

Zhiwu Zhang

Associate Professor

Department of Crop and Soil Sciences

Washington State University

403C Plant Science Building, Pullman, WA 99164, USA

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

Curriculum Vitae

SUMMARY: *I am an Associate Professor in the Department of Crop and Soil Sciences at Washington State University (WSU). I have a multidisciplinary background with two Ph.D. degrees, one in Statistical Genetics and one in Animal Breeding. Since 2005, I have published over 100 peer-reviewed articles and received over 21,000 citations with an h-index of 4 (Google Scholar). My research focus is the development of innovative analytical methods and computing tools using statistics, statistical learning, machine learning, and artificial intelligence (AI) to advance genomic and phenomic research toward the sustainability of food production and healthcare management. The developed software packages directly interact with public stakeholders, including TASSEL, GAPIT, FarmCPU, BLINK, iPAT, and MMAP for genomics, GRID, GridFree, and ROOSTER for phenomic computer vision, and AI4Everyone for general audience to develop AI systems without requiring programming skills. Since joining WSU in 2014, I have received 14 grants from a variety of sources, including WSU, Murdock Foundation, USDA, NSF, and DOE, which total \$3M in direct funding for my lab plus \$5M in funding for collaborative research. In 2015, I developed a graduate-level course in Statistical Genomics, which I have taught for six cycles. I am recognized as an academic editor (PLoS One), journal reviewer (Nature Genetics, Nature Methods, and PLoS Genetics), and grant panelist (USDA, NSF, Canadian Alberta Innovates, BBSRC, and Swiss National Science Foundation). I was invited to write a review on software engineering for Briefings in Bioinformatics and two articles for Plant Breeding Reviews. I have been invited to give presentations and workshops in multiple countries, including the US, Canada, Sweden, the UK, France, Thailand, and China. Since 2018, I have been the workshop organizer for the annual international Conference of Plant and Animal Genome. In 2021, I received CAHNRS' Early Career Excellence Award at WSU.*

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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 (2005-2010), 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

USDA

8/1/2020-7/31/2023 (PI)

“FACT: Predicting Wheat Hagberg Falling Number from Near Infrared Spectrometers” (Award number 2020-67021-32460), \$500,000 (1, 2, 3, 5, 6).

USDA

2/15/2019-2/14/2023 (PI)

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

USDA

9/1/2018-8/31/2022 (PI)

“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).

Washington Grain Commission

5/1/2021-6/30/2024 (PI)

“Intelligent Prediction and Association Tool to Facilitate Wheat Breeding” (Award number 134574-001), \$293,463 (1, 2, 3, 5, 6).

NSF

8/1/2020-7/31/2022 (Co-PI, PI: Dr. Thomas W Okita)

“EAGER: The RNA Landscape as defined by RNA binding proteins” (Award number ISO 2029933), \$300,000 (2, 3, 4, 5, 6).

Washington Wheat Foundation

1/1/2018-12/31/2021 (PI)

“Equipment for wheat research”, Total direct cost: \$28,738 (\$3,000, 2018; \$6,738, 2019; \$7,000, 2020; \$7,000, 2021, and \$5000, 2022), (1, 2, 3, 5, 6).

NSF

5/16/2017-5/15/2021 (Co-PI, PI: Dr. Ananth-Kalyanaraman)

“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).

DOE

8/1/2016-7/31/2021 (Co-PI, PI: Dr. Jack Brown)

“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).

USDA

2/15/2016-2/14/2021 (Co-PI, PI: Dr. Arron Carter)

“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).

USDA

10/15/2015-10/14/2020 (Co-PI, PI: Dr. Camille Steber)

“Molecular Genetic Architectures for Increasing Pre-harvest Sprouting Tolerance in White Wheat” (Award number 2015-05798), \$422,000. (2, 4, 5, 6).

M.J. Murdock Charitable Trust

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

“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).

Washington Grain Commission

5/1/2018-6/30/2021 (PI)

“Intelligent Prediction and Association Tool to Facilitate Wheat Breeding” (Award number 126593), \$259,848 (1, 2, 3, 5, 6).

Washington Grain Commission

5/1/2015-6/30/2018 (PI)

“Intelligent Prediction and Association Tool to Facilitate Wheat Breeding” (Award number 126593), \$220,667 (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).

National Institutes of Health (1R21AR055228-01A1)

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

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

National Natural Science Foundation, China (39200088)

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

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

Intramural Funding

University of Georgia Research Foundation

10/1/2021-9/30/2022 (Co-PI, PI: Zenglu Li)

“An intelligent and high-throughput imaging system for soybean cyst nematode phenotyping” (Project No. 2220-172-0150, Subaward No. SUB00002652), \$15,000 (direct cost). (2, 3, 4, 5, 6).

Emerging Research Issues at Washington State University

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

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

CAHNRS Undergraduate Internships at Washington State University

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

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

Office of Research at Washington State University

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

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

Cornell Advanced Technology - Biotechnology

7/1/2006-6/30/2007 (Co-PI, PI: Dr. Rory Todhunter)

“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>.

2023: [Flyer](#), [syllabus](#), [student evaluation](#), [slides](#), [R code](#), and [homework](#)

2021: [Flyer](#), [syllabus](#), [student evaluation](#), [slides](#), [R code](#), and [homework](#)

2020: [Flyer](#), [syllabus](#), [student evaluation](#), [slides](#), [R code](#), and [homework](#)

2018: [Flyer](#), [syllabus](#), [student evaluation](#), [slides](#), [R code](#), and [homework](#)

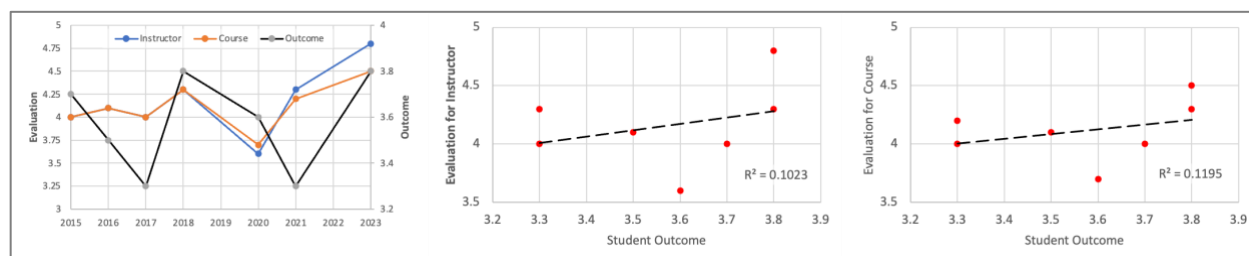
2017: [Syllabus](#), [student evaluation](#), [slides](#), [R code](#), and [homework](#)
 2016: [Flyer](#), [syllabus](#), [student evaluation](#), [slides](#), [R code](#), and [homework](#)
 2015: [Flyer](#), [syllabus](#), and [student evaluation](#)

Summary of Student Evaluation on Statistical Genomics (2015-2023)

Year	Credit	Student		Student learned*		Instructor#		Course#	
		Number	Response	Mean	Median	Mean	Median	Mean	Median
2015	1	11	27%	3.7	4.0	4.0	4.0	4.0	4.0
2016	3	19	79%	3.5	4.0	4.1	4.0	4.1	4.0
2017	3	7	100%	3.3	3.0	4.0	4.0	4.0	4.0
2018	3	13	100%	3.8	4.0	4.3	4.0	4.3	4.0
2020	3	9	100%	3.6	4.0	3.6	4.0	3.7	4.0
2021	3	6	100%	3.3	3.0	4.3	4.0	4.2	4.5
2023	3	9	67%	3.8	4.0	4.8	5.0	4.5	5.0

*4-Great deal, 3- Fair amount, 2-Little, 1-Not much

#5-Outstanding, 4-Above average, 3-Average, 2-Below average, 1-Poor



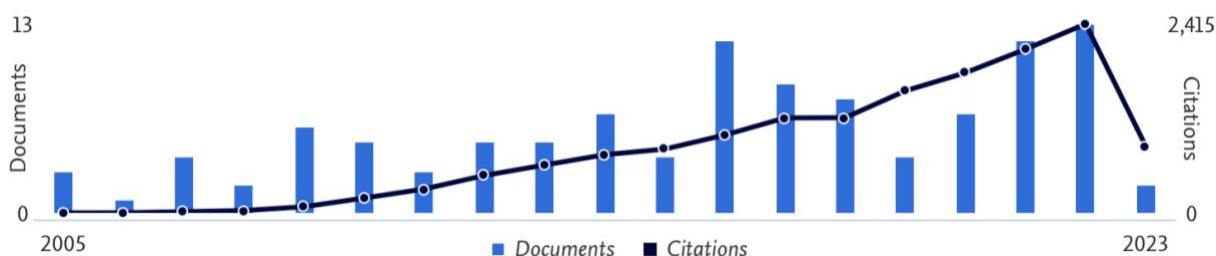
2008-2009 **Course Project Supervisor** for *Applied Statistical Analysis* (STSCI 501–502) at Cornell University. Principal Component Analysis and Mixed Linear Model in SAS were taught. The project generated a publication in the *Journal of Applied Statistics* (2012, 40:235–251).

1995-1997 **Teaching Assistant** for *Statistical Methods for Biologists* at Michigan State University
 STT 464 Statistical Methods for Biologists I (Instructor: Rob Templeman)
 STT 464 Statistical Methods for Biologists II (Instructor: Rob Templeman)

1982-1985 **Instructor** for *Genetics* and *Biological Statistics* at Jilin Agricultural College. Each course was taught for three semesters.

PUBLICATIONS

ORCID: [0000-0002-5784-9684](https://orcid.org/0000-0002-5784-9684), [Web of Science](#) (h-index = 38, citations > 14,000), [Google Scholar](#) (h-index = 49, citations > 21,000), [Scopus](#) (h-index=40, citations >15,000) * = corresponding authorship, and # = equal authorship. First or corresponding authorship rate: 41.7% (last five years) and 42.7% (all-time).



Peer-reviewed articles

2023 (4 article)

112. Zhou Tang, Meinan Wang, Michael Schirrmann, Karl-Heinz Dammer, Xianran Li, Robert Brueggeman, Sindhuja Sankaran, Arron H Carter, Michael O Pumphrey, Yang Hu*, Xianming Chen*, and **Zhiwu Zhang***, **Affordable High Throughput Field Detection of Wheat Stripe Rust Using Deep Learning with Semi-Automated Image Labeling**. Computers and Electronics in Agriculture, 2023, <https://doi.org/10.1016/j.compag.2023.107709>
111. Bosen Zhang, Haiyan Huang, Laura E. Tibbs-Cortes, Adam Vanous, Zhiwu Zhang, Karen Sanguinet, Kimberly A. Garland-Campbell, Jianming Yu, Xianran Li, **Streamline unsupervised machine learning to survey and graph indel-based haplotypes from pan-genomes**. Molecular Plant, 2023, <https://doi.org/10.1016/j.molp.2023.05.005>
110. Chun-Peng James Chen*, Yang Hu, Xianran Li, Craig F. Morris, Stephen Delwiche, Arron H. Carter, Camille Steber, **Zhiwu Zhang**, **An independent validation reveals the potential to predict Hagberg–Perten falling number using spectrometers**. The Plant Phenome Journal, 2023, <https://doi.org/10.1002/ppj2.20070>
109. Zhou Tang, Yang Hu*, and **Zhiwu Zhang***, **ROOSTER: An image labeler and classifier through interactive recurrent annotation**. F1000Researchy, 2023, <https://doi.org/10.12688/f1000research.127953.1>

2022 (12 articles)

108. Yang Hu, Stephanie M Sjoberg, Chunpen James Chen, Amber L Hauvermale, Craig F Morris, Stephen R Delwiche, Ashley E Cannon, Camille M Steber*, **Zhiwu Zhang***, **As the number falls, alternatives to the Hagberg–Perten falling number method: A review**. Comprehensive Reviews in Food Science and Food Safety, 2022, <https://doi.org/10.1111/1541-4337.12959>.
107. Yao Zhou, Zhiyang Zhang, Zhigui Bao, Hongbo Li, Yaqing Lyu, Yanjun Zan, Yaoyao Wu, Lin Cheng, Yuhan Fang, Kun Wu, Jinzhe Zhang, Hongjun Lyu, Tao Lin, Qiang Gao, Surya Saha, Lukas Mueller, Zhangjun Fei, Thomas Städler, Shizhong Xu, **Zhiwu Zhang**, Doug Speed & Sanwen Huang*, **Graph pangenome captures missing heritability and empowers tomato breeding**. Nature, 2022, <http://dx.doi.org/10.1038/s41586-022-04808-9>.

106. Xianran Li, Tingting Guo, Guihua Bai, **Zhiwu Zhang**, Deven See, Juliet Marshall, Kimberly A Garland-Campbell, Jianming Yu, **Genetics-inspired data-driven approaches explain and predict crop performance fluctuations attributed to changing climatic conditions.** *Molecular Plant*, 2022, <https://doi.org/10.1016/j.molp.2022.01.001>.
105. Chun-Peng J Chen, Gota Morota, Kiho Lee, **Zhiwu Zhang**, Hao Cheng, **VTag: a Semi-Supervised Pipeline for Tracking Pig Activity with a Single Top-View Camera.** *Journal of Animal Science*, 2022, <https://doi.org/10.1093/jas/skac147>.
104. Fan Zhang, Junmei Kang, Ruicai Long, Mingna Li, Yan Sun, Fei He, Xueqian Jiang, Changfu Yang, Xijiang Yang, Jie Kong, Yiwen Wang, Zhen Wang, **Zhiwu Zhang***, and Qingchuan Yang, **Application of machine learning to explore the genomic prediction accuracy of fall dormancy in autotetraploid alfalfa.** *Horticulture Research*, 2022, <https://doi.org/10.1093/hr/uhac225>.
103. Wesley Crump, Cameron Peace, Zhiwu Zhang, Per McCord, **Fruit cracking and firmness DNA test development and evaluation in sweet cherry.** *Fruit Research*, 2022, <https://doi.org/10.48130/FruRes-2022-0014>.
102. YP Fu, YT Dai, KWT Chethana, ZH Li, L Sun, CT Li, HL Yu, RH Yang, Q Tan, DP Bao, YJ Deng, SX Wang, YF Wang, FH Tian, LL Qi, LL Shu, PS Jia, LC Chen, MY Chen, QX Hu, H Tan, TT Song, **ZW Zhang**, G Bonito, GI Zervakis, SJ Xiao, KD Hyde, Y Li, XH Yuan, **Large-scale genome investigations reveal insights into domestication of cultivated mushrooms.** *Mycosphere*, 2022, DOI: [10.5943/mycosphere/si/1f/4](https://doi.org/10.5943/mycosphere/si/1f/4).
101. KS Sandhu, LF Merrick, S Sankaran, **Zhiwu Zhang**, Arron Carter, **Prospectus of Genomic Selection and Phenomics in Cereal, Legume and Oilseed Breeding Programs.** *Frontiers in Genetics*, 2022, <https://doi.org/10.3389/fgene.2021.829131>.
100. Chenggen Chu, Shichen Wang, Jackie C Rudd, Amir MH Ibrahim, Qingwu Xue, Ravindra N Devkota, Jason A Baker, Shannon Baker, Bryan Simoneaux, Geraldine Opena, Haixiao Dong, Xiaoxiao Liu, Kirk E Jessup, Ming-Shun Chen, Kele Hui, Richard Metz, Charles D Johnson, **Zhiwu Zhang**, Shuyu Liu, **A new strategy for using historical imbalanced yield data to conduct genome-wide association studies and develop genomic prediction models for wheat breeding.** *Molecular Breeding*, 2022, <https://doi.org/10.1007/s11032-022-01287-8>.
99. LF Merrick, AB Burke, **Zhiwu Zhang**, and Arron Carter, **Comparison of Single-Trait and Multi-Trait Genome-Wide Association Models and Inclusion of Correlated Traits in the Dissection of the Genetic Architecture of a Complex Trait in a Breeding Program.** *Frontiers in Plant Science*, 2022, <https://doi.org/10.3389/fpls.2021.772907>.
98. William Wesley Crump, Cameron Peace, **Zhiwu Zhang**, and Per McCord, **Detection of breeding-relevant fruit cracking and fruit firmness QTLs in sweet cherry via pedigree-based and genome-wide association approaches.** *Frontiers in Plant Science*, 2022, <https://doi.org/10.3389/fpls.2022.823250>.
97. Ruicai Long, Fan Zhang, **Zhiwu Zhang**, Mingna Li, Lin Chen, Xue Wang, Wenwen Liu, Tiejun Zhang, Long-Xi Yu, Fei He, Xueqian Jiang, Xijiang Yang, Changfu Yang, Zhen Wang, Junmei Kang, Qingchuan Yang, **Genome assembly of alfalfa cultivar zhongmu-4 and identification of SNPs associated with agronomic traits.** *Genomics, Proteomics & Bioinformatics*, 2022, <https://doi.org/10.1016/j.gpb.2022.01.002>.

2021 (10 articles)

96. Yang Hu, and **Zhiwu Zhang***, **GridFree: a python package of imageanalysis for interactive grain counting and measuring**. *Plant Physiology*, 2021, <https://doi.org/10.1093/plphys/kiab226>.
95. Zhou Tang, Atit Parajuli, Chunpeng James Chen, Yang Hu, Samuel Revolinski, Cesar Augusto Medina, Sen Lin, **Zhiwu Zhang*** and Long-Xi Yu*. **Validation of UAV-based alfalfa biomass predictability using photogrammetry with fully automatic plot segmentation**. *Scientific Reports*, 2021, [doi: 10.1038/s41598-021-82797-x](https://doi.org/10.1038/s41598-021-82797-x).
94. Jiabo Wang* and **Zhiwu Zhang***, **GAPIT Version 3: Boosting Power and Accuracy for Genomic Association and Prediction**. *Genomics, Proteomics and Bioinformatics*, 2021, <https://doi.org/10.1016/j.gpb.2021.08.005>.
93. Lilin Yin, Haohao Zhang, Zhenshuang Tang, Jingya Xu, Dong Yin, **Zhiwu Zhang**, Xiaohui Yuan, Mengjin Zhu, Shuhong Zhao, Xinyun Li, Xiaolei Liu, **rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated tool for Genome-Wide Association Study**. *Genomics, Phenomics and Bioinformatics*, 2021, <https://doi.org/10.1016/j.gpb.2020.10.007>.
92. Laura Tibbs Cortes, **Zhiwu Zhang**, and Jianming Yu. **Status and prospects of genome-wide association studies in plants**. *The Plant Genome*, 2021, [DOI: 10.1002/tpg2.20077](https://doi.org/10.1002/tpg2.20077).
91. Matthew T. McGowan, **Zhiwu Zhang** & Stephen P. Ficklin, **Chromosomal characteristics of salt stress heritable gene expression in the rice genome**. *BMC Genomic Data*, 2021, <https://doi.org/10.1186/s12863-021-00970-7>.
90. Karansher Singh Sandhu, Dennis Nicuh Lozada, **Zhiwu Zhang**, Michael O Pumphrey, Arron Hyrum Carter. **Deep Learning for Predicting Complex Traits in Spring Wheat Breeding Program**. *Frontiers in Plant Science*, 2021, [doi: 10.3389/fpls.2020.613325](https://doi.org/10.3389/fpls.2020.613325).
89. Haixiao Dong, He Li, Yingjie Xue, Shengzhong Su, Shipeng Li, Xiaohui Shan, Hongkui Liu, Nan Jiang, Xuyang Wu, **Zhiwu Zhang** and Yaping Yuan*. **E183K Mutation in Chalcone Synthase C2 Causes Protein Aggregation and Maize Colorless**. *Frontier of Plant Science*, 2021, <https://doi.org/10.3389/fpls.2021.679654>.
88. Kelly Swarts, Eva Bauer, Jeffrey C Glaubitz, Tiffany Ho, Lynn Johnson, Yongxiang Li, Yu Li, Zachary Miller, Cinta Romay, Chris-Carolin Schön, Tianyu Wang, **Zhiwu Zhang**, Edward S Buckler, Peter Bradbury. **Joint analysis of days to flowering reveals independent temperate adaptations in maize**. *Heredity*, 2021, <https://www.nature.com/articles/s41437-021-00422-z>.
87. Chandler R. Keller, Yang Hu, Kelsey F. Ruud, Anika E. VanDeen, Steve R. Martinez, Barry T. Kahn, Zhiwu Zhang, Roland K. Chen and Weimin Li. **Human Breast Extracellular Matrix Microstructures and Protein Hydrogel 3D Cultures of Mammary Epithelial Cells**. *Cancers*, 2021, <https://www.mdpi.com/2072-6694/13/22/5857>.

2020 (8 articles)

86. Wei Huang, Ping Zheng, Zhenhai Cui, Zhuo Li, Yifeng Gao, Helong Yu, You Tang, Xiaohui Yuan, and **Zhiwu Zhang***. **MMAP: A Cloud Computing Platform for Mining the Maximum Accuracy of Predicting Phenotypes from Genotypes**. *Bioinformatics*, 2020, <https://doi.org/10.1093/bioinformatics/btaa824>.
85. Ying Wu, Fan Lin, Yao Zhou, Jie Wang, Shuai Sun, Bin Wang, Zhibin Zhang, Guo Li, Xiuyun Lin, Xutong Wang, Yue Sun, Qianli Dong, Chunming Xu, Lei Gong, Jonathan F Wendel*,

- Zhiwu Zhang*, Bao Liu*. **Genomic mosaicism due to homoeologous exchange generates extensive phenotypic diversity in nascent allopolyploids.** National Science Review, 2020, <https://doi.org/10.1093/nsr/nwaa277>.
84. James Chen and Zhiwu Zhang. **GRID: A Python Package for Field Plot Phenotyping Using Aerial Images.** Remote Sensing, 2020, <https://www.mdpi.com/2072-4292/12/11/1697>.
83. Liyuan Liu, Jinghang Zhou, Chunpeng James Chen, Juan Zhang, Wan Wen, Jia Tian, Zhiwu Zhang*, Yaling Gu*. **GWAS-Based Identification of New Loci for Milk Yield, Fat, and Protein in Holstein Cattle.** Animals, 2020, <https://doi.org/10.3390/ani10112048>.
82. Zhenhai Cui, H Dong, A Zhang, Y Ruan, S Jiang, Y He, and Zhiwu Zhang*. **Assessment of the Potential for Genomic Selection To Improve Husk Traits in Maize.** G3: Genes, Genomes, Genetics, 2020, <https://doi.org/10.1534/g3.120.401600>.
81. Zhenhai Cui, H Dong, A Zhang, Y Ruan, S Jiang, Y He, and Zhiwu Zhang*. **Denser Markers and Advanced Statistical Method Identified More Genetic Loci Associated with Husk Traits in Maize.** Scientific Reports, 2020, <https://doi.org/10.1038/s41598-020-65164-0>.
80. Lu Liu, Meinan Wang, Zhiwu Zhang, Deven R See, Xianming Chen. **Identification of Stripe Rust Resistance Loci in US Spring Wheat Cultivars and Breeding Lines Using Genome-wide Association Mapping and Yr Gene Markers.** Plant Disease, 2020, <https://doi.org/10.1094/PDIS-11-19-2402-RE>.
79. Feixiong Luo, Kate Evans, John L Norelli, Zhiwu Zhang, Cameron Peace. **Prospects for achieving durable disease resistance with elite fruit quality in apple breeding.** Tree Genetics & Genomes, 2020, <https://doi.org/10.1007/s11295-020-1414-x>.

2019 (5 articles)

78. 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*, 2019. <https://doi.org/10.1093/gigascience/giy154>.
77. Jinghang Zhou, Liyuan Liu, Chunpeng James Chen, Menghua Zhang, Xin Lu, Zhiwu Zhang*, Xixia Huang* and Yuangang Shi*. **Genome-wide association study of milk and reproductive traits in dual-purpose Xinjiang Brown cattle.** *BMC Genomics*, 2019. <https://doi.org/10.1186/s12864-019-6224-x>.
76. Ying-hui Li, Delin Li, Yong-qing Jiao, James C Schnable, Yan-fei Li, Hui-hui Li, Huai-zhu Chen, Hui-long Hong, Ting Zhang, Bin Liu, Zhang-xiong Liu, Qing-bo You, Yu Tian, Yong Guo, Rong-xia Guan, Li-juan Zhang, Ru-zhen Chang, Zhiwu Zhang, Jochen Reif, Xin-an Zhou, Patrick S Schnable, Li-juan Qiu. **Identification of loci controlling adaptation in Chinese soya bean landraces via a combination of conventional and bioclimatic GWAS.** *Plant biotechnology journal*, 2019. <https://doi.org/10.1111/pbi.13206>.
75. Yueting Dai, Xiao Li, Bing Song, Sun Lei, Chentao Yang, Xin Zhang, Yanfeng Wang, Zhiwu Zhang, Yongping Fu, Yu Li. **Genomic Analyses Provide Insights into the Evolutionary History and Genetic Diversity of Auricularia species.** *Frontiers in Microbiology*, 2019. <https://doi.org/10.3389/fmicb.2019.02255>.
74. Lei Sun, Yuhua Fu, Yang Yang, Xinxin Wang, Weijie Cui, Dan Li, Xiaohui Yuan, Zhiwu Zhang, Yongping Fu, Yu Li. **Genomic Analyses Reveal Evidence of Independent Evolution, Demographic History, and Extreme Environment Adaptation of Tibetan Plateau *Agaricus bisporus*.** *Front. Microbiology*, 2019. <https://doi.org/10.3389/fmicb.2019.01786>.

2018 (8 articles)

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>.
72. 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>.
71. 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>.
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>.
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>.
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>.
67. Shantel A. Martinez¹, 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>.
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>.

2017 (7 articles)

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>.
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>.
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>.
 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>.
 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>.
 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>.
 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>.
- 2016 (12 articles)
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>
 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).

2015 (5 articles)

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, 209(2): 871-84 <https://doi.org/10.1111/nph.13626> (1, 2, 3, 5, 6).
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 (7 articles)

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).
30. Guo T, Li H, Yan J, Tang J, Li J, **Zhiwu Zhang**, Zhang L, Wang J. **Performance prediction of F1 hybrids between recombinant inbred lines derived from two elite maize inbred lines.** *Theor Appl Genet Appl Genet* 2013, **126**:189–201, <https://doi.org/10.1007/s00122-012-1973-9> (1, 5, 6).

2012

29. Fitzpatrick CL, Krotscheck U, Thompson MS, Todhunter RJ, **Zhiwu Zhang**. **Evaluation of Tibial Torsion in Yorkshire Terriers with and without Medial Patellar Luxation.** *Vet Surg* 2012, **41**:966–972, <https://doi.org/10.1111/j.1532-950X.2012.01041.x> (4, 5, 6).
28. Lipka AE, Tian F, Wang Q, Peiffer J, Li M, Bradbury PJ, Gore MA, Buckler ES, **Zhiwu Zhang***. **GAPIT: genome association and prediction integrated tool.** *Bioinformatics* 2012, **28**:2397–2399, <https://doi.org/10.1093/bioinformatics/bts444> (1, 3, 4, 5, 6).
27. Zhu L, Chen S, Jiang Z, **Zhiwu Zhang**, Ku H-C, Li X, McCann M, Harris S, Lust G, Jones P, Todhunter R. **Identification of quantitative trait loci for canine hip dysplasia by two sequential multipoint linkage analyses.** *J Appl Stat* 2012:1719–1731, <https://doi.org/10.1080/02664763.2012.673121> (1, 2, 3, 5, 6).
26. Jer-Ming Chia, Chi Song, Peter J Bradbury, Denise Costich, Natalia de Leon, John Doebley, Robert J Elshire, Brandon Gaut, Laura Geller, Jeffrey C Glaubitz, Michael Gore, Kate E Guill, Jim Holland, Matthew B Hufford, Jinsheng Lai, Meng Li, Xin Liu, Yanli Lu, Richard McCombie, Rebecca Nelson, Jesse Poland, Boddupalli M Prasanna, Tanja Pyhäjärvi, Tingzhao Rong, Rajandeep S Sekhon, Qi Sun, Maud I Tenailon, Feng Tian, Jun Wang, Xun Xu, **Zhiwu Zhang**, Shawn M Kaeppler, Jeffrey Ross-Ibarra, Michael D McMullen, Edward S Buckler, Gengyun Zhang, Yunbi Xu & Doreen Ware. **Maize HapMap2 identifies extant variation from a genome in flux.** *Nat Genet* 2012, **44**:803–807, <https://doi.org/10.1038/ng.2313> (4, 5, 6).

2011

25. Guo G, Zhou Z, Wang Y, Zhao K, Zhu L, Lust G, Hunter L, FriedenberG S, Li J, Zhang Y, Harris S, Jones P, Sandler J, Krotscheck U, Todhunter R, **Zhiwu Zhang***. **Canine hip dysplasia is predictable by genotyping**. *Osteoarthr Cartil* 2011, **19**:420–429, <https://doi.org/10.1016/j.joca.2010.12.011> (1, 2, 3, 4, 5, 6).
24. FriedenberG SG, Zhu L, **Zhiwu Zhang**, van den Berg Foels W, Schweitzer PA, Wang W, Fisher PJ, Dykes NL, Corey E, Vernier-Singer M, Foels WB, Jung SW, Sheng X, Hunter LS, McDonough SP, Lust G, Bliss SP, Krotscheck U, Gunn TM, Todhunter RJ. **Evaluation of a fibrillin 2 gene haplotype associated with hip dysplasia and incipient osteoarthritis in dogs**. *Am J Vet Res* 2011, **72**:530–540, <https://doi.org/10.2460/ajvr.72.4.530> (1, 2, 3, 4, 5, 6).
23. Setter TL, Yan J, Warburton M, Ribaut JM, Xu Y, Sawkins M, Buckler ES, **Zhiwu Zhang**, Gore MA. **Genetic association mapping identifies single nucleotide polymorphisms in genes that affect abscisic acid levels in maize floral tissues during drought**. *J Exp Bot* 2011, **62**:701–716, <https://doi.org/10.1093/jxb/erq308> (4, 5, 6).

2010

22. **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, <https://doi.org/10.1038/ng.546> (1, 3, 4, 5, 6).
21. Huang X, Wei X, Sang T, Zhao Q, Feng Q, Zhao Y, Li C, Zhu C, Lu T, **Zhiwu Zhang**, Li M, Fan D, Guo Y, Wang A, Wang L, Deng L, Li W, Lu Y, Weng Q, Liu K, Huang T, Zhou T, Jing Y, Lin Z, Buckler ES, Qian Q, Zhang QF, Li J, Han B. **Genome-wide association studies of 14 agronomic traits in rice landraces**. *Nat Genet* 2010, **42**:961–967, <https://doi.org/10.1038/ng.695> (4, 5, 6).
20. Zhang N, Gibon Y, Gur A, Chen C, Lepak N, Höhne M, **Zhiwu Zhang**, Kroon D, Tschöep H, Stitt M, Buckler E. **Fine quantitative trait loci mapping of carbon and nitrogen metabolism enzyme activities and seedling biomass in the maize IBM mapping population**. *Plant Physiol* 2010, **154**:1753–1765, <https://doi.org/10.1104/pp.110.165787> (3, 4, 5, 6).
19. Zhou Z, Sheng X, **Zhiwu Zhang***, Zhao K, Zhu L, Guo G, FriedenberG SG, Hunter LS, Vandenberg-Foels WS, Hornbuckle WE, Krotscheck U, Corey E, Moise NS, Dykes NL, Li J, Xu S, Du L, Wang Y, Sandler J, Acland GM, Lust G, Todhunter RJ. **Differential genetic regulation of canine hip dysplasia and osteoarthritis**. *PLoS One* 2010, **5**:e13219, <https://doi.org/10.1371/journal.pone.0013219> (1, 2, 3, 4, 5, 6).
18. Hou Y, Wang Y, Lust G, Zhu L, **Zhiwu Zhang***, 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, <https://doi.org/10.1371/journal.pone.0009410> (1, 2, 3, 4, 5, 6).

2009

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, <https://doi.org/10.1093/bib/bbp050> (1, 3, 4, 5, 6).

16. Zhu L, **Zhiwu Zhang**, 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, <https://doi.org/10.1016/j.tvjl.2009.02.008> (1, 2, 3, 4, 5, 6).
15. Buckler ES*, Holland JB*, Bradbury PJ, Acharya CB, Brown PJ, Browne C, Ersoz E, Flint-Garcia S, Garcia A, Glaubitz JC, Goodman MM, Harjes C, Guill K, Kroon DE, Larsson S, Lepak NK, Li H, Mitchell SE, Pressoir G, Peiffer JA, Rosas MO, Rocheford TR, Romay MC, Romero S, Salvo S, Sanchez Villeda H, da Silva HS, Sun Q, Tian F, UpadayaYula N, Doreen Ware, Heather Yates, Jianming Yu, **Zhiwu Zhang**, Stephen Kresovich*, Michael D. McMullen*. **The genetic architecture of maize flowering time**. *Science* 2009, **325**:714–718, <https://doi.org/10.1126/science.1174276> (3, 4, 5, 6).
14. Myles S, Peiffer J, Brown PJ, Ersoz ES, **Zhiwu Zhang**, Costich DE, Buckler ES. **Association Mapping: Critical Considerations Shift from Genotyping to Experimental Design**. *Plant Cell* 2009, **21**:2194–2202, <https://doi.org/10.1105/tpc.109.068437> (3, 4, 5, 6).
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, <https://doi.org/10.2460/ajvr.70.4.483> (1, 2, 3, 4, 5, 6).
12. Yu J, **Zhang Z**, Zhu C, Tabanao DA, Pressoir G, Tuinstra MR, Kresovich S, Todhunter RJ, Buckler ES. **Simulation Appraisal of the Adequacy of Number of Background Markers for Relationship Estimation in Association Mapping**. *Plant Genome* 2009, **2**:63–77, <https://doi.org/10.3835/plantgenome2008.09.0009> (3, 4, 5, 6).
11. **Zhang Z**, Li CX, Todhunter RJ, Lust G, Goonewardene L, Wang ZQ. **An algorithm to sort complex pedigrees chronologically without birthdates**. *J Anim Vet Adv* 2009, **8**:177–182, <http://medwelljournals.com/abstract/?doi=javaa.2009.177.182> (1, 2, 3, 4, 5, 6).

2008

10. Mateescu RG, Burton-wurster NI, Tsai K, Phavaphutanon J, **Zhang Z**, Murphy KE, Lust G, Todhunter RJ. **Identification of quantitative trait loci for osteoarthritis of hip joints in dogs**. *AJVR* 2008, **69**:1294–1300, <https://doi.org/10.2460/ajvr.69.10.1294> (1, 2, 3, 4, 5, 6).
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, <https://doi.org/10.1111/j.1365-2052.2007.01691.x> (1, 2, 3, 4, 5, 6).

2007

8. Bradbury PJ#, **Zhang Z**#, Kroon DE#, Casstevens TM, Ramdoss Y, Buckler ES. **TASSEL: software for association mapping of complex traits in diverse samples**. *Bioinformatics* 2007, **23**:2633–2635, <https://doi.org/10.1093/bioinformatics/btm308> (1, 3, 4, 5, 6).
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, <https://doi.org/10.1016/j.ygeno.2007.04.004> (4, 5, 6).

6. **Zhang Z**, Todhunter RJ, Buckler ES, Van Vleck LD. **Technical note: Use of marker-based relationships with multiple-trait derivative-free restricted maximal likelihood.** *J Anim Sci* 2007, **85**:881–885, <https://doi.org/10.2527/jas.2006-656> (1, 3, 4, 5, 6).
5. Hays L, **Zhang Z**, Mateescu RG, Lust G, Burton-Wurster NI, Todhunter RJ. **Quantitative genetics of secondary hip joint osteoarthritis in a Labrador Retriever-Greyhound pedigree.** *Am J Vet Res* 2007, **68**:35–41, <https://doi.org/10.2460/ajvr.68.1.35> (4, 5, 6).

2006

4. Michal JJ, **Zhang Zhiwu**, Gaskins CT, Jiang Z. **The bovine fatty acid binding protein 4 gene is significantly associated with marbling and subcutaneous fat depth in Wagyu x Limousin F2 crosses.** *Anim Genet* 2006, **37**:400–402, <https://doi.org/10.1111/j.1365-2052.2006.01464.x> (4, 5, 6).

2005

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).
2. Dikeman ME, Pollak EJ, **Zhang Z**, Moser DW, Gill CA, Dressler EA. **Phenotypic ranges and relationships among carcass and meat palatability traits for fourteen cattle breeds , and heritabilities and expected progeny differences for Warner-Bratzler shear force in three beef cattle breeds (the online version of this article).** *J Anim Sci* 2005, **83**:2461–2467, <https://doi.org/10.2527/2005.83102461x> (4, 5, 6).
1. Todhunter RJ, Mateescu R, Lust G, Burton-Wurster NI, Dykes NL, Bliss SP, Williams AJ, Vernier-Singer M, Corey E, Harjes C, Quaas RL, **Zhang Z**, Gilbert RO, Volkman D, Casella G, Wu R, Acland GM. **Quantitative trait loci for hip dysplasia in a crossbreed canine pedigree.** *Mamm Genome* 2005, **16**:720–730, <https://doi.org/10.1007/s00335-005-0004-4> (4, 5, 6).

Book Chapter (7)

7. Chunpeng Chen, Jessica Rutkoski , James Schnable , Seth Murray , Lizhi Wang , Xiuliang Jin, Benjamin Stich , Jose Crossa , Ben Hayes, and **Zhiwu Zhang***. **Role of the Genomics-Phenomics-Agronomy Paradigm in Plant Breeding.** *Plant Breeding Review Vol 46* (eds. Irwin Goldman), John Wiley & Sons, Inc. 2022. <https://doi.org/10.1002/9781119874157.ch10>. Also available at [Preprint](#) and [Publication](#).
6. Jiabo Wang, Jianming yu, Alex Lipka, and **Zhiwu Zhang***. **Interpretation of Manhattan Plots and Other Outputs of Genome-Wide Association Studies.** *Genome Wide Association Studies Methods in Molecular Biology*, vol 2481, 2022. Humana, New York, NY. https://doi.org/10.1007/978-1-0716-2237-7_5
5. Jiabo Wang, You Tan, and **Zhiwu Zhang***. **Performing Genome-Wide Association Studies with Multiple Models Using GAPIT.** In: *Torkamaneh, D., Belzile, F. (eds) Genome-Wide Association Studies. Methods in Molecular Biology*, vol 2481, 2022. Humana, New York, NY. https://doi.org/10.1007/978-1-0716-2237-7_13

4. Matthew McGowan, Jiabo Wang, Haixiao Dong, Xiaolei Liu, Yi Jia, Xianfeng Wang, Hiroyoshi Iwata, Yutao Li, Alexander E Lipka, and **Zhiwu Zhang***. **Ideas in Genomic Selection with the Potential to Transform Plant Molecular Breeding: A Review**. *Plant Breeding Review Vol 45* (eds. Irwin Goldman), John Wiley & Sons, Inc. 2021. pp. 273-320, <https://doi.org/10.1002/9781119828235.ch7>, also available as [Preprint](#), [Publication](#), and [Google Book](#).
3. Atit Parajuli, Long-Xi Yu, Michael Peel, Deven See, Steve Wagner, Steve Norberg, and **Zhiwu Zhang***. **Self-incompatibility, Inbreeding Depression, and Potential to Develop Inbred Lines in Alfalfa**. *The Alfalfa Genome* (eds. Long-Xi Yu and Chittaranjan Kole), Springer Press. 2021. pp. 255-269, available as [Preprint](#) and [Publication](#), or [Google Book](#).
2. Haixiao Dong, Zhao Li, Guanghui Hu, Yaping Yuan, and **Zhiwu Zhang***. **The Genetic Architecture and Breeding Towards Cold Tolerance in Maize: Review**. *Molecular Breeding in Wheat, Maize and Sorghum* (eds. Mohammad Anwar Hossain, Mobashwer Alam, Saman Seneweera, and Sujay Rakshit), CABI Press. 2021, <https://www.cabi.org/bookshop/book/9781789245431/>, or [Google Book](#).
1. 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**. *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

5. Matthew T. McGowan, Paul D. Mihalyov, Michael O. Pumphrey, Stephen P. Ficklin and **Zhiwu Zhang**, Calling SNPs Out of DNA Array for Diverse Hexaploid Wheat Population by Using Gaussian Mixture Models, Proceedings of the 11th World Congress on Genetics Applied to Livestock Production, Auckland, New Zealand, February 7-11, 2018, <http://www.wcgalp.org/system/files/proceedings/2018/calling-snps-out-dna-array-diverse-hexaploid-wheat-population-using-gaussian-mixture-models.pdf>
4. Chunpeng James Chen and **Zhiwu Zhang***, GWAS and GS Are as Easy as Clicking and Dragging with iPat, Proceedings of the 11th World Congress on Genetics Applied to Livestock Production, Auckland, New Zealand, February 7-11, 2018, <http://www.wcgalp.org/system/files/proceedings/2018/gwas-and-gs-are-easy-clicking-and-dragging-ipat.pdf>
3. 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, [Download here](#).
2. 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, [Download here.](#)

1. **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.wcgalp.org/system/files/proceedings/2002/simulation-study-effects-incorporating-external-genetic-evaluation-results.pdf>

Peer-reviewed articles in Chinese

18. Sun B, Chen Y, Xu S, **Zhang Z**. **Effect of Simmental sire line on linear type traits in crossbreeding with Mongolian cattle.** *Acta Vet Zootech Sin* 1998, **29**:221–224.
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.** *Hereditas* 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.
14. Wang Y, Xu S, **Zhang Z**, Lu J. **Effect of interval and antiseptics on milk composition.** *J Chinese Dairy Sci* 1994:45–48.
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.
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.

Extension articles

6. **Zhang Z**, Watch for stripe rust with smartphones, February, 2022, https://wheatlife.org/wp-content/uploads/2022/03/02_WL_Feb22web.pdf, page 51
5. **Zhang Z**, Party game ignites satellite, drone research effort, Wheat Life, October 2019, https://wheatlife.org/Issues/09_WLOct19web.pdf, page 50-51
4. **Zhang Z**, Empowering breeders for success, Wheat Life, November 2018, https://wheatlife.org/Issues/10_WLNov18web.pdf, page 41-43
3. **Zhang Z**, Genomics tools turbocharge classical breeding, Wheat Life, November 2017, http://wheatlife.org/Issues/08_WLAugSep17web.pdf, page 63-65
2. **Zhang Z**, Educational tour is fun and filling, Wheat Life, February 2017, https://wheatlife.org/Issues/02_WLFeb17web.pdf, page 53-54
1. **Zhang Z**, Juggling thousands of balls, Wheat Life, November 2016, page 43-44

SOFTWARE RELEASED

I have developed multiple 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 9,000 returning users. These packages include the widely-used GAPIT, which has received over 2,000 citations.

- **GridFree**: To count and measure specific objects in images with supervised classification using principal components. See publication on [Plant Physiology](#) by Yang Hu and Zhiwu Zhang. More information is provided on the GRID website: <https://zzlab.net/GRID> (1, 2, 3, 4, 5, 6).
- **GRID**: To automatic extract plot information on images with grid patterns. See publication on [Remote Sensing](#) by Chunpeng James Chen and Zhiwu Zhang. More information is provided on the GRID website: <https://zzlab.net/GRID> (1, 2, 3, 4, 5, 6).

- **MMAP**: Mining the Maximum Accuracy of prediction. See publication on [Bioinformatics by Huang et al.](#) More information is provided on the MMAP website: <http://zzlab.net/MMAP>. (1, 2, 3, 4, 5, 6).
- **iPat**: Intelligent Prediction and Association Tool. See publication on [Bioinformatics by Chen and Zhang](#). 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. See [publication by Huang and et al.](#) 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).

INVITED PRESENTATIONS

- 2020 **International Plant & Animal Genome Conference XXVIII, *High Throughput Image Techniques in Breeding***, San Diego, January 11, 2020.
- 2019 **University of Georgia, *See beyond what we can see***, Athens, GA, August 30, 2019.
International Plant & Animal Genome Conference XXVII, *iPat, a tool to perform gene mapping and genomic prediction*, San Diego, January 12, 2019.
Chinese Academy of Agricultural Sciences, *See beyond what we can see*, Beijing, China, November 10, 2019.
- 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.

- University of Idaho, Saving the Babies from the Bathwater in Genome-Wide Association Studies**, Moscow, Idaho, January 19, 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, June 18-21, 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/PastMathBiologySeminar.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.
- 6th 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: 4, graduated students: 6)

Meijing Liang: 2021-present, Ph.D. Student. Research Project: Genomic prediction.

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.

Matthew McGowan: 2016-2022, Ph.D. Student. Research Project: Genotype calling for SNP and structural variation, Current: Scientist at KromaTiD.

Chun-Peng Chen: 2016-2021, Ph.D. Student. Research Project: Intelligent Prediction and Association Tool, Current: Assistant Professor at Virginia Tech.

Samuel Revolinkski: 2018-2019, M.S. Student. Research Project: High throughput phenotyping. Current: Postdoctoral Research Associate at Washington State University.

Yuanhong Song: 2017-2019, M.S. Student. Research Project: Explain variables of NDVI on satellite imagery, Current: Data Scientist at Bayer R&D Services LLC.

Jiabo Wuang: 2014-2018, Ph.D. Dissertation: Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. Current: Assistant professor at Sichuan Minzu University.

Yao Zhou: 2014-2017, Ph.D. Dissertation: Systematic bias of correlation coefficient may explain negative accuracy of genomic prediction. Current: Professor, Institute of Plant Science at Chinese Academy of 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

Hatice Sari: 2022-present, Postdoctoral Researcher. Research Project: Genome wide association study and genomic prediction.

Renan Uhdre: 2022-present, Postdoctoral Researcher. Research Project: Genome wide association study and genomic prediction.

Yang Hu: 2019-2022, Postdoctoral Researcher. Research Project: Hyperspectral image analysis and artificial intelligence.

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: Research Scientist at University of North Texas, Health Science Center at Fort Worth.

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

Visiting scientists

Shipeng Li: 2018-2019, Visiting Professor. Research Project: Meta analyses on gene expression in maize.

Zhenhai Cui: 2018-2019, Visiting Professor. Research Project: Gene mapping for husk in maize.

Yongping Fu: 2014-2015, Visiting Professor. Research Project: Gene profiling of mushroom.

Xiaohui Yuan: 2014-2015, Visiting Professor. Research Project: High performance computing.

Mengjin Zhu: 2014-2015, Visiting Professor. Research Project: Genome-wide association study.

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.

Visiting students

Taseer Naqvi: 2022, Visiting student. Research Project: Genomic research in wheat.

Fan Zhang: 2020-2021, Visiting student. Research Project: Genomic research in alfalfa.

Sorour Arzhang: 2019-2020, Visiting Student. Research Project: Genome-wide association study in maize.

Arfa Anjun: 2018-2019, Visiting Student. Research Project: Bioinformatics.

Reena Rani: 2018-2019, Visiting Student. Research Project: GWAS in soybean.

Iqra Ishaag: 2018-2019, Visiting Student. Research Project: GWAS in wheat.

Liyuan Liu: 2018-2019, Visiting Student. Research Project: Genome-wide association study.

Jinghang Zhou: 2018-2019, 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.

Hsuan Chen: 2014-2015, Visiting Ph.D. Student. Research Project: Statistical genomics.

Zhao Li: 2014-2015, Visiting Ph.D. Student. Research Project: Freezing tolerance of maize.

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.

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 advisory committee

1. Swarnita Chakraborty (Molecular Plant Science, Dr. Nairanjana Dasgupta) 2020-
2. John Hadish (Molecular Plant Science, Dr. Stephen Ficklin) 2018-
3. Joseph Daniel Crawford (Biology, Dr. Asaph Cousins) 2018-2022
4. Karansher Singh Sandhu (Crop and Soil, Dr. Arron Carter) 2018-2022
5. Lance Merrick (Crop and Soil, Dr. Mike Pumphrey) 2018-2022
6. Cristina Ocana Gallegos (Crop and Soil, Dr. Kevin Murphy) 2018-2022
7. Samuel Prather (Crop and Soil, Dr. Mike Pumphrey) 2018-2022
8. William Crump (Horticulture, Dr. Per Hilding McCord) 2018-2022
9. Evan Craine (Horticulture, Dr. Scot Hulbert) 2018-2022
10. Feixiong Luo (Horticulture, Dr. Cameron Peace) 2016-2019
11. Ragupathi Nagarajan (CSS, Dr. Kulvinder Gill) 2014-2017
12. Stephanie Sjoberg (CSS, Dr. Arron Carter) 2016-2019
13. Wilson Craine (CSS, Dr. Scot Hulbert) 2016-2021
14. Ahsan Khan (CSS, Dr. Kulvinder Gill) 2015-2019
15. Md Nurul Amin (CSS, Dr. Rebecca McGee) 2015-2017

PROFESSIONAL SERVICE

Academic Editor

PLoS One

Guest Editor

PLoS Genetics

Ad Hoc Reviewer (Number of manuscripts reviewed)

Nature Genetics (7)	Genetics (1)
Nature Methods (1)	Heredity (1)
Nature Communications (4)	Theoretical and Applied Genetics (1)
Nature Plants (1)	Plant Genome (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)

Committee Memberships

Bioinformatics Certificate Oversight Committee, 2018-present, Washington State University, Pullman, WA (<https://sbs.wsu.edu/graduate-certificate-in-bioinformatics>)
Executive Committee Member, Molecular Plant Sciences Program, 2017-2022, Washington State University, Pullman, WA.
Vice Chair of Hatch Fund Project in Plant Breeding, 2017-2021, Washington State University, Pullman, WA.
Department Website Committee Member, 2016-2019, Washington State University, Pullman, WA.
Department Mentoring Taskforce Committee Member, 2018-2019, Washington State University, Pullman, WA.
Board Member for Community of Emerald Pointe, 2017-2019, 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.
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.
Judge of Showcase for Undergraduate Research and Creative Activities, Washington State University, 2017
Judge of Showcase for Undergraduate Research and Creative Activities, Washington State University, 2018
Judge of Research Exposition, The Graduate and Professional Student Association, Washington State University, 2019
Judge of Student Poster Awards, Plant Science Symposium at Washington State University, 2019

PROFESSIONAL MEMBERSHIP

American Association for the Advancement of Science (AAAS)
American Association Agronomy (ASA)

AWARDS AND RECONGNITIONS

- **WSU CAHNRS Early Career Excellence Award, [2021](#)**

- **Workshop Organizer** for the International Plant & Animal Genome Conference, [2018](#), [2019](#), [2020](#), [2022](#), and [2023](#).
- **Long Service Award** from PLOS ONE Editorial Board, February 28, 2023.
- **Recognition Award** from the Nature Publication Group for contribution to referencing papers, 2012.
- **The most cited author of PLoS Genetics in 2016**
<https://exaly.com/journal/13871/plos-genetics/top-authors/2016>
- **The third most cited author at Cornell University in 2010**
<https://exaly.com/institution/123787/cornell-university/top-authors/2010>
- **The sixth most cited author at Washington State University in 2016**
<https://exaly.com/institution/126424/washington-state-university/top-authors/2016>
- **Young Scientist Scholarship**, the 5th World Congress of Genetics Applied to Livestock Production, Canadian International Development Agency, Canada (August 1994).

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.