

Jianming Yu

Department of Agronomy, Iowa State University, 2104 Agronomy Hall, Ames, IA 50011-1051
Phone: 515-294-2757 Fax: 515-294-3163 E-mail: jmyu@iastate.edu

Professional Experience

2017–date Professor, Dept. of Agronomy, Iowa State Univ.
2013–date 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. Applied Plant Sciences, Univ. of Minnesota
1998–2000 M.S. Agronomy, Kansas State Univ.
1990–1994 B.S. Agronomy, Northwest Agriculture and Forestry Univ.

Honors and Awards

2018 Highly Cited Researcher, Clarivate Analytics
2018 Fellow, American Association for the Advancement of Science (AAAS)
2018 Fellow, Crop Science Society of America (CSSA)
2018 Editor's Citation for Excellence, *The Plant Genome*
2018 Raymond and Mary Baker Agronomic Excellence Award, Agronomy, Iowa State Univ.
2017 Mid-Career Achievement in Research Award, Iowa State Univ.
2017 Mid-Career Achievement in Research Award, College of Agriculture and Life Sciences, Iowa State Univ.
2015–date Faculty Scholar of Plant Sciences Institute, Iowa State Univ.
2014 Emerging Leader in Plant Sciences, Univ. of Minnesota
2010 Young Crop Scientist Award, Crop Science Society of America
2010 Early Career Professional Award, American Society of Agronomy – Crop Science Society of America – Soil Science Society of America
2004 Summer Institute in Statistical Genetics Scholarship, North Carolina State Univ.
2003 Gerald O. Mott Award, Crop Science Society of America
2003 H.K. Hayes Graduate Student Award, Dept. of Agronomy & Plant Genetics, Univ. of Minnesota
2002–2003 Doctoral Dissertation Fellowship, Graduate School, Univ. of Minnesota
2000–2002 Troyer/Darwin Fellowship, Dept. of Agronomy & Plant Genetics, Univ. of Minnesota
2001 Gamma Sigma Delta, the Honor Society of Agriculture
1999 Dan M. Rodger's Graduate Scholarship, Dept. of Agronomy, Kansas State Univ.
1991–1994 Outstanding Undergraduate Scholarship, Dept. of Agronomy, Northwest Agriculture and Forestry Univ.

Research Summary

Jianming Yu is Professor and Pioneer Distinguished Chair in Maize 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 maize breeding. 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 trait dissection and crop improvement. Yu is a Faculty Scholar of [Plant Sciences Institute](#) and a member of [Raymond F. Baker Center for Plant Breeding](#).

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](#)). 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 nongenetic contributions to quantitative trait variation in maize ([Genome Research 22:2436-2444](#)).
- 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.
- Developed the mixed model method 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.

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](#)).
- 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 major breeding companies.

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](#)). 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 ([Nature Genetics 44:720-724](#)).
- Cloned the *Tan1* gene in sorghum underlying a trait with incomplete domestication ([PNAS 109:10281-10286](#)).

Other Significant Research

- Revealed the patterns in DNA base composition divergence ([Nucleic Acids Research 43:3614-3625](#)).
- Revealed the patterns in chromosome size variation ([Molecular Biology and Evolution 28:1901-1911](#)) across multiple species.

Invited Talks (98 = 69 National + 29 International)

1. 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).
2. May 13, 2021. Quantitative genetics: current status and history. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China** (Virtual).
3. Feb. 27, 2021. Genome-wide associate studies, genomic selection, and genome editing, but what about environment? Corn Breeding Research Meeting Virtual.
4. 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.
5. Apr. 1, 2020. Pattern finding for a better understanding of genes, organisms, and environments. Bayer Crop Science Zoom Seminar Series.
6. Nov. 29, 2019. Genome-wide association studies and discovery of tannins' role in agroecosystems. Shanghai Chenshan Plant Science Research Center, Shanghai, **China**.
7. Nov. 29, 2019. An integrated understanding of genes, organisms, and environments. Shanghai Institute of Plant Physiology and Ecology, Chinese Academy of Sciences, Shanghai, **China**.
8. 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**.
9. Sept. 13, 2019. ([YouTube](#)) Integrating design, analytics, and genomics in crop improvement. University of Nebraska - Lincoln, Lincoln, NE.
10. Aug. 29, 2019. Design thinking, data mining, and the complex genotype-environment-phenotype relationship. Corteva, Johnston, IA.
11. Jun. 20, 2019. Genomic selection, plant breeding design, and optimization. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
12. May 31, 2019. ([YouTube](#)) Towards a better understanding of genes, organisms, and

- environments. Cornell University, Ithaca, NY.
13. 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.
 14. Feb. 25, 2019. A unified synthesis framework of genes, organisms, and environments for gene discovery and performance forecasting. Purdue University, West Lafayette, IN.
 15. 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.
 16. Dec. 13, 2018. Establishing a unified framework for genomic prediction of untested genotypes in untested environments. BASF, Morrisville, NC.
 17. Nov. 28, 2018. Uncovering patterns behind phenotypic plasticity for gene discovery and trait prediction. Colorado State University, Fort Collins, CO.
 18. 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**.
 19. 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**.
 20. 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**.
 21. Jul. 20, 2018. Genomic and environmental determinants and their interplay underlying phenotypic plasticity. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
 22. Apr. 20, 2018. ([YouTube](#)) Pattern discovery, predictive modeling, and design in plant breeding and genetics, Clemson Integrated Plant Sciences Symposium, Clemson, SC.
 23. Apr. 6, 2018. Genomic and environmental determinants underlying phenotypic plasticity. Texas A&M University, College Station, TX.
 24. Dec. 6, 2017. Exploring the genotype-phenotype relationship for germplasm enhancement. Germplasm Enhancement of Maize (GEM) Cooperator's Meeting, Chicago, IL.
 25. Nov. 15, 2017. Quantitative Genetics and Maize Breeding. ISU Plant Breeding Mini Retreat. Ames, IA
 26. 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**).
 27. Jul. 3, 2017. Design thinking and data mining in genetics and breeding. China Agricultural University, Beijing, **China**.
 28. Jun. 29, 2017. Design and application in genome-wide association studies and genomic selection. Henan University, Kaifeng, Henan, **China**.
 29. 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.
 30. 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.

31. Nov. 29, 2016. Optimal design in complex trait dissection and genomic prediction. Design Optimal Genetics Improvement and Agronomic Systems. Ames, IA.
32. Nov. 18, 2016. Breeding strategies with genomic selection. Hi Fidelity Genetics, Durham, NC.
33. Nov. 17, 2016. Genomic selection: Continuing the journey of excellence of plant breeding. Bayer CropScience, Morrisville, NC.
34. 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.
35. Aug. 30, 2016. Parallel evolution of alleles, genes, chromosomes, and taxa. Bioinformatics Seminar, Department of Statistics, Purdue University., West Lafayette, IN.
36. Jul. 14, 2016. Genetics of heterosis and plant breeding methods. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
37. Jul. 9, 2016. Genotype and phenotype relationship for different biological questions. Shandong Agricultural University, Tai'an, Shandong, **China**.
38. 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.
39. Apr. 28, 2016. Genomic prediction contributes to a promising global strategy to evaluate plant germplasm in genebanks. Noble Foundation, Ardmore, OK.
40. 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.
41. Jan. 9, 2016. Evolutionary patterns of chromosomes and genomes. Evolution of Genome Size workshop, Plant and Animal Genome XXIV Conference, San Diego, CA.
42. Sept. 2, 2015. Genetic dissection and genomic prediction of quantitative traits. Department of Bioagricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO.
43. 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.
44. 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.
45. Nov. 10, 2014. Leveraging genomics and phenomics for a better understanding of genotype-phenotype relationship. Center for Sorghum Improvement, Kansas State University, Manhattan, KS.
46. 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.
47. 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.
48. Sept. 8, 2014. Quantitative perspectives in gene cloning, genotype by environment interaction, and germplasm enhancement. Interdepartmental Plant Group seminar series, Columbia, MO.
49. Jun. 30, 2014. Genomic selection and model prediction as an integrated breeding strategy. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.

50. 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.
51. 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.
52. Mar. 18, 2014. The significance of quantitative genetics in the high throughput era. Workshop at Center of Maize Improvement, China Agricultural University, Beijing, **China**.
53. Oct. 16, 2013. Parallel evolution of alleles, genes, chromosomes, and genomes. Genetic, Genomics, and Bioinformatics Program, University of California-Riverside, Riverside, CA.
54. Sept. 24, 2013. Genic and nongenic contributions to natural variation of maize quantitative traits in maize, Plant Genomics Congress USA, St. Louis, MO.
55. Aug. 9, 2013. The frequency issue in current genetics and genomics analysis. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
56. Jul. 31, 2013. Understanding the role of frequency in “complex” trait dissection in plants and humans. Huazhong Agricultural University, Wuhan, Hubei, **China**.
57. 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.
58. Jan. 29, 2013. Interdisciplinary genetics analysis across plants, animals, and human. Department of Animal Sciences, Iowa State University, Ames, IA.
59. 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.
60. 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.
61. 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.
62. 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**.
63. 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.
64. Apr. 23, 2012. Genome-wide association studies in crops and comparative genomics for gene cloning. Oklahoma State University, Stillwater, OK.
65. 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.
66. Oct. 28, 2011. Opportunities and challenges of genome-wide association studies for plant breeding. Plant Breeding and Genetics Symposium, University of Wisconsin, Madison, WI.
67. Oct. 18, 2011. Enhancing gene discovery and plant breeding by combining genomic technology and genetic design. Chromatin, Lubbock, TX.
68. 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.

69. Sept. 8, 2011. Juggling between going genome-wide and nailing down the gene. Department of Plant Pathology, Kansas State University, Manhattan KS.
70. Jul. 4, 2011. Resequencing-based genome-wide association study and meta-genome analysis of chromosome evolution. Chinese Academy of Agricultural Sciences, Beijing, **China**.
71. Jul. 1, 2011. From meta-genome analyses to genome-wide signals to genes underlying complex traits. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
72. Jun. 22, 2011. What we can do with all these genome sequences and genomic technologies? China Agricultural University, Beijing, **China**.
73. Jun. 21, 2011. Genomics-assisted complex trait dissection and crop improvement. Institute of Crop Improvement, Tianjin Academy of Agricultural Research, Tianjin, **China**.
74. 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.
75. 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.
76. Aug. 11, 2010. AFRI National Cereal Germplasm Phenotyping - Future for public sorghum research. Great Plains Sorghum Conference, Mead, NE.
77. Apr. 5, 2010. Quantitative genetics in next generation genomics and plant breeding. Department of Agronomy, Purdue University, West Lafayette, IN.
78. 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.
79. 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.
80. Sept. 1, 2009. Dissecting and selecting for complex traits. Monsanto, Ankeny, IA.
81. Aug. 18, 2009. Genomic mapping, genetic design, and genomewide selection in plants. Mendel Genetics, Lafayette, IN.
82. Jun. 23, 2009. Genomic mapping and next-generation genetics in plants. China Agriculture University, Beijing, **China**.
83. Jun. 25, 2009. Genomic mapping and next-generation genetics in plants. Chinese Academy of Agricultural Sciences, Beijing, **China**.
84. Jun. 25, 2009. Genomic mapping and next-generation genetics in plants. Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, **China**.
85. Jun. 29, 2009. Genomic mapping in plants. Northwest Agriculture and Forestry University, Yangling, Shaanxi, **China**.
86. Mar. 3, 2009. Realizing the potential of genetic diversity and genomic technology in plant breeding. Montana State University, Bozeman, MT.
87. Feb. 25, 2009. Translational genomics in sorghum. Joint SICNA/NSP, Grapevine, TX.
88. Jan. 7, 2009. Assembling and scrambling the genomes for gene discovery. Exelixis Plant Sciences, Portland, OR.
89. 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**.

90. Sept. 3-4, 2008. Sweet sorghum improvement, Great Plains Sorghum Conference, Manhattan, KS.
91. Feb. 5, 2008. Strategies and methods for genome-wide association and genome-wide selection. Dow AgroSciences, Indianapolis, IN.
92. Jan. 16, 2008. Towards genome-wide association mapping and selection. Sorghum and Millet Workshop, Plant and Animal Genome XIV Conference, San Diego, CA.
93. Jul. 19-20, 2007. Association mapping in sorghum: progress and prospects. Great Plains Sorghum Conference, College Station, TX.
94. Oct. 25-26, 2006. Complex trait dissection through association mapping. Genomic Mapping Workshop, USDA-ARS, Lubbock, TX.
95. Jun. 2006. Association mapping in plants and animals. Summer Institute in Statistical Genetics, Washington State Univ. Seattle, WA.
96. Mar. 6, 2006. Association mapping in maize. The 42nd Illinois Corn Breeder's School, Urbana, IL.
97. Jan. 15, 2006. Association mapping accounting for multiple levels of relatedness. QTL Cloning Workshop, *Plant and Animal Genome XIV Conference*, San Diego, CA.
98. 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.

Teaching Experience

2014-2021, Instructor, ISU AGRON 621, Advanced Plant Breeding

2020-2021, Instructor, ISU AGRON 600A, Plant Breeding Seminar

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 (25)

Graduate Students (12), Postdoctoral Research Associates (8), and Visiting Students/Scholars (5)

No	Name	Degree/ Postdoc	Place	Duration	Research Area	Current Employment
12	Mahule-Elyse- Boris Alladassi	Ph.D.	ISU	2018-	Plant Breeding & Genetics	Iowa State University
11	Laura Tibbs Cortes	Ph.D.	ISU	2017-	Genetics & Genomics	Iowa State University
10	Jialu Wei	Ph.D.	ISU	2017-	Plant Breeding & Genetics	Iowa State University

9	James McNellie	Ph.D.	ISU	2016-	Genetics & Genomics	Iowa State University
8	Qi Mu	Ph.D.	ISU	2016-2021	Plant Breeding & Genetics	Iowa State University
7	Jinyu Wang	Ph.D.	ISU	2014-2019	Plant Biology	Data Analyst, Guardant Health
6	Matt Dziejewit	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, AgReliant
3	Sivakumar Sukumaran	Ph.D.	KSU	2008-2012	Plant Breeding & Genetics	Scientist & Lead, CIMMYT
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
<hr/>						
8	Hongwei Zhang	Postdoc	ISU	2016-2021	Plant Breeding & Genetics	Maze Breeder, Stine Seeds
7	Tingting Guo	Postdoc Staff	ISU	2016-2019 2019-2021	Quantitative Genetics	(Transition)
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	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
<hr/>						
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

Leadership Activities and Professional Contributions

Associate Editor, *Genetics* (2020-present)

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

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

Associate Editor, *Molecular Breeding* (2018-present)
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)
Technical Steering Group, Germplasm Enhancement of Maize (2017-present)
Advisory Board, Genome to Phenome Bridge project funded by Foundation for Food and Agriculture Research (2019-present)
Scientific Organizing Committee: CROPS 2019, CROPS 2017, and CROPS 2015, HudsonAlpha Institute for Biotechnology (2014-present)
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, 2022-01-01 - 2024-12-31
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 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
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)
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: 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: Plant Breeding for Agricultural Production and Conventional Breeding for Cultivar
Development, USDA-NIFA AFRI (2021)

Review Panel: Crop Production, Binational Agricultural Research & Development Fund (BARD)
(2017)

Review Panel: Physiology of Agricultural Plants, USDA-NIFA AFRI (2016)

Review Panel: Plant Genome Research Program, NSF (2013)

Review Panel: Molecular and Cellular Evolution, NSF (2011)

Review Panel: Agricultural and Food Research Initiative, Plant Breeding and Education, USDA (2009)

Review Panel: National Research Initiative Plant Genome Program, USDA-CSREES (2007)

Review Panel: National Research Initiative Coordinated Agriculture Project (CAP), USDA-CSREES
(2007)

Grant Reviewer: Swiss National Science Foundation (2019, 2020)

Grant Reviewer: Deutsche Forschungsgemeinschaft (DFG) German Research Foundation (2019,
2020)

Grant reviewer: Plant Genome Research Program (2019), Molecular and Cellular Evolution (2015),
NSF

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 Genetics*, *Nature Biotechnology*, *Nature Review Genetics*,
PNAS, *Genome Biology*, *Nature Communications*, *Nature Plants*, *Genome Research*, *Molecular
Biology and Evolution*, *Molecular Plant*, *Plant Cell*, *Genetics*, *PLOS Genetics*, *Theoretical and*

Applied Genetics, Heredity, Crop Science, 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: Judge for the Postdoctoral Research Excellence Award (2019); 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: Department Enhancement Program (DEP) Implementation Committee (Chair, 2019-2020); Junior/Senior Curriculum Committee (2020-present); Research Committee for Departmental Review (2018-2019); Awards Committee for Plant Breeding Program (Chair, 2016-present); Monsanto 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).

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, ISU Plant Breeding Symposium Organization Group (2013-present)

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

Grants Funded (\$7 million directly to Yu's program, \$27 million total)

Peer-Reviewed Journal Publications (96)


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



1. 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* (online first).
2. 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. News release: [Sensing what plants sense: Integrated framework helps scientists explain biology and predict crop performance](#).
3. 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.
4. 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.
5. 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.
6. Tibbs Cortes, L., Z. Zhang, and **J. Yu***. 2021. Status and prospects of genome-wide association studies in plants. *Plant Genome* 14:e20077.
7. 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.
8. 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](#).
9. 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.
10. 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.
11. 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](#).


12. 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.
13. 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.
14. 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](#).
15. 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.
16. 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](#).
17. 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](#)
18. 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.
19. Dzievit, M., X. Li, and J. Yu*. 2019. Dissection of leaf angle variation in maize through genetic mapping and meta-analysis. *Plant Genome* 12:180024.
20. 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](#)
21. McNellie, J.P., J. Chen*, X. Li, and J. Yu*. 2018. Genetic mapping of foliar and tassel heat stress tolerance in maize. *Crop Science* 58:2484-2493.
22. Lyra, D.H., Í.S.C. Granato, P.P.P. Morais, F.C. Alves, A.R.M. dos Santos, X. Yu, T. Guo, J. Yu, R. Fritsche-Neto*. 2018. Controlling population structure in the genomic prediction of tropical maize hybrids. *Molecular Breeding* 38:126.
23. Liu S., J.C. Schnable, A. Ott, C.T. Yeh, N.M. Springer, J. Yu, G.J. Muehlbauer, M.C.P. Timmermans, M.J. Scanlon, and P.S. Schnable*. 2018. Intragenic meiotic crossovers generate novel alleles with transgressive expression levels. *Molecular Biology and Evolution* 35:2762-2772.
24. Li, Xin, T. Guo, Q. Mu, Xianran Li*, and J. Yu*. 2018. Genomic and environmental determinants and their interplay underlying phenotypic plasticity. *Proceedings of National Academy of Sciences USA* 115:6679-6684. News release: [Scientists find 'patterns in the noise' that could help make more accurate crop performance predictions](#)
25. Zhang, Z., X. Zhang, Z. Lin, J. Wang, M. Xu, J. Lai, J. Yu, and Z. Lin. 2018. The genetic architecture

- of maize nodal root number during domestication. *Plant Journal* 93:1032-1044.
26. Gage, J.L., D. Jarquin, C. Romay, A. Lorenz, E.S. Buckler, S. Kaeppler, ..., **J. Yu**, ..., and Natalia de Leon*. 2017. The effect of artificial selection on phenotypic plasticity in maize. *Nature Communications* 8:1348.
 27. Bouchet, S., M.O. Olatoye, S.R. Marla, R. Perumal, T. Tesso, **J. Yu**, and M. Tuinstra, and G.P. Morris*. 2017. Increased power to dissect adaptive traits in global sorghum diversity using a nested association mapping population. *Genetics* 206:573-585.
 28. Lin, M., D. Zhang, S. Liu, G. Zhang, **J. Yu**, A.K. Fritz, and G. Bai*. 2016. Genome-wide association analysis on pre-harvest sprouting resistance and grain color in US winter wheat. *BMC genomics* 17:794.
 29. Yu, X., X. Li, T. Guo, C. Zhu, Y. Wu, S.E. Mitchell, K.L. Roozeboom, D. Wang, M.L. Wang, G.A. Pederson, T.T. Tesso, P.S. Schnable, R. Bernardo, and **J. Yu***. 2016. Genomic prediction contributing to a promising global strategy to turbocharge genebanks. *Nature Plants* 2:16150. News and Views from the journal: [Plant breeding: Effective use of genetic diversity](#). News release: [New strategy to accelerate plant breeding by turbocharging gene banks](#)
 30. Wang, M.L.* , M. Dziejewit, Z. Chen, J.B. Morris, J.E. Norris, N.A. Barkley, B. Tonnis, G.A. Pederson, and **J. Yu***. 2016. Genetic diversity and population structure of castor (*Ricinus communis* L.) germplasm within the U.S. collection assessed with EST-SSR markers. *Genome* 60:193-200.
 31. Sukumaran, S., Xin Li, Xianran Li, C. Zhu, G. Bai, R. Perumal, M.R. Tuinstra, P.V.V. Prasad, S.E. Mitchell, T.T. Tesso, and **J. Yu***. 2016. QTL mapping for grain yield, flowering time, and stay-green traits in sorghum using genotyping-by-sequencing markers. *Crop Science* 56:1429-1442.
 32. Adeyanju, A., **J. Yu**, C. Little, W. Rooney, P. Klein, J.J. Burke, and T. Tesso*. 2016. Sorghum recombinant inbred lines segregating for stay-green QTLs and leaf dhurrin content show differential reaction to stalk rot diseases. *Crop Science* 56:1429-1442.
 33. Yang, J., H. Jiang, C.-T. Yeh, **J. Yu**, J.A. Jeddelloh, D. Nettleton, P.S. Schnable*. 2015. Extreme phenotype-genome-wide association study (XP-GWAS): a method for identifying trait-associated variants by sequencing pools of individuals selected from a diversity panel. *Plant Journal* 84:587-596.
 34. Leiboff, S., X. Li, H. Alvis, N. Todt, J. Yang, X. Li, X. Yu, G.J. Muehlbauer, M.C.P. Timmermans, **J. Yu**, P.S. Schnable, and M.J. Scanlon*. 2015. Genetic control of morphometric diversity in the maize shoot apical meristem. *Nature Communications* 6:8974. *Selected as an Editors' Choice by MaizeGDB, 01/16*
 35. Li, Xin, Xianran Li, E. Fridman, T.T. Tesso, and **J. Yu***. 2015. Dissecting repulsion linkage in the dwarfing gene Dw3 region for sorghum plant height provides insights into heterosis. *Proceedings of National Academy of Sciences USA* 112:11823-11828. News release: [Iowa State University agronomist explores the genetics that allow hybrid plants to perform better than parents; Sorghum height research offers insight for wider crop improvement](#)
 36. Tabanao, D.A.*, A.E. Pocse dio, J.C. Yabes, M.C. Niño, R.A. Millas, N. Rosandra, L. Sevilla, Y. Xiao, and **J. Yu**. 2015. Genetic diversity and population structure in a rice breeding panel based on single nucleotide polymorphism and simple sequence repeat markers. *Plant Genetics Resources* 13:195-205.
 37. Adeyanju, A., C. Little, **J. Yu**, and T. Tesso*. 2015. Genome-wide association study on resistance to stalk rot diseases in grain sorghum. *G3-Genes, Genomes, Genetics* 5:1165-1175.
 38. Thompson, A.M., **J. Yu**, M.C.P. Timmermans, P. Schnable, J.C. Crants, M.J. Scanlon, G.J. Muehlbauer*. 2015. Diversity of maize shoot apical meristem architecture and its relationship to plant morphology. *G3-Genes, Genomes, Genetics* 5:819-827.

39. Li, X., M.J. Scanlon, and J. Yu*. 2015. Evolutionary patterns of DNA base composition and correlation to polymorphisms in DNA repair systems. *Nucleic Acids Research* 43:3614-3625. News release: [Researchers find patterns in evolving genomes of thousands of species](#)
40. Lipka, A.E.*, C.B. Kandianis, M.E. Hudson, J. Yu, J. Drnevich, P.J. Bradbury, and M.A. Gore. 2015. From association to prediction: statistical methods for the dissection and selection of complex traits in plants. *Current Opinion in Plant Biology* 24:110-118.
41. Xu, F., L. Zhou, K. Zhang, J. Yu, and D. Wang*. 2015. Rapid determination of both structural polysaccharides and soluble sugars in sorghum biomass using near-infrared spectroscopy. *BioEnergy Research* 8:130-136. *2015 Applied Energy Award for Highly Cited Paper*
42. Li, M., X. Liu, P. Bradbury, J. Yu, Y.-M. Zhang, R.J. Todhunter, E.S. Buckler, and Z. Zhang*. 2014. Enrichment of statistical power for genome-wide association studies. *BMC Biology* 12:73.
43. Wang, M.L.*, M. Cole, B. Tonnis, D. Pinnow, Z. Xin, J. Davis, Y.-C. Hung, J. Yu, G.A. Pederson, and G. Eggleston. 2014. Comparison of stem damage and carbohydrate composition in the stem juice between sugarcane and sweet sorghum harvested before and after late fall frost. *Journal of Sustainable Bioenergy Systems* 4:161-174.
44. Zhang, D., R.L. Bowden, J. Yu, B.F. Carver, G. Bai*. 2014. Association analysis of stem rust resistance in U.S. winter wheat. *PLOS One* 9:e103747.
45. Thompson, A.M., J.E. Crants, P.S. Schnable, J. Yu, M.C.P. Timmermans, N.M. Springer, M.J. Scanlon, G.J. Muehlbauer*. 2014. Genetic control of maize shoot apical meristem architecture. *G3-Genes, Genomes, Genetics* 4:1327-1337.
46. Li, L., S.R. Eichten, R. Shimizu, K. Petsch, C.T. Yeh, W. Wu, A.M. Chetoor, S.A. Givan, R.A. Cole, J.E. Fowler, M.M.S. Evans, M.J. Scanlon, J. Yu, P.S. Schnable, M.C.P. Timmermans, N.M. Springer, G.J. Muehlbauer*. 2014. Genome-wide discovery and characterization of maize long non-coding RNAs. *Genome Biology* 15:R40. *Selected as an Editors' Choice by MaizeGDB, 07/14.*
47. Narayanan, S.*, R.M. Aiken, P.V. Prasad, Z. Xin, G. Paul, and J. Yu. 2014. A simple quantitative model to predict leaf area index in sorghum. *Agronomy Journal* 106:219-226.
48. Morris, G.P.*, D.H. Rhodes, Z. Brenton, P. Ramu, V.M. Thayil, S. Deshpande, C.T. Hash, C. Acharya, S.E. Mitchell, E.S. Buckler, J. Yu, and S. Kresovich. 2013. Dissecting genome-wide association signals for loss-of-function phenotypes in sorghum flavonoid pigmentation traits. *G3-Genes, Genomes, Genetics* 3:2085-2094.
49. Liu, S., S.K. Sehgal, J. Li, M. Lin, H.N. Trick, J. Yu, B.S. Gill, and G. Bai*. 2013. Cloning and characterization of a critical regulator for pre-harvest sprouting in wheat. *Genetics* 195:263-273. News release: [PHS gene prevents wheat from sprouting: Fewer crop losses anticipated](#)
50. Yu, X., G. Bai, S. Liu, N. Luo, Y. Wang, D.S. Richmond, P.M. Pijut, S.A. Jackson, J. Yu, and Y. Jiang*. 2013. Association of candidate genes with drought tolerance traits in diverse perennial ryegrass accessions. *Journal of Experimental Botany* 64:1537-1551.
51. Li, L., K. Petsch, R. Shimizu, S. Liu, W.W. Xu, K. Ying, J. Yu, M.J. Scanlon, P.S. Schnable, M.C.P. Timmermans, N.M. Springer, and G.J. Muehlbauer*. 2013. Mendelian and non-Mendelian regulation of gene expression in maize. *PLOS Genetics* 9: e1003202.  *Selected as an Editors' Choice by MaizeGDB, 02/13*
52. Xu, F., J. Yu, T. Tesso, F. Dowell, and D. Wang*. 2013. Qualitative and quantitative analysis of lignocellulosic biomass using infrared techniques: A mini-review. *Applied Energy* 104:801-809.
53. Li, C., M. Chen, S. Chao, J. Yu, and G. Bai*. 2013. Identification of a novel gene, H34, in wheat using recombinant inbred lines and single nucleotide polymorphism markers. *Theoretical and Applied Genetics* 126:2065-2071.

54. Narayanan, S.*, R.M. Aiken, P.V.V. Prasad, Z. Xin, and J. Yu. 2013. Water and radiation use efficiencies in sorghum. *Agronomy Journal* 105:649-656.
55. Wang, M.*, Z. Xin, B. Tonniss, G. Farrell, D. Pinnow, Z. Chen, J. Davis, J. Yu, Y. Hung, and G. Pederson. 2012. Evaluation of sweet sorghum as a feedstock by multiple harvests for sustainable bioenergy production. *Journal of Sustainable Bioenergy Systems* 2:122-137.
56. Sukumaran, S., W. Xiang, S.R. Bean, J.F. Pedersen, S. Kresovich, M.R. Tuinstra, T.T. Tesso, M.T. Hamblin, and J. Yu*. 2012. Association mapping for grain quality in a diverse sorghum collection. *Plant Genome* 5:126-135.
57. Takacs, E.M., J. Li, C., Du, L. Ponnala, D. Janick-Buckner, J. Yu, G.J. Muehlbauer, P.S. Schnable, M.C.P. Timmermans, Q. Sun, D. Nettleton, and M.J. Scanlon*. 2012. Ontogeny of the maize shoot apical meristem. *Plant Cell* 8:3219-3234.  Selected as an Editors' Choice by *MaizeGDB*, 10/12
58. Li, X., C. Zhu, C.-T. Yeh, W. Wu, K. Petsch, E. Takacs, F. Tian, G. Bai, E.S. Buckler, G.J. Muehlbauer, M.C.P. Timmermans, M.J. Scanlon, P.S. Schnable* and J. Yu*. 2012. Genic and non-genic contributions to natural variation of quantitative traits in maize. *Genome Research* 22:2436-2444. Selected as an Editors' Choice by *MaizeGDB*, 8/12. News Release: [Prioritizing rather than canvassing entire plant genome may lead to improved crops](#)
59. Wu, Y., X. Li, W. Xiang, C. Zhu, Z. Lin, Y. Wu, J. Li, S. Pandravada, D.D. Ridder, G. Bai, M.L. Wang, H.N. Trick, S.R. Bean, M.R. Tuinstra, T.T. Tesso and J. Yu*. 2012. Presence of tannins in sorghum grains is conditioned by different natural alleles of *Tannin1*. *Proceedings of National Academy of Sciences USA* 109:10281-10286. News release: [Tannins in sorghum and benefits focus of genetic research](#)
60. Lin, Z., X. Li, L.M. Shannon, C.-T. Yeh, M.L. Wang, G. Bai, Z. Peng, J. Li, H.N. Trick, T.E. Clemente, J. Doebley, P.S. Schnable, M.R. Tuinstra, T.T. Tesso, F. White, J. Yu*. 2012. Parallel domestication of the *Shattering1* genes in cereals. *Nature Genetics* 44:720–724.  Selected as an Editors' Choice by *MaizeGDB* 7/12 News and Views from the journal: [One gene's shattering effect](#). News release: [Genes underlying the key domestication process in sorghum and other cereals](#)
61. Li, X., C. Zhu, J. Wang, and J. Yu*. 2012. Computer simulation in plant breeding. *Advances in Agronomy* 116:217-262.
62. Wang, M.L.*, S. Sukumaran, N.A. Barkley, Z. Chen, C.Y. Chen, B. Guo, R.N. Pittman, H.T. Stalker, C.C. Holbrook, G.A. Pederson, and J. Yu*. 2011. Population structure and marker-trait association analysis of the U.S. peanut (*Arachis hypogaea* L.) mini-core collection. *Theoretical and Applied Genetics* 123:1307-1317.
63. Zhang, D., G. Bai*, R.M. Hunger, W.W. Bockus, J. Yu, B.F. Carver, and G. Brown-Guedira. 2011. Association study of resistance to *soilborne wheat mosaic virus* in U.S. winter wheat. *Phytopathology* 101:1322-1329.
64. Zhu, C., X. Li, and J. Yu*. 2011. Integrating rare-variant testing, function prediction, and gene network in composite resequencing-based genome-wide association studies (CR-GWAS). *G3-Genes, Genomes, Genetics* 1:233-243.
65. Nelson, J.C.*, S. Wang, Y. Wu, X. Li, G. Antony, F.F. White, J. Yu. 2011. Single-nucleotide polymorphism discovery by high-throughput sequencing in sorghum. *BMC Genomics* 12:352.
66. Mutava, R.N., P.V.V. Prasad*, M.R. Tuinstra, K.D. Kofoid, and J. Yu. 2011. Characterization of sorghum genotypes for traits related to drought tolerance. *Field Crops Research* 123:10-18.
67. Li, X., C. Zhu, Z. Lin, Y. Wu, D. Zhang, G. Bai, W. Song, J. Ma, G.J. Muehlbauer, M.J. Scanlon, M.

- Zhang, and **J. Yu***. 2011. Chromosome size in diploid eukaryotic species centers on the average length with a conserved boundary. *Molecular Biology and Evolution* 28:1901–1911. News release: [Chromosomes' big picture: Similarities found in genomes across multiple species; Platypus still out of place](#)
68. Wisser, R.J.* , J.M. Kolkman, M.E. Patzoldt, J.B. Holland, **J. Yu**, M. Krakowsky, R.J. Nelson, and P.J. Balint-Kurti. 2011. Multivariate analysis of maize disease resistances suggests a pleiotropic genetic basis and implicates a glutathione S-transferase gene. *Proceedings of National Academy of Sciences USA* 108:7339-7344.
 69. Zhang, D., G. Bai*, C. Zhu, **J. Yu**, and B. Carver. 2010. Genetic diversity, population structure and linkage disequilibrium in U.S. elite winter wheat (*Triticum aestivum* L.). *Plant Genome* 3:117-127.
 70. Sun, G., C. Zhu, S. Yang, W. Song, M.H. Kramer, H.-P. Piepho, and **J. Yu***. 2010. Variation explained in mixed model association mapping. *Heredity* 105:333-340.
 71. Zhang, Z.* , E. Ersoz, C.-Q. Lai, R.J. Todhunter, H.K. Tiwari, M.A. Gore, P.J. Bradbury, **J. Yu**, D.K. Arnett, J.M. Ordovas, and E.S. Buckler. 2010. Mixed linear model approach adapted for genome-wide association studies. *Nature Genetics* 42:355-360.
 72. Wu, X., S. Scott, J.L. Propheter, W.L. Rooney, **J. Yu**, and D. Wang*. 2010. Features and fermentation performance of sweet sorghum juice after harvest. *Industrial Crops and Products* 31:164-170.
 73. Tian, Z., Q. Qian, Q. Liu, M. Yan, X. Liu, C. Yan, G. Liu, Z. Gao, S. Tang, D. Zeng, Y. Wang, **J. Yu***, M. Gu*, and J. Li*. 2009. Allelic diversities in rice starch biosynthesis lead to a diverse array of rice eating and cooking qualities. *Proceedings of National Academy of Sciences USA* 106:21760-21765.
 74. Wang, M.L.* , C. Zhu, N.A. Barkley, Z. Chen, J.E. Erpelding, S.C. Murray, M.R. Tuinstra, T. Tesso, G.A. Pederson, and **J. Yu***. 2009. Genetic diversity and population structure analysis of the accessions in the US historic sweet sorghum collection. *Theoretical and Applied Genetics* 102:13-23.
 75. Buckler, E.S.* , J.B. Holland*, P.J. Bradbury, C.B. Acharya, P.J. Brown, C. Browne, E. Ersoz, S. Flint-Garcia, A. Garcia, J.C. Glaubitz, M.M. Goodman, C. Harjes, K. Guill, D.E. Kroon, S. Larsson, N.K. Lepak, H. Li, S.E. Mitchell, G. Pressoir, J.A. Peiffer, M.O. Rosas, T.R. Rocheford, M.C. Romay, S. Romero, S. Salvo, H.S. da Villeda, Q. Sun, F. Tian, N. Upadyayula, D. Ware, H. Yates, **J. Yu**, Z. Zhang, S. Kresovich*, and M.D. Mullen* 2009. The genetic architecture of maize flowering time. *Science* 325:714-718.
 76. Zhu, C., and **J. Yu***. 2009. Nonmetric multidimensional scaling corrects for population structure in association mapping with different sample types. *Genetics* 182:875-888.
 77. **Yu, J.***, Z. Zhang, C. Zhu, D. Tabanao, G. Pressoir, M.R. Tuinstra, S. Kresovich, R.J. Todhunter, and E.S. Buckler. 2009. Simulation appraisal of the adequacy of number of background markers for relationship estimation in association mapping. *Plant Genome* 2:63-77.
 78. **Yu, J.*** 2009. Realizing the potential of ultrahigh throughput genomic technologies in plant breeding. *Plant Genome* 2:2.
 79. Ochanda, N., **J. Yu***, P.J. Bramel, A. Menkir, M.R. Tuinstra, and M.D. Witt. 2009. Selection before backcross during exotic germplasm introgression. *Field Crops Research* 112:37-42.
 80. Zhu, C., M. Gore, E.S. Buckler, and **J. Yu***. 2008. Status and prospects of association mapping in Plants. *Plant Genome* 1:5-20.
 81. **Yu, J.**, J.B. Holland, M.D. McMullen, and E.S. Buckler*. 2008. Genetic design and statistical power of nested association mapping in maize. *Genetics* 138:539-551.

82. Weber, A., R.M. Clark, L. Vaughn, J.D.J. Sánchez-Gonzalez, **J. Yu**, B.S. Yandell, P. Bradbury, and J.F. Doebley*. 2007. Major regulatory genes in maize contribute to standing variation in Teosinte (*Zea mays* ssp. *parviglumis*). *Genetics* 177:2349–2359.
83. Tabanao, D.A., **J. Yu**, and R. Bernardo*. 2007. Multilocus epistasis, linkage, and genetic variance in breeding populations with few parents. *Theoretical and Applied Genetics* 115:335-342.
84. Bernardo, R.* , and **J. Yu**. 2007. Prospects for genomewide selection for quantitative traits in maize. *Crop Science* 47:1082-1090.
85. Yang, X.H., J.B. Yan, Y.P. Zheng, **J. Yu**, and J.S. Li*. 2007. Reviews of association analysis of quantitative traits in plants. *Acta Agronomica Sinica* 33:523-530.
86. Stich, B., **J. Yu**, A.E. Melchinger*, H.-P. Piepho, F. Utz, H.P. Maurer, and E.S. Buckler*. 2007. Power to detect high-order epistatic interactions in a metabolic pathway using a new mapping strategy. *Genetics* 176:563-570.
87. **Yu, J.**, and E.S. Buckler*. 2006. Genetic association mapping and genome organization of maize. *Current Opinion in Biotechnology* 17:155-160.
88. Arbelbide, M., **J. Yu**, and R. Bernardo*. 2006. Power of mixed-model QTL mapping from phenotypic, pedigree, and marker data in self-pollinated crops. *Theoretical and Applied Genetics* 112:876-884.
89. **Yu, J.**, G. Pressoir, W.H. Briggs, I. Vroh Bi, M. Yamasaki, J.F. Doebley, M.D. McMullen, B.S. Gaut, D. Nielsen, J.B. Holland, S. Kresovich, and E.S. Buckler*. 2006. A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. *Nature Genetics* 38:203-208. 
90. Flint-Garcia, S.A., A. Thillet, **J. Yu**, G. Pressoir, S.M. Romero, S.E. Mitchell, J.F. Doebley, S. Kresovich, M.M. Goodman, and E.S. Buckler*. 2005. Maize association population: a high resolution platform for QTL dissection. *Plant Journal* 44:1054-1064.
91. **Yu, J.**, M. Arbelbide, and R. Bernardo*. 2005. Power of in silico QTL mapping from phenotypic, pedigree, and marker data in a hybrid breeding program. *Theoretical and Applied Genetics* 110:1061-1067.
92. **Yu, J.**, and R. Bernardo*. 2004. Metabolic control analysis as a mechanism for maintaining genetic variance during advanced cycle breeding. *Theoretical and Applied Genetics* 108:1614-1619.
93. **Yu, J.**, and R. Bernardo*. 2004. Changes in genetic variance during advanced cycle breeding in maize. *Crop Science* 44:405-410.
94. **Yu, J.**, M.R. Tuinstra*, M.M. Claassen, W.B. Gordon, and M.D. Witt. 2004. Analysis of cold tolerance in sorghum under controlled environment conditions. *Field Crops Research* 85:21-30.
95. **Yu, J.**, H. Lu, and R. Bernardo*. 2001. Inconsistency between SSR groupings and genetic backgrounds of white corn inbreds. *Maydica* 46:133-139.
96. **Yu, J.**, and M.R. Tuinstra*. 2001. Genetic analysis of seedling growth under cold temperature stress in grain sorghum. *Crop Science* 41:1438-1443.

Book Chapters, Proceedings, Book Reviews, and Research Highlights (10)

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

1. Baltensperger, D., M. Basu, Z. Dou, S. Flis, D. Galligan, M. Matlock, C. Morgan, D. Reed, C.W. Rice, G. Shurson, J.M. Tricarico, A.M. Thompson, A. Thomson, J.A. Thomasson, and **J. Yu**. 2021

The Role of Agricultural Science and Technology in Climate 21 Project Implementation, Council for Agricultural Science and Technology. https://climate21.org/documents/C21_USDA.pdf

2. **X. Li**, and **J. Yu***. 2021. Retrofitting elite cultivars with an ancestral allele for sustainable agriculture. *Science China Life Sciences* 64, <https://doi.org/10.1007/s11427-021-1923-0>.
3. **Sukumaran, S.**, and **J. Yu***. 2014. Association mapping of genetic resources: Achievements and future perspectives. In R. Tuberosa et al. (ed.) *Genomics of Plant Genetic Resources*, 207-235.
4. **Yu, J.***, M.T. Hamblin, and M.R. Tuinstra. 2013. Association genetics strategies and resources. In A. Paterson (ed.) *Genetics and Genomics of the Saccharinae*. *Plant Genetics and Genomics: Crops and Models* 11:187-203. Springer Verlag.
5. Ersoz, E., **J. Yu**, and E.S. Buckler. 2009. Applications of linkage disequilibrium and association mapping in maize. In A.L. Kriz and B.A. Larkins (ed.) *Molecular Genetic Approaches to Maize Improvement, Biotechnology in Agriculture and Forestry*, Vol 63, 173-195. Springer Verlag.
6. Sorrells, M.E., and **J. Yu**. 2009. Linkage disequilibrium and association mapping in the Triticeae. In C. Feuillet and G.J. Muehlbauer (ed.) *Genetics and Genomics of the Triticeae*, 655-683. Springer Verlag.
7. Wu, X., S. Scott, J.L. Prophet, W.L. Rooney, **J. Yu**, and D. Wang. 2008. Features and fermentation performance of sweet sorghum juice after harvest. 2008 Providence, Rhode Island, Jun. 29 – Jul. 2, 2008.
8. Ersoz, E., **J. Yu**, and E.S. Buckler. 2008. Applications of linkage disequilibrium and association mapping in crop plants. In R. Varshney and R. Tuberosa (ed.) *Genomics-Assisted Crop Improvement: Vol 1: Genomics Approaches and Platforms*, 97-120. Springer Verlag.
9. Bernardo, R., M. Arbelbide, B. Parisseaux, and J. Yu. 2005. In silico QTL mapping with phenotypic, pedigree, and genomic data in plant breeding programs. *Proceedings of the 10th International Congress of "The Society for the Advancement of Breeding Researches in Asia and Oceania"*.
10. **Yu, J***. 2007. *Plant Breeding: The Arnel R. Hallauer International Symposium*. By Kendall R. Lamkey and Michael Lee. Ames, IA: Blackwell Publishing, 2006. *Great Plains Research* 17:236-237.