

# Zhiwu Zhang

Associate Professor

Washington Grain Commission Distinguished Professorship for Statistical Genomics

Department of Crop and Soil Sciences

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## Curriculum Vitae

**SUMMARY:** *I have a multidisciplinary background with two Ph.D. degrees, one in Statistical Genetics and one in Animal Breeding. Currently, I am an Assistant Professor with an Endowment of Distinguished Professorship for Statistical Genomics from the Washington Grain Commission (WGC). Since 2005, I have published over 70 peer-reviewed articles, have received over 8,700 citations, and have an h-index of 29 (Google Scholar). My 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 statistical methods include the Compressed Mixed Linear Model for Genome-Wide Association Studies (GWAS); the released software computing packages include the widely-used TASSEL, GAPIT, and FarmCPU. Since joining WSU in 2014, I have received 11 awards and grants from a variety of sources, including WSU, WGC, Murdock Foundation, USDA, NSF, and DOE, which total \$1.8M in direct funding for my lab plus \$6M in funding for collaborative research. In 2015, I developed a graduate-level course in Statistical Genomics, which I have taught for four cycles. I am recognized internationally as an academic editor, journal article reviewer, grant review panelist, international conference workshop organizer, and invited speaker in multiple countries.*

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## EDUCATION

- 1995-1998      Ph.D., *Statistical Genetics*  
**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., *Animal Breeding and Genetics*  
**Northeast Agricultural University**, Harbin, China  
Dissertation: Theory of genetic resources conservation and its application in Chinese Swine populations
- 1985-1988      M.S., *Animal Breeding and Genetics*  
**Jilin Agricultural University**, Changchun, China  
Dissertation: The method of minimizing inbreeding in domestic animals
- 1978-1982      B.S., *Animal Science*  
**Jilin Agricultural University**, Changchun, China

## PROFESSIONAL POSITIONS

- 2019-Present      **Associate Professor**  
Department of Crop and Soil Sciences, Washington State University, Pullman, WA, USA
- 2014-2018      **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 Science and Technology University, Jilin, China

## **GRANT SUPPORT**

*Notes for grants, publications, and software: 1 = Developed initial idea, 2 = Obtained or provided funds/resources, 3 = Collected data, 4 = Analyzed data, 5 = Wrote/created product, and 6 = Edited product.*

### ***Extramural Funding***

2/15/2019-2/14/2022 (PI)

#### **USDA**

“Genomics-Enabled Satellite Phenomics For Wheat Breeding In The Palouse” (Award number 2019-67013-29171), \$500,000 (1, 2, 3, 5, 6).

9/1/2018-8/31/2021 (PI)

#### **USDA**

“Genomics Enabled Purging Selection to Develop 200 Alfalfa Inbred Lines Toward High Yield Hybrid Production” (Award number 2018-70005-28792), \$295,000 (1, 2, 3, 5, 6).

5/1/2015-6/30/2021 (PI)

#### **Washington Grain Commission**

“Intelligent Prediction and Association Tool to Facilitate Wheat Breeding” (Award number 134574-001, renew), \$480,515 (1, 2, 3, 5, 6).

5/16/2017-5/15/2020 (Co-PI, PI: Dr. Ananth-Kalyanaraman)

#### **NSF**

“A Scalable Framework for Visual Exploration and Hypotheses Extraction of Phenomics Data using Topological Analytics” (Award number DBI 1661348), \$783,163 (\$109,400 to Dr. Zhang). (2, 3, 4, 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” (Award number DESC0016366), \$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 2015-05798), \$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” (Award number 2016049:MNL), \$480,000. (2, 3, 4, 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).

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).

***Intramural Funding***

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).

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).

7/1/2006-6/30/2007 (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).

**TEACHING EXPERIENCE**

- 2015-present **Instructor** for *Statistical Genomics* at Washington State University. The course was initiated as one credit in the Department of Crop and Soil Sciences (CROP\_SCI 512) in 2015. The following year, the course was promoted to an annual, three-credit course and listed as CROP\_SCI 545. Currently, the course is cross-listed by multiple departments from multiple colleges, including the Department of Animal Sciences (ANIM SCI 545), the Department of Horticulture (HORT 545), and the Department of Plant Pathology (PL P 545) from the College of Agriculture, Human, and Natural Resource Sciences, and the School of Biology (BIOLOGY 545) from the College of Art and Sciences. The course syllabus, teaching documents and student evaluations are available on the course website: <http://zzlab.net/teaching>.  
2018: [Flyer](#), [syllabus](#), [student evaluation](#), [slides](#), [R code](#), and [homework](#)  
2017: [Syllabus](#), [student evaluation](#), [slides](#), [R code](#), and [homework](#)  
2016: [Flyer](#), [syllabus](#), [student evaluation](#), [slides](#), [R code](#), and [homework](#)  
2015: [Flyer](#), [syllabus](#), and [student evaluation](#)
- 2008-2009 **Course Project Supervisor** for *Applied Statistical Analysis* (STSCI 501–502) at Cornell University. Principal Component 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 **Teaching Assistant** for *Statistics for Biology* at Michigan State University
- 1982-1985 **Instructor** for *Genetics* and *Biological Statistics* at Jilin Agricultural College. Each course was taught for three semesters.

**PUBLICATIONS**

(*h-index* = 31, *i10-index* = 55; 9,510 citations (Google Scholar). \* = corresponding authorship.)

**Peer-reviewed articles**

2018

74. Meng Huang, Xiaolei Liu, Yao Zhou, Ryan M. Summers and **Zhiwu Zhang\***. **BLINK: A Package for Next Level of Genome Wide Association Studies with Both Individuals and Markers in the Millions**. *GigaScience*, 2018 (accepted with major revision)  
<https://doi.org/10.1101/227249> (1, 2, 3, 5, 6).
73. Chunpeng Chen and **Zhiwu Zhang\***. **iPat: Intelligent Prediction and Association Tool for Genomic Research**. *Bioinformatics*, 2018, bty015,  
<https://doi.org/10.1093/bioinformatics/bty015> (1, 2, 3, 5, 6).

72. Haixiao Dong, Rui Wang, Yaping Yuan, James Anderson, Michael O Pumphrey, **Zhiwu Zhang\*** and Jianli Chen\*. **Evaluation of the Potential for Genomic Selection to Improve Spring Wheat Resistance to Fusarium Head Blight in the Pacific Northwest.** *Frontiers in Plant Science*, 2018, <https://www.frontiersin.org/articles/10.3389/fpls.2018.00911/abstract> (1, 2, 3, 5, 6).
71. Jiabo Wang, Zhengkui Zhou, Zhe Zhang, Hui Li, Di Liu, Qin Zhang, Peter J. Bradbury, Edward S. Buckler & **Zhiwu Zhang\***. **Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits.** *Heredity*, 2018, <https://doi.org/10.1038/s41437-018-0075-0> (1, 2, 3, 5, 6).
70. Jinita Sthapit Kandel, Meng Huang, Zhiwu Zhang, Daniel Z. Skinner, and Deven R. See\*. **Genetic diversity of clinal freezing tolerance variation in winter wheat landraces.** *Agronomy*, 2018, <https://doi.org/10.3390/agronomy8060095> (2, 4, 6).
69. Kendra Lyn Jernigan, Jayfred Gaham Godoy, Meng Huang, Yao Zhou, Craig Morris, Kimberly Garland-Campbell, **Zhiwu Zhang**, Arron H Carter Carter\*. **Association mapping for end-use quality traits in Pacific Northwest adapted soft white winter wheat.** *Frontiers in Plant Science*, 2018, <https://doi.org/10.3389/fpls.2018.00271> (2, 4, 6).
68. Yong-xiang Li, Lin Chen, Chunhui Li, Peter J. Bradbury, Yun-su Shi, Yanchun Song, Dengfeng Zhang, **Zhiwu Zhang**, Edward S. Buckler, Yu Li and Tianyu Wang. **Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize.** *Scientific Report*, 2018, <https://doi.org/10.1038/s41598-018-25304-z> (5, 6).
67. Shantel A. Martinez<sup>1</sup>, Jayfred Godoy, Meng Huang, **Zhiwu Zhang**, Arron H. Carter, Kimberly A. Garland Campbell and Camille M. Steber. **Genome-wide Association Mapping for Tolerance to Preharvest Sprouting and Low Falling Numbers in Wheat.** *Frontiers in Plant Science*, 2018, <https://doi.org/10.3389/fpls.2018.00141> (2, 4, 6).
66. Ying Wu, Yue Sun, Shuai Sun, Guo Li, Jie Wang, Bin Wang, Xiuyun Lin, Meng Huang, Zhiyun Gong, Karen A Sanguinet, **Zhiwu Zhang**, Band ao Liu. **Aneuploidization under segmental allotetraploidy in rice and its phenotypic manifestation.** *Theoretical and Applied Genetics*, 2018, <https://doi.org/10.1007/s00122-018-3077-7> (2, 4, 6).

## 2017

65. Simerjeet Kaur, Xu Zhang, Amita Mohan, Haixiao Dong, Prashant Vikram, Sukhwinder Singh, **Zhiwu Zhang**, Kulvinder S Gill, Kanwarpal S Dhugga, Jaswinder Singh. **Genome-Wide Association Study Reveals Novel Genes Associated with Culm Cellulose Content in Bread Wheat (*Triticum aestivum*, L.).** *Frontiers in Plant Science*, 2017, 8:1913, <https://doi.org/10.3389/fpls.2017.01913> (2, 4, 6).

64. Chao Fang, Yanming Ma, Shiwen Wu, Zheng Wang, Rui Yang, Guanghui Hu, Zhengkui Zhou, Hong Yu, Min Zhang, Yi Pan, Guoan Zhou, Haixiang Ren, Weiguang Du, Hongrui Yan, Yanping Wang, Dezhi Han, Yanting Shen, Shulin Liu, Tengfei Liu, Jixiang Zhang, Hao Qin, Jia Yuan, Xiaohui Yuan, Fanjiang Kong, Baohui Liu, Jiayang Li, **Zhiwu Zhang\***, Guodong Wang\*, Baoge Zhu\* & Zhixi Tian\*. **Genome-wide association study dissects the genetic network underlying agronomical traits in soybean.** *Genome Biology*, 2017, 18:161, <https://doi.org/10.1186/s13059-017-1289-9> (2, 4, 6).
63. Guanghui Hu, Zhao Li1, Yuncai Lu, Chunxia Li, Shichen Gong, Shuqin Yan, Guoliang Li, Mingquan Wang, Honglei Ren, Haitao Guan, Zhengwei Zhang, Jinpeng Zou, Dongling Qin, Mengzhu Chai , Juping Yu , Yu Li, Deguang Yang, Tianyu Wang, **Zhiwu Zhang\***. **Genome-wide association study Identifies multiple Genetic Loci on Chilling Resistance during Germination in Maize.** *Scientific Report*, 2017, <https://doi.org/10.1038/s41598-017-08049-z> (1, 2, 6).
62. Yongping Fu, Yueting Dai, Chentao Yang, Peng Wei, Bing Song, Yang Yang, Lei Sun, **Zhiwu Zhang\*** & Yu Li\*. **Comparative Transcriptome Analysis Identified Candidate Genes Related to Bailinggu Mushroom Formation and Genetic Markers for Genetic Analyses and Breeding.** *Scientific Report*, 2017, <https://doi.org/10.1038/s41598-017-08049-z> (1, 2, 6).
61. Kebede T. Muleta, Peter Bulli, **Zhiwu Zhang**, Xianming Chen, and Michael Pumphrey\*. **Unlocking Diversity in Germplasm Collections via Genomic Selection: A Case Study Based on Quantitative Adult Plant Resistance to Stripe Rust in Spring Wheat.** *Plant Genome*, 2017, <https://doi.org/10.3835/plantgenome2016.12.0124> (4, 6).
60. Xu Zhang, Qin Chu, Gang Guo, Ganghui Dong, Xizhi Li, Qin Zhang, Shengli Zhang, **Zhiwu Zhang\***, Yachun Wang\*. **Genome-wide association studies identified multiple genetic loci for body size at four growth stages in Chinese Holstein cattle.** *PLoS One*, 2017, 12(4): e0175971, <https://doi.org/10.1371/journal.pone.0175971> (1, 2, 6).
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, <https://doi.org/10.1186/s12711-017-0299-0> (1, 2, 6).

## 2016

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, <https://doi.org/10.1186/s12864-016-3170-8> (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*. 2016, <https://doi.org/10.1105/tpc.15.00919> (2, 4, 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, <https://doi.org/10.3390/ijms17101568> (1, 2, 3, 4, 5, 6).
55. Chunhui Li, Yongxiang Li, Y Shi, Y Song, D Zhang, ES Buckler\*, **Zhiwu Zhang\***, Yu Li\*, Tianyu 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, <https://doi.org/10.1007/s00122-016-2739-6> (1, 2, 3, 4, 5, 6).
54. Yao Zhou, MI Vales, Aoxue Wang, **Zhiwu Zhang\***. **Systematic bias of correlation coefficient may explain negative accuracy of genomic prediction**. *Briefings in Bioinformatics* 2016, <https://doi.org/10.1093/bib/bbx133> (1, 2, 3, 4, 5, 6).
53. Yong-Ping Fu, Yuan Liang, Yue-Ting Dai, Chen-Tao Yang, Ming-Zheng Duan, Zhuo Zhang, Song-Nian Hu\*, **Zhiwu Zhang\***, Yu Li\*. **De Novo Sequencing and Transcriptome Analysis of *Pleurotus eryngii* subsp. *tuoliensis* (Bailinggu) Mycelia in Response to Cold Stimulation**. *Molecules* 2016, 21(5), 560; <https://doi.org/10.3390/molecules21050560> (1, 2, 3, 5, 6).
52. Yong-xiang Li; 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, <https://doi.org/10.1111/tpj.13174> (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, <https://doi.org/10.3835/plantgenome2015.11.0120> (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, <https://doi.org/10.1371/journal.pgen.1005767> (1, 2, 3, 5, 6).
49. Li Zhao, Guanghui Hu, Xiangfeng Liu, Yao Zhou, Yu Li, Xu Zhang, Xiaohui Yuan, Qian Zhang, Deguang Yang\*, Tianyu Wang\*, **Zhiwu Zhang\***. **Transcriptome Sequencing Identified**



**Genes and Gene Ontologies Associated with Early Freezing Tolerance in Maize.** *Frontiers in Plant Science* 2016, 7, 1477, <https://doi.org/10.3389/fpls.2016.01477> (1, 2, 3, 5, 6).

48. Wu, Xun, Yongxiang Li, Yunsu Shi, Yanchun Song, Dengfeng Zhang, Chunhui Li, Edward S. Buckler, Yu Li\*, **Zhiwu Zhang\*** and Tianyu Wang\*: **Joint-linkage mapping and GWAS reveal extensive genetic loci that regulate male inflorescence size in maize.** *Plant Biotechnology Journal* 2016, 1–12, <https://doi.org/10.1111/pbi.12519> (1, 2, 3, 5, 6).
47. Krotscheck, Ursula, Samantha A. Nelson, Rory J. Todhunter, Marisa Stone, and **Zhiwu Zhang.** **Long Term Functional Outcome of Tibial Tuberosity Advancement vs. Tibial Plateau Leveling Osteotomy and Extracapsular Repair in a Heterogeneous Population of Dogs.** *Veterinary Surgery* 2016, **45(2)**: 261-8, <https://doi.org/10.1111/vsu.12445> (4, 5, 6).
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* 2016, 209(2): 871-84 <https://doi.org/10.1111/nph.13626> (1, 2, 3, 5, 6).

#### 2015

45. Li C, Li Y, Bradbury PJ, Wu X, Shi Y, Song Y, Zhang D, Rodgers-Melnick E, Buckler ES, **Zhiwu Zhang\***, Li Y\*, Wang T\*. **Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize.** *BMC Biology*, 2015, **13**:78, <https://doi.org/10.1186/s12915-015-0187-4> (1, 2, 3, 5, 6).
44. Jiang Z, Zhou X, Li R, Michal JJ, Zhang S, Dodson M V., **Zhiwu Zhang**, Harland RM. **Whole transcriptome analysis with sequencing: methods, challenges and potential solutions.** *Cell and Molecular Life Sciences*, 2015, **72**:3425–3439 <https://doi.org/10.1007/s00018-015-1934-y> (5, 6).
43. Yingpeng Han, Xue Zhao, Guanglu Cao, Yan Wang, Yinghui Li, Dongyuan Liu, Weili Teng, **Zhiwu Zhang**, Dongmei Li, Lijuan Qiu, Hongkun Zheng, Wenbin Li. **Genetic characteristics of soybean resistance to HG type 0 and HG type 1.2. 3.5. 7 of the cyst nematode analyzed by genome-wide association mapping.** *BMC genomics*, 2015, **16(1)** 1: <https://doi.org/10.1371/journal.pone.0121624> (1, 2, 3, 5, 6).
42. Li C, Y Li, Y Shi, Y Song, D Zhang, ES Buckler, **Zhiwu Zhang**, T Wang, Y Li. **Genetic Control of the Leaf Angle and Leaf Orientation Value as Revealed by Ultra-High Density Maps in Three Connected Maize Populations.** *PLoS One* 2015, **10(3)**: <https://doi.org/10.1371/journal.pone.0121624> (1, 2, 3, 5, 6).

#### 2014

41. Li M, Liu X, Bradbury P, Yu J, Zhang Y-M, Todhunter RJ, Buckler ES, **Zhiwu Zhang\***. **Enrichment of statistical power for genome-wide association studies.** *BMC Biol* 2014, **12**:73, <https://doi.org/10.1186/s12915-014-0073-5> (1, 2, 3, 5, 6).
40. Zhu Dandan, Liu Xiaolei, Max Rothschild, Shuhong Zhao, **Zhiwu Zhang**, Fan Bin. **Genome-wide association study of the backfat thickness trait in two pig populations.** *Frontiers of Agricultural Science and Engineering*, 2014, **1** (2) 91-95:e107684, <https://doi.org/10.15302/J-FASE-2014005> (4, 5, 6).
39. Wang Q, Tian F, Pan Y, Buckler ES, **Zhiwu Zhang\***. **A SUPER Powerful Method for Genome Wide Association Study.** *PLoS One* 2014, **9**:e107684, <https://doi.org/10.1371/journal.pone.0107684> (1, 2, 3, 4, 5, 6).
38. Yang Y, Wang Q, Chen Q, Liao R, Zhang X, Yang H, Zheng Y, **Zhiwu Zhang\***, Yuchun Pan\*. **A new genotype imputation method with tolerance to high missing rate and rare variants.** *PLoS One* 2014, **9**, <https://doi.org/10.1371/journal.pone.0101025> (1, 2, 3, 4, 5, 6).
37. Boyko A, Brooks S, Behan-Braman A, Castelhana M, Corey E, Oliveira K, Swinburne J, Todhunter R, **Zhiwu Zhang**, Ainsworth D, Robinson N. **Genomic analysis establishes correlation between growth and laryngeal neuropathy in Thoroughbreds.** *BMC Genomics* 2014, **15**:259, <https://doi.org/10.1186/1471-2164-15-259> (1, 2, 5, 6).
36. Peiffer JA, Romay MC, Gore MA, Flint-Garcia SA, **Zhiwu Zhang**, Millard MJ, Gardner CAC, McMullen MD, Holland JB, Bradbury PJ, Buckler ES. **The genetic architecture of maize height.** *Genetics* 2014, **196**:1337–1356, <https://doi.org/10.1534/genetics.113.159152> (3, 4, 5, 6).
35. Caniato FF, Hamblin MT, Guimaraes CT, **Zhiwu Zhang**, Schaffert RE, Kochian L V., Magalhaes J V. **Association mapping provides insights into the origin and the fine structure of the sorghum aluminum tolerance locus, AltSB.** *PLoS One* 2014, **9**, <https://doi.org/10.1371/journal.pone.0087438> (4, 5, 6).

### 2013

34. Hou Y, Wang Y, Lu X, Zhang X, Zhao Q, Todhunter RJ, **Zhiwu Zhang\***. **Monitoring Hip and Elbow Dysplasia Achieved Modest Genetic Improvement of 74 Dog Breeds over 40 Years in USA.** *PLoS One* 2013, **8**:e76390, <https://doi.org/10.1371/journal.pone.0076390> (1, 2, 3, 4, 5, 6).
33. Chen Q, Ma Y, Yang Y, Chen Z, Liao R, Xie X, Wang Z, He P, Tu Y, Zhang X, Yang C, Yang H, Yu F, Zheng Y, **Zhiwu Zhang**, Wang Q, Pan Y. **Genotyping by Genome Reducing and Sequencing for Outbred Animals.** *PLoS One* 2013, **8**, <https://doi.org/10.1371/journal.pone.0067500> (5, 6).

32. Duan F, Ogden D, Xu L, Liu K, Lust G, Sandler J, Dykes NL, Zhu L, Harris S, Jones P, Todhunter RJ, **Zhiwu Zhang**. **Principal component analysis of canine hip dysplasia phenotypes and their statistical power for genome-wide association mapping.** *J Appl Stat* 2013, **40**:235–251, <https://doi.org/10.1080/02664763.2012.740617> (1, 2, 3, 4, 5, 6).
31. Nelson SA, Krotscheck U, Rawlinson J, Todhunter RJ, **Zhiwu Zhang**, Mohammed H. **Long-Term Functional Outcome of Tibial Plateau Leveling Osteotomy Versus Extracapsular Repair in a Heterogeneous Population of Dogs.** *Vet Surg* 2013, **42**:38–50, <https://doi.org/10.1111/j.1532-950X.2012.01052.x> (4, 5, 6).
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9. Zhu L, **Zhang Z**, Feng F, Schweitzer P, Phavaphutanon J, Vernier-Singer M, Corey E, Friedenbergs S, Mateescu R, Williams A, Lust G, Acland G, Todhunter R. **Single nucleotide**

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3. Mateescu RG, **Zhang Z**, Tsai K, Phavaphutanon J, Burton-Wurster NI, Lust G, Quaas R, Murphy K, Acland GM, Todhunter RJ. **Analysis of allele fidelity, polymorphic information content, and density of microsatellites in a genome-wide screening for hip dysplasia in a crossbreed pedigree**. *J Hered* 2005, **96**:847–853, <https://doi.org/10.1093/jhered/esi109> (4, 5, 6).
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**Journal Impact Factor(JIF) (2016) and number of Zhang papers published**

<b>Journal</b>	<b># Papers</b>	<b>JIF (2016)</b>
SCIENCE	1	37.205
NATURE GENETICS	3	27.959
GENOME BIOLOGY	1	11.908
PLANT CELL	2	8.688
PLANT BIOTECHNOLOGY JOURNAL	1	7.443
NEW PHYTOLOGIST	1	7.33
BIOINFORMATICS	3	7.307
GIGASCIENCE	1	6.871
BMC BIOLOGY	2	6.779
PLANT PHYSIOLOGY	1	6.456
PLOS GENETICS	1	6.1
PLANT JOURNAL	1	5.901
JOURNAL OF EXPERIMENTAL BOTANY	1	5.83
CELLULAR AND MOLECULAR LIFE SCIENCES	1	5.788
BRIEFINGS IN BIOINFORMATICS	2	5.134
OSTEOARTHRITIS AND CARTILAGE	1	4.742
GENETICS	1	4.556
FRONTIERS IN PLANT SCIENCE	5	4.298
SCIENTIFIC REPORTS	3	4.259
THEORETICAL AND APPLIED GENETICS	3	4.132
HEREDITY	1	3.961
BMC GENOMICS	3	3.729
INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES	1	3.326
GENETICS SELECTION EVOLUTION	1	2.964
MOLECULES	1	2.861
PLOS ONE	9	2.806
GENOMICS	1	2.801
PLANT GENOME	3	2.736
MAMMALIAN GENOME	1	2.509
JOURNAL OF HEREDITY	1	2.432
AGRONOMY	1	2.380
JOURNAL OF ANIMAL SCIENCE	2	1.863
ANIMAL GENETICS	2	1.815
VETERINARY JOURNAL	5	1.802
VETERINARY SURGERY	3	1.215
JOURNAL OF APPLIED STATISTICS	2	0.664
J ANIM VET ADV	1	0.39



FRONTIERS OF AGRICULTURAL SCIENCE AND ENGINEERING	1	NA
<b>Total</b>	<b>74</b>	

### **Book Chapter**

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, <https://cshmonographs.org/index.php/monographs/article/viewArticle/4583>.

### **Referenced-non-peer-reviewed articles**

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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 Dovc, 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, [Download here](#).

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17. Meng A, Qi S, Yu R, Wang R, Cai Z, Jiao Sh, Xin C, **Zhang Z**. **Analysis of DNA fingerprints of Fengjing Pig and Xiang Pig**. *Hereiditas* 1995, **17**:19–22.
16. **Zhang Z**, Tao L, Zhou M, Xu X, Zhang Y. **A management system to improve accuracy of milk yield**. *J Chinese Dairy Sci* 1994:14–16.
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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13. **Zhang Z**, Sheng Z. **A mathematical model of systemic conservation of livestock genetic resources and applications**. *Acta Vet Zootech Sin* 1994, **25**:306–310.



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.**
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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.**

## SOFTWARE RELEASED

I have developed seven computer software packages for public use and two for private use. Most of the public software packages are hosted on the Zhiwu Zhang Lab website (<http://zzlab.net>). The website has received over 6,000 users, with ~30 unique users daily. These packages include the widely-used TASSEL and GAPIT, which have received over 15 and 200 citations, respectively.

- iPat: Intelligent Prediction and Association Tool. More information is provided on the iPat website: <http://zzlab.net/iPat>. (1, 2, 3, 4, 5, 6).

- **BLINK: Bayesian-information and Linkage-disequilibrium Iteratively Nested Keyway.** More information is provided on the BLINK website: <http://zzlab.net/blink>.
- **FarmCPU: Software for Genome-Wide Association Studies.** See [publication by Liu et al. in PLoS Genetics](#). More information is provided on the FarmCPU website: <http://zzlab.net/FarmCPU>. (1, 2, 3, 4, 5, 6).
- **GAPIT: Genome Association and Prediction Integrated Tool.** See publications by [Lipka et al. in Bioinformatics](#) and [Tang et al. in Plant Genome](#). More information is provided on the 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. in Bioinformatics](#). More information is provided on the 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. in 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 on the TASSEL website: <http://statgen.neau.edu.cn/SeqPed>. (1, 2, 3, 4, 5, 6).

## INVITED PRESENTATIONS

- 2018      **International Plant & Animal Genome Conference XXVI, *Gene Mapping by Segregation: From Mendel to BSA and Beyond***, San Diego, January 15, 2018.
- International Conference of Genetics Applied to Livestock Production, *GWAS and GS Are as Easy as Clicking and Dragging with iPat***, Auckland, New Zealand, February 10-14, 2018.
- 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, June18-21, 2017.
- International Plant & Animal Genome Conference XXV, *BLUP Alphabet for Genomic Prediction***, San Diego, CA, January 14-18, 2017.
- 2016      **Iowa State University, *Saving the Babies from the 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 the 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 the Bathwater in Genome-Wide Association Studies*, February 11, 2015.
- International Plant & Animal Genome Conference 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 **International Plant & Animal Genome Conference XXI (Statistical Genomics Workshop)**, *Kinship Evolution for Genome Prediction and Association Studies*. San Diego, CA, January 13, 2013.  
<https://pag.confex.com/pag/xxi/webprogram/Session1586.html>
- 2012 **International Plant & Animal Genome Conference 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 Studies*, Beijing, China, July 2, 2011.
- 2010 **Cornell University Center for Vertebrate Genomics**, *Canine Dysplasia is Predictable by Genotyping*, Ithaca, NY, November 9, 2010.

**6<sup>th</sup> SJTU\_CU Workshop on Modern Agriculture and Biotechnology, Adaptation of Mixed Model for Genome-Wide Association Studies**, Shanghai, China, October 9-11, 2010.

**Center for Agricultural biotechnology, Kasetsart University, Adaptation of Mixed Model for Genome-Wide Association Studies**, 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 Studies**, 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 Studies**, 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**

- **Genome-Wide Association Studies**, Chansha Agricultural University, Changsha, China, July 27-30, 2017. Website: <http://zzlab.net/GWAS2017CHANGSHA>.
- **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 Studies**, Department of Agronomy, Iowa State University, Ames, IA, 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. Website: <http://zzlab.net/WSUGWAS>.
- **Methods and Tools for Genome-Wide Association Studies**, College of Veterinary Medicine, Cornell University, Ithaca, NY, June 14, 2013.
- **Genomic Mapping Workshop**, USDA ARS, Lubbock, TX, Oct 25-26, 2006.

#### **ADVISOR, SUPERVISOR, AND MENTOR ROLES**

**Major advisor (current students: 6, graduated students: 4)**

**Atit Parajuli** 2019-present, Ph.D. Student. Research Project: Development of 200 inbred alfalfa lines.

**Zhou Tang:** 2019-present, Ph.D. Student. Research Project: Wheat variety recognition on satellite imagery.

**Samuel Revolinski:** 2017-present, Ph.D. Student. Research Project: Transforming satellite imagery into reference of genomic selection of plant breeding.

**Yuanhong Song:** 2017-present, M.S. Student. Research Project: Explain variables of NDVI on satellite imagery.

**Matthew McGowan:** 2016-present, Ph.D. Student. Research Project: Genotype calling for SNP and structural variation.

**Chun-Peng Chen:** 2016-present, Ph.D. Student. Research Project: Intelligent Prediction and Association Tool.

**Meijing Liang:** 2015-present, Ph.D. Student. Research Project: Genomic prediction.

**Jiabo Wuang:** 2014-2018, Ph.D. Dissertation: Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. Current: Associate Professor at Heilongjiang Academy of Agricultural Sciences.

**Yao Zhou:** 2014-2017, Ph.D. Dissertation: Systematic bias of correlation coefficient may explain negative accuracy of genomic prediction. Current: Postdoc at Chinese Academy of Agricultural Sciences.

**You Tang:** 2014-2017, Ph.D. Dissertation: GAPIT Version 2: An enhanced integrated tool for genomic association and prediction. Current: Professor at Jilin Agricultural College

**Guanghui Hu:** 2013-2017, Ph.D. Dissertation: Genome-wide association study identified multiple genetic loci on chilling resistance during germination in maize. Current: Professor at Heilongjiang Academy of Agricultural Sciences.

***Staff, postdoctoral researchers, and undergraduate students***

**Isabel Vales:** 2014-2015, Research Scientist. Research Area: Genomic prediction. Dr. Vales is now an Associate Professor at Texas A&M University.

**Meng Huang:** 2014-2017, Postdoctoral Researcher. Research Project: Genome-wide association study on complex traits. Current: Postdoc at Purdue University.

**Ryan Summers:** 2014-2018, Undergraduate Student. Research Project: Non-CPU computation.

***Visiting scientists and students***

**Shipeng Li:** 2018-present, Visiting Professor. Research Project: Meta analyses on gene expression in maize.

**Zhenhai Cui:** 2018-present, Visiting Professor. Research Project: Gene mapping for husk in maize.

**Liyuan Liu:** 2018-present, Visiting Student. Research Project: Genome-wide association study.

**Jinghang Zhou:** 2018-present, Visiting Student. Research Project: Genome-wide association study.

**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.

**Qishan Wang:** 2011, Visiting Scientist. Research Project: An improved mixed linear model for genome-wide association studies. The manuscript is in the process of preparation. Dr. Wang 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”, PLoS One 2010, 5(10): e13219. doi:10.1371/journal.pone.0013219. Current: Assistant Professor of Genetics at Beijing Agricultural College.

***Graduate committee member***

Evan Craine (Horticulture, Dr. Scot Hulbert) 2018-  
 Wilson Craine (Horticulture, Dr. Scot Hulbert) 2017-  
 Feixiong Luo (Horticulture, Dr. Cameron Peace) 2016-  
 Ragupathi Nagarajan (CSS, Dr. Kulvinder Gill) 2014-2017  
 Stephanie Sjoberg (CSS, Dr. Arron Carter) 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) 2015-2017

**PROFESSIONAL SERVICE**

***Academic Editor***

PLoS One

***Ad Hoc Reviewer*** (Number of manuscripts reviewed)

Nature Genetics (7)	Genetics (1)
Nature Methods (1)	Heredity (1)
Nature Communications (1)	Theoretical and Applied Genetics (1)
Nature Plants (1)	Plant Genome (1)
PNAS (1)	Animal Genetics (1)

Annals of Human Genetics (1)  
Annals of Applied Statistics (1)  
Genome Research (1)  
PLoS Genetics (3)  
PLoS One (5)  
GigaScience (1)

Bioinformatics (3)  
Journal of Animal Science (1)  
Journal of Human Genetics (1)  
PLoS Computation Biology (1)  
G3 (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.  
Bioinformatics Certificate Oversight Committee, 2018-present, Washington State University, Pullman, WA (<https://sbs.wsu.edu/graduate-certificate-in-bioinformatics>)  
Department Website Committee Member, 2016-present, Washington State University, Pullman, WA.  
Board Member for Community of Emerald Pointe, 2017-present, Management of Real Estate Property, Pullman, WA.  
Employee Assembly for Minorities, 2002-2003, Cornell University.  
Employee Assembly for Communications, 2001-2002, Cornell University.

### ***Volunteer and Leadership Activities***

Wrote an article for Wheat Life (published February 2017) to help recruit farmers to attend the Pacific Northwest Portland Tour.  
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.

## **PROFESSIONAL MEMBERSHIP**

American Association for the Advancement of Science (AAAS)

## **AWARDS AND RECONGNITIONS**

**Workshop Organizer** for the International Plant & Animal Genome Conference, 2018.  
**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 Models**: Linear models are among the most frequently used, well and poorly, of statistical models. Simple and multiple regression analysis and the analysis of variance are statistical methodologies based on linear models. These methods provide a means of studying the relationship between one dependent variable and explanatory variables when the dependent variable is also affected by some random error.
- 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 **Computers 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.