Zhiwu Zhang

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SUMMARY: *As a Professor in the Department of Crop and Soil Sciences at Washington State University (WSU), I have a multidisciplinary background with dual Ph.D. degrees, one in Statistical Genetics and one in Animal Breeding. Since 2005, I have published over 130 peer-reviewed articles and book chapters garnering over 33,000 citations with an h-index of 57 on Google Scholar. My research is dedicated to developing 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 secured 15 grants from a variety of sources, including WSU, Murdock Foundation, USDA, NSF, and DOE, which total $3.8M 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 seven cycles. I am recognized as an Associate editor (PLoS Genetics), journal reviewer (Nature Genetics, Nature Methods, and PLoS Genetics), and grant panelist (USDA, NSF, Natural Sciences and Engineering Research Council of Canada, 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. I was honored with the CAHNRS' Early Career Excellence Award at WSU in 2021 and the Highly Cited Award by Clarivate in 2025.*

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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

2025-Present	**Professor** Department of Crop and Soil Sciences, Washington State University, Pullman, WA, USA
2019-2024	**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** Institute for Genomic Diversity (2005-2010) and Department of Animal Science (2002-2005), 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

Extramural Funding

NSF
10/1/2025-9/30/2028 (PI)
"AI-ENGAGE: Harnessing AI for Precision Genomic Selection Models in Wheat" (Award number 2520271), $400,000.

USDA
8/1/2024-10/31/2027 (Co-PI)
"Use of New Technology to Improve Chickpea Seed Nutritional Content" (Award number 5820902039), $157,050.

USDA
8/1/2022-10/31/2026 (Co-PI)
"Targeted Genomic Assisted Improvement of Seed Protein Concentration" (Award number 5820902024), $326,509.

Washington Grain Commission
7/1/2021-6/30/2026 (PI)
"Intelligent Prediction and Association Tool to Facilitate Wheat Breeding" (Award number 134574-001), $293,463.

Washington Research Foundation Commercialization Gap Fund
1/1/2024-12/31/2025 (PI)
"Computer Aided Grain Inspection of Club Wheat Identification" (Award number PG00022460), $50,000.

USDA
8/1/2020-7/31/2025 (PI)
"FACT: Predicting Wheat Hagberg Falling Number from Near Infrared Spectrometers" (Award number 2020-67021-32460), $500,000.

Washington Research Foundation Commercialization Gap Fund
1/1/2022-12/31/2024 (PI)
"A fast wheat quality inspection method" (Award number PG00020471), $40,000.

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.

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.

NSF
8/1/2020-8/31/2024 (Co-PI, PI: Dr. Thomas W Okita)
"EAGER: The RNA Landscape as defined by RNA binding proteins" (Award number ISO 2029933), $600,000.

Washington Wheat Foundation
1/1/2018-12/31/2022 (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).

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).

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).

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).

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.

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.

Washington Grain Commission

5/1/2018-6/30/2021 (PI)
"Intelligent Prediction and Association Tool to Facilitate Wheat Breeding" (Award number 126593), $259,848.

Washington Grain Commission
5/1/2015-6/30/2018 (PI)
"Intelligent Prediction and Association Tool to Facilitate Wheat Breeding" (Award number 126593), $220,667.

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.

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.

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).

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).

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).

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).

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).

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.

TEACHING EXPERIENCE

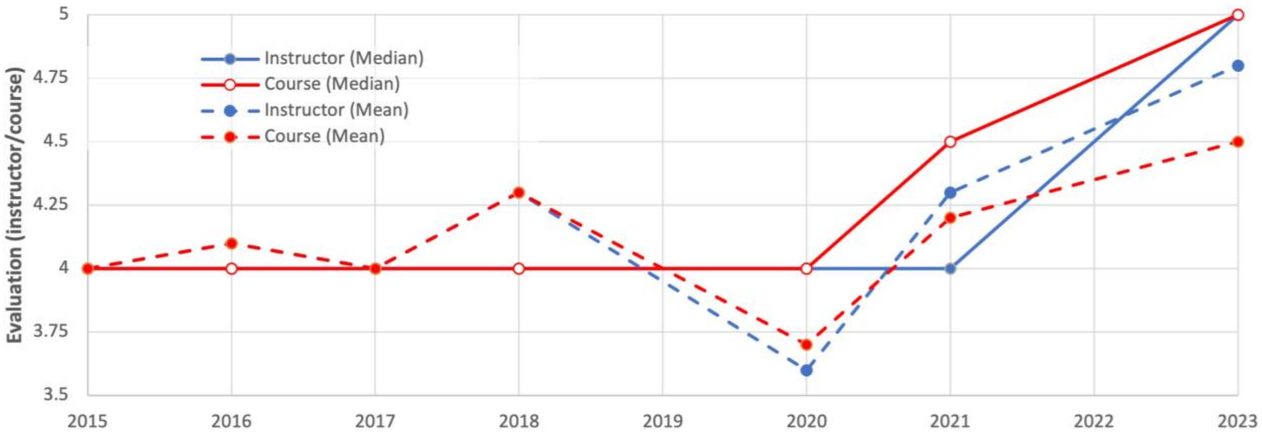
2015-present **Instructor** for *Statistical Genomics* at Washington State University. The course was initiated as one credit course in the Department of Crop and Soil Sciences (CROP_SCI 512) in 2015. The following year, the course was promoted to a three-credit course and listed as CROP_SCI 545. Currently, 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.

2025: Flyer, syllabus, student evaluation, slides, R code, and homework
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	12	75%	3.6	4.0	3.6	4.0	3.7	4.0
2021	3	7	85%	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, Web of Science (h-index=46, citations >21,000), Scopus (h-index=49, citations >22,000), Google Scholar (h-index = 57, citations > 32,000) * = corresponding authorship, and # = equal authorship. First or corresponding authorship rate: 41.7% (last five years) and 42.7% (all-time).*

Peer-reviewed articles

2025 (8 articles)

132. Zhen Zuo, Mingliang Li, Defu Liu, Qi Li, Bin Huang, Guanshi Ye, Jiabo Wang, You Tang*, **Zhiwu Zhang***, **GWAS Procedures for Gene Mapping in Diverse Populations with Complex Structures.** Bio-protocol, 2025, https://doi.org/10.21769/BioProtoc.5284

131. Fan Zhang, Chunxue Wei, Xiaoya Shi, Shuo Cao, Xiaodong Xu, Zhiyao Ma, Yanling Peng, Rida Arshad, Hui Xue, Zhen Zhang, Wei Zhang, Yanshuai Xu, Yang Dong, Lianzhu Zhou, Xuejing Cao, Mengrui Du, Xu Wang, Zhiwu Zhang, Ruicai Long, Junmei Kang, Yongfeng Zhou, Qingchuan Yang, **Medicago super-pangenome reveals adaptive advantages and evolutionary constraints in autotetraploid alfalfa.** Nature Communication, 2025, https://www.nature.com/articles/s41467-025-67280-9

130. Linqian Han, Xiaoming Wang, Ryan Benke, Laura E. Tibbs-Cortes, Peng Zhao, Karen A. Sanguinet, Zhiwu Zhang, Shengbao Xu, Jianming Yu & Xianran Li, **Integrated phenomic and**

genomic analyses unveil modes of altered phenotypic plasticity during wheat improvement. Genome Biology, 2025, https://doi.org/10.1186/s13059-025-03740-1

129. Markus Lange, Amber N. Parrish, Iris Lange, Yanmei Xiao, Iovanna Pandelova, Haixiao Dong, **Zhiwu Zhang**, Sümeyye Carkit-Yilmaz, Thomas M. Davis, Matthias Wüst, Narayanan Srividya, Kelly J. Vining, **Transgressive segregation affects essential oil composition in a model mint population.** New Phytologist, 2025, https://doi.org/10.1111/nph.70305
128. Brandon J Weihs, Zhou Tang, Somshubhra Roy, Zezhong Tian, Deborah Jo Heuschele, Zhiwu Zhang, Cranos Williams, Zhou Zhang, Garett Heineck, Swayamjit Saha, Zhanyou Xu, **No More Laborious Stem Counting: AI-powered Computer Vision Enables Identification and Quantification of Solid and Hollow Alfalfa Stems at the Pixel Level.** Smart Agricultural Technology, 2025, https://doi.org/10.1016/j.atech.2025.101278
127. Yu Gan , Zhenya Liu , Fan Zhang , Qi Xu , Xu Wang , Hui Xue , Xiangnian Su , Wenqi Ma , Qiming Long , Anqi Ma , Guizhou Huang , Wenwen Liu , Xiaodong Xu , Lei Sun , Yingchun Zhang , Yuting Liu , Xinyue Fang , Chaochao Li , Xuanwen Yang , Pengcheng Wei , Xiucai Fan , Chuan Zhang , Pengpai Zhang , Chonghuai Liu , Lianzhu Zhou , **Zhiwu Zhang** , Yiwen Wang , Zhongjie Liu , Yongfeng Zhou, **Deep learning empowers genomic selection of pest-resistant grapevine.** Horticulture Ressearch, 2025, https://doi.org/10.1093/hr/uhaf128
126. Hatice Sari, Clarice J. Coyne, Michael A. Grusak, Veselina Valkov, Zhiwu Zhang, Rebecca J. McGee, Dorrie Main, Nonoy Bandillo, Jonah Hart, Britton M. Bourland, Renan Uhdre, Marilyn L. Warburton, **Genome-Wide Association Study of Seed Mineral Nutrients in Peas.** The plant Genome, 2025, https://doi.org/10.1002/tpg2.70137
125. Lizhi Tan, Xinyu Cai, Yuan Kong, Zexuan Liu, Zilong Wen, Lina Bu, Yuzhan Wang, Xiaojun Liu, Zhiwu Zhang, Jianlin Han, Dandan Wang, Yiqiang Zhao, **Genome-wide analyses reveal intricate genetic mechanisms underlying egg production efficiency in chickens.** Journal of Animal Science and Biotechnology, 2025, https://doi.org/10.1186/s40104-025-01245-2

2024 (10 articles)

124. Renan Uhdre, Clarice J Coyne, Britton Bourland, Julia Piaskowski, Ping Zheng, Girish M Ganjyal, Zhiwu Zhang, Rebecca J McGee, Dorrie Main, Nonoy Bandillo, Mario Morales, Yu Ma, Chengci Chen, William Franck, Adam Thrash, Marilyn L Warburton, **Association study of crude seed protein and fat concentration in a USDA pea diversity panel.** Plant Genome, 2025, https://doi.org/10.1002/tpg2.20485
123. Fan Zhang, Ruicai Long, Zhiyao Ma, Hua Xiao, Xiaodong Xu, Zhongjie Liu, Chunxue Wei, Yiwen Wang, Yanling Peng, Xuanwen Yang, Xiaoya Shi, Shuo Cao, Mingna Li, Ming Xu, Fei He, Xueqian Jiang, Tiejun Zhang, Zhen Wang, Xianran Li, Long-Xi Yu, Junmei Kang, **Zhiwu Zhang***, Yongfeng Zhou*, Qingchuan Yang*, **Evolutionary genomics of climatic adaptation and resilience to climate change in alfalfa.** Mollecular Plant, 2024, https://doi.org/10.1016/j.molp.2024.04.013
122. Atit Parajuli, Bhabesh Borphukan, Karen A Sanguinet*, **Zhiwu Zhang***, **In silico analysis identified bZIP transcription factors genes responsive to abiotic stress in Alfalfa (Medicago sativa L.).** BMC genomics 25 (1), 1-16, 2024, https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-024-10277-3

121. Cheng He, Jacob D. Washburn, Nathaniel Schleif, Yangfan Hao, Heidi Kaeppler, Shawn M. Kaeppler, Zhiwu Zhang, Jinliang Yang, Sanzhen Liu, **Trait association and prediction through integrative k-mer analysis.** The Plant Journal, 2024, https://doi.org/10.1111/tpj.17012
120. Brandon J Weihs, Zhou Tang, Zezhong Tian, Deborah Jo Heuschele, Aftab Siddique, Thomas H Terrill, Zhou Zhang, Larry M York, **Zhiwu Zhang***, Zhanyou Xu*, **Phenotyping alfalfa (Medicago sativa L.) root structure architecture via integrating confident machine learning with ResNet-18.** Plant Phenomics, 2024, https://spj.science.org/doi/pdf/10.34133/plantphenomics.0251
119. Brandon J Weihs, Deborah J Heuschele, Zhou Tang, Larry York, **Zhiwu Zhang**, Zhanyou Xu, **The State of the Art in Root System Architecture Image Analysis Using Artificial Intelligence: A Review.** Plant Phenomics, 2024, https://doi.org/10.34133/plantphenomics.0178
118. Cristina Ocaña-Gallegos, Meijing Liang, Emma McGinty, Zhiwu Zhang, Kevin M Murphy, Amber L Hauvermale, **Preharvest Sprouting in Quinoa: A New Screening Method Adapted to Panicles and GWAS Components.** Plants, 2024, https://doi.org/10.3390/plants13101297
117. Per McCord, W Wesley Crump, **Zhiwu Zhang**, Cameron Peace, **Improving fruit size in sweet cherry via association mapping and genomic prediction.** Tree Genetics & Genomes, 2024, https://link.springer.com/article/10.1007/s11295-024-01660-y
116. Bosen Zhang, Amber L Hauvermale, Zhiwu Zhang, Alison Thompson, Clark Neely, Aaron Esser, Michael Pumphrey, Kimberly Garland-Campbell, Jianming Yu, Camille Steber, Xianran Li, **Harnessing enviromics to predict climate-impacted high-profile traits to assist informed decisions in agriculture.** Food and Energy Security, 2024, https://doi.org/10.1002/fes3.544
115. Hatice Sari, Renan Uhdre, Lyle Wallace, Clarice J. Coyne, Britton Bourland, Zhiwu Zhang, M. Russo, Alecia Kiszonas, and Marilyn L. Warburton, **Genome-wide association study in Chickpea (Cicerarietinum L.) for yield and nutritional components.** Euphytica, 2024, https://doi.org/10.1007/s10681-024-03338-x
114. Lina Bu, Yuzhe Wang, Lizhi Tan, Zilong Wen, Xiaoxiang Hu, Zhiwu Zhang, Yiqiang Zhao, **Haplotype analysis incorporating ancestral origins identified novel genetic loci associated with chicken body weight using an advanced intercross line.** Genetics, Selection, Evolution, 56:78, 2024, https://doi.org/10.1186/s12711-024-00946-y.

2023 (6 articles)

113. Lanzhi Li, Xingfei Zheng, JiaboWang, Xueli Zhang, Xiaogang He,Liwen Xiong, Shufeng Song, Jing Su, Ying Diao, Zheming Yuan, **Zhiwu Zhang*** & Zhongli Hu*, **Joint analysis of phenotype-effect-generation identifies loci associated with grain quality traits in rice hybrids.** Nature Communication, 2023, https://doi.org/10.1038/s41467-023-39534-x
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.** F1000Research, 12:137, 2023, https://doi.org/10.12688/f1000research.127953.1
108. 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.

2022 (11 articles)

107. 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.
106. 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.
105. 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.
104. 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.
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, https://mycosphere.org/pdf/MYCOSPHERE_si_1f_4.pdf
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, 186(4),2239–2252, 2021, https://doi.org/10.1093/plphys/kiab226.
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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. 2023. **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 Wise 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.
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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

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2. 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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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**. *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.

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.

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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

7. **Zhang Z**, Boosting Wheat Production with AI, December, 2023, https://wagrains.org/articles/boosting-wheat-production-with-ai/
6. **Zhang Z**, Watch for stripe rust with smartphones, Wheat Life, April, 2022, https://wagrains.org/articles/watch-for-stripe-rust-with-smartphones/
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 15,000 returning users. These packages include the widely-used GAPIT, which has received over 2,000 citations.

- **AI4Everyone**: To allow general citizens to develop wide range of artificial intelligence systems without requirement of computer programming skills. Users can customize neural network architecture by simply typing, clicking and dragging numbers, buttons and objects. More information is provided on the GRID AI4Everyone: https://zzlab.net/AI4EVER.
- **LADDER**: To allow general citizens to develop computer vision systems without requirement of computer programming skills. This plat form integrates both training and prediction. Users can label their images and let the computer learn what the users want to identify objects on images they provide. More information is provided on the GRID website: https://zzlab.net/GRID.
- **ROOSTER**: To detect wheat strip rust using neural networks. More information can be found in publication on Computers and Electronics in Agriculture and the GRID website: https://zzlab.net/ROOSTER.
- **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.
- **GRID**: To automatic extract plot information on images with grid patterns. More information can be found in publication on Remote Sensing and the GRID website: https://zzlab.net/GRID.
- **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.
- **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.
- **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.
- **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.
- **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.

- **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.

INVITED PRESENTATIONS (Total: 39)

2026 Decoding the Genomic Prediction Maze: A Benchmark of 18,000 Analyses Reveals Feature-Trait Compatibility Dominates Stability and Accuracy. International Conference of Plant and Animal Genome, Sandiego, United State, Jan 10, 2026

Accelerating Image-Based Phenotyping: Build Your Own AI Vision Tool Easily with Ladder. International Conference of Plant and Animal Genome, Sandiego, United State, Jan 11, 2026

AI4EVER: A User-Friendly Platform to Bridge Deep Learning and Genomic Selection. International Conference of Plant and Animal Genome, Sandiego, United State, Jan 11, 2026

2025 AI In The Statistics Ecosystem: From Research Assistance To Educational Disruption. World Statistics Congress, The Hague, Netherland, October 5-9, 2025

Master Computer Vision: Create Your Own AI to Recognize Anything from Scratch. Washington State 4-H Teen Conference, Pullman, WA, June 25, 2025

Overcoming Catastrophic Forgetting in Neural Networks: Leveraging LADDER to Customize Smart Agriculture Applications. PNNL-WSU Discuss, Discourse, Disseminate with Data (D4) Seminar, May 15, 2025

2024 Boosting Agriculture with Artificial Intelligence, Department of Crop and Soil Sciences, Washington State University, Pullman, Washington, Sep 16, 2024

International Conference of Quantitative Genetics (7th), Emerging Marker Assisted Selection and Genomic Selection, Vienna, Austria, July 22-26, 2024.

Translational Omics Working Group, Untangling False Positives, Statistical Power, Populations Structure, and Kinship in GWAS, USDA SCINet Scientific Computing, July 11, 2024. Recording (Passcode: KDsfXZ6@).

North America Alfalfa Improvement Conference, Genomics Enabled Purging Selection to Develop 200 Alfalfa Inbred Lines Toward High Yield Hybrid Production, Pasco, WA, USA, June 24-26, 2024.

Cornell University, Confusion and prospection of Genomic Prediction to Incorporate Genome Wide Association Study, Departmental Seminar for Plant Breeding, Ithaca, NY, USA, January 23, 2024.

International Conference of Plant and Animal Genome, Modeling Complex Data Structure in GWAS Using BLINK, San Diego, USA, January 15, 2024.

2023 **64th World Statistics Conference**, AI Winter of Genomic Prediction, Ottawa, Canada. July 16-20, 2023.

International Conference of Plant and Animal Genome, Software Engineering for Genomic and Phenomic Research, San Diego, USA, January 15, 2023.

Washington State University, Confusion and prospection of Genomic Prediction to Incorporate Genome Wide Association Study, Gest lecture for Venkata Krishna Jandhyala on *Seminar in Statistics (State 591), Department of Statistics,* October 18, 2023.

2022 **International Plant & Animal Genome Conference XXIX**, *Bulk Sequencing Identified Numerous Genetic Loci Associated with Alfalfa Growth Vigor during Self-Pollination Inbreeding*, San Diego, January 8-12, 2022.

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*, 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/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

- **Genomic Prediction***, Chinese Academy of Forestry, Beijing*, China, September 6-10, 2023 (Eighty participants onsite and over 1,000 online). Website: Genomic Prediction Workshop.
- **Co-instructor with Patrick Carter, High Throughput Genomic Data analyses***, Southeast Nationality University, Chendu*, China, November 11-15, 2019.
- **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.

Zhou Tang: 2019-2024, Ph.D. Student. Research Project: Speed up precision agriculture with artificial intelligence empowered phenomics. Postdoc at University of Florida.

Atit Parajuli 2019-2023, Ph.D. Student. Research Project: Development of 200 inbred alfalfa lines. Postdoc at Iowa State University.

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 inteligence. Dr. Hu is now a scientist at Bayer.

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. Dr. Huang is now a Research Scientist at University or 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. Zhaslan Akhmetov (Crop Science, Dr. Karen Sanguinet) 2023-
2. Swarnita Chakraborty (Molecular Plant Science, Dr. Nairanjana Dasgupta) 2020-2023
3. John Hadish (Molecular Plant Science, Dr. Stephen Ficklin) 2018-2023
4. Joseph Daniel Crawford (Biology, Dr. Asaph Cousins) 2018-2022
5. Karansher Singh Sandhu (Crop and Soil, Dr. Arron Carter) 2018-2022
6. Lance Merrick (Crop and Soil, Dr. Mike Pumphrey) 2018-2022
7. Cristina Ocana Gallegos (Crop and Soil, Dr. Kevin Murphy) 2018-2022
8. Samuel Prather (Crop and Soil, Dr. Mike Pumphrey) 2018-2022
9. William Crump (Horticulture, Dr. Per Hilding McCord) 2018-2022
10. Evan Craine (Horticulture, Dr. Scot Hulbert) 2018-2022
11. Feixiong Luo (Horticulture, Dr. Cameron Peace) 2016-2019
12. Ragupathi Nagarajan (CSS, Dr. Kulvinder Gill) 2014-2017
13. Stephanie Sjoberg (CSS, Dr. Arron Carter) 2016-2019
14. Wilson Craine (CSS, Dr. Scot Hulbert) 2016-2021
15. Ahsan Khan (CSS, Dr. Kulvinder Gill) 2015-2019
16. Md Nurul Amin (CSS, Dr. Rebecca McGee) 2015-2017

PROFESSIONAL SERVICE

Editorial Board

PLoS Genetics (https://journals.plos.org/plosgenetics/static/editorial-board?)

Editorial Board (https://journals.plos.org/plosone/static/editorial-board?)

PLoS One

Grant Panelist

USDA
NSF
Natural Sciences and Engineering Research Council of Canada
Biotechnology and Biological Sciences Research Council (UK)
Swiss National Science Foundation

Ad Hoc Reviewer (Number of manuscripts reviewed)

Nature Genetics (7)

Genetics (1)

Nature Methods (1)
Nature Communications (4)
Nature Plants (1)
PNAS (1)
Annals of Human Genetics (1)
Annals of Applied Statistics (1)
Genome Research (1)
PLoS Genetics (3)
PLoS One (5)
GigaScience (1)
Heredity (1)
Theoretical and Applied Genetics (2)
Plant Genome (1)
Animal Genetics (1)
Bioinformatics (3)
Journal of Animal Science (1)
Journal of Human Genetics (1)
PLoS Computation Biology (1)
G3 (2)

Committee Memberships

Promotion and Tenure Advisory Committee, 2024-2026, CAHNRS, Washington State University, Pullman, WA.
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 the Graduate and Professional Student Association (GPSA) Research Exposition, Washington State University, 2025
Judge of the Graduate and Professional Student Association (GPSA) Research Exposition, Washington State University, 2024

Judge of the Graduate and Professional Student Association (GPSA) Research Exposition, Washington State University, 2019
Judge of Showcase for Undergraduate Research and Creative Activities, Washington State University, 2024
Judge of Showcase for Undergraduate Research and Creative Activities, Washington State University, 2023
Judge of Showcase for Undergraduate Research and Creative Activities, Washington State University, 2019
Judge of Showcase for Undergraduate Research and Creative Activities, Washington State University, 2018
Judge of Showcase for Undergraduate Research and Creative Activities, Washington State University, 2017
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

- **Clarivate Highly Cited Award Recipient**, 2025
- **WSU CAHNRS Early Career Excellence Award**, 2021 (The purpose of this award is to acknowledge outstanding contributions in research, teaching and/or extension in any CAHNRS discipline during the early phases of a faculty member's academic career. Eligible candidates must have less than ten years of experience in a faculty appointment)
- **IPS Chair** of 65th World Statistics Conference, Statistical Concourse of Machine Learning and Artificial Intelligence, The Hague, Austria. October 5-9, 2025.
- **IPS Chair** of 65th World Statistics Conference, ChatGPT: Challenges And Opportunities To Statistical Research And Education, The Hague, Austria. October 5-9, 2025.
- **IPS Chair** of 64th World Statistics Conference, Statistical Concourse of Machine Learning and Artificial Intelligence, Ottawa, Canada. July 16-20, 2023.
- **Workshop Organizer** for the International Plant & Animal Genome Conference, 2018, 2019, 2020, 2022, 2023, 2024, 2025, and 2026.
- **The most cited author in Plant Genome in 2021** https://exaly.com/journal/26819/plant-genome/top-authors/most-cited/2021
- **The most cited author in Plant Genome in 2016** https://exaly.com/journal/26819/plant-genome/top-authors/most-cited/2016
- **The most cited author of PLoS Genetics in 2016** https://exaly.com/journal/13871/plos-genetics/top-authors/most-cited/2016
- **The second cited author of Bioinformatics in 2007** https://exaly.com/journal/12899/bioinformatics/top-authors/most-cited/2007

- **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.. 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 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 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.