

Jianming Yu

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Professional Experience

2017–date	Professor & Pioneer Distinguished Chair in Maize Breeding, Dept. of Agronomy, Iowa State University
2013–2017	Associate Professor & Pioneer Distinguished Chair in Maize Breeding, Dept. of Agronomy, Iowa State University
2010–2012	Associate Professor, Dept. of Agronomy, Kansas State University
2006–2010	Assistant Professor, Dept. of Agronomy, Kansas State University
2004–2006	Postdoctoral Research Associate, Institute for Genomic Diversity, Cornell
2003–2004	Postdoctoral Research Associate, Dept. of Agronomy & Plant Genetics, Univ. of Minnesota
2000–2003	Graduate Research Assistant, Dept. of Agronomy & Plant Genetics, Univ. of Minnesota
1998–2000	Graduate Research Assistant, Dept. of Agronomy, Kansas State University
1994–1998	Research Assistant, Res. & Dev. Dept., China National Seed Group Corp., Beijing, China

Education

2000–2003	Ph.D. Applied Plant Sciences, Univ. of Minnesota
1998–2000	M.S. Agronomy, Kansas State University
1990–1994	B.S. Agronomy, Northwest Agriculture and Forestry Univ., China

Honors and Awards

2018	Fellow, American Association for the Advancement of Science
2018	Fellow, Crop Science Society of America
2018	Editor's Citation for Excellence, <i>The Plant Genome</i>
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, University 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 and 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. Yu's research integrates knowledge in Plant Breeding, Quantitative Genetics, Genomics, Molecular Genetics, and Statistics, and has the ultimate goal of developing and implementing new strategies and methods in trait dissection and crop improvement. Current research includes Genome-Wide Association Studies (GWAS) with diverse germplasm or multiple designed mapping populations (such as Nested Association Mapping, NAM; or meta-QTL analysis), Genomic Selection (GS; or Genome-Wide Selection GWS) to efficiently integrate high throughput genotyping into various breeding processes, Gene Cloning for traits with agronomic and domestication importance, Genotype-by-Environment Interaction (GEI) and Epistasis dissection to causal polymorphic sites, Genome and Chromosome Size Evolution across taxonomic groups, and Genome-Wide Base Composition changes and underlying principles.

In 2018, Yu's program developed an integrated framework for gene discovery underlying phenotypic plasticity and performance prediction across environments ([PNAS 115:6679-6684](#)). This work was regarded as having the potential to be a landmark paper in genotype-by-environment interaction, phenotypic plasticity, and norm of reaction. In 2016, Yu's team demonstrated that a comprehensive strategy based on genomic selection and other relevant technologies can be designed to mine the natural heritage stored in numerous gene banks ([Nature Plants 2:16150](#)). In 2015, his research team published the first complete case of heterosis due to pseudo-overdominance ([PNAS 112:11823-11828](#)). Other significant research contributions include identifying the *Shattering1* gene and its homologs underlying the parallel domestication of multiple cereal species ([Nature Genetics 44:720-724](#)), quantifying genic and nongenic contributions to quantitative trait variation in maize ([Genome Research 22:2436-2444](#)), cloning of the *Tan1* gene in sorghum underlying a trait with incomplete domestication ([PNAS 109:10281-10286](#)). In addition, his team revealed the patterns in DNA base composition divergence ([Nucleic Acids Research 43:3614-3625](#)) in 2015 and chromosome size variation ([Molecular Biology and Evolution 28:1901-1911](#)) across multiple species in 2011. Yu's significant research contributions also include pioneering genomic selection (GS) research in crops ([Crop Science 47:1082-1090](#)), the state-of-the-art breeding methodology; outlining the nested association mapping (NAM) strategy ([Genetics 138:539-551](#)), an approach being replicated in multiple crops; and developing the mixed model method for genome-wide association studies (GWAS) ([Nature Genetics 38:203-208](#)), the standard method framework for complex trait dissection.

Invited Talks (82 = 59 National + 23 International)

Selected Leadership Activities and Professional Contributions

Associate Editor, *Molecular Breeding* (2018-present), *Plant Genome* (2012-2017), *Theoretical and Applied Genetics* (2007-2011), *Crop Science* (2008-2010)

[Maize Genetics Executive Committee](#) (2015-2019: Chair 2018, Vice-Chair 2017)

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

Scientific Organizing Committee: CROPS 2019, CROPS 2017, CROPS 2015, HudsonAlpha Institute for Biotechnology.

Advisory Panel, Plant Genomics Congress USA (2014-2016)

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

Crop Science Society of America, C-8, Plant Genetic Resources, (Chair-Elect 2015, Chair 2016, Past-Chair 2017); Crop Science Research Award Committee (2016-2017); Tengtou Agricultural

Science Award Committee (Chair 2015; member 2014-2017); Selection Committee for Young Crop Scientists Award (Chair, 2013; member, 2011, 2012); Gerald O. Mott Scholarship Committee (2005-2007)

Workshop Organizer (2013-present): Genomic Selection and Genome-Wide Association Studies, *Plant & Animal Genome*, San Diego, CA.

Review Panel: Corp Production, Binational Agricultural Research & Development Fund (BARD) (2017); Physiology of Agricultural Plants, USDA-NIFA AFRI (2016); Plant Genome Research Program, NSF (2013); Molecular and Cellular Evolution, NSF (2011); Agricultural and Food Research Initiative, Plant Breeding and Education, USDA (2009); National Research Initiative Plant Genome Program, USDA-CSREES (2007); National Research Initiative Coordinated Agriculture Project (CAP), USDA-CSREES (2007)

Selected Peer-Reviewed Journal Publications

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

[Google Scholar, h-index = 38, total citation =11,648](#)

1. Guo, T., X. Yu, X. Li, H. Zhang, C. Zhu, S. Flint-Garcia, M.D. McMullen, J.B. Holland, R.J. Wisser, and J. Yu*. 2019. Optimal designs for genomic selection in hybrid crops. *Molecular Plant*. News Release: [Data mining brings new clarity to plant breeding](#)
2. 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](#)
3. 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](#)
4. 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*
5. 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](#)
6. 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](#)
7. 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](#)
8. 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](#)
9. 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, and 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](#)
10. 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.
11. 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](#)
12. 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.
13. 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.
14. 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.
15. 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.
16. Zhu, C. and J. Yu*. 2009. Nonmetric multidimensional scaling corrects for population structure in association mapping with different sample types. **Genetics** 182:875-888.
17. 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.
18. 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.
19. Bernardo, R.* and J. Yu. 2007. Prospects for genomewide selection for quantitative traits in maize. **Crop Science** 47:1082-1090.
20. 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. 