

# CURRICULUM VITAE OF JIXIANG WU

## CONTACT INFORMATION

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Associate Professor of Quantitative Genetics/Biostatistics  
Plant Science Department  
South Dakota State University,  
Box 2140C  
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## EDUCATION HISTORY

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- 2003      Ph. D., Agronomy (Quantitative Genetics and Plant Breeding)  
Mississippi State University, Mississippi State, MS  
Dissertation: Genetic variation, conditional analysis, and QTL mapping for agronomic and fiber traits in upland cotton  
Advisor: Dr. Johnie N. Jenkins
- 2003      M.S., Statistics  
Mississippi State University, Mississippi State, MS  
Project: Multivariable conditional analyses under a mixed linear model: methodology and application  
Advisor: Dr. Dongfeng Wu
- 2001      Ph.D., Genetics and Plant Breeding (Statistical Genetics)  
Zhejiang University, Hangzhou, P. R. China  
Dissertation: Comparisons on properties of marker linkage and QTL mapping between two methods of RI line development  
Advisor: Dr. Jun Zhu
- 1994      M.S., Genetics and Plant Breeding (Quantitative Genetics)  
Zhejiang Agricultural University, Hangzhou, P. R. China  
Theses: Genetic analysis on yield and fiber traits of F<sub>2</sub> hybrid in upland cotton  
Advisor: Dr. Jun Zhu
- 1991      B. S., Genetics and Plant Breeding  
Zhejiang Agricultural University, Hangzhou, P. R. China

## EXTENDED EDUCATION

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- “Statistics for spatio-temporal data”, April 26, 2015. Manhattan, KS
- “Genetic association mapping” April 27, 2014. Manhattan, KS
- “Applied Statistics in Agriculture Short Course” April 28, 2013. Manhattan, KS
- “Bayesian analysis for linear mixed models”, April 29, 2012, Manhatta, KS.

- “Living with generalized linear mixed models in agriculture” May 1, 2011. Manhattan, KS
- “Applied Survival Analysis”, April 25, 2010. Kansas State University, Manhattan, KS
- “Analysis of Messy Data”, April 19, 2009. Kansas State University, Manhattan, KS
- “Computational Biology Certificate”, May 2008, Mississippi State University
- “Methods and Models for Categorical Data in Agriculture”, April 26, 2008. Kansas State University, Manhattan, KS
- “Spatial Statistics” December 11, 2006. USDA/ARS, Stoneville, MS
- “Genomics Mapping” October 25-26, 2006. USDA/ARS, Lubbock, TX
- “Statistical Data Mining Using SAS Macro Applications” April 25, 2004. Kansas State University, Manhattan, KS
- “Summer Institute in Statistical Genetics” May 28- June 15, 2002. North Carolina State University, Raleigh, NC
- “Neural Network Modeling Data Mining.” May 3, 2000. Kansas State University. Manhattan, KS.
- “Models and Designs for Agricultural Mixture Experiments.” April 30, 2000. Kansas State University, Manhattan, KS.

### **PROFESSIONAL EXPERIENCE**

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July 2015-current	Associate Professor (Tenured), Plant Science Department, South Dakota State University, Brookings, SD
2009-June 2015	Assistant Professor, Plant Science Department, South Dakota State University, Brookings, SD
2004-2009	Research Associate, Department of Plant and Soil Sciences, Mississippi State University, MS.
2001-2003	Research Assistant, Department of Plant and Soil Sciences, Mississippi State University
1998-2001	Visiting Scholar, Department of Plant and Soil Sciences, Mississippi State University. Mississippi State, MS
1994-1998	Instructor and Researcher, Department of Agronomy, Zhejiang Agricultural University Hangzhou, P. R. China.

### **AWARDS**

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1994	“New Methods of Genetic Study for Crop Quantitative Traits”, Second-place award (Advanced technology)” from China Ministry of Education Department as a co-contributor
2001	“Seed Trait Genetic Models with Corresponding Statistical Methods and the Application in Crop Breeding”, Second-place award from the Committee of China Institute of Higher Education as a co-contributor

## RESEARCH ACHIEVEMENTS

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- Developed a generalized genetic model frame for various types of genetic designs and data structures using the mixed linear model approaches.
- Developed a generalized linear model system for various linear mixed model analyses
- Proposed a generalized conditional model and approach for developmental genetics and complex trait analysis
- Proposed a generalized experimental design frame for various experimental designs including augmented experimental design
- Developed and released an R package **minque** for various linear model analyses and experimental designs
- Developed and released an R package **qgtools** for various genetic mating designs, genetic models, and data structures
- Developed and released an R package **linkim** for missing marker imputation based on linkage mapping information
- Developed algorithms for constructing large-scale linkage mapping with improved accuracy and speed (an R package is under development)
- Developed algorithms for high-dimensional marker association mapping and genome-wide selection with high-order epistasis detection (an R package is under development)

## RESEARCH EXPERIENCE

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- Linear mixed model approaches and irregular data analysis
- Plant breeding
- Quantitative genetics and genetic modeling
- Experienced in experimental designs including augmented experimental designs
- Linkage mapping
- Genome-wide association mapping algorithms with high-order epistasis and applications
- Computational statistics/genetics and Monte Carlo simulations
- Computer programming with C++, SAS, and R,
- Computer tool development
- Resampling techniques including permutation, jackknifing, and bootstrapping

## RESEARCH ACTIVITIES

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### Current Activities

- Genetic association mapping methodologies and applications in cotton, wheat, barley, soybean, and tree

- Augmented experimental designs for field error control: models, methodologies, and applications in spring wheat and cotton
- Yield stability analysis: methodologies and applications in soybean, winter wheat, and spring wheat
- Quantitative genetic analysis for wheat, barley, wheat, cupplant, cordgrass, soybean, cotton, and pea
- Computer tool development and update

### Previous Activities

- Genetic Modeling for Seed Traits and Applications in Cotton Nutritional Components (Mississippi State University, MAFES special funding, collaborated with Drs. J. N. Jenkins, J. N. McCarty, and P. Thaxton)
- Germplasm Enhancement and Genetic Improvement of Cotton (USDA-ARS CRIS project, collaborate with Drs. J. N. Jenkins, J. C. McCarty, S. Saha, and M. Wubben).
- Development of Precision Agriculture Systems for Cotton Production (USDA-ARS CRIS project, collaborate with Drs. J. N. Jenkins and J. Willers, and J. McKinion).
- Chromosome associations with cotton yield and fiber traits using chromosome substitution lines (Cotton Incorporated founded project, collaborated with Dr. T. Wallace).
- Germplasm Enhancement and Genetic Improvement of Cotton (USDA-ARS CRIS project, collaborate with Drs. J. N. Jenkins, J. C. McCarty, and S. Saha).

### **TEACHING AND ADVISING**

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#### Courses I have Taughted

- “Genetic data analysis with R” (FA2016), Plant Science Department, South Dakota State University
- “Data analysis with R” (Spring 2015 and 2016), Plant Science Department, South Dakota State University
- “Design of experimnents” (Fall 2013 and 2014; summer 2015, Spring 2016), Department of Mathematics and Statistics, South Dakota State University
- “Linear model analysis with R” (Fall 2014, Spring 2016), Departments of Mathematics and Statistics and of Plant Science, South Dakota State University
- “Quantitative genetics” (Fall 2010,2011, 2013,2015, 2016), Plant Science Department and Department of Mathematics and Statistics, South Dakota State University.
- “Computational genetics” (Spring 2012), Plant Science Department and Department of Mathematics and Statistics, South Dakota State University.
- “Generalized linear models and application” (Spring 2011), Plant Science Department and Department of Mathematics and Statistics, South Dakota State University.

- “Biometrical genetics for plant breeding” (Spring 2005), Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS.
- “Linear models and analytical methods” (Fall 1995, 1996, and 1997), Department of Agronomy, Zhejiang Agricultural University, Hangzhou, China.
- “Plant breeding” (Fall 94 and Spring 1998), Department of Agronomy, Zhejiang Agricultural University, Hangzhou, China.
- “General genetics” (Spring 1997) Department of Agronomy, Zhejiang Agricultural University, Hangzhou, China.

#### Advising activities

- Yi Xu (MS in Plant Science, graduated in spring 2014): working on high-dimensional genetic association mapping, now a Ph.D. student in Biostatistics at the University of Alabama at Birmingham. Completed thesis: “Genetic association mapping: missing markers, Epistatic effects, and applications”
- Kaushal Raj Chaudhary (MS in Statistics, Graduated in 2013): working on soybean stability analysis (graduated in summer 2013, now employed with Sanford). Completed thesis: “Stability analysis for soybean in Eastern South Dakota Environments”
- Krishna Bondalapati (Ph.D in Statistics, graduated in 2013): working on applied statistics with emphasis on field variation control (graduated in fall 2013, now employed in Bayer Inc.). Completed dissertation: “Improving genetic analysis with augmented experimental design”
- Adams Kusi Appiah (MS in Statistics, Graduated in summer 2015): working on P-treatment based yield components. Completed thesis: “Soybean yield and yield component response to phosphorus fertilization and variety trial analyses in South Dakota”
- Rebecca Helget (MS in Plant Science, graduated in Summer 2016): working on soybean production
- Nan Nan (MS in Statistics, expected to graduate in 2017): working on applications of linear mixed model approaches and wheat breeding data

#### **PROFESSIONAL ACTIVITIES AND SERVICES**

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##### Paper review activities

I am a regular reviewer for the following 25 journals:

Journal of Biometrics & Biostatistics, Journal of Statistical Computation and Simulation, Genetics, Journal of Heridity, Crop Science, Plant Breeding, Applied Statistics in Agriculture, American Journal of Plant Science, The New Zealand Journal of Crop and Horticultural Science, Euphytica, Journal of Cotton Science, Biochemical Systematics and Ecology, Chinese Science Bulletin, Gene, Heridity, Journal of Biocomputing, Journal of Open Statistics, PLOS, PONE, Theoretical and Applied Genetics, Scientia, Horticulturae, and Statistics Inference and Interface

### Editorial service

I am currently serving on editorial board for the following four journals:

Journal of Applied Bioinformatics & Computational Biology (currently as Editor-in-Chief), journal of geoinformatics geostatistics, Advances in Agriculture, and Australian Journal of Crop Science;

### Workshops

- Provided two workshops related to using novel and flexible linear mixed model approaches for various quantitative genetics data analyses in 2010
- Provided two workshops related to data analysis with R at the first and second SDSU Research Biological Computation Symposiums (2013 and 2014)

### Professional Affiliations

- East North American Region (ENAR/The International Biometric Society)
- The Genetics Society of America
- Sigma Xi, The Scientific Research Society
- International Cotton Genome Initiative
- Association of Societies of Agronomy

### **FUNDING HISTORY**

#### Proposals funded

01/2017 -12/2018	Elucidation of competition patterns among three perennial biofuel feedstock species in the North Central USA. USDA-NIFA-Sun Grants (Role: PI, \$89,447)
07/2016- 06/2017	Achieving 100 Bu/A soybean yields: on-farm research and sharing high yield protocols with South Dakota soybean producers. SD Soybean Research and Promotion Council (Role: Co-PI, \$283,478)
10/2015 -09/2017	Accelerating Genetic Improvement for Oat milling and Nutritional Quality. USDA-NIFA (Role: Co-PI, \$150,000)
11/2009 -09/2014	Development and application of new quantitative genetic methodologies to the improvement of plants and animals. USDA (Role: PI, \$25,000)
09/2014 -08/2019	Developing and using novel statistical approaches and computer tools to improve genetic data analysis (USDA-CRIS, hatch project, PI, \$25,000)

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07/2012 -06/2013	Stability evaluation for soybean genotypes in South Dakota environment. South Dakota Soybean Research & Promotion Council (Role: PI, \$39,398)
07/2011 -06/2012	Stability evaluation for soybean genotypes in South Dakota environment. South Dakota Soybean Research & Promotion Council (Role: PI, \$19,162)
01/2012 -12/2012	Developing stable, high-yielding winter wheat varieties for South Dakota. South Dakota Wheat Commission. (Role: CoPI with PI William Berzosky, \$97,929)
07/2013 -06/2014	Critically Evaluating the Interpretation of Soybean Plant Tissue Analysis in the 21st Century. South Dakota Soybean Research & Promotion Council (Role: CoPI with Nathan Mueller, \$132,876)
08/2013 -10/2015	A New Approach to Producing Biomass Feedstocks from Marginal Land and Reclaiming Salt Impacted Soils in the North Central USA. Suns Grants (CoPI with Arvid Boe, ~\$125,000)
04/2012 -03/2013	An integrated approach for association mapping with high order epistatic effects. South Dakota State University (PI, \$2,500)
2007-2008:	“Genetics and breeding technologies to improve cottonseed oil and protein levels and plant seed quality”, Research Initiate Program, MSU (Role: PI, \$45,400; Co-investigators: Drs. P. Thaxton, J. C. McCarty, and J. N. Jenkins)
2006-2007:	“Yield and fiber trait improvement using recently developed cotton chromosome substitution germplasm lines”, Cotton Incorporated State Support Program (Role: PI, \$21,642; Co-investigator: Dr. T. Wallace)
1996-1999:	“Development of Germplasm with special fiber quality in upland cotton”, China Agricultural Department/ “95” Project (Role: Co-investigator with Dr. J. Zhu, 42,000 RMB)
1995-1997:	“Genetic study and the utilization of intraspecific heterosis in upland cotton”, Natural Science Foundation/Zhejiang Province (Role: Co-investigator with Dr. J. Zhu, 42,000 RMB)

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### Proposals under pending

1. NRT-INFEWS: Training next-generation scientists with experimental, theoretical, and operational competencies for sustainable precision agriculture (Letter of Intent) (Co-PI with K. Muthukumarappan, NSF).

### **PUBLICATIONS AND PRESENTATIONS**

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#### Released computer tools with users' manuals

1. Xu, Y. and J. **Wu**. 2014. linkim: Linkage information based genotype imputation method. Available at <http://cran.r-project.org/web/packages/linkim/index.html>

2. **Wu, J.** 2014. minque: An R Package for Linear Mixed Model Analyses. Available at <http://cran.r-project.org/web/packages/minque/index.html>
3. **Wu, J., J. Jenkins, and J. McCarty.** 2014. qgtools: Tools for Quantitative Genetics Data Analyses. Available at <http://cran.r-project.org/web/packages/qgtools/index.html>

### Book chapters

1. Saha, S., D.M. Stelly, D. A. Raska, J. **Wu**, J. N. Jenkins, J. C. McCarty, A. Makamov, V. Gotmare, I. Y. Abdurakhmonov, and B. T. Campbell. 2011. Chromosome substitution lines: concept, development and utilization in the genetic improvement of Upland cotton. In the Book of "Plant Breeding" (edited by I. Y. Abdurakhmonov, Chapter 6) P107-128.
2. **Wu, J., J. Zhu, and J. N. Jenkins,** 2003. Mixed Linear Model Approaches in Quantitative Genetic Models (book chapter) In: *Formulars, Software, and Techniques for Genetics and Breeders*. The Haworth Reference Press Inc. New York.

### Peer-reviewed publications

#### FY2016

1. Campbell, B. T., J. Greene, J. **Wu**, and D. C. Jones. 2016. Genetic variation for agronomic and fiber quality traits in a population derived from high-quality cotton germplasm. *Crop Science*. doi:10.2135/cropsci2015.10.0657

#### FY2015

1. Rasul, G., K.D. Glover, P.G. Krishnan, J. **Wu**, W.A. Berzonsky, and A.M.H. Ibrahim. 2015. Additive-dominance genetic model analyses for late-maturity alpha-amylase activity in a bread wheat factorial crossing population. *Genetica* 143(6): 671-680.
2. Bondalapati, K.D., J. N. Jenkins, J. C. McCarty, and J. **Wu**. 2015. Field experimental design comparisons to detect field effects associated with agronomic traits in upland cotton. *Euphytica* 206(3): 747-757 (corresponding author).
3. Assefa, T., J. **Wu**, and A. Boe. 2015. Genetic Variation for Achene Traits in Cup Plant (*Silphium perfoliatum* L.). *Open Journal of Genetics* 5: 71-82.
4. Similien, R. M., T. P. Trooien, J. **Wu**, and A. Boe. 2015. Impact of Harvest Management on Forage Production and Nutrient Removal by Smooth Bromegrass on a Vegetated Treatment Area. *American Journal of Plant Sciences* 6(9): 1550-1559.
5. Assefa, T., J. **Wu**, K. A. Albrecht, P. J. Johnson, and A. Boe. 2015. Genetic Variation for Biomass and Related Morphological Traits in Cup Plant (*Silphium perfoliatum* L.). *American Journal of Plant Sciences* 6(8): 1098-1108.
6. Zhang, J. Q. Song, P. B. Cregan, R. L. Nelson, X. Wang, J. **Wu**, and G. L. Jiang. 2015. Genome-wide association study for flowering time, maturity dates and plant height in early maturing soybean (*Glycine max*) germplasm. *BMC Genomics* 16:217.
7. Xu Y., Y. Wu, M. G. Gonda, and J. **Wu**. 2015. A Linkage based Imputation Method for Missing SNP Markers in Association Mapping. *Journal of Applied Bioinformatics and Computational Biology* 4:1. doi:10.4172/2329-9533.1000115 (corresponding author) .

#### FY2014

1. Fang, D.D., J. N. Jenkins, D.D. Deng, J. C. McCarty, P. Li, and J. **Wu**. 2014. Quantitative trait loci analysis of fiber quality traits using a random-mated recombinant inbred population in Upland cotton (*Gossypium hirsutum* L.). *BMC genomics* 15 (1), 397
2. Asefa, T., J. **Wu**, S.E. Beebe, I.M. Rao, D. Marcomin, and R.J. Claude. 2014. Improving adaptation to drought stress in small red common bean: phenotypic differences and predicted genotypic effects on grain yield, yield components and harvest index. *Euphytica* (accepted with DOI 10.1007/s10681-014-1242-x)
3. Bondalapati, K., J. **Wu**, K. Glover. 2014. An augmented additive-dominance (AD) model for analysis of multi-parental spring wheat F2 hybrids. *Australian Journal of Crop Science* (in press)
4. Campbell, B.T., J. Greene, J. **Wu**, and D.C. Jones. 2014 Assessing the breeding potential of day-neutral converted racestock germplasm in the Pee Dee cotton germplasm enhancement program. *Euphytica* 195:453-465.

#### FY2013

5. **Wu**, J., K. Bondalapati, K. Glover, W. Berzonsky, J. N. Jenkins, J. C. McCarty. 2013. Genetic analysis without replications: model evaluation and application in spring wheat. *Euphytica*. 190:447-458.
6. Campbell, B., D. Weaver, R. Sharpe, J. **Wu**, and D. Jone. 2013. Breeding potential of elite Pee Dee germplasm in Upland cotton breeding programs. *Crop Science* 53:894-905.
7. Zeng, L., and J. **Wu**. 2013. Genetic effects and genetic values of fiber properties in F2 and F3 hybrids between germplasm lines and high yield cultivars. *Euphytica* 190: 459-469.
8. Saha, S., J. **Wu**, J. N. Jenkins, J. C. McCarty, D. M. Stelly. 2013. Interspecific chromosomal effects on agronomic traits in *Gossypium hirsutum* by AD analysis using intermated *G. barbadense* chromosome substitution lines. *Theoretical and Applied Genetics*. 126:109-117.

#### FY2012

9. **Wu**, J., L. Zhang, W. D. Johnson. 2012. The Permutation Test as an Ancillary Procedure for Comparing Zero-inflated Continuous Distributions. *Open Journal of Statistics* 2:274-280.
10. Rasul, G., G. D. Humphreys, J. **Wu**, A. Brûlé-Babel, B. Fofana, and K. D. Glover. 2012. Evaluation of pre-harvest sprouting traits in a collection of spring wheat germplasm using genotype and genotype x environment interaction model. *Plant Breeding* 131:244-251.
11. Willers J.L., J. **Wu**, C. O'Hara, and J. N. Jenkins. 2012. A categorical, improper probability method for combining NDVI and LiDAR elevation information for potential cotton precision agricultural applications. *Computers and Electronics in Agriculture* 82: 15-22.
12. Liang, M., D. Hole, J. **Wu**, T. Blake, and Y. Wu. 2012. Expression and functional analysis of NUCLEAR FACTOR-Y, subunit B genes in barley. *Planta* 235: 779-791.

#### FY2011

13. Saha, S. J. **Wu**, J. N. Jenkins, J. C. McCarty, R. Hayes, D. M. Stelly. 2011. Delineation of interspecific epistasis on fiber quality traits in *Gossypium hirsutum* by ADAA analysis of intermated *G. barbadense* chromosome substitution lines. *Theoretical and Applied Genetics* 122: 1351-1361.
14. Jenkins J. N., J. C. McCarty, J. **Wu**, R. Hayes, D. M. Stelly, 2012. Genetic effects of nine *Gossypium barbadense* L. chromosome substitution lines in top crosses with five elite Upland cotton *G. hirsutum* L. cultivars. *Euphytica* 187: 161-173.

15. **Wu, J.**, J. N. Jenkins, M. C. McCarty, X-Y. Lou. 2011. Comparisons of Four Approximation Algorithms for Large-Scale Linkage Map Construction. *Theoretical and Applied Genetics* 123: 649-655.
16. **Wu, J.**, X-Y Lou, M. Gonda. 2011. Stochastic deletion-insertion algorithm to construct dense linkage maps. *Statistics and Its Interface* 4(3): 381–388.

#### FY2010

17. **Wu, J.** J. N. Jenkins, J. C. McCarty, S. Saha. 2010. Genetic effects of individual chromosomes in cotton cultivars detected by using chromosome substitution lines as genetic probes. *Genetica*: 138:1171–1179.
18. Saha, S., **Wu, J.**, Jenkins, J.N., McCarty Jr., J.C., Hayes, R.W., Stelly, D. 2010. Genetic dissection of chromosome substitution lines of cotton to discover novel *Gossypium barbadense* L. alleles for improvement of agronomic traits. *Theoretical and Applied Genetics* 120:1193-1205.
19. An, C., J.N. Jenkins, J. **Wu**, Y. Guo, and J. C. McCarty. 2010. Use of fiber and fuzz mutants to detect QTL for yield components, seed, and fiber traits of upland cotton. *Euphytica* 172:21-34.
20. **Wu, J.**, McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. *Theoretical and Applied Genetics* 120:1473-1483.
21. **Wu, J.**, McCarty, J.C., Jenkins, J.N., Meredith, W. R. 2010. Breeding potential of introgressions into upland cotton: genetic effects and heterosis. *Plant Breeding* 129: 526-532.
22. Zhang, L., **Wu, J.**, W. D. Johnson, 2010. Empirical study of six tests for equality of populations with zero-inflated continuous distributions. *Communications in Statistics-Simulation and Computation*. 39: 1181-1196.

#### FY2009

23. **Wu, J.**, O. A. Gutierrez, J. N. Jenkins, J. C. McCarty, and J. Zhu. 2009. Quantitative analysis and QTL mapping for agronomic and fiber traits in an RI population of upland cotton. *Euphytica* 165: 231-245.
24. **Wu, J.**, J. N. Jenkins, J. C. McCarty, and P. Thaxton. 2009. Seed trait associations with *Gossypium barbadense* L. line chromosomes in a *G. hirsutum* L. background. *Euphytica* 167: 371-380.
25. **Wu, J.**, J. C. McCarty, S. Saha, J. N. Jenkins, and R. Hayes. 2009. Genetic changes in plant growth and their associations with chromosomes from *Gossypium barbadense* L. in *G. hirsutum* L. *Genetica* 137: 57-66.
26. Jenkins, J. N., J. C. McCarty, J. **Wu**, and O. A. Gutierrez. 2009. Genetic variance components and genetic effects among eleven diverse upland cotton lines and their F<sub>2</sub> hybrids *Euphytica* 167: 397-408.

#### FY2008

27. **Wu, J.** J. N. Jenkins, J. C. McCarty, S. Saha, and R. Percy. 2008. Genetic association of lint yield with its components in cotton chromosome substitution lines. *Euphytica* 164: 199-207.
28. McCarty, J. C., J. **Wu**, J. N. Jenkins. 2008. Genetic associations of cotton yield with its component traits in derived primitive accessions crossed by elite Upland cultivars using the conditional ADA genetic model. *Euphytica* 161: 337–352.

29. Saha, S., J. N. Jenkins, J. **Wu**, J. C. McCarty, and D. Stelly. 2008. Genetic analysis of agronomic and fiber traits using four interspecific chromosome lines. *Plant Breeding* 127: 612-618.  
FY2007
30. Jenkins, J. N., J. C. McCarty, J. **Wu**, S. Saha, O. Guitierrez, R. Hayes, and D. Stelly. 2007. Genetic effects of thirteen *Gossypium barbadense* L. chromosome substitution lines in topcrosses with upland cotton cultivars: II. Fiber quality traits. *Crop Science* 47: 561-572.
31. **Wu**, J., J. N. Jenkins, J. C. McCarty, M. Zhong, and M. Swindle. 2007. AFLP marker associations with agronomic and fiber traits in cotton. *Euphytica* 153: 153-163.
32. McCarty, J. C., J. **Wu**, and J. N. Jenkins. 2007. Use of primitive derived cotton accessions for agronomic and fiber traits improvement: variance components and genetic effects. *Crop Science* 47: 100-110.

FY2006

33. Jenkins, J. N., J. **Wu**, J. C. McCarty, S. Saha, O. Gutierrez, R. Hayes, and D. M. Stelly. 2006. Genetic evaluation for thirteen chromosome substitution lines crossed with five commercial cultivars: yield traits. *Crop Science* 46: 1169-1178.
34. **Wu**, J., D. Wu, J. N. Jenkins, and J. C. McCarty. 2006a. A recursive approach to detect multivariate conditional variance components and random effects. *Computational Statistics and Data Analysis*. 50: 285-300.
35. **Wu**, J., J. N. Jenkins, J. C. McCarty, S. Saha, and D.M. Stelly. 2006c. A new genetic model to determine chromosomal effects in chromosome substitution lines and other genmplasms. *Theoretical and Applied Genetics*. 112: 391-399.
36. **Wu**, J., J. N. Jenkins, Jack C. McCarty, and D. Wu. 2006b Variance component estimation using the ADAA model when genotypes vary across environments. *Crop Science* 46: 174-179.
37. Gutiérrez, O. A., D. T. Bowman, C. B. Cole, J. N. Jenkins, J. C. McCarty, J.**Wu**, and C. E. Watson. 2006. Development of random mating populations using bulked-pollen methodology: cotton as a model. *Journal of Cotton Science* 10: 175-179.
38. McCarty, J. C., J. **Wu**, and J. N. Jenkins. 2006a. Genetic diversity for agronomic and fiber traits in day-neutral primitive cotton germplasm accessions. *Euphytica* 148: 283-293.
39. McCarty, J. C., J. **Wu**, S. Saha, J. N. Jenkins, and R. Hayes. 2006b. Effects of chromosome 5sh from *Gossypium barbadence* L. on flower production in *G. hirsutum* L. *Euphytica* 152: 99-107.
40. Saha S., J. N. Jenkins, J. **Wu**, J. C. McCarty, R.G. Percy, R. G. Cantrell, and D. M. Stelly. 2006. Effect of chromosome specific introgression in Upland cotton on fiber and agronomic traits. *Genetics* 172: 1927-1938.

FY2005

41. McCarty, J. C., J. **Wu**, J. N. Jenkins, X. Mo. 2005b. Evaluating American and China cotton cultivars and their crosses for improvement. *Journal of Cotton Science (China)* 17(1): 47-55.

42. **Wu, J.**, J. N. Jenkins, J. C. McCarty, and C. E. Watson. 2005a. Comparisons of two statistical models for evaluating boll retention in cotton. *Agronomy Journal* 97: 1291-1294.
43. **Wu, J.**, J. Zhu, J. N. Jenkins, and J. C. McCarty. 2005b. Constructing linkage maps with achiasmatic gametogenesis. *Acta Genetica Sinica*. 32: 608-615.

#### FY2004

44. **Wu, J.**, J. N. Jenkins, J. C. McCarty Jr., and J. Zhu. 2004. Genetic association of yield with its component traits for upland cotton recombinant inbred lines. *Euphytica* 140: 171-179.
45. McCarty, J. C. Jr., J. N. Jenkins, and J. **Wu**. 2004a. Primitive accession germplasm by cultivar crosses as sources for cotton improvement I: Phenotypic values and variance components. *Crop Science* 44: 1226-1230.
46. McCarty, J. C. Jr., J. N. Jenkins, and J. **Wu**. 2004b. Primitive accession germplasm by cultivar crosses as sources for cotton improvement II: Genetic effects and genotype values. *Crop Science* 44: 1231-1235.
47. Saha, S., J. **Wu**, J. N. Jenkins, J. C. McCarty Jr., O. A. Gutiérrez, R. G. Percy, D. A. Raska, and D. M. Stelly, 2004. Association of agronomic and fiber traits with specific Pima 3-79 chromosomes in a TM-1 Background. *Journal of Cotton Science*. 8: 162-169.

#### FY2003

48. Cheatham, C. L., J. N. Jenkins, J. C. McCarty Jr., C. E. Watson, and J. **Wu**. 2003. Genetic variance and combining ability of crosses of American cultivars, Australian cultivars, and wild cottons. *Journal of Cotton Science* 7: 16-22.
49. **Wu, J.**, J. N. Jenkins, and J. Zhu, J. C. McCarty Jr. and C. E. Watson. 2003a. Comparisons of QTL mapping properties for two methods of recombinant inbred line development. *Euphytica* 132: 159-166.
50. **Wu, J.**, J. N. Jenkins, and J. Zhu, J. C. McCarty Jr. and C. E. Watson. 2003b. Monte Carlo simulations on marker grouping and ordering. *Theoretical and Applied Genetics* 107: 568-573.

#### FY2000 and before

51. Chen, Q., J. Zhu, J. **Wu**. 2000. Genetic study on seed cotton yield at different boll setting stages and fruiting sites in upland cotton. *Scientia Agricultura Sinica* 33(4):97-99.
52. Huang, S., J. **Wu**, Y. Chen, Z. Zhen. 2000. Analysis of genotype × environment interaction effects for unbalanced data in late rice regional trial. *Acta Agricultural Shanghai* 16(2): 50-53.
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[Presentations \(Over 60 at national and international conferences/meetings\)](#)