

Zhiwu Zhang

Assistant Professor

Washington Grain Commission Distinguished Professorship for Statistical Genomics

Department of Crop and Soil Sciences

Washington State University

105 Johnson Hall, Pullman, WA 99164, USA

Email: Zhiwu.Zhang@WSU.edu, Phone: (509) 335-2899, Website: <http://zzlab.net>

Curriculum Vitae

SUMMARY: *Dr. Zhang holds the Washington Wheat Distinguished Professorship for Statistical Genomics and has an interdisciplinary background, including one Ph.D. in Animal Breeding and Genetics, one Ph.D. in Statistical Genetics, and Postdoctoral training in Computational Biology. His research focus is the development of innovative, cutting-edge statistical methods and computing tools to advance genomic research toward the sustainability of food production and healthcare management. The developed methods include the Compressed Mixed Linear Model (CMLM) for Genome-Wide Association Study (GWAS) and FarmCPU GWAS methods. The software packages include well-known TASSEL and GAPIT, which are used by thousands of users, and have received over 1,000 citations. These methods and tools not only continually improve the accuracy of genomic prediction—increasing the probability of finding genes controlling human diseases and agriculturally important traits—but also continually reduce computing time. Dr. Zhang's research has generated over 50 publications within the last 10 years. His methods and tools are readily available and being used for immediate applications such as the development of a molecular breeding platform to improve wheat yield, quality, and resistance to biotic and abiotic stress. Dr. Zhang has received over one million dollars of funding from Washington State University (WSU), Washington Grain Commission (WGC), USDA, and DOE.*

EDUCATION

- | | |
|-----------|---|
| 1995-1998 | Ph.D., <i>Statistical Genetics</i>
Michigan State University , East Lansing, MI, USA
Dissertation: Power and accuracy of detecting linkage between quantitative trait loci and genetic markers |
| 1988-1991 | Ph.D., <i>Animal Breeding and Genetics</i>
Northeast Agricultural University , Harbin, China
Dissertation: Theory of genetic resources conservation and its application in Chinese Swine populations |
| 1985-1988 | M.S., <i>Animal Breeding and Genetics</i>
Jilin Agricultural University , Changchun, China
Dissertation: The method of minimizing inbreeding in domestic animals |
| 1978-1982 | B.S., <i>Animal Science</i>
Jilin Agricultural University , Changchun, China |

APPOINTMENTS

- 2014-Present **Assistant Professor**
Department of Crop and Soil Sciences, Washington State University,
Pullman, WA, USA
- 2011-2013 **Senior Research Associate**
Institute for Genomic Diversity, Cornell University, Ithaca, NY, USA
- 2002-2010 **Research Associate**
Department of Animal Science (2002-2005) and Institute for Genomic
Diversity (2006-2010), Cornell University, Ithaca, NY, USA
- 1998-2001 **Postdoctoral Fellow**
Department of Animal Science, Cornell University, Ithaca, NY, USA
- 1993-1994 **Associate Professor**
Institute of Animal Science, Chinese Academy of Agricultural Science,
Beijing, China
- 1991-1993 **Assistant Professor**
Institute of Animal Science, Chinese Academy of Agricultural Science,
Beijing, China
- 1982-1985 **Lecturer**
Jilin Agricultural College, Jilin, China

Footnotes for publication, funding and software: 1) Developed the initial idea; 2) Obtained or provided funds/resources; 3) Collected data; 4) Analyzed data; 5) Wrote/created product; and, 6) Edited product.

PUBLICATIONS (PEER REVIEWED)

Total Citations = 5792; H-index = 23; i10-index = 38 (accessed from Google Scholar, February 10, 2017); Corresponding authorship are indicated by an "" (20 articles); 2015 Impact factor (IF) is reported. Total IF: 234.367*

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59. Hui Zhang, Wei Na, Hong-Li Zhang, Ning Wang, Zhi-Qiang Du, Shou-Zhi Wang, Zhi-Peng Wang, Zhiwu Zhang* and Hui Li*, **TCF21 is related to testis growth and development in broiler chickens**. *Genet Sel Evol* 2017, DOI 10.1186/s12711-017-0299-0. IF= 2.895. (1,2,6).
58. Chunhui Li, Baocheng Sun, Yongxiang Li, Cheng Liu, Xun Wu, Dengfeng Zhang, Yunsu Shi, Yanchun Song, Edward S Buckler*, **Zhiwu Zhang***, Tianyu Wang*, Yu Li*, **Numerous genetic loci identified for drought tolerance in the maize nested association mapping populations**. *BMC genomics* 2016, 17 (1), 894. IF= 3.867. (1,2,3,5,6).

57. Annett Richter, Claudia Schaff, **Zhiwu Zhang**, Alexander E Lipka, Feng Tian, Tobias G Köllner, Christiane Schnee, Susanne Preiss, Sandra Irmisch, Georg Jander, Wilhelm Boland, Jonathan Gershenzon, Edward S Buckler, Jorg Degenhardt*. **Characterization of biosynthetic pathways for the production of the volatile homoterpenes DMNT and TMTT in *Zea mays***. *The Plant Cell* tpc. 2016, 00919.2015. IF= 8.538. (1,2,3,4,5,6).
56. Yongping Fu, Xinxin Wang, Dan Li, Yuan Liu, Bing Song, Chunlan Zhang, Qi Wang, Meiyuan Chen, **Zhiwu Zhang***, Yu Li*. **Identification of Resistance to Wet Bubble Disease and Genetic Diversity in Wild and Cultivated Strains of *Agaricus bisporus***. *International Journal of Molecular Sciences* 2016, 17 (10), 1568. IF= 3.257. (1,2,3,5,6).
55. C Li, Y Li, Y Shi, Y Song, D Zhang, ES Buckler*, **Z Zhang***, Y Li*, T Wang*. **Analysis of recombination QTLs, segregation distortion, and epistasis for fitness in maize multiple populations using ultra-high-density markers**. *Theoretical and Applied Genetics* 2016, 129 (9), 1775-1784. IF= 3.264. (1,2,3,5,6).
54. Y Zhou, MI Vales, A Wang, **Z Zhang***. **Systematic bias of correlation coefficient may explain negative accuracy of genomic prediction**. *Briefings in Bioinformatics* 2016, bbw064. IF= 8.399. (1,2,3,5,6).
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52. Li Yong-xiang; Chunhui Li, Peter J. Bradbury, Xiaolei Liu, Fei Lu, M. Cinta Romay, Jeffrey C. Glaubitz, Xun Wu, Bo Peng, Yunsu Shi, Yanchun Song, Dengfeng Zhang, Edward S. Buckler*, **Zhiwu Zhang***, Yu Li* & Tianyu Wang*. **Identification of genetic variants associated with maize flowering time using an extremely large multi-genetic background population**. *The Plant Journal* 2016, DOI: 10.1111/tpj.13174. IF= 6.280. (1,2,3,5,6).
51. You Tang, Xiaolei Liu, Jiabo Wang, Meng Li, Qishan Wang, Feng Tian, Zhongbin Su, Yuchun Pan, Di Liu, Alexander E. Lipka, Edward S. Buckler, and **Zhiwu Zhang***. **GAPIT Version 2: An Enhanced Integrated Tool for Genomic Association and Prediction**. *The Plant Genome* 2016, 9(2) 1-9. IF= 3.509. (1,2,3,5,6).
50. Xiaolei Liu, Meng Huang, Bin Fan, Edward S. Buckler, and **Zhiwu Zhang***: **Iterative Usage of Fixed and Random Effect Models for Powerful and Efficient Genome-Wide Association Studies**. *PLoS Genetics* 2016, DOI: 10.1371/journal.pgen.1005767. IF= 6.661. (1,2,3,5,6).
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46. Yingpeng Han, Xue Zhao, Dongyuan Liu, Yinghui Li, David A. Lightfoot, Zhijiang Yang, Lin Zhao, Gang Zhou, Zhikun Wang, Long Huang, **Zhiwu Zhang**, Lijuan Qiu, Hongkun Zheng, Wenbin Li. **Domestication footprints anchor genomic regions of agronomic importance in soybeans.** *New Phytologist* 2015, **10.1111/nph.13626**. IF= 7.672. (1,2,3,5,6).
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37. Boyko A, Brooks S, Behan-Braman A, Castelhana M, Corey E, Oliveira K, Swinburne J, Todhunter R, Zhang Z, Ainsworth D, Robinson N: **Genomic analysis establishes correlation between growth and laryngeal neuropathy in Thoroughbreds.** *BMC Genomics* 2014, **15**:259. IF= 3.867. (1,2,4,5,6).
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34. Hou Y, Wang Y, Lu X, Zhang X, Zhao Q, Todhunter RJ, *Zhang Z. **Monitoring Hip and Elbow Dysplasia Achieved Modest Genetic Improvement of 74 Dog Breeds over 40 Years in USA.** *PLoS One* 2013, **8**:e76390. IF= 2.234. (1,2,3,5,6).
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19. *Zhang Z, Ersoz E, Lai CQ, Todhunter RJ, Tiwari HK, Gore MA, Bradbury PJ, Yu J, Arnett DK, Ordovas JM, Buckler ES. **Mixed linear model approach adapted for genome-wide association studies.** *Nat Genet* 2010, **42**:355–360. IF= 31.616. (1,3,4,5,6).

18. Hou Y, Wang Y, Lust G, Zhu L, *Zhang Z, Todhunter RJ: **Retrospective analysis for genetic improvement of hip joints of cohort labrador retrievers in the United States: 1970-2007.** *PLoS One* 2010, **5**:e9410. IF= 2.234. (1,2,3,4,5,6).
17. *Zhang Z, Buckler ES, Casstevens TM, Bradbury PJ: **Software engineering the mixed model for genome-wide association studies on large samples.** *Br Bioinform* 2009, **10**:664–675. IF= 8.399. (1,3,4,5,6).
16. Zhu L, Zhang Z, Friedenberg S, Jung SW, Phavaphutanon J, Vernier-Singer M, Corey E, Mateescu R, Dykes N, Sandler J, Acland G, Lust G, Todhunter R. **The long (and winding) road to gene discovery for canine hip dysplasia.** *Vet J* 2009, **181**:97–110. IF= 1.142. (1,2,3,4,5,6).
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13. Zhang Z, Zhu L, Sandler J, Friedenberg SS, Egelhoff J, Williams AJ, Dykes NL, Hornbuckle W, Krotscheck U, Moise NS, Lust G, Todhunter RJ. **Estimation of heritabilities, genetic correlations, and breeding values of four traits that collectively define hip dysplasia in dogs.** *Am J Vet Res* 2009, **70**:483–492. IF= 1.124. (1,2,3,4,5,6).
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9. Zhu L, Zhang Z, Feng F, Schweitzer P, Phavaphutanon J, Vernier-Singer M, Corey E, Friedenberg S, Mateescu R, Williams A, Lust G, Acland G, Todhunter R. **Single nucleotide polymorphisms refine QTL intervals for hip joint laxity in dogs.** *Anim Genet* 2008, **39**:141-146. IF= 2.605. (1,2,3,4,5,6).

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7. Liu T, Todhunter RJ, Wu S, Hou W, Mateescu R, **Zhang Z**, Burton-Wurster NI, Acland GM, Lust G, Wu R. **A random model for mapping imprinted quantitative trait loci in a structured pedigree: an implication for mapping canine hip dysplasia.** *Genomics* 2007, **90**:276–284. IF= 3.327. (4,5,6).
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PUBLICATIONS (BOOK CHAPTERS)

Mateescu RG, Tsai K, **Zhang Z**, Burton-Wurster NI, Lust G, Dykes N, Acland GM, Quaas RL, Murphy K, Todhunter RJ. QTL Mapping Using Cross Breed Pedigrees: Strategies for Canine Hip Dysplasia. In *The Dog and Its Genome* (eds. E.A. Ostrander, U. Giger, K. Lindblad-Toh), Cold Spring Harbor Press. 2005. pp. 407-438.

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PUBLICATIONS (REFERENCED NON-PEER-REVIEWED)

Total: 3; first author: 1

3. **Zhang Z**, RL Quaas, EJ Pollak, Simulation study on the effects of incorporating external genetic evaluations results, Proceedings of the 7th World Congress on Genetics Applied to Livestock Production, Montpellier, France, August 19-23, 2002, CD-ROM Commun, 20-14, http://www.lagoa.com.br/images/upload/Zhang_Quaas_Pollack_2002.pdf
2. Quaas RL, **Z Zhang**, Multiple-breed genetic evaluation in the US beef cattle context: methodology, Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte, Minas Gerais, Brazil, 13-18 August, 2006. CD-ROM Commun, 24-12, <https://www.cabdirect.org/cabdirect/FullTextPDF/2006/20063170188.pdf>
1. Jiang Zhihua, Tanja Kunej, Tito A Wibowo, Jennifer J Michal, **Zhiwu Zhang**, Charles Thorne Gaskins, Jerry J Reeves, Jan Roger Busboom, P Dovic, RW Wright Jr, The basal nucleus-encoded mitochondrial transcription genes and meat quality in beef cattle, Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte, Minas Gerais, Brazil, 13-18 August, 2006. CD-ROM Commun, 22-24, <https://www.cabdirect.org/cabdirect/FullTextPDF/2006/20063170035.pdf>

PUBLICATIONS (IN CHINESE, PEER REVIEWED)

Total: 18; first author: 11

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15. Tang D, **Zhang Z**, Xu S. **Path analysis on AKP, Ca and P in serum and milk composition in Simmental cattle.** *J Gansu Anim Sci* 1994:8–11.
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12. **Zhang Z**, Yu R, Wang R, Fang Z, Zheng Y. **Estimates of gene effects and effective gene number on litter size in pig.** *Acta Genet Sin* 1994, **21**:275–280.
11. Xu S, **Zhang Z**, Wan Y, Cai M, Zhao C. **A systemic model of conservation, selection and utilization of Fuzhou Cattle.** *J Chinese Beef* 1993, **68**:15–8.

10. **Zhang Z**, Tang D, Xu S, Lu J, Wang Y, Wang Y, Yang L, Shao Z, Jian E, Qian S, Liu Y, Zhang ZX. **The distribution of AKP, Ca and P in Serum of Simmental cattle.** *J Chinese Dairy Sci* 1993:40–44.
9. **Zhang Z.** **Modeling of Eco-Breeding system in livestock.** *Eco Agric Res* 1993:48–51.
8. Tang D, **Zhang Z**, Xu S, Lu J, Wang Y, Yang X. **The Relationship between blood serum amylase and milk composition.** *J Chinese Beef* 1993, **64**:20–22.
7. **Zhang Z**, Sheng Z, Feng W. **Strategies and scheme to conserve genetic resources of Chinese Pigs.** *Chinese J Anim Sci* 1993, **29**:5–7.
6. **Zhang Z.** **A statistical method for standardized transferability.** *J Chinese Simmental Cattle* 1993:37–39.
5. **Zhang Z.** **Decision support system of screening pig breed for conservation.** *Comput Appl Agric* 1993:27–30.
4. **Zhang Z**, Cai Y, He Y, Jin X. **Group mating model with quadratic program and its application in minimizing inbreeding.** *Chinese Acta Vet Zootech* 1991, **22**:42–48.
3. **Zhang Z.** **Recursive algorithm to calculate individual relationship.** *J Northeast Agric Univ* 1991, **22**:231–235.
2. Zhao G, **Zhang Z**, Cai Y, He Y, Jin X. **A method of non-linear estimate of effective size of Min Pig population conserved.** *Heilongjiang Anim Vet Sci* 1990:5–6.
1. **Zhang Z**, Cai Y, He Y, Jin X. **Minimizing inbreeding of population by selecting mating pairs.** *J Jilin Agric Univ* 1990, **12**:61–65.

FUNDING AWARDS

Total funding directly to Dr. Zhang since starting faculty position: \$1.27 million

Endowment of Washington Grain Commission

"Distinguished Professorship in Statistical Genomics" since 2015 with annual revenue of ~\$60,000. (1,2,3,5,6).

5/1/2015-12/31/2018 (PI)

Washington Grain Commission

"Intelligent Prediction and Association Tool to Facilitate Wheat Breeding", \$220,667 (direct cost). (1,2,3,5,6).

1/1/2017-12/31/2019 (Co-PI, PI: Dr. Jack Brown)

DOE

"Developing Non-food Grade Brassica Biofuel Feedstock Cultivars with High Yield, Oil Content, and Quality for Low-Input Production Dryland Systems", \$1,200,000 (\$332,925 to Dr. Zhang). (2,3,4,5,6).

1/1/2016-12/31/2019 (Co-PI, PI: Dr. Arron Carter)

USDA

“Next Generation Variety Development and Education for Grains, Apples, Alternative Crops, and Cool Season Legumes” (award number 2016-68004-24770), \$3,000,000 (\$234,705 to Dr. Zhang). (2,3,4,5,6).

1/1/2016-12/31/2019 (Co-PI, PI: Dr. Camille Steber)

USDA

“Molecular Genetic Architectures for Increasing Pre-harvest Sprouting Tolerance in White Wheat” (award number 123555-002), \$422,000. (2,4,5,6).

1/1/2017-12/31/2019 (Co-PI, PI: Dr. Kiwamu Tanaka)

M.J. Murdock Charitable Trust

“Acquisition of an Automated Phenotyping System to Enable the Next Generation of Plant Phenomics-Genomics Study”, \$480,000. (2,3,4,5,6).

7/1/2015-12/30/2016 (Co-PI, PI: Dr. Zhihua Jiang)

Office of Research at Washington State University

“Neurogenetics and Neurogenomics of Addiction Vulnerability”, \$22,500 (direct cost). (2,3,4,5,6).

1/30/2015-7/1/2017 (PI)

Emerging Research Issues at Washington State University

“A Single Step Approach to Map Genes Underlying Phenotypes in Multiple Environments”, \$80,000 (direct cost). (1,2,3,5,6).

5/1/2015-12/30/2015 (PI)

CAHNRS Undergraduate Internships at Washington State University

“Upgrading Software to Enhance Biological and Agricultural Research”, \$6,500 (direct cost). (1,2,3,5,6).

8/27/2011-8/26/2014 (Co-PI, PI: Dr. Dorothy Ainsworth)

Harry M. Zweig Memorial Fund for Equine Research

“The Genetic Basis of Recurrent Laryngeal Neuropathy (RLN) in Thoroughbreds”, \$297,000. (2,4,5,6).

12/01/2008-11/20/2010 (Co-PI, PI: Dr. Rory Todhunter)

National Institutes of Health (1R21AR055228-01A1)

“Fibrillin 2 and Developmental Genetics of Hip Dysplasia in a Canine Model”, \$225,000 (direct cost). (2,3,4,5,6).

4/20/2008-4/19/2011 (PI)

American Simmental Association

“Multiple Breed Genetic Evaluation System”, \$35,000 annual direct costs. (1,2,4,5,6).

4/20/2005-4/19/2008 (PI)

American Simmental Association

“Multiple Breed Genetic Evaluation System”, \$25,000 annual direct costs. (1,2,4,5,6).

07/01/2006-6/30/2007 (Co-PI, PI: Dr. Rory Todhunter)

Cornell Advanced Technology - Biotechnology

“Incipient Events in Osteoarthritis: Models, Microarrays, SNPs, and Natural Diseases”, \$50,000 annual direct costs. (2,4,5,6).

01/01/1993-12/31/1995 (PI)

National Natural Science Foundation, China (39200088)

“Study on the Genetic Conservation for the Population Undergoing Selection”, 40,000 RMB (Chinese currency, renminbi). (1,2,3,4,5,6).

SOFTWARE DEVELOPED

Developed seven software packages for public and two for private. Most of the public software packages are hosted at Zhiwu Zhang Lab website (<http://zzlab.net>). The website receives over six thousand users. There are ~30 unique users daily. These packages include the widely-used packages: TASSEL and GAPIT. They have received over fifteen and two hundred citations, respectively.

- iPat: Intelligent Prediction and Association Tool. More information is provided at iPat website: <http://zzlab.net/iPat>. (1,2,3).
- BLINK: **Bayesian-information and Linkage-disequilibrium Iteratively Nested Keyway**. More information is provided at BLINK website: <http://zzlab.net/blink>.
- FarmCPU: Software for Genome Wide Association Study. See [publication by Liu et al. on PLoS Genetics](#). More information is provided at FarmCPU website: <http://zzlab.net/FarmCPU>. (1,2,3,5,6).
- GAPIT: Genome Association and Prediction Integrated Tool. See publications by [Lipka et al on Bioinformatics](#) and [Tang et al. on Plant Genome](#). More information is provided at GAPIT website: <http://zzlab.net/GAPIT>. (1,2,3,4,5,6).
- TASSEL: The mixed model component for QTL association analysis to incorporate kinship. See [publication by Bradbury et al. on Bioinformatics](#). More information is provided at TASSEL website: <http://www.maizegenetics.net/tassel>. (4,5,6).
- MTDFREML – MTDFARM: To perform multiple trait genetic analysis using arbitrary kinship including pedigree and marker based kinship. See [publication by Zhang et al. on Journal of Animal Science](#). More details can be found at: <http://zzlab.net/MTDFREML>. (1,2,3,4,5,6).
- Incorporating external information into genetic evaluation using Bayesian approach. The algorithm was implemented in the computer software: Beef Genetic Evaluation with Incorporation of External Information (Private: owned by American Simmental Association for official genetic evaluation). (4,5,6).
- Multiple breed genetic evaluation for carcass traits (Private: owned by American Simmental Association for official genetic evaluation). (4,5,6).

- Determination of chronological identification without birth date. The algorithm was implemented in [SeqPed](#). More information is provided at TASSEL website: <http://statgen.neau.edu.cn/SeqPed>. (1,2,3,4,5,6).

INVITED PRESENTATIONS

- 2017 **Keynote Speaker, Incubating BLUP Method for Full Spectrum of Complex Traits, Umeå Plant Science Centre, Swedish University of Agricultural Sciences, SE-901 83 Umeå, June 18-21, 2017**
- International Conference of Plant and Animal Genome XXV, BLUP Alphabet for Genomic Prediction, San Diego, CA, January 14-18, 2017**
- 2016 **Iowa State University, Saving the Babies from Bathwater in Genome-Wide Association Studies, Ames, IA, March 27-29, 2016**
- Mathematical Biology Seminar at Washington State University. Upgrade the Compartments of Mixed Linear Model to Reduce Both False Positives and False Negatives in Gene Mapping, Pullman, September 20, 2016**
<http://www.math.wsu.edu/faculty/xueying/MathBiologySeminar.html>
- 2015 **Agricultural Genomics 2015 — from Variation to Improved Production, Saving the Babies from Bathwater in Genome-Wide Association Studies, Shenzhen, China, November 16-18, 2015**
<http://www.nature.com/natureconferences/ag2015/speakers.html>
- University of California at Riverside Saving the Babies from Bathwater in Genome-Wide Association Studies, February 11, 2015**
- Plant and Animal Genomics XXIII (Statistical Genomics Workshop): Getting Power Back from Population Structure and Kinship in Genome-Wide Association Studies, San Diego, CA, April 11, 2015**
<https://pag.confex.com/pag/xxiii/webprogram/Session2712.html>
- 2014 **Presentation Series from Experts: Dissecting Genetic Architecture of Complex Traits. Heilongjiang Academy of Agricultural Science, Harbin, China, April 9, 2014**
- 2013 **Plant and Animal Genomics XXI (Statistical Genomics Workshop): Kinship Evolution for Genome Prediction and Association Study. San Diego, CA, January 13, 2013** <https://pag.confex.com/pag/xxi/webprogram/Session1586.html>
- 2012 **Plant and Animal Genomics XX (Statistical Genomics Workshop): Integration of Genome Association And Prediction, San Diego, CA, January 15, 2012** <https://pag.confex.com/pag/xx/webprogram/Session1069.html>
- 2011 **Nanjing Agricultural University, National Soybean Improvement Center, Integration of Genome Association And Prediction, Nanjing, China, July 5, 2011**
- China Agricultural University, National Maize Improvement Center, Advances of Statistical Methods for Genome-Wide Association Study, Beijing, China, July 2, 2011**

- 2010 **Cornell University Center for Vertebrate Genomics, *Canine Dysplasia is Predictable by Genotyping***, Ithaca, NY, November 9, 2010
- 6th SJTU_CU Workshop on Modern Agriculture and Biotechnology, *Adaptation of Mixed Model for Genome-Wide Association Study***, Shanghai, China, October 9-11, 2010
- Center for Agricultural biotechnology, Kasetsart University, *Adaptation of Mixed Model for Genome-Wide Association Study***, Kamphaeng Saen Campus, Thailand, March 20, 2010
- Plant Breeding for Commercial Organization Workshop, Kasetsart University, *Molecular breeding***, Kamphaeng Saen Campus, Thailand, March 22, 2010
- 2009 **Department of Agronomy, University of Nebraska, *Adaptation of Mixed Model for Genome-Wide Association Study***, Lincoln, NE, November 20, 2009
- 2008 **Nutrition and Genomics Laboratory, JM-USDA Human Nutrition Research Center on Aging at Tufts University, *Mixed Model for Genome-Wide Association Study***, Boston, MA, November 14, 2008
- 2007 **62nd Northeastern Corn Improvement Conference, Cornell University, *Association Mapping by Using TASSEL Software to Incorporate Background QTL Effect***, Ithaca, NY, February 16, 2007

INSTRUCTED WORKSHOPS

- **Genomic Prediction**, Northeast Agricultural University, Harbin, China, December 26-29, 2016. Website: <http://zzlab.net/GS2016Harbin>
- **Genome Wide Association Studies**, Huazhong Agricultural University, Harbin, China, July 4-9, 2016. Website: <http://zzlab.net/GWAS2016WUHAN>
- **Assessment of Statistical Power and False Discovery in Genome Wide Association Study**, Department of Agronomy, Iowa State University, Ames, IO, March 27-28, 2016. Website: <http://zzlab.net/WorkshopISU>
- **Mapping Genes by Using Genome Wide Association Studies**, Washington State University, Pullman, WA, February 23-27, 2015
- **Methods and Tools for Genome Wide Association Studies**, Collage of Veterinary Medicine, Cornell University, Ithaca, MY, June 14, 2013
- **Genomic Mapping Workshop**, USDA ARS, Lubbock, TX, Oct 25-26, 2006,

RESEARCH ADVISEES

Current

- Meng Huang:** 2014-present, Postdoctoral Researcher. Research Project: Genome-wide association study on complex traits.
- Matthew McGowan:** 2016-present, Ph.D. Student. Research Project: Genotype Calling for SNP and Structural Variation.
- Chris Watson:** 2016-present, Ph.D. Student. Research Project: Genotype Imputation for Sequencing Data
- Chun-Peng Chen:** 2016-present, M.S. Student. Research Project: Intelligent Prediction and Association Tool
- Ryan Summers:** 2014-present, Undergraduate Student. Research Project: None CPU computation.
- Yao Zhou:** 2014-present, Ph.D. Student. Research Project: High dimensional genetic effect.
- Jiabo Wuang:** 2014-present, Ph.D. Student. Research Project: Genomic prediction.
- You Tang:** 2014-present, Ph.D. Student. Research Project: Mining the maximum accuracy of prediction.
- Guanghui Hu:** 2013-present, Ph.D. Student. Research Project: Dissection of genetic architecture of cold tolerance in maize.
- Meijing Liang:** 2015-present, Ph.D. Student. Research Project: Genomic prediction.

Past

- Isabel Vales:** 2014-2015, Research Scientist. Research Area: Genomic prediction. She is now an Associate Professor at Texas A&M.
- Joseph G Homan:** 2014-2016, Undergraduate Student. Research Project: Remote access on mobile devices.
- Xu Zhang:** 2014-2016, Visiting Ph.D. Student. Research Project: Identification of genes controlling cattle growth.
- Ying Wu:** 2015-2016, Visiting Ph.D. Student. Research Project: Identification of genes controlling agronomic traits in rice.
- Zhao Li:** 2014-2015, Visiting Ph.D. Student. Research Project: Freezing tolerance of maize.
- Yongping Fu:** 2014-2015, Visiting Professor. Research Project: Gene profiling of mushroom.
- Mengjin Zhu:** 2014-2015, Visiting Professor. Research Project: Genome-wide association study.
- Xiaolei Liu:** 2013-2015, Visiting Ph.D. Student. Research Project: Iterative Usage of Fixed and Random Effect Models for Powerful and Efficient Genome-Wide Association Studies.
- Yongxiang Li:** 2012, Visiting Scientist. Research Project: Genome-wide association study for genetic resistance for northern and southern leaf blight in maize.
- Alexander Lipka:** 2010-2014, Postdoctoral Researcher. Research Project: GAPIT: genome association and prediction integrated tool. He is now an assistant professor at University of Illinois.
- Qishan Wang:** 2011, Visiting Scientist. Research Project: An improved mixed linear model for genome-wide association study. The manuscript is in the process of preparation. He is currently an associate professor at Shanghai Jiaotong University, China.

Meng Li: 2009-2011, Visiting Ph.D. Student. Research Project and the title of the related publication is “Enrichment of statistical power for genome-wide association studies”, *BMC Biology* 2014, 12:73.

Zhengkui Zhou: 2009-2011, Visiting Ph.D. Student. Research Project and the title of the related publication is “Differential Genetic Regulation of Canine Hip Dysplasia and Osteoarthritis”, *PLoS One* 2010, 5(10): e13219. doi:10.1371/journal.pone.0013219.

Xihui Sheng: 2009-2010, Visiting Ph.D. Student. Research Project and the title of the related publication is “Differential Genetic Regulation of Canine Hip Dysplasia and Osteoarthritis”. She is currently an assistant professor of genetics at Beijing Agriculture College.

Yali Hou: 2007-2010, Visiting Ph.D. Student. Research Project and the title of the related publication is “Retrospective Analysis for Genetic Improvement of Hip Joints of Cohort Labrador Retrievers in the United States: 1970–2007”. *PLoS One*, 2010 5(2): e9410.

Gang Guo: 2007-2010, Visiting Ph.D. Student. Research Project and the title of the related publication is “Canine Hip Dysplasia is Predictable by Genotyping”, *Osteoarthritis and Cartilage*, 2011, (19) 420-429. He is currently a research scientist at Beijing Sanyuan Breeding Technology Co., Ltd.

Daniel Ogden: 2007-2009, Veterinary Resident. Research Project and the title of the related publication is “Principal component analysis of canine hip dysplasia phenotypes and their statistical power for genome-wide association mapping”, *Journal of Applied Statistics*, Vol. 40, No. 2, February 2013, 235–251. He is currently an assistant professor of veterinary surgery at Louisiana State University.

TEACHING

2017 Spring **Statistical Genomics (CROP_SCI 545)**, Washington State University (*Instructor*)

2016 Spring **Statistical Genomics (CROP_SCI 545)**, Washington State University (*Instructor*)

2015 Fall **Genome-Wide Association Study (CROP_SCI 512 Topics in Crop Science)**, Washington State University (*Instructor*)

2008-2009 **Applied Statistical Analysis (STSCI 501–502)**, Cornell University (*course project supervisor*). Principal Components Analysis and Mixed Linear Model in SAS were taught. The project generated a publication in the *Journal of Applied Statistics* (2012, 40:235–251).

1995-1997 **Statistics for Biology (I and II)**, Michigan State University, **Teaching Assistant**

1982-1985 **Genetics**, Jilin Agricultural College (*Instructor*, three semesters)
Biological Statistics, Jilin Agricultural College (*Instructor*, three semesters)

PROFESSIONAL ORGANIZATION MEMBERSHIP

American Association for the Advancement of Science (AAAS)

SERVICE

Academic Editor
 PLoS One

Ad Hoc Reviewer (Number of manuscripts reviewed)

Nature Genetics (7)	Genetics (1)
Nature Method (1)	Heredity (1)
Nature Communication (1)	Theoretical and Applied Genetics (1)
PNAS (1)	Animal Genetics (1)
Annals of Human Genetics (1)	Bioinformatics (3)
Annals of Applied Statistics (1)	Journal of Animal Science (1)
Genome Research (1)	Journal of Human Genetics (1)
PLoS Genetics(3)	PLoS Computation Biology (1)
PLoS One (5)	G3 (1)
GigaScience (1)	Plant Genome (1)
Theoretical and Applied Genetics (1)	

Committee Memberships

Executive Committee Member, Molecular Plant Sciences Program, 2017-present, Washington State University, Pullman, WA
Vice Chair of Hatch fund project in Plant Breeding, 2017-present, Washington State University, Pullman, WA
Department Website Committee Member, 2016-present, Washington State University, Pullman, WA
Board Member for Community of Emerald Pointe, 2017-present, Management of real state property, Pullman, WA
Employee Assembly for Minorities, 2002-2003, Cornell University
Employee Assembly for Communication, 2001-2002, Cornell University

Volunteer and Leadership

Wrote an article for Wheat Life for recruiting farmers to attend Pacific Northwest Portland Tour published on Wheat Life, February, 2017.
Substitute Mathematics Teacher, 2007-2008, Northeast Elementary School, Ithaca Public School System, Ithaca, NY
Volunteer Safety Guard for Public Skating, 2000-2002, The Rink at Lansing, NY
Advisor of Panda Coed Volleyball, Cornell (<http://sao.cornell.edu/SO/org/10-11/248>)
President of the Ph.D. Graduate Student Association, 1988-1990, Northeast Agricultural University, Harbin, China
President of the Graduate Student Association, 1985-1987, Jilin Agricultural University, Changchun, China

Graduate Advisory Committees

Feixiong Luo (Horticulture, Dr. Cameron Peace) 2016-
Ragupathi Nagarajan (CSS, Dr. Kulvinder Gill) 2014-
Stephanie Sjoberg (CSS, Dr. Arron Carter) 2016-
Wilson Craine (CSS, Dr. Scot Hulbert) 2016-
Ahsan Khan (CSS, Dr. Kulvinder Gill) 2015-
Joseph Daniel Crawford (School of Biology, Dr. Asaph Cousins) 2017-
Md Nurul Amin (CSS, Dr. Rebecca McGee) 2015-

AWARDS

Recognition award from the Nature Publication Group for contribution to referencing papers, 2012

Young Scientist Scholarship, the 5th World Congress of Genetics Applied to Livestock Production, Canadian International Development Agency, Canada (August, 1994)

Outstanding paper, National Natural Science Foundation, China, December 1993

COURSEWORK

Michigan State University (Ph.D.)

STT 441 ***Probability and Statistics-Probability***: Probability models and basic statistics at an intermediate mathematical level. Discrete, continuous, univariate, and multivariate distributions. Random variables. Normal approximation. Sampling distributions, parameter estimation, and elementary tests of hypotheses.

STT 442 ***Probability and Statistics- Statistics***: Estimation, tests of hypotheses, confidence intervals. Goodness of fit, non-parametric methods. Linear models, multiple regression, ANOVA.

STT 825 ***Sample surveys***: Application of statistical sampling theory to survey designs. Simple random, stratified, and systematic samples. Sub-sampling, double sampling. Ratio and regression estimators.

STT 841 ***Linear Statistical Model***: Probability models and basic statistics at an intermediate mathematical level. Discrete, continuous, univariate, and multivariate distributions. Random variables. Normal approximation. Sampling distributions, parameter estimation, and elementary tests of hypotheses.

STT 842 ***Categorical data analysis***: Analysis of categorical and ordinal data: contingency tables; chi square tests; exact tests; log-linear models; measures of association; logistic regression; generalized linear models.

ANS 943 ***Techniques of Analyzing Unbalanced Research Data***: Linear model techniques to analyze biological research data characterized by missing and unequal number of observations in classes. Simultaneous consideration of multiple factors. Prediction of breeding values and estimation of population parameters from variance and covariance components.

Cornell University (Postdoctoral Employee Continuing Education)

COMS 211 ***Computer and Programming***: Project course that introduces students to the ways of software engineering using the Java programming language. The course requires the design and implementation of several large programs.

COMS 213 ***C++ Programming***: An intermediate introduction to the C++ programming language and the C/C++ standard libraries. Topics include basic statements, declarations, and types; stream I/O; user-defined classes and types; derived classes, inheritance, and

object-oriented programming; exceptions and templates. Recommended for students who plan to take advanced courses in computer science that require familiarity with C++ or C.

- COMS 280 ***Discrete Structures***: Covers the mathematics that underlies most of computer science. Topics include mathematical induction; logical proof; propositional and predicate calculus; combinatorics and discrete mathematics; basic probability theory; basic number theory; sets, functions, and relations; partially ordered sets; and graphs. These topics are discussed in the context of applications to many areas of computer science, including game playing, the RSA cryptosystem, data mining, load balancing in distributed systems, properties of the Internet and World Wide Web, and web searching.
- COMS 381 ***Introduction to Theory of Computing***: Introduction to the modern theory of computing: automata theory, formal languages, and effective computability.
- COMS 432 ***Introduction to Database Systems***: Introduction to modern database systems. Concepts covered include storage structures, access methods, query languages, query processing and optimization, transaction management, recovery, database design, XML, and XQuery. The course focuses on the design and internals of modern database systems.
- COMS 482 ***Introduction to Analysis of Algorithms***: Develops techniques used in the design and analysis of algorithms, with an emphasis on problems arising in computing applications. Example applications are drawn from systems and networks, artificial intelligence, computer vision, data mining, and computational biology. This course covers four major algorithm design techniques (greedy algorithms, divide-and-conquer, dynamic programming, and network flow), computational complexity focusing on NP-completeness, and algorithmic techniques for intractable problems (including identification of structured special cases, approximation algorithms, and local search heuristics).
- COMS 501 ***Software Engineering***: Introduction to the practical problems of specifying, designing, and building large, reliable software systems. Students work in teams on projects for real clients. This work includes a feasibility study, requirements analysis, object-oriented design, implementation, testing, and delivery to the client. Additional topics covered in lectures include professionalism, project management, and the legal framework for software development.
- NGL 288 ***Expository Writing***: ENGL 288 offers guidance and an audience for students who wish to gain skill in expository writing—the common term for critical, reflective, and literary nonfiction. Each section provides a context for writing defined by a form of exposition, a disciplinary area, a practice, or a topic intimately related to the written medium. Course members will read in relevant published material and write and revise their own work regularly, while reviewing and responding to one another's. Since these seminar-sized courses depend on members' full participation, regular attendance and submission of written work are required. Students and instructors will confer individually throughout the semester.
- ENGLF 212 ***English as a Second Language-Research paper writing***: For the major writing assignment of this course, students must have a real project that is required for their graduate work. This can be a thesis proposal; a pre-thesis; part of a thesis, such as the literature review or discussion section; a paper for another course or a series of shorter papers (by permission of the other instructor); or a paper for publication. Time

limitations make it difficult to deal with work over 20 pages in length. Course work involves practice in paraphrase, summary, the production of cohesive, coherent prose, vocabulary use, and grammatical structure. Frequent individual conferences are a necessary part of the course. Separate sections for social sciences/humanities and for science/technology.

HOBBIES

Skiing, ice skating, rollerblading, fishing, hiking, biking, gardening, volleyball, tennis, and photography