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A. Education and Training

University of Hawaii at Manoa	Plant Molecular Biology	Ph.D.	2001
University of Chicago	Computer Science	MS	2003
Beijing Forestry University, P.R. China	Forest Genetics	MS	1989
Beijing Forestry University, P.R. China	Agricultural Science	BS	1986
University of Alabama at Birmingham	Biostatistics	Post-doc	2004-2005
University of Minnesota	Bioinformatics	Post-doc	2003-2004

B. Professional Appointments:

2018 ~ now Full Professor, Michigan Technological University, Houghton, MI
2014 ~ 2018 Associate Professor, Michigan Technological University, Houghton, MI
2008 ~ 2014 Assistant Professor, Michigan Technological University, Houghton, MI
2006 ~ 2008 Omics Data Analyst, WiCell, In, Madison, WI
2005 ~ 2006 Bioinformatics Scientist, Operon Biotechnologies, Inc., Huntsville, AL
2004 ~ 2005 Postdoc, Biostatistics, University of Alabama, Birmingham, AL
2003 ~ 2004 Postdoc, Bioinformatics, University of Minnesota, Minneapolis, MN
1996 ~ 2001 Research Assistant, Plant Molecular Biology, University of Hawaii at Manoa, Honolulu, HI
1995 ~ 1996 Research Assistant, Plant Genetics, University of Hawaii at Manoa, Honolulu, HI
1989 ~ 1995 Assistant Professor, and Lecturer, Forest Genetics, Beijing Forestry University

C. Publications (Google Scholar Citations = 6183, h-index=32, * Correspondence/co-correspondence author)

- 1) Liu, W., C. Liu, S. Chen, M. Wang, X. Wang, Y. Yu, R. Sederoff, **H. Wei**, X. You, G. Qu and S. Chen. 2024. A nearly gapless, highly contiguous reference genome for a doubled haploid line of *Populus ussuriensis*, enabling advanced genomic studies. *Forestry Research* (in press). doi: [10.48130/forres-0024-0016](https://doi.org/10.48130/forres-0024-0016)
- 2) (Review article) Wei, Z. and **H. Wei** *. 2024. Deciphering the intricate hierarchical gene regulatory network: unraveling multi-level regulation and modifications driving secondary cell wall formation. *Horticulture Research* 11(2) <https://doi.org/10.1093/hr/uhad281>.

- 3) Islam, M.K., S. T. Mummadi, S, Liu, and H. **Wei** *. 2023. Regulation of regeneration in *Arabidopsis thaliana*. **aBiotech** 4: 332-351 <https://link.springer.com/article/10.1007/s42994-023-00121-9>
- 4) Cao, X., L. Zhang, M. Zhao, C. He, K. Zhang, S. Liu, Q. Sha* and **H. Wei***. 2023. TGPred: Efficient methods for predicting target genes of a transcription factor by integrating statistics, machine learning, and optimization. **NAR Genomics and Bioinformatics** 5(3):1-13
<https://doi.org/10.1093/nargab/lqad083>
- 5) Gu, C., R. Han, C. Liu, G. Fang, Q. Yuan, Z. Zheng, Q. Yu, J. Jiang, S. Liu, **H. Wei***, Q. Zhang* and G. Liu *. 2023. Heritable epigenetic modification of BpPIN1 is associated with leaf shapes in *Betula pendula*. **Tree Physiology** 43(10):1811-1124 tpad085, <https://doi.org/10.1093/treephys/tpad085>
- 6) Li, J., C. Li., Y. Deng, **H. Wei** and S. Lu, 2023. Characteristics of *Salvia miltiorrhiza* methylome and the regulatory mechanism of DNA methylation in tanshinone biosynthesis. **Horticulture Research** 10(7). <https://doi.org/10.1093/hr/uhad114>
- 7) Zhao, M., Z. Peng, Y. Qin, T. M. Tamang, L. Zhang, B. Tian, Y. Chen, Y. Liu, J. Zhang, G. Lin, H. Zheng, C. He, K. Lv, A. Klaus, C. Marcon, F. Hochholdinger, H. Trick, M.J. Cho, S. Park, Y. Liu, **H. Wei**, J. Zheng, F. White, and S. Liu. 2023. Bacterium-enabled transient gene activation by artificial transcription factors for resolving gene regulation in maize. **Plant Cell** 35(8):2736-2749.
<https://doi.org/10.1093/plcell/koad155>
- 8) Li, J., F. Han, T. Yuan, W. Li, Y. Li, H. X. Wu, **H. Wei** and S. Niu. 2023. The methylation landscape of giga-genome and the epigenetic timer of age in Chinese pine. **Nature Communication** 14, 1947.
<https://doi.org/10.1038/s41467-023-37684-6>
- 9) Wang, L., L. Wang, T. Ye, J. Zhao, L. Wang, **H. Wei**, P. Liu, and M. Liu. 2023. Autotetraploidization alters morphology, photosynthesis, cytological characteristics and fruit quality in sour jujube. **Plants** 12, 1106. <https://doi.org/10.3390/plants12051106>
- 10) Liu, Y., R. Wang, J. Yu, S. Huang, Y. Zhang, **H. Wei** and Z. Wei. 2023. Genome-Wide identification and characterization of auxin response factor (ARF) gene family involved in wood formation and response to exogenous hormone treatment in *Populus trichocarpa*. **International Journal of Molecular Sciences** 24(1):740. <https://doi.org/10.3390/ijms24010740>
- 11) Zhang, Y., J. Yu, X. Xu, R. Wang, Y. Liu, S. Huang, **H. Wei** and Z. Wei. 2022. Molecular mechanisms of diverse auxin responses during plant growth and development (Review Article). **International Journal of Molecular Sciences** 23, 12459. <https://doi.org/10.3390/ijms232012495>
- 12) Wei, M., M. Zhang, J. Sun, Y. Zhao, S. Pak, M. Ma, Y. Chen, H. Lu, J. Yang, **H. Wei**, Y. Li, C. Li. 2022. PuHox52 promoted coordinated uptake of nitrate, phosphate and iron under nitrogen deficiency in *Populus ussuriensis*. **Journal of Integrative Plant Biology** 65(3):791-809.
<https://doi.org/10.1111/jipb.13389>

- 13) Borthakur, D., V. Busov, X. H. Cao, Q. Du, O. Gailing, F. Isik, J.H. Ko, C. Li, Q. Li, S. Niu, G. Qu, T.H. G. Vu, X.R. Wang, Z. Wei, L. Zhang and **H. Wei** *. 2022. Current status and trends of forest genomics (Review Article). *Forestry Research* 2:11 doi: <https://www.maxapress.com//article/doi/10.48130/FR-2022-0011>
- 14) Huang, X., W. Wang, T. Gong, D. A. Wickell, L.Y. Kuo, X. Zhang, J. Wen, H. Kim, F. Lu, H. Li, W. Wu, W. Fan, S. Chen, X. Bao, L. Li, D. Zhang, L. Jiang, X. Peng, X. Dai, X. Yan, Z. Liao, J. Ralph, R. R. Sederoff, **H. Wei** *, P. Zhu *, F. Li*, R. Ming * and Q. Li *. 2022. The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. *Nature Plants* 8:500-512. <https://doi.org/10.1038/s41477-022-01146-6>
- 15) Wang, H., S. Pak, J. Yang, Y. Wu, W. Li, H. Feng, J. Yang, **H. Wei** * and C. Li *. 2022. Two high hierarchical regulators, PuMYB40 and PuWRKY75, control the low phosphorus driven adventitious root formation in *Populus ussuriensis*. *Plant Biotechnology Journal* 20(8):1561-1577 <https://doi.org/10.1111/pbi.13833>.
- 16) Niu, S*, J. Li, W. Bo, W. Yang, A. Zuccolo, S. Giacomello, J. Ma, F. Han, X. Chen, J. Yang, Y. Song, Y. Nie, B. Zhou, P. Wang, Q. Zuo, H. Zhang, J. Wang, L. Wang, Z. Liu, X. Zhang, T. Liu, S. Pei, Z. Li, Y. Hu, Y. Yang, W. Li, J. Lin, Y. Zan, L. Zhou, T. Yuan, W. Li, Y. Li, **H. Wei** * and H. X. Wu*. 2022. The Chinese pine genome and methylome unveil key features of conifer evolution. *Cell* 185(1):204-217. <https://doi.org/10.1016/j.cell.2021.12.006>
- 17) Kang X and Wei H. 2022. Breeding polyploid *Populus*: progress and perspective (Review Article). *Forestry Research* 1: 4 doi: [10.48130/FR-2022-0004](https://doi.org/10.48130/FR-2022-0004)
- 18) Tao, S., P. Liu, Y. Shi, Y. Feng, J. Gao, L. Chen, A. Zhang, X. Cheng, **H. Wei**, T. Zhang, and W. Zhang. 2022. Single cell transcriptome and network analyses unveil key transcription factors regulating mesophyll cell development in maize. *Genes* 13, 374. <https://doi.org/10.3390/genes13020374>
- 19) Ren, M., Y. Zhang, R. Wang, Y. Liu, M. Li, X. Wang, X. Chen, X. Luan, H. Zhang, **H. Wei**, C. Yang, Z. Wei. 2022. PtrHAT22, as a higher hierarchy regulator, coordinately regulates secondary cell wall component biosynthesis in *Populus trichocarpa*. *Plant Science* 316 (2022) 111170. <https://doi.org/10.1016/j.plantsci.2021.111170>
- 20) Gao, C., **H. Wei** and K. Zhang. 2021. LORSEN: fast and efficient eQTL mapping with low rank penalized regression. *Frontier of Genetics*. 12:690926. <https://doi.org/10.3389/fgene.2021.690926>
- 21) Lv, K., **H. Wei** and G. Liu. 2021. A R2R3-MYB transcription factor gene, *BpMYB123*, regulates *BpLEA14* to improve drought tolerance in *Betula platyphylla*. *Frontier of Plant Science* 12:791390. doi: 10.3389/fpls.2021.791390 <https://doi.org/10.3389/fpls.2021.791390>
- 22) Lin, G, C. He, J. Zheng, D.H. Koo, H. Le, H. Zheng, T. M. Tamang, J. Lin, Y. Liu, M. Zhao, Y. Hao, F.

- McFrand, B. Wang, Y. Qin, H. Tang, D.R. McCarty, **H. Wei**, M.J. Cho, S. Park, H. Kaepler, S. Kaepler, N. Springer, Y/ Liu, P.S. Schnable, G. Wang, F. F. White, S. Liu. 2021. Chromosome-level genome assembly of a regenerable maize Inbred line A188. **Genome Biology** **22**, 175 (2021). <https://doi.org/10.1186/s13059-021-02396-x>
- 23) Gao, J., P. Zhang, W. Wu, **H. Wei*** and W. Zhang*. 2021. Toward an understanding of the detection, and function of R-loops in plants (Review paper). **Journal of Experimental Botany** **72**(18):6110-6122. <https://doi.org/10.1093/jxb/erab280>. (Review)
- 24) Wang, R., M. Ren, S. Tian, C. Liu, H. Cheng, Y. Liu, H. Zhang, S. Muhammad, **H. Wei**, Z. Wei. 2021. Transcriptome-wide identification and characterization of microRNAs in diverse phases of wood formation in *Populus trichocarpa*. **G3: Genes, Genomes, Genetics** **11**(8). <https://doi.org/10.1093/g3journal/jkab195>.
- 25) Wang, Q., X. Dai, H. Pang, Y. Cheng, X. Huang, H. Li, X. Yan, F. Lu, **H. Wei**, R. R. Sederoff, Q. Li. 2021. BEL1-like homeodomain protein BLH6a is a negative regulator of CAld5H2 in syringyl monolignol biosynthesis in poplar. **Frontiers in Plant Science** **12**:695223 <https://doi.org/10.3389/fpls.2021.695223>
- 26) Hong, J., C. Gunasekara, C. He, C., S. Liu, J. Huang and **H. Wei ***. 2021. Identification of biological pathway and process regulators using sparse partial least squares and triple-gene mutual interaction. **Scientific Reports** **11**, Article number: 13174. <https://doi.org/10.1038/s41598-021-92610-4>
- 27) Lv, K., W. Wu, **H. Wei**, G. Liu*. 2021. A systems biology approach identifies *Bp/ERF1* as a regulator of cold tolerance in *Betula platyphylla*. **Forestry Research** **1**: 13 doi: [10.48130/FR-2021-0013](https://doi.org/10.48130/FR-2021-0013)
- 28) Wu, W., K. Du, X. Kang* and **H. Wei***. 2021. The diverse roles of cytokinins in regulating leaf development (Review). **Horticulture Research** **8**:118. <https://doi.org/10.1038/s41438-021-00558-3>
- 29) Wu, W., Liao, T., Du, K., **Wei, H.** and Kang, X. 2021. Transcriptome comparison of different ploidy reveals the mechanism of photosynthetic efficiency superiority of triploid poplar. **Genomics** **113**(4): 2211-2220.
- 30) Ren, M., Y. Zhang, C. Liu, Y. Liu, S. Tian, H. Cheng, H. Zhang, **H. Wei**, and Z. Wei*. 2021. Characterization of a high hierarchical regulator, PtrGATA12, functioning in differentially regulating secondary wall component biosynthesis in *Populus trichocarpa*. **Frontier of Plant Science** **12** Article 657787. <https://doi.org/10.3389/fpls.2021.657787>.
- 31) Li, J., Y. Wang, **H. Wei** and X. Kang. 2021. Comparative proteomic analysis provides insight into the molecular mechanism of vegetative growth advantage in allotriploid *Populus*. **Genomics** **113**(3):1180-1192.

- 32) Deng, W., K. Zhang, C. He, S. Liu and **H. Wei** *. 2021. HB-PLS: A statistical method for identifying biological process or pathway regulators by integrating Huber loss and Berhu penalty with partial least squares regression. *Forestry Research*. 1: 6 doi: 10.48130/FR-2021-0006.
- 33) Lv, Kaiwen, **H. Wei**, and Guifeng Liu. 2021. A R2R3-MYB transcription factor gene, BpMYB123 regulates BpLEA14 to improve drought tolerance in *Betula platyphyll*. *Frontier of Plant Science* 12:791390. doi: 10.3389/fpls.2021.791390.
- 34) Zhao, M., P. Zhao, Y. Qin, L. Zhang, B.Tian, Y. Chen, Y. Liu, G. Lin, H. Zheng, C. He, K. Lv, H.N. Trick, Y. Liu, M. Cho, S. Park, **H. Wei**, J. Zheng, F. F. White, S. Liu. 2021. Bacterium-enabled transient gene activation by artificial transcription factor for resolving gene regulation in maize. bioRxiv doi: <https://doi.org/10.1101/2021.02.05.429970>.
- 35) Wu, W., J. Li, Q. Wang, K. Lv, K. Du, W. Zhang, Q. Li, X. Kang* and **H. Wei***. 2021. Growth-regulating factor 5 (GRF5)-mediated gene regulatory network promotes leaf growth and expansion in triploid poplar. *New Phytologist* 230: 612–628. <https://doi.org/10.1111/nph.17179>
- 36) Chen, S., G., Y. Wang, L. Yu, T. Zheng, S. Wang, Z. Yue, J. Jiang, S. Kumari, C. Zheng, H. Tang, J. Li, Y. Li, J. Chen, W. Zhang, H. Kuang, J. Robertson, P. Zhao, H. Li, S. Shu, Y. Yordanov, H. Huang, D. Goodstein, Y. Gai, Q. Qi, J. Min, C. Xu, S. Wang, G. Qu, A. Paterson, D. Sankoff, **H. Wei**, G. Liu and C. Yang. 2021. Genome sequence and evolution of *Betula platyphylla*. *Horticulture Research* 8: 37(2021). <https://doi.org/10.1038/s41438-021-00481-7>
- 37) Cheng, Y, L. Wang, M. Abbas, X. Huang, Q. Wang, A. Wu, **H. Wei**, S. Peng, X. Dai, and Q. Li. 2021. MicroRNA319-mediated gene regulatory network impacts leaf development and morphogenesis in poplar. *Forestry Research* 1: 4, doi: 10.48130/FR-2021-0004
- 38) **Wei, H.** 2021. Inaugural editorial. *Forestry Research* (10.48130/FR-2021-0001).
- 39) Wei, M., Q. Liu, Z. Wang, J. Yang, W. Li, Y. Chen, H. Lu, J. Nie, B. Liu, K. Lv, X. Mao, S. Chen, J. Sanders, **H. Wei*** and Chenghao Li *. 2020. PuHox52-mediated hierarchical multilayered gene regulatory network promotes adventitious root formation in *Populus ussuriensis*. *New Phytologist*. 228(4): 1369-1385. <https://nph.onlinelibrary.wiley.com/doi/full/10.1111/nph.16778>
- 40) Li, Y., **H. Wei**, J. Yang, L. K. Du, J. Li, Y. Zhang, T. Qiu, Z. Liu, Y. Ren, L. Song, X. Kang. 2020. High quality de novo assembly of the *Eucommia ulmoides* haploid genome provides new insights into the evolution and rubber biosynthesis. *Horticulture Research*. 7:183. <https://doi.org/10.1038/s41438-020-00406-w>
- 41) Li, J. Y. Wang, **H. Wei** and X. Kang. 2020. Comparative proteomic analysis of leaf development in allotriploid *Populus* originated from first-division restitution (FDR). *Forests* 2020, 11(11), 1154;

- 42) Lv, K., **H. Wei**, J. Jiang, 2020. Overexpression of *BpIERD15* enhances drought tolerance in *Betula platyphylla*. **Forests** 11(9): 978.
- 43) He, C., G. Lin, **H. Wei**, H. Tang, F. F. White, B. Valent, and S. Liu. 2020. Factorial estimating assembly base errors using *k*-mer abundance difference (KAD) between short reads and genome assembled sequences. **NAR Genomics and Bioinformatics** Vol. 2, No. 3: 1-14.
<https://doi.org/10.1093/nargab/lqaa075>
- 44) Zhang, Y., C. Liu, H. Cheng, S. Tian, Y. Liu, S. Wang, H. Zhang, M. Saqib, **H. Wei**, Z. Wei*. 2020. The DNA methylation and its effects on gene expression during primary to secondary growth in poplar stems. **BMC Genomics**. 21:489. <https://doi.org/10.1186/s12864-020-06902-6>
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- 46) Zhang, P., Y. Feng, **H. Wei*** and W. Zhang*. 2019. R-loop identification and profiling in plants. **Trends in Plant Science** 24(10):971-972.
- 47) Fang, Y, L. Chen, K. Lin, Y. Feng, P. Zhang, J. Sanders, X. Pan, Y. Wu, X. Wang, Z. Su, C. Chen, **H. Wei***, W. Zhang*. 2019. Characterization of functional relationships of R-loops with gene transcription and epigenetic modifications in rice. **Genome Research** 29(8):1287-1297.
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- 50) Wang, L. Z. Luo, L. Wang, W. Deng, **H. Wei**, P. Liu, M. Liu. 2019. Morphological, cytological and nutritional changes of autotetraploid compared to its diploid counterpart in Chinese jujube (*Ziziphus jujuba* Mill.). **Scientia Horticulture** 249: 263-270.
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- 103) **Wei H.** 1989. Studies on juvenile-mature correlation between quantitative traits and early selection ages of *Ulmus pumila*. *Journal of Inner Mongolia Forestry College*. Vol.11.

D. Patents

- 1) Albert, H and **H. Wei**. Sugarcane Ubi9 gene promoter and methods of use thereof. 2004, U.S. Patent No. 6706948 (<http://www.uspto.gov>).

- 2) Albert, H and **H. Wei**. Promoter of the sugarcane Ubi9 gene. 2004. U.S. Patent No. 6686513 B1 (<http://www.uspto.gov>).
- 3) Albert, H and **H. Wei**. Promoter of the sugarcane Ubi4 Gene. 2003. U.S. Patent No. 6638766 (<http://www.uspto.gov>).

E. Bioinformatics Software and Tools

(Note that sys.bio.mtu.edu server is currently under re-construction and not available)

1. **TF-Finder**: A tool for identifying genes involved in a biological process. *BMC Bioinformatics*, 2010. (<http://sys.bio.mtu.edu/software.php>). (Correspondence author)
2. **TF-Cluster** A tool for identifying genes that govern biological process and complex trait. *BMC System Biology*, 2011. (Correspondence author) (https://github.com/hwei0805/TF_CollaborativeNet).
3. **DeGNServer** (<http://plantgrn.noble.org/DeGNServer/>). *Biomed Research International*, 2013.
4. **GPLUXUS** (<http://plantgrn.noble.org/GPLEXUS/>). *Nucleic Acid Research*, 2013
5. **Coexpression**: Eight gene association methods for constructing co-expression network. PloS One 2012. (Correspondence author) (R script: <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0050411>)
6. **Pop's Pipes** (<http://sys.bio.mtu.edu/index.php>). *Tree Genetics & Genome*, 2014 (Correspondence author)
7. **Blossom Plasmid Vector** (<https://blossom.ffr.mtu.edu/index.php>). A tool for designing plasmid vectors that target microRNAs for degradation. *Molecular Plant*. 2018.
8. **ExactSearch**: A web-based plant motif search tool. *Plant Method* 2016. (Corresponding author) <http://sys.bio.mtu.edu/motif/index.php>.
9. **BWERF**: Backward elimination random forests for constructing multilayered gene regulatory networks. *PLoS ONE* 2017: 12(2): e0171532. (Correspondence author). R package is available at: <https://doi.org/10.1371/journal.pone.0171532.s004> (zip)
10. **SSGA** and **MSGa**: two seed-growing algorithms for constructing collaborative subnetworks. *Scientific Reports*. 2017. (Correspondence author) <https://www.nature.com/articles/s41598-017-01556-z>
11. **TF-Miner**: <http://sys.bio.mtu.edu/cluster/>. Submitted to *BMC Genomics* (Correspondence author)
12. **Top-down GGM algorithm**: An algorithm that uses Gaussian Graphical Model to construct hierarchical gene regulatory network-mediated by one regulator. *BMC Bioinformatics* 2016: 17:132. <http://sys.bio.mtu.edu/topdown/> (Correspondence author)
13. **Bottom-up GGM algorithm**: An algorithm that uses Gaussian Graphical Model to construct of an hierarchical gene regulatory network that governs a biological process/pathway. *BMC Bioinformatics* 2016: 17:132. (Correspondence author). <http://sys.bio.mtu.edu/topdown/>

14. **TGMI**: An algorithm for identifying pathway regulators. Mar 2018. (R package is available on NAR Web page). *Nucleic Acids Research*. 46(11):e67. (Correspondence author)
http://sys.bio.mtu.edu/sample_output/TGMI/
15. **JRmGRN**: Joint reconstruction of multiple gene regulatory networks with common hub genes using OMICS data from multiple tissues or conditions (R package is available on Bioinformatics Web page). 2018. *Bioinformatics* 5;34(20):3470-3478. (Correspondence author)
R Package: <https://github.com/wenpingd>
16. **HB-PLS**: Huber loss and Berhu penalty with Partial Least Square (PLS) for identifying pathway regulators. 2021. *Forestry Research*. (Correspondence author) <https://github.com/hwei0805/>
17. **LORSEN** (low rank penalized regression method): a fast and efficient eQTL mapping method. *Frontier Genetics*. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8636089/>
18. **Huber-ENET, Huber-Lasso, Huber-Net, MSE-ENET, MSE-Lasso, and MSE-Net**. A highly effective package that comprises six methods for predicting target genes of a transcription factor of interest using OMICS data. 2023. *NAR Genomics and Bioinformatic*. (Correspondence author)
R code: <https://zenodo.org/record/8297854>; Python: <https://zenodo.org/record/>
19. **Web Portal: Genomic Surveillance and Epidemiology in the Upper Peninsula** (Team leader)
<https://mtu.bxngs.com/web/index.php>

F. Teaching

- FW5092 Experimental Design, Spring 2018, 2022, and 2024.
 FW4099 Programming Skills for Bioinformatics, Fall 2009, 2011, 2013, 2015, 2019, and 2023.
 FW5082 Gene Expression Data Analysis, Fall 2010, 2012, 2018, and 2020.
 CS2321 Data Structure in Java, Spring 2011.
 FW5084 Data Representation with R, Spring 2012, 2021 and 2023.
 BMB6030 Advanced Molecular Biology Lab, Spring 2013, 2014 and 2015.
 FW3320 Fundamental of Genetics, Spring 2013.
 FW3200 Forest Biometrics and Data Analysis, Spring 2014, 2015 and 2016.

G. Graduate Students

Current:

- Ph.D. Md Khairul Islam, Computational Science & Engineering, Fall 2022 – now

Past:

- Ph.D. Wenping Deng, 2018, Bioinformatics, Huawei, Inc. China.
 Ph.D. Chathura Gunasekara, 2017, Computational Science & Engineering, Baylor College, USA.
 Ph.D. Sapna Kumari, 2013, Mathematics, FDA, Maryland. USA.
 MS Sai Teja Mummadi, 2023, Computer Science.
 MS Joshua Marshall, 2019, Computer Science, The Jackson Laboratory. CT, USA
 MS Avinash Subramanian, 2017, Computer Science, Midwest Veterinary Inc. MN, USA.
 MS Jialin Lei, 2017, Computer Science, Amazon, CA. USA
 MS Saeed Binsabaan, 2014, Molecular Biology. Tobacco Industry, Saudi Arabia
 MS Xiang Li, 2012, Computer Science, Senior Developer, Anthem, Inc. Virginia. USA.
 MS Hang Zhang, 2011, Computer Science, Web Developer at US Biotek Laboratories. USA.

MS Yang Li, 2011, Molecular Biology. Beijing Pharmaceutical Company, China.

Committees:

Biology:

Christine Zawaski, Ph.D. 2009; Fuyu Xu, Ph.D., 2009; Zijun Xu, Ph.D., 2009; Yiru, Chen, Ph.D. 2012; Surendar Dhadi, Ph.D., Biology, 2012; Yiru Chen, Ph.D. 2012, Kefeng Li, Ph.D., 2012, Rafi Shaik, Ph.D., 2013; Sermsawat Tunlaya-Anukit, Ph.D. NCSU (external) 2014, Weilue He, Ph.D. 2015; Lukai Zhai, Ph.D. 2018; Mujeeb Shittu, Ph.D., 2021; Deepak Kumar, MS, 2010; Mengmeng Qiao, MS. 2015, Priyanka Dipak Kadav, MS, 2015, Chelsea Elizabeth Mundell, MS, 2016, James Rauschendorfer, MS, 2017; Ryan Williams, MS, 2019, Will Dion, MS, 2020, and Emma Burke, MS, 2023.

Mathematics:

Xiaoqi Cui, Ph.D., 2010; Beini Jiang, Ph.D., 2012; Erin Thomas, Ph.D. 2012, Xiaoyu Liang, Ph.D. 2018, Cheng Gao, Ph.D., 2021; Xiaoqing Gao, Ph.D. 2023, Tessa Kriz, MS, 2021

Bioinformatics and Data Science:

William Roland, MS, 2021; Zayne Knuth, 2022, Ling Zhang, 2021

H. Editorial Board Members of Scientific Journals

- 1) Editor-in-Chief, **Forestry Research**, 2020 ~ present
<http://www.maxapress.com/journal/forres>
- 2) Associate Editor for **Horticulture Research**, 2022 ~ Present
<https://academic.oup.com/hr/pages/editorial-board>
- 3) Associate Editor for **Frontier of Plant Science: Plant Biotechnology**, 2011 ~ present.
<https://www.frontiersin.org/journals/plant-science/sections/plant-biotechnology#editorial-board>
- 4) Guest Co-editor. Forestry Biosafety (6 articles published). 2022. Frontiers in Bioengineering.
- 5) Guest Co-editor. Molecular mechanisms of Fruit Quality Formation in Fruit Trees. 2023. Frontier in Plant Science.
- 6) Member of the American Association for the Advancement of Science (AAAS).
- 7) Member of American Association of Plant Biology (ASPB).
- 8) Tenure, Promotion, and Reappointment (TPR) Committee, 2018-Present.

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