

Professor in Plant Bioinformatics and Molecular Biology  
College of Forest Resources and Environmental Science (home)  
Department of Computer Science (Adjunct)  
Department of Mathematics (Adjunct)  
Michigan Technological University  
Houghton, MI 49931  
1400 Townsend Drive, Houghton, MI 49931  
Tel: (906) 487-1473; Fax: (906)487-2915  
Email: [hairong@mtu.edu](mailto:hairong@mtu.edu)

## A. Current Research Interests

- Regulation of plant regeneration
- Plant adventitious rooting
- Wood formation and bioenergy
- Development of algorithms for gene regulatory network construction
- Plant functional genomics
- Development of bioinformatics tool and software for Identifying genes regulating complex traits
- Genome assembly and annotation
- R-loop and gene regulation
- Machine learning and deep Learning
- SARS-CoV-2 variant detection

## B. Education and Training

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

## C. 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 Microarray Data Analyst, WiCell Research Institute, Inc., Madison, WI  
2005 ~ 2006 Microarray Design 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, 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

**D. Publications & Patents (Citations = 5438. \* Correspondence/co-correspondence)**

- 1) Li, J., F. Han, T. Yuan, W. Li, Y. Li, H. X. Wu, **H. Wei** and S. Niu. 2023. Epigenetic timer of age in giga-genome of Chinese pine. *Nature Communication* (Accepted) (**JIF = 17.69**)
- 2) 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>
- 3) 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> (**JIF = 6.21**)
- 4) 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> (**JIF = 6.21**)
- 5) 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*. <https://doi.org/10.1111/jipb.13389> (**JIF = 9.1**)
- 6) 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>
- 7) 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. (**JIF = 17.35**) <https://doi.org/10.1038/s41477-022-01146-6>
- 8) 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*, pp. 1-17 (**JIF = 13.2**) <https://doi.org/10.1111/pbi.13833>
- 9) 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. (**JIF = 41.58**) <https://doi.org/10.1016/j.cell.2021.12.006>
- 10) 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)
- 11) 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>
- 12) 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>
- 13) 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>
- 14) 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 (**JIF 5.75**). <https://doi.org/10.3389/fpls.2021.791390>
- 15) 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. Kaeppler, S. Kaeppler, 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). (**JIF =13.58**) <https://doi.org/10.1186/s13059-021-02396-x>
- 16) 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. (**JIF =6.99**). <https://doi.org/10.1093/jxb/erab280>. (Review)
- 17) 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** <https://doi.org/10.1093/g3journal/jkab195>.
- 18) 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 (**JIF 5.75**). <https://doi.org/10.3389/fpls.2021.695223>

- 19) 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>
- 20) 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)
- 21) Wu, W., K. Du, X. Kang\* and **H. Wei**\*. 2021. The diverse roles of cytokinins in regulating leaf development (Review). **Horticulture Research** 8:118 (**JIF =6.67**)  
<https://doi.org/10.1038/s41438-021-00558-3>
- 22) 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 (**JIF =6.2**).
- 23) 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> (**JIF 5.75**).
- 24) 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. (**JIF =6.2**).
- 25) 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.
- 26) 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. (**JIF 5.75**).
- 27) 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>.
- 28) 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. (**JIF =10.15**) <https://doi.org/10.1111/nph.17179>
- 29) 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) (**JIF =6.67**). <https://doi.org/10.1038/s41438-021-00481-7>
- 30) 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
- 31) **Wei, H.** 2021. Inaugural editorial. *Forestry Research* (10.48130/FR-2021-0001).
- 32) 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. (**JIF =10.15**) <https://nph.onlinelibrary.wiley.com/doi/full/10.1111/nph.16778>
- 33) 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 (**JIF =6.67**) <https://doi.org/10.1038/s41438-020-00406-w>
- 34) 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;
- 35) Lv, K., **H. Wei**, J. Jiang, 2020. Overexpression of *BpIERD15* enhances drought tolerance in *Betula platyphylla*. *Forests* 11(9): 978.
- 36) 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>
- 37) 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>
- 38) Lv, K., J. Li, K. Zhao, S. Chen, J. Nie, W. Zhang, G. Liu\* and **H. Wei\***. 2019. Overexpression of an AP2/ERF family gene, BpERF13, in birch enhances cold tolerance through upregulating CBF genes and mitigating reactive oxygen species. *Plant Science* 292:110375.
- 39) 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. (**JIF =14.42**)

- 40) 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. (**JIF =11.1**) <https://doi.org/10.1101/gr.246009.118>
- 41) **Wei. H\***. 2019. Construction of a hierarchical gene regulatory network centered around a transcription factor (Review). *Briefings in Bioinformatics* 20(3):1021-1031. (**JIF =9.3**). <http://www.genome.org/cgi/doi/10.1101/gr.246009.118>
- 42) Wang, L, Z. Luo, Z. Liu, J. Zhao, W. Deng, **H. Wei**, P. Liu, M. Liu. 2019. Genome size variation within species of Chinese jujube (*Ziziphus jujuba* Mill.) and its wild ancestor sour jujube. *Forests* 10(5):460
- 43) Li, M, S. Wang, L. Liu, T. Lu, Y. Liu, Y. Zhang, M. Ren, **H. Wei**, Z. Wei. 2019. Overexpression of PsnSuSy1, 2 genes enhance secondary cell wall thickening, vegetative growth, and mechanical strength in transgenic tobacco. *Plant Molecular Biology*, 100(3):215-230.
- 44) 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.
- 45) Gunasekara, C, K. Zhang, W. Deng, L. Brown and **H. Wei\***. 2018. TGMI: an efficient algorithm for identifying pathway regulators through evaluation of triple-gene mutual interaction. *Nucleic Acids Res.* 46(11):e67. (**JIF = 11.57**) <https://doi.org/10.1093/nar/gky210>
- 46) Deng, W., K. Zhang, S. Liu, P. Zhao and S. Xu and **H. Wei\***. 2018. JRmGRN: Joint reconstruction of multiple gene regulatory networks with common hub genes using data from multiple tissues or conditions. *Bioinformatics* 34(20):3470-3478. (**JIF =7.3**). <https://doi.org/10.1093/bioinformatics/bty354>
- 47) Zheng, J., C. He, Y. Qin, G. Lin, D. Park, M. Sun, J. Li, X. Lu, C. Zhang, C. Zhang, D. D Bade, CT “Eddy” Yeh, E. Zeng, **H. Wei**, P. S. Schnable, G. Wang, S. Liu. 2019. Co-expression analysis aids in the identification of new genes in the epicuticular wax pathway. *Plant Journal* 97: 530-542 (**JIF =5.8**)
- 48) Peng, T., M. Qiao, H. Liu, S. Teotia, Y. Zhao, D. Zhao, L. Shi, B. Le, K. Rogers, C. Gunasekara, H. Duan, Y. Gu, L. Tian, Z. Zhang, F. Meng, L. Huang, Q. Chen, Z. Wang, J. Tang, X. Tang, X. Chen\*, **H. Wei\***, Q. Zhao\* and G. Tang\*. 2018. A resource for inactivation of microRNAs using short tandem target mimic technology in model and crop plants. *Molecular Plant* 11(11):1400-1417. (**JIF =9.3**). <https://doi.org/10.1016/j.molp.2018.09.003>
- 49) Liu, Z., J. Zhu, X. Yang, H. Wu, Q. Wei, **H. Wei**, H. Zhang\*. 2018. Growth performance, ion organ-level relations and osmotic regulation of *Elaeagnus angustifolia* in response to salt stress. *PLoS ONE* 13(1): e0191552.

- 50) Lu, T., L. Liu, M. Wei, Y. Liu, Z. Qu, C. Yang, **H. Wei\*** and Z. Wei\*. 2018. The effect of poplar PsnGS1 overexpression on growth and secondary cell wall and fibre characteristics in tobacco. *Frontier of Plant Science* 9:9. doi: 10.3389/fpls.2018.00009.
- 51) Dash, M, Y. Yordan, T. Georgieva, **H. Wei** and V. Busov\*. 2018. Gene network analysis of poplar root transcriptome in response to drought stress identifies a PtaJAZ3 and PtaRAP2.6 centered hierarchical network. *PLoS ONE* 13(12): e0208560. <https://doi.org/10.1371/journal.pone.0208560>
- 52) Ji, X. S. Chen, J. Li, W. Deng, Z. Wei and **H. Wei\***. 2017. SSGA and MSGA: two seed-growing algorithms for constructing collaborative subnetworks. *Scientific Reports*. 7:1446, DOI:10.1038/s41598-017-01556-z (**JIF =5.3**).
- 53) Liu, Y., M. Wei, C. Hou, T. Lu, L. Liu, **H. Wei**, Y. Cheng and Z. Wei. 2017. Functional characterization of Populus PsnSHN2 in coordinate regulation secondary wall components in tobacco. *Scientific Reports* 7(1):42. doi: 10.1038/s41598-017-00093-z (**JIF =5.3**).
- 54) Mitchell, C.L., C.E. Latuszek, K. R. Vogel, I. M. Greenlund, R. E. Hobmeier, O. K. Ingram, S. R. Dufek, J. L. Pecore, F. R. Nip, Z. J. Johnson, X. Ji, **H. Wei**, O. Gailing, and T. Werner. 2017.  $\alpha$ -amanitin resistance in *Drosophila melanogaster*: a genome-wide association approach. *PLoS ONE*. 12(2): e0173162. doi:10.1371/journal.pone.0173162.
- 55) Deng, W., K. Zhang, V. Busov and **H. Wei\***. 2017. Recursive random forest algorithm for constructing multilayered hierarchical gene regulatory networks that govern biological pathways. *PLoS ONE* 12(2):e0171532. DOI:10.1371/journal.pone.0171532.
- 56) Ma, H., G.M. Weber, H. Wei, and J. Yao. 2016. Identification of mitochondrial genome-encoded small RNAs related to egg deterioration caused by post-ovulatory aging in rainbow trout. *Marine Biotechnology* 18(5): 584-597
- 57) Dash, M, Y. Yordan, S. Kumari, T. Georgieva, H. Wei and V. Busov. 2016. A network of genes associated with poplar root development in response to low nitrogen. *Plant Signaling & Behavior* 11(8):e1214792.
- 58) Tang, F. **H. Wei**, S. Zhao, L. Wang, H. Zheng, M. Lu. 2016. Identification of microRNAs involved in regeneration of the secondary vascular system in *Populus tomentosa* Carr. *Frontiers in Plant Science*. 2016, 7(Article 724):1-17
- 59) Gunasekara, C., A. Subramanian, Avvari, R. K., B. Li, Chen, S. and **H. Wei\***. 2016. ExactSearch: A web-based plant motif search tool (<http://sys.bio.mtu.edu/motif/index.php>). *Plant Methods* 12:26
- 60) Kumari, S., W. Deng, C. Gunasekara, V. Chiang, H.S. Chen, H. Ma, X. Davis, and **H. Wei\***. 2016. Bottom-up GGM algorithm for constructing multilayered hierarchical gene regulatory networks that govern biological pathways or processes. *BMC Bioinformatics* 17: 132

- 61) Dash, M, Y. Yordan, S. Kumari, T. Georgieva, **H. Wei** and V. Busov. 2015. A system biology approach identifies new regulators of poplar root development under low nitrogen. *Plant Journal* 84(2): 335-46 (**JIF = 5.97**). <https://doi.org/10.1111/tpj.13002>
- 62) Li, J. **H. Wei**, T. Liu, X. Dai, P.X. Zhao. 2015. Legume: An integrative platform for comparative genomics and transcriptomics of model legumes. Frans J. de Bruijn (eds). Biological Nitrogen Fixation. Vol2. Wiley-Black.
- 63) Wei, Z, Z. Qu, L. Zhang, S. Zhao, Z. Bi, X. Ji, X. Wang and **H. Wei\***. 2015. Overexpression of poplar xylem sucrose synthase in tobacco leads to a thickened cell wall and increased height. *PLoS ONE*. 10(3):e0120669.
- 64) Ma, H., M. Weber, M. Hostuttler, **H. Wei**, L. Wang and J. Yao. 2015. MicroRNA expression profiles from eggs of different qualities associated with post-ovulatory ageing in rainbow trout. *BMC Genomics*. 16:201. doi:10.1186/s12864-015-1400-0.
- 65) Wei, Z., Z. Qu, C. Hou, Y. Liu, L. Zhang, C. Yang and **H. Wei\***. 2015. Genetic diversity and paternal analysis of open-pollinated progenies of Larix olgensis seed orchard. *Journal of Nature and Science*. Vol.1 No.1 E19.
- 66) Yang, C and **H. Wei\***. 2014. Designing microarray and RNA-seq experiments for greater systems biology discovery in modern plant genomics (Review Article). *Molecular Plant* 8, 196–206. (**JIF =8.8**). <https://doi.org/10.1093/mp/ssu136>
- 67) Zhang, W., R. Wei, S. Chen, J. Jiang, H. Li, H. Huang, G. Yang, S. Wang, H. Wei and G. Liu. 2014. Functional Characterization of Cinnamoyl-CoA Reductase (CCR) in Birch (*Betula platyphylla* × *Betula pendula*) through overexpression and suppression analysis. *Physiologia Plantarum* 154(2):283-96. .
- 68) Li, X, C. Gunasekara, Y. Guo, H. Zhang, L. Lei, S. Tunlaya-Anukit, V. Busov, V. Chiang, and **H. Wei\***. 2014. Pop's Pipes: poplar gene expression data analysis pipelines (<http://sys.bio.mtu.edu/index.php>). *Tree Genetics & Genome*. 10:1093-1101.
- 69) Mitchell, C. M. Saul, L. Lei, **H. Wei**, and T. Werner. 2014. The mechanisms underlying  $\alpha$ -amanitin resistance in *Drosophila melanogaster*: a microarray analysis. *PLoS ONE* 9(4): e93489.
- 70) Wang, S., W. Yao, **H. Wei**, T. Jiang, and B. Zhou. 2014. Expression patterns of ERF genes underlying abiotic stresses in dihaploid *Populus simonii* X *P. nigra*. *The Scientific World Journal*. Vol. 2014, Article ID 745091.
- 71) **Wei, H.Y.** Yordan, S. Kumari, T. Georgieva, V. Busov. 2013. Genetic networks involved in poplar root response to low nitrogen. *Plant Signal and Behavior*. 8(11). pii: e27211



- 72) Lin, Y.C., Li, W., Sun, Y.H., Kumari, S., **Wei, H.**, Li, Q.Z., Tunlaya-Anukit, S., Sederoff, R.R., and Chiang, V.L. 2013. SND1 transcription factor-directed quantitative functional hierarchical genetic regulatory network in wood formation in *Populus trichocarpa*. *Plant Cell* 25(11) 4324-4341. (**JIF =10.22**).
- 73) Li, J., **H. Wei**, T. Liu and P. Zhao. 2013. GPLEXUS: Enable genome-scale gene regulatory network analysis for plants through ultrafast mutual information computing and filtering. *Nucleic Acids Research* 42(5): e32 doi:10.1093/nar/gkt983. (**JIF = 8.3**).
- 74) **Wei, H.**, Y. Yordan, T. Georgieva, X. Li, V. Busov. 2013. Nitrogen deprivation promotes *Populus* root growth via global transcriptomic reprogramming and activation of hierarchical genetic networks. *New Phytologist*. 200 (2):483-497. (**JIF =6.5**). <https://doi.org/10.1111/nph.12375>
- 75) Li, J., **H. Wei** and P. X. Zhao. 2013. DeGNServer: Deciphering genome-scale gene networks through high performance reverse engineering analysis. *Biomed Research International* Vol. 2013 (856325):110.
- 76) Lu, S., Q. Li, **H. Wei**, M.J. Chang, S.T. Anukit, H. Kim, Liu, J., J. Song, Y.H. Sun, L. Yuan, T.F. Yeh, I. Peszlen, J. Ralph. R. R. Sederoff, V. L. Chiang. 2013. Ptr-miR397a is a negative regulator of laccase genes affecting lignin content in *Populus trichocarpa*. *Proc Natl Acad Sci USA* 110 (26) 10848-10853. (**JIF =9.9**). <https://doi.org/10.1073/pnas.1308936110>
- 77) Liu, Z., H. Zhang, X. Yang, and H. Wei. 2013. Effect of Soil Salinity on growth, ion relations and compatible solute accumulation of two sumac species: *Rhus glabra* and *Rhus trilobata*. *Communications in Soil Science and Plant Analysis*. 44(21): 3187-3204.
- 78) Wei, H\*. J. Gou, Y. Yordanov, H. Zhang, R. Thakur, W. Jones, A. Burton. 2013. Global transcriptome profiling of aspen trees under elevated [CO<sub>2</sub>] for identifying potential molecular mechanisms responsible for enhanced growth. *Journal of Plant Research*. V126, No 2: 305-320.
- 79) Kumari, S., J. Nie., H.S. Chen, R. Stewart, H. Ma, X. Li, M. Lu, W.M. Taylor, and **H. Wei\***. 2012. Evaluation of gene association methods for coexpression network construction and biological knowledge discovery. *PLoS ONE* 7(11): e50411. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3511551/>
- 80) Ma. H. Houttler, C., H. Wei, M. Recroad III, J. Yao. 2012. Characterization of the rainbow trout oocyte microRNA transcriptome (*Oncorhynchus mykiss*). *PLoS ONE* 7(6): e39649. doi:10.1371/journal.pone.0039649.
- 81) Nie, J., R. Stewart, F. Ruan, J. Thomson, H. Zhang, X. Cui and **H. Wei\***. 2011. TF-Cluster: a pipeline for identifying functionally coordinated transcription factors via network decomposition of the shared coexpression connectivity matrix (SCCM). *BMC Systems Biology*, 5:53. <https://doi.org/10.1186/1752-0509-5-53>.

- 82) Cui, X, T. Wang, H.S. Chen, V. Busov and **H. Wei\***. 2010. TF-Finder: A software package for identifying transcription factors involved in biological processes using microarray data and existing knowledge base. *BMC Bioinformatics*, 11:425. <https://doi.org/10.1186/1471-2105-11-425>
- 83) **Wei, H.**, P. F. Kuan, S. Tian, C. Yang, J. Nie, S. Sengupta, V. Ruotti, G. Jonsdottir, S. Keles, J. Thomson and R. Stewart. 2008. A study of the relationships between oligonucleotide properties and hybridization intensities in NimbleGen platform. *Nucleic Acids Res*, Vol. 36, No. 9:2926-2938. (*JIF* =7.2). <https://doi.org/10.1093/nar/nfn133>
- 84) Ming, R., S. Hou, Y. Feng, Q. Yu, A. Dionne-Laporte, J. Saw, P. Senin, W. Wang, S. Salzberg, X. Wang, Lyons, D. Rice, M. Riley, R. Skelton, J. Murray, C. Chen, M. Eustice, E. Tong, H. Albert, R. E. Paull, M.-L. Wang, Y. Zhu, M. Schatz, N. Nagarajan, R. Agbayani, P. Guan, A. Blas, J. Wang, J.-K. Na, T. Michael, E. V. Shakirov, B. Haas, J. Thimmapuram, D. Nelson, H. Tang, J. E. Bowers, J. Suzuki, S. Tripathi, K. Neupane, **H. Wei**, R. Singh, B. Irikura, N. Jiang, W. Zhang, K. Wall, G. Presting, A. Gschwend, Y. Li, A. Windsor, R. N. Pérez, M. J. Torres, F. A. Feltus, B. Porter, M. Paidi, M.-C. Luo, L. Liu, D. Christopher, P. H. Moore, T. Sugimura, C. dePamphilis, J. Jiang, M. Schuler, T. Mitchell-Olds, D. Shippen, J. Palmer, M. R. Freeling, A. H. Paterson, D. Gonsalves, L. Wang and M. Alam. 2008. The draft genome of the transgenic tropical fruit tree papaya (*Carica papaya* Linnaeus). *Nature*, Vol. 452, No. 7190:991996. (*JIF* =31). <https://doi.org/10.1038/nature06856>
- 85) Pan, P., S. Tian, J. Nie, C. Yang, V. Ruotti, **H. Wei**, G. Jonsdottir, R. Stewart, and J. Thomson. 2007. Whole genome analysis of Histone H3 lysine 4 and lysine 27 methylation in human embryonic stem cells. *Cell Stem Cell*, Vol. 1, No 3:299~312. (*JIF* =25.0) <https://doi.org/10.1016/j.stem.2007.08.003>
- 86) **Wei, H.**, S. Persson, T. Mehta, V. Srinivasasainagendra, L. Chen, G. Page, C. Somerville, A. Loraine. 2006. Transcriptional coordination of the metabolic network in *Arabidopsis thaliana*. *Plant Physiology* 142(2):762-74. (*JIF* =7.08). <https://doi.org/10.1104/pp.106.080358>
- 87) Persson, S., **H. Wei**, J. Milne, G. Page, C. Somerville. 2005. Identification of genes required for cellulose synthesis by regression analysis of public microarray data sets. *Proc Natl Acad Sci USA*, 102: 86338638. (Faculty 1000 evaluation) (*JIF* =9.9). <https://doi.org/10.1073/pnas.0503392102>
- 88) **Wei, H.**, Y. Kaznessis. 2005. Inferring gene regulatory relationships by combining target-target pattern recognition and regulator-specific motif examination. *Biotechnology and Bioengineering*. Vol. 89, No1: 53-77.
- 89) **Wei, H.** & Yiannis Kaznessis. 2004. Inferring gene regulatory networks using microarray data and SQL SERVER. Minnesota Supercomputing Institute Research Bulletin. Vol. 20, NO 2: 1-3.
- 90) Lee, K.M., S. Bhawan, T. Majima, **H. Wei**, V. Kumar. 2003. Cutting Edge: The NK cell receptor 2B4 augments Ag-specific CTL activity through CD48 ligation on neighboring T cells. *Journal of Immunology*. Vol.170, No 10: 4881. (*JIF* =6.31). <https://doi.org/10.4049/jimmunol.170.10.4881>

- 91) **Wei, H.**, H. Albert and P. Moore. 2003. Comparative expression analysis of two sugarcane polyubiquitin promoters and flanking sequences in transgenic plants. *Journal of Plant Physiology* 160, 1241-1251.
- 92) **Wei, H.**, H. Albert and P. Moore. 1999. Differential expression of sugarcane polyubiquitin gene and isolation of promoters from two highly expressed members of the gene family. *Journal of Plant Physiology*, Vol. 155, p513-519.
- 93) Albert, H and **H. Wei**. Sugarcane Ubi9 gene promoter and methods of use thereof. 2004, U.S. Patent No. 6706948 (<http://www.uspto.gov>).
- 94) Albert, H and **H. Wei**. Promoter of the sugarcane Ubi9 gene. 2004. U.S. Patent No. 6686513 B1 (<http://www.uspto.gov>).
- 95) Albert, H and **H. Wei**. Promoter of the sugarcane Ubi4 Gene. 2003. U.S. Patent No. 6638766 (<http://www.uspto.gov>).
- 96) **Wei, H.** F. Li., Y. Zhu, T. Dong. 1995. Some correlations between leaf structures of elms and resistance to leaf beetles. *Journal of Beijing Forestry University* (English edition). Vol.4, No. 1, pp.17-26.
- 97) **Wei, H.** 1994. Heterosis and cross breeding of forest trees (review). *Journal of Heibei Forestry College*. Vol.9, No.1, pp. 92-96.
- 98) **Wei, H.**, and Y., Zhu. 1991. Breeding strategies of *Ulmus pumila*. Genetic Improvement on Broadleaf Trees. Huang, M and Tu, Z (eds). Scientific and Technical Document Publisher, pp. 263-270.
- 99) **Wei, H.**1990. Comparison of genetics gain between two breeding strategies: clonal selection and seed orchard. *Forestry Science and Technology*. Vol. 236. No.1, pp 13-14.
- 100) **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.

## E. SOFTWARE AND COMPUTING TOOLS

(Note that sys.bio.mtu.edu is currently under re-construction)

1. **TF-Finder** (<http://sys.bio.mtu.edu/software.php>). *BMC Bioinformatics*, 2010.
2. **TF-Cluster** ([https://github.com/hwei0805/TF\\_CollaborativeNet](https://github.com/hwei0805/TF_CollaborativeNet)). *BMC System Biology*, 2011
3. **DeGNServer** (<http://plantgrn.noble.org/DeGNServer/>). *Biomed Research International*, 2013.
4. **GPLUXUS** (<http://plantgrn.noble.org/GPLEXUS/>). *Nucleic Acid Research*, 2013
5. **Coexpress**: Eight gene association methods for constructing co-expression network  
(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

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. <http://sys.bio.mtu.edu/motif/index.php>. *Plant Method* 2016. (Corresponding author)
9. **BWERF**: Backward elimination random forests for constructing multilayered gene regulatory networks. *PLoS ONE* 2017: 12(2): e0171532. R package is available at: (<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0171532>)
10. **SSGA** and **MSGa**: two seed-growing algorithms for constructing collaborative subnetworks. *Scientific Reports*. 2017. <https://www.nature.com/articles/s41598-017-01556-z>
11. **TF-Miner**: <http://sys.bio.mtu.edu/cluster/>. Submitted to *BMC Genomics*
12. **Top-down and Bottom-up GGM**. *BMC Bioinformatics* 2016: 17:132. <http://sys.bio.mtu.edu/topdown/>
13. **TGMI**: An algorithm for identifying pathway regulators. Mar 2018. (R package is available on NAR Web page). *Nucleic Acids Research*. 46(11):e67. [http://sys.bio.mtu.edu/sample\\_output/TGMI/](http://sys.bio.mtu.edu/sample_output/TGMI/)
14. **JRmGRN**: Joint reconstruction of multiple gene regulatory networks with common hub genes (R package is available on Bioinformatics Web page). 2018. *Bioinformatics* 5;34(20):3470-3478. <https://github.com/wenpingd>
15. **HB-PLS**: Huber loss and Berhu penalty with Partial Least Square (PLS) for identifying pathway regulators. 2021 *Forestry Research*. <https://github.com/hwei0805/>
16. **LORSEN** (low rank penalized regression method): a fast and efficient eQTL mapping method. DOI: 10.3389/fgene.2021.690926. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8636089/>
17. **Huber-ENET, Huber-Lasso, Huber-Net, MSE-ENET, MSE-Lasso, and MSE-Net**. A package that comprises six methods for predicting target genes of a transcription factor of interest using OMICS data. (Submitted to *Bioinformatics* on Sept 19, 2022) <https://github.com/xueweic/TGPred>

## E. Invited Presentations

- 1) **2020. Wei, H.**, The Plant & Animal Genome XXIII, "A Statistics, Machine Learning and Optimization Combined Approach Toward Identifying Hub Genes from Multi-Source Gene Expression Data," San Diego. (January 10, 2020 - January 14, 2020), (Oral).
- 2) **2019. Wei, H.**, ASPB Annual Conference, "Joint reconstruction of multiple gene regulatory networks with spatial data," American Society of Plant Biology, San Jose. (August 3, 2019 - August 7, 2019), (Poster).

- 3) **2019. Wei, H.**, Department of Plant Biology Seminar Series, Identification of Genes that Govern Biological Pathways and Processes through Network Construction and Decomposition. Michigan State University. East Lansing, (Feb 23, 2019), (Oral)
- 4) **2019. Wei, H.**, ASPB Annual Conference, "TGMI: A highly efficient algorithm for identifying biological pathway and process regulators using conditional mutual information," American Society of Plant Biology, San Jose. (August 3, 2019 - August 7, 2019), (Poster).
- 5) **2017. Wei, H.**, Department of Plant Pathology Seminar Series, "Novel biological discovery through gene network construction and decomposition," Kansas State University, Manhattan, KS. (February 9, 2017), (Oral).
- 6) **2017. Wei, H.**, Plant & Animal Genome Conference, "Genome and Evolution of *Betula platyphylla*," San Diego. (January 14, 2017 - January 18, 2017), (Poster).
- 7) **2016. Wei, H.** (Co-Chair), ABI NSF Workshop, "Towards building hierarchical gene regulatory networks that govern biological pathways and complex traits," Ardmore, Oklahoma. (April 29, 2016 - April 30, 2016), (Oral).
- 8) **2015. Wei, H.** (Organizer), The ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB), "Extraction of novel biological knowledge from large genomics data. Workshop on genomics and metagenomics data mining," Atlanta. (August 9, 2015 - August 13, 2015), (Oral).
- 9) **2015. Wei, H.** (Presenter Only), Plant & Animal Genome Conference, "Identifying genes controlling complex traits in forest trees via network construction and decomposition," San Diego. (January 14, 2015 - January 18, 2015), (Oral).
- 10) **2014. Wei, H.** (Presenter Only), Department of Plant Biology Seminar Series, "Identification of genes controlling complex traits through network construction and decomposition," University of South Dakota, Vermillion, South Dakota. (September 29, 2014), (Oral).
- 11) **2014. Wei, H.**, Seminar Series, "Identification of gene controlling root growth and development under low nitrogen," Beijing Forestry University. (May 23, 2014), (Oral).
- 12) **2013. Wei, H.**, Plant Genomics Congress, "Direct identification of genes controlling complex traits from gene expression data," St. Louis, Missouri, (September 23, 2013 - September 24, 2013), (Oral).

## G. TEACHING

FW5092 Experimental Design, Spring 2018, and 2022  
 FW4099 Programming Skills for Bioinformatics, Fall 2009, 2011, 2013, 2015, 2019, and 2021  
 FW5082 Gene Expression Data Analysis, Fall 2010, 2012, 2018, and 2020  
 CS2321 Data Structure in Java, Spring 2011  
 FW5510 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

## H. GRADUATE STUDENTS

Current:

Ph.D. Md Khairul Islam, Computational Science & Engineering, Fall 2022 - now  
 MS Sai Meja Mummadi, Computer Science. Sept 2021- now.

Past: Ph.D. Wenping Deng, 2018, Forest Molecular Genetics (Bioinformatics), Huawei, Inc. China  
 Ph.D. Chathura Gunasekare, 2017, Computational Science & Engineering, Baylor College, USA  
 Ph.D. Sapna Kumari, 2013, Mathematics, FDA, Maryland. 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.

## I. 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)

**J. EXTRAMURAL FUNDING:** A total of \$14,538,533 from ABI/NSF, Plant Genome/NSF, DOE, MDHHS, MI and USDA as PI and Co-PI. \$8,109,729 to Michigan Tech. \$2,254,099 to me.