

Xiao Wang

Curriculum Vitae

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ORCID: 0000-0002-7380-1832

Current appointment

2026.08 - present

Lecturer · College of Life Sciences / Houji Laboratory, Shanxi Agricultural University

Research interests

Plant metabolomics; multi-omics integration; crop quality and specialized metabolism; bioinformatics software development.

Education

2017.09 - 2021.06

Ph.D., Crop Germplasm Resources

Cotton Research Institute, Chinese Academy of Agricultural Sciences

2013.09 - 2016.06

M.Sc., Biochemistry and Molecular Biology

College of Life Sciences, Shanxi Agricultural University

2009.09 - 2013.06

B.Sc., Biotechnology

College of Information, Shanxi Agricultural University

Research experience

2021.07 - 2026.05

Postdoctoral Researcher, Plant Metabolomics

Henan University, State Key Laboratory of Crop Stress Adaptation and Improvement

2016.04 - 2017.09

Project Assistant

Cotton Research Institute, Chinese Academy of Agricultural Sciences

Funding & awards

Principal investigator, Henan Postdoctoral Research Funding Project HN2022138: molecular mechanisms of Arabidopsis F-box mutants using large-scale pseudo-targeted metabolomics (awarded 2023; CNY 100,000; completed).

Second Prize, 2025 Henan Department of Education Science and Technology Achievement Evaluation (research paper category), for MetMiner; certificate no. 09969 (2025).

Software copyright

WGCNA-shinyapp V1.0.0 · 2024SR2121189 · 2024-12-18.

Co-copyright holder.

Patent applications (co-inventor)

- ZmPMT1 for identifying maize haplotypes with high polyunsaturated fatty-acid content · 202511182165X
- GhBGLU gene, VIGS vector, host cells and applications · 2024119695078
- GhGSTL3 gene, VIGS vector, host cells and applications · 2024119358360
- GhMATE27 for regulating upland cotton fiber quality and drought tolerance · 2024114850683

Teaching areas & technical skills

Teaching areas: biochemistry, molecular biology, molecular genetics, bioinformatics, plant metabolomics and plant genomics.

R · Shiny · Snakemake · LC-MS · mGWAS · RSEM · EMMAX / GAPIT · MaxQuant

Publications

2026 · TidyMass2: advancing LC-MS untargeted metabolomics through metabolite origin inference and metabolic feature-based functional module analysis

Wang, X., Liu, Y., Jiang, C., Huang, Z., Yan, H., Wong, S. H., Johnson, C. H., Zhang, J., Ge, Y., Zhang, F., Zhang, J., Lai, R., Gao, P., Zhang, X., & Shen, X.

Nature Communications, 17(1), 1755 First author

doi: 10.1038/s41467-026-68464-7

2025 · A CRY1-HY5-MYB signaling cascade fine-tunes guard cell reactive oxygen species levels and triggers stomatal opening

Chang, Y., Shi, M., Wang, X., Cheng, H., Zhang, J., Liu, H., Wu, H., Ou, X., Yu, K., Zhang, X., Day, B., Miao, C., Zhao, Y., & Jiang, K.

The Plant Cell, 37(4), koaf064 Co-first author

doi: 10.1093/plcell/koaf064

2025 · Multi-omics dissection of transgressive expressed mechanism to reveal fiber yield heterosis in cotton (*Gossypium hirsutum*)

Geng, X., Wang, X., Dong, N., Qin, T., Ren, S., Sun, R., Chen, J., Yang, Q., Jia, Y., Sun, J., Peng, Z., Li, H., Hu, D., Pan, Z., Chen, B., Wang, L., He, S., Wang, Q., & Du, X.

Industrial Crops and Products, 238, 122398 Co-first author

doi: 10.1016/j.indcrop.2025.122398

2025 · Integrated metabolomic and transcriptomic analyses identify MYB genes regulating key metabolites and agronomic traits in upland cotton *Gossypium hirsutum*

Zhang, X., Tian, X., Gao, X., Sun, G., Peng, Z., Geng, X., Peng, J., Dai, P., Wang, X., Li, H., Wang, Z., Pan, Z., Jia, Y., Chen, B., Hu, D., Wang, L., Pang, B., Xing, A., Lu, S., ... Du, X.

Nature Genetics, 57(11), 2819-2830 Co-author

doi: 10.1038/s41588-025-02363-3

2025 · Modulation of lignin and anthocyanin homeostasis by GTP cyclohydrolase1 in maize

Zhang, M., Li, X., Wang, X., Jiang, S., Zhang, J., Sun, M., Zhou, Z., Zhang, J., Li, M., Lv, Y., Qi, E., Tian, Z., Zhu, H., Zhang, X., Zhao, X., Xu, C., Lübberstedt, T., Zhang, X., Yang, X., ... Liu, H.

Plant Biotechnology Journal, 23(7), 2449-2463 Co-author

doi: 10.1111/pbi.70061

2025 · The R2R3-MYB transcription factor GhMYB315 associates with GhVQ28 to enhance *Verticillium* wilt resistance in upland cotton by regulating phenylpropanoid metabolism

Guo, Y., Qian, Y., Fu, Y., Miao, K., Wang, X., Tian, H., Fu, R., Yang, F., Guo, J., Li, K., Jia, K.-P., Botella, J. R., & Miao, Y.

The Plant Journal, 124(3), e70562 Co-author

doi: 10.1111/tpj.70562

2025 · Exploring metabolite diversity in global rapeseed germplasm: insights into ecotypes, geographical influences, and correlations with diabetes

Wang, P., Zhai, Y., Wang, Y., Zhao, B., Wang, X., Liu, F., Yang, C., Zhang, S., Liu, H., Zhang, X., & Wang, D.

BMC Plant Biology, 26(1), 37 Co-author

doi: 10.1186/s12870-025-07830-x

2025 · Absciscic acid plays a pivotal role in stomatal defense at the early infection of *Verticillium dahliae* in *Gossypium hirsutum*

Xue, S., Li, K., Zhang, H., Xu, S., Dou, Y., Li, L., Ning, Y., Wang, X., Jia, K., Botella, J. R., & Miao, Y.

Environmental and Experimental Botany, 240, 106282 Co-author

doi: 10.1016/j.envexpbot.2025.106282

2025 · Identification of UDP-glucosyltransferase involved in the biosynthesis of phloridzin in *Gossypium hirsutum*

Zhang, X., Tian, X., Luo, J., Wang, X., He, S., Sun, G., Dong, R., Dai, P., Wang, X., Pan, Z., Chen, B., Hu, D., Wang, L., Pang, B., Xing, A., Fu, G., Wang, B., Cui, J., Ma, L., & Du, X.

The Plant Journal, 121(3), e17248 Co-author

doi: 10.1111/tpj.17248

2024 · MetMiner: A user-friendly pipeline for large-scale plant metabolomics data analysis

Wang, X., Liang, S., Yang, W., Yu, K., Liang, F., Zhao, B., Zhu, X., Zhou, C., Mur, L. A. J., Roberts, J. A., Zhang, J., & Zhang, X.

Journal of Integrative Plant Biology, 66(11), 2329-2345 First author

doi: 10.1111/jipb.13774

2024 · Integrative Dissection of Lignin Composition in Tartary Buckwheat Seed Hulls for Enhanced Dehulling Efficiency

Yang, W., Duan, H., Yu, K., Hou, S., Kang, Y., Wang, X., Hao, J., Liu, L., Zhang, Y., Luo, L., Zhao, Y., Zhang, J., Lan, C., Wang, N., Zhang, X., Tang, J., Zhao, Q., Sun, Z., & Zhang, X.

Advanced Science, 11(20), e2400916 Co-author

doi: 10.1002/advs.202400916

2024 · Mitochondrial VOLTAGE-DEPENDENT ANION CHANNEL 3 regulates stomatal closure by abscisic acid signaling

Qin, H., Yang, W., Liu, Z., Ouyang, Y., Wang, X., Duan, H., Zhao, B., Wang, S., Zhang, J., Chang, Y., Jiang, K., Yu, K., & Zhang, X.

Plant Physiology, 194(2), 1041-1058 Co-author

doi: 10.1093/plphys/kiad516

2023 · Metabolome and transcriptome signatures shed light on the anti-obesity effect of Polygonatum sibiricum

Ou, X., Wang, X., Zhao, B., Zhao, Y., Liu, H., Chang, Y., Wang, Z., Yang, W., Zhang, X., & Yu, K.

Frontiers in Plant Science, 14, 1181861 Co-first author

doi: 10.3389/fpls.2023.1181861

2023 · TBtools-II: A “one for all, all for one” bioinformatics platform for biological big-data mining

Chen, C., Wu, Y., Li, J., Wang, X., Zeng, Z., Xu, J., Liu, Y., Feng, J., Chen, H., He, Y., & Xia, R.

Molecular Plant, 16(11), 1733-1742 Co-author

doi: 10.1016/j.molp.2023.09.010

2023 · Cell type-specific proteomics uncovers a RAF15-SnRK2.6/OST1 kinase cascade in guard cells

Wang, H., Wang, Y., Sang, T., Lin, Z., Li, R., Ren, W., Shen, X., Zhao, B., Wang, X., Zhang, X., Zhou, S., Dai, S., Hu, H., Song, C.-P., & Wang, P.

Journal of Integrative Plant Biology, 65(9), 2122-2137 Co-author

doi: 10.1111/jipb.13536

2023 · Genome-wide analysis of the serine carboxypeptidase-like protein family reveals Ga09G1039 is involved in fiber elongation in cotton

Fu, G., Chen, B., Pei, X., Wang, X., Wang, X., Nazir, M. F., Wang, J., Zhang, X., Xing, A., Pan, Z., Lin, Z., Peng, Z., He, S., & Du, X.

Plant Physiology and Biochemistry, 201, 107759 Co-author

doi: 10.1016/j.plaphy.2023.107759

2022 · The Kelch-F-box protein SMALL AND GLOSSY LEAVES 1 (SAGL1) negatively influences salicylic acid biosynthesis in *Arabidopsis thaliana* by promoting the turn-over of transcription factor SYSTEMIC ACQUIRED RESISTANCE DEFICIENT 1 (SARD1)

Yu, K., Yang, W., Zhao, B., Wang, L., Zhang, P., Ouyang, Y., Chang, Y., Chen, G., Zhang, J., Wang, S., Wang, X., Wang, P., Wang, W., Roberts, J. A., Jiang, K., Mur, L. A. J., & Zhang, X.

New Phytologist, 235(3), 885-897 Co-author

doi: 10.1111/nph.18197

2021 · Genome-wide profiling of circular RNAs in the hybridization of two elite inbred lines of *Gossypium hirsutum*

Wang, X., Qin, T., Peng, Z., Zhang, Y., Yang, Q., Geng, X., Salih, H., Sun, J., He, S., Wang, Q., & Du, X.

Industrial Crops and Products, 170, 113754 First author

doi: 10.1016/j.indcrop.2021.113754

2021 · Identification, characterization and expression profiling of circular RNAs in the early cotton fiber developmental stages

Salih, H., Wang, X., Chen, B., Jia, Y., Gong, W., & Du, X.

Genomics, 113(1), 356-365 Co-first author

doi: 10.1016/j.ygeno.2020.12.023

2021 · Large-fragment insertion activates gene GaFZ (Ga08G0121) and is associated with the fuzz and trichome reduction in cotton (*Gossypium arboreum*)

Wang, X., Miao, Y., Cai, Y., Sun, G., Jia, Y., Song, S., Pan, Z., Zhang, Y., Wang, L., Fu, G., Gao, Q., Ji, G., Wang, P., Chen, B., Peng, Z., Zhang, X., Wang, X., Ding, Y., Hu, D., ... Du, X.

Plant Biotechnology Journal, 19(6), 1110-1124 Co-author

doi: 10.1111/pbi.13532

2021 · CottonGVD: A Comprehensive Genomic Variation Database for Cultivated Cottons

Peng, Z., Li, H., Sun, G., Dai, P., Geng, X., Wang, X., Zhang, X., Wang, Z., Jia, Y., Pan, Z., Chen, B., Du, X., & He, S.

Frontiers in Plant Science, 12, 803736 Co-author

doi: 10.3389/fpls.2021.803736

2021 · Multi-Omics Analyses Reveal Systemic Insights into Maize Vivipary

Wang, Y., Zhang, J., Sun, M., He, C., Yu, K., Zhao, B., Li, R., Li, J., Yang, Z., Wang, X., Duan, H., Fu, J., Liu, S., Zhang, X., & Zheng, J.

Plants, 10(11), 2437 Co-author

doi: 10.3390/plants10112437

2020 · Expression patterns and functional divergence of homologous genes accompanied by polyploidization in cotton (*Gossypium hirsutum* L.)

Peng, Z., Cheng, H., Sun, G., Pan, Z., Wang, X., Geng, X., He, S., & Du, X.

Science China Life Sciences, 63(10), 1565-1579 Co-author

doi: 10.1007/s11427-019-1618-7