Board, Stine Seeds, Texas Corn, Kansas Grain Sorghum Commission, National Sorghum Checkoff, and internal funding sources.

Peer-Reviewed Journal Publications (114)

(Students/postdocs/staff of Yu's program; *, corresponding author)

[Google Scholar, h-index = 60, total citation = 24,358](#)



1. Zhang, H., D. Li, K.R. Lamkey, W.H. Stine, J. Yu*, and H.H. Stine*. 2024. New maize inbred development method I: Inter-heterotic group composite and tester choice. *Crop Science* (online first).
2. Gou, X., Y. Shao; H. Shi; J. Yu, X. Li*, and T. Guo*. 2024. Evolutionary patterns of DNA base composition at polymorphic sites highlight the role of the environment in shaping barley and rice genomes. *The Plant Genome* (online first).
3. Adak, A., S.C. Murray*, J.I. Varela, V. Infante, J. Wilker, C.I. Calderón, N. Subramanian, N. de Leon, J. Yu, M.A. Stull; M. Brun, J. Hill, C.D. Johnson, O. Riera-Lizarazu, W.L. Rooney, and H. Zhang. 2024. Photoperiod associated late flowering reaction norm: Dissecting loci and genomic-environment associated prediction in maize. *Field Crops Research* 31:109380.
4. Negus, K.L., X. Li, S.M. Welch, and J. Yu*. 2024. The role of artificial intelligence in crop improvement. *Advances in Agronomy* 184:1-66. (Book series functioning as a journal)
5. Dziejewicz, M.J., X. Li, and J. Yu*. 2024. Genetic mapping of dynamic control of leaf angle across multiple canopy levels in maize. *The Plant Genome* 17:e20423.
6. Guo, T*, J. Wei, X. Li, and J. Yu*. 2024. Environmental context of phenotypic plasticity in flowering time in sorghum and rice. *Journal Experimental Botany* 75:1004-1015. **Insight article by the journal:** [Importance of phenotypic plasticity in crop resilience](#).
7. Tibbs-Cortes, L.E., T. Guo., X. Li, R. Tanaka, A.E. Vanous, D. Peters, C. Gardner, M. Magallanes-Lundback, N.T. Deason, D. DellaPenna, M.A. Gore, and J. Yu*. 2023. Genomic prediction of tocochromanols in exotic-derived maize. *The Plant Genome* 16:e20286.
8. Tanaka, R., D. Wu, Xiaolei Li, L.E. Tibbs-Cortes, J.C. Wood, M. Magallanes-Lundback, N. Bornowski, J.P. Hamilton, B. Vaillancourt, X. Li, N.T. Deason, G.R. Schoenbaum, C.R. Buell, D. DellaPenna, J. Yu, and M.A. Gore*. 2023. Leveraging prior biological knowledge improves prediction of tocochromanols in maize grain. *The Plant Genome* 16:e20276.
9. Elli, E.F., J. Edwards, J. Yu, S. Trifunovic, D.M. Eudy, K.R. Kosola, P.S. Schnable, K.R. Lamkey, S.V. Archontoulis*. 2023. Maize leaf angle genetic gain is slowing down in the last decades. *Crop Science* 63:3520-3533.
10. Zhang, B., H. Huang, L.E. Tibbs-Cortes, A.E. Vanous, Z. Zhang, K. Sanguinet, K.A. Garland-Campbell, J. Yu, and X. Li*. 2023. Streamline unsupervised machine learning to survey and graph indel-based haplotypes from pan-genomes. *Molecular Plant* 16:975-978.
11. Xiang, L., J. Gai, Y. Bo, J. Yu., P.S. Schnable, and T. Lie*. 2023. Field-based robotic leaf angle detection and characterization of maize plants using stereo vision and deep convolutional neural networks. *Journal of Field Robotics* 40:1034-1053.
12. Wu, D., Xiaolei Li, R. Tanaka, J.C. Wood, L.E. Tibbs-Cortes, M. Magallanes-Lundback, N. Bornowski, J.P. Hamilton, B. Vaillancourt, C.H. Diepenbrock, Xianran Li, N.T. Deason, G.R. Schoenbaum, J. Yu, C.R. Buell, and D. DellaPenna, and M.A. Gore*. 2022. Combining GWAS

- and TWAS to identify candidate causal genes for tocochromanol levels in maize grain. *Genetics* 221:iyac091.
13. Dos Santos, C.L., L. Abendroth, J.A. Coulter, E.D. Nafziger, A. Suyker, **J. Yu**, P.S. Schnable, and S. Archontoulis*. 2022. Maize leaf appearance rates: a synthesis from the US Corn Belt. *Frontiers in Plant Science* 13:872738.
 14. Li, X.* , T. Guo, G. Bai, G., Z. Zhang, D. See, J. Marshall, K.A. Garland-Campbell, and **J. Yu**. 2022. Genetics-inspired data-driven approaches explain and predict crop performance fluctuations attributed to changing climatic conditions. *Molecular Plant* 15:203-206. **Spotlight by the journal:** [Prediction of and for new environments: What's your model?](#)
 15. Qi, M., T. Guo, X. Li*, and **J. Yu***. 2022. Phenotypic plasticity in plant height shaped by interaction between genetic loci and diurnal temperature range. *New Phytologist* 233:1768-1779. News release: [Under the hood: How environment interact with genome during plant development.](#)
 16. Onogi, A.* , D. Sekine, A. Kaga, S. Nakano, T. Yamada, **J. Yu**, and S. Ninomiya. 2021. A method for identifying environmental stimuli and genes responsible for genotype-by-environment interactions from a large-scale multi-environment data set. *Frontiers in Genetics* 12:803636.
 17. Dzievit, M.J., T. Guo, X. Li, and **J. Yu***. 2021. Comprehensive analytical and empirical evaluation of genomic prediction across diverse accessions in maize. *The Plant Genome* 14:e20160.
 18. Wang, J., X. Li, T. Guo, M.J. Dzievit, X. Yu, P. Liu, K.P. Price, and **J. Yu***. 2021. Genetic dissection of seasonal vegetation index dynamics in maize through aerial based high-throughput phenotyping. *The Plant Genome* 14:e20155.
 19. M.B. Hufford, A.S. Seetharam, M.R. Woodhouse, K.M. Chougule, S. Ou, J. Liu, W.A. Ricci, T. Guo, A. Olson, Y. Qiu, R.D. Coletta, S. Tittes, A.I. Hudson, A.P. Marand, S. Wei, Z. Lu, B. Wang, M.K. Tello-Ruiz, R.D. Piri, N. Wang, D.W. Kim, Y. Zeng, C.H. O'Connor, X. Li, A.M. Gilbert, E. Baggs, K.V. Krasileva, J.L. Portwood, E.K.S. Cannon, C.M. Andorf, N. Manchanda, S.J. Snodgrass, D.E. Hufnagel, Q. Jiang, S. Pedersen, M.L. Syring, D.A. Kudrna, V. Llaca, K. Fengler, R.J. Schmitz, J. Ross-Ibarra, **J. Yu**, J.I. Gent, C.N. Hirsch, D. Ware, R.K. Dawe*. 2021. De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. *Science* 373:655-662.
 20. Li, X., T. Guo, J. Wang, W.A. Bekele, S. Sukumaran, A.E. Vanous, J.P. McNellie, L. Tibbs Cortes, M.S. Lopes, K.R. Lamkey, M.E. Westgate, J. McKay, S.V. Archontoulis, M.P. Reynolds, N.A. Tinker, P.S. Schnable, and **J. Yu***. 2021. An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. *Molecular Plant* 14:874-887. **Spotlight by the journal:** [Prediction of and for new environments: What's your model?](#) News release: [Sensing what plants sense: Integrated framework helps scientists explain biology and predict crop performance.](#)
 21. Varshney, R.K*., A. Bohra, **J. Yu**, A. Graner, Q. Zhang, and M.E. Sorrells. 2021. Designing future crops: genomics-assisted breeding comes of age. *Trends in Plant Science* 26:631-649.
 22. Perumal, R.* , G.P. Morris, S.V. Krishna Jagadish, C.R. Little, T.T. Tesso, S.R. Bean, **J. Yu**, P.V. Vara Prasad, and M.R. Tuinstra. 2021. Registration of the Sorghum [*Sorghum bicolor* (L.) Moench] Nested Association Mapping (NAM) Population in RTx430 Background. *Journal of Plant Registration* 15:395-402.
 23. Kusmec, A., Z. Zheng, S.V. Archontoulis, B. Ganapathysubramanian, G. Hu; L. Wang, **J. Yu**, and P.S. Schnable*. 2021. Interdisciplinary strategies to enable data-driven plant breeding in a changing climate. *One Earth* 4:372-383.
 24. Tibbs Cortes, L., Z. Zhang, and **J. Yu***. 2021. Status and prospects of genome-wide association studies in plants. *The Plant Genome* 14:e20077.

25. Jarquín D.*, N. de Leon, M.C. Romay, M.O. Bohn, E.S. Buckler, I.A. Ciampitti, J.W. Edwards, D. Ertl, S. Flint-Garcia, M.A. Gore, C. Graham, C.N. Hirsch, J.B. Holland, D.C. Hooker, S.M. Kaeppler, J. Knoll, E.C. Lee, C.J. Lawrence-Dill, J.P. Lynch, S.P. Moose, S.C. Murray, R. Nelson, T.R. Rocheford, J.C. Schnable, P.S. Schnable, M. Smith, N.M. Springer, P. Thomison, M.R. Tuinstra, R.J. Wisser, W. Xu, **J. Yu**, and A.J. Lorenz. 2021. Utility of climatic information via combining ability models to improve genomic prediction for yield within the genomes to fields maize project. *Frontier in Genetics* 11:819.
26. Yu, X., S. Leiboff, X. Li, T. Guo, N. Ronning, X. Zhang, G.J. Muehlbauer, M.C.P. Timmermans, P.S. Schnable, M.J. Scanlon, and **J. Yu***. 2020. Genomic prediction of maize micro-phenotypes provides insights for optimizing selection and mining diversity. *Plant Biotechnology Journal* 18:2456-2465. News release: [Making sense of a universe of corn genetics](#).
27. Tonnis, B., M.L. Wang*, X. Li, J. Wang, N. Puppala, S. Tallury, and **J. Yu**. 2020. Peanut *FAD2* genotype and growing location interactions significantly affect the level of Oleic Acid in seeds. *Journal of the American Oil Chemist's Society* 97:1001-101.
28. Jarquin, D.* , H. Kajiya-Kanegae, C. Taishen, S. Yabe, R. Persa, **J. Yu**, H. Nakagawa, M. Yamasaki, and H. Iwata*. 2020. Coupling day length data and genomic prediction tools for predicting time related traits under complex scenarios. *Scientific Reports* 10:13382.
29. Guo, T., Q. Mu, J. Wang, A.E. Vanous, A. Onogi, H. Iwata, X. Li*, and **J. Yu***. 2020. Dynamic effects of flowering-time genes underlying phenotypic plasticity in rice. *Genome Research* 30:673-683. News release: [Patterns in crop data reveal new insight about plants and their environments](#).
30. Char, S.N., J. Wei, Q. Mu, X. Li, Z. Zhang, **J. Yu**, and B. Yang*. 2020. An Agrobacterium-delivered CRISPR/Cas9 system for targeted mutagenesis in sorghum. *Plant Biotechnology Journal* 18:319-321.
31. Zhang, Z., X. Zhang, Z. Lin, J. Wang, H. Liu, L. Zhou, S. Zhong, Y. Li, C. Zhu, J. Lai, X. Li, **J. Yu**, and Z. Lin*. 2020. A large transposon insertion in the *stiff1* promoter controls stiff stalk in maize. *Plant Cell* 32:152-165.
32. Wu, Yuye, T. Guo, Q. Mu, J. Wang, Xin Li, Yun Wu, B. Tian, M.L. Wang, G. Bai, R. Perumal, H.N. Trick, S.R. Bean, I.M. Dweikat, M.R. Tuinstra, G. Morris, T.T. Tesso, **J. Yu***, and Xianran Li*. 2019. Allelochemicals targeted to balance competing selections in African agroecosystems. *Nature Plants* 5:1229-1236. **News and Views from the journal:** [When bitter is better](#). News release: [Sorghum study illuminates relationship between humans, crops and the environment in domestication](#).
33. Knauer, S., M. Javelle, L. Li, X. Li, X. Ma, S. Kumari, K. Wimalanathan, S. Kumari, R. Johnston, S. Leiboff, R. Meeley, P.S. Schnable, D. Ware, C. Lawrence-Dill, **J. Yu**, G.J. Muehlbauer, M.J. Scanlon, and M.C.P. Timmermans*. 2019. A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. *Genome Research* 29:1962-1973.
34. Su, Z., A. Bernardo, B. Tian, H. Chen, S. Wang, H. Ma, S. Cai, D. Liu, D. Zhang, T. Li, H. Trick, P. St. Amand, **J. Yu**, Z. Zhang, and G. Bai*. 2019. A deletion mutation in *TaHRC* confers *Fhb1* resistance to fusarium head blight in wheat. *Nature Genetics* 51:1099-1105. **News and Views from the journal:** [A new player contributing to durable Fusarium resistance](#).
35. Wang, J., X. Li*, K.D. Kim, M.J. Scanlon, S.A. Jackson, N.M. Springer, and **J. Yu***. 2019. Genome-wide nucleotide patterns and potential mechanisms of genome divergence following domestication in maize and soybean. *Genome Biology* 20:74. News release: [Research sheds light on genomic features that make plants good candidates for domestication](#).
36. Andorf, C., W.D. Beavis, M. Hufford, S. Smith, W.P. Suza, K. Wang, M. Woodhouse, **J. Yu**, and T.

- Lübberstedt*. 2019. Technological advances in maize breeding: Past, present and future. *Theoretical and Applied Genetics* 132:817-849.
37. Dziewit, M., X. Li, and **J. Yu***. 2019. Dissection of leaf angle variation in maize through genetic mapping and meta-analysis. *The Plant Genome* 12:180024.
 38. Guo, T., X. Yu, X. Li, H. Zhang, C. Zhu, S. Flint-Garcia, M.D. McMullen, J.B. Holland, S.J. Szalman, R.J. Wisser, and **J. Yu***. 2019. Optimal designs for genomic selection in hybrid crops. *Molecular Plant* 12:390-401. News release: [Data mining brings new clarity to plant breeding](#).
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