

王骁

学术简历

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现任职务

2026.08 - 至今
讲师 · 山西农业大学 · 生命科学学院 / 后稷实验室

研究领域

植物代谢组学、多组学整合、作物品质与植物次生代谢、生物信息软件开发。

教育经历

2017.09 - 2021.06

博士 · 作物种质资源学
中国农业科学院棉花研究所

2013.09 - 2016.06

硕士 · 生物化学与分子生物学
山西农业大学生命科学学院

2009.09 - 2013.06

学士 · 生物技术
山西农业大学信息学院

科研经历

2021.07 - 2026.05

博士后 · 植物代谢组学
河南大学 · 省部共建作物逆境适应与改良国家重点实验室

2016.04 - 2017.09

项目助理
中国农业科学院棉花研究所

项目与奖励

主持河南省博士后科研资助项目：拟靶代谢组学批量研究拟南芥 F-box 突变体分子机制（HN2022138，2023 年立项，10 万元，已结项）。

2025 年度河南省教育厅科技成果评定（科技论文类）二等奖：MetMiner；认定编号：豫教〔2025〕09969。

软件著作权

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

共同著作权人。

专利申请（共同发明人）

- ZmPMT1 基因在鉴定玉米籽粒多不饱和脂肪酸优异单倍型中的应用 · 202511182165X
- 一种基因 GhBGLU 及其 VIGS 载体、宿主细胞和应用 · 2024119695078
- 一种基因 GhGSTL3 及其 VIGS 载体、宿主细胞和应用 · 2024119358360
- GhMATE27 在调控陆地棉纤维品质和棉花植株抗旱性中的应用 · 2024114850683

教学与技术能力

可承担课程：生物化学、分子生物学、分子遗传学、生物信息学、植物代谢组学、植物基因组学。

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

论文

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 第一作者

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 共同第一作者

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 共同第一作者

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 合作论文

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., L. Ü bberstedt, T., Zhang, X., Yang, X., ... Liu, H.

Plant Biotechnology Journal, 23(7), 2449-2463 合作论文

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 合作论文

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 合作论文

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 合作论文

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 合作论文

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 第一作者

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 合作论文

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 合作论文

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 共同第一作者

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 合作论文

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 合作论文

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 合作论文

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 合作论文

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 第一作者

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 共同第一作者

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 合作论文

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 合作论文

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 合作论文

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 合作论文

doi: 10.1007/s11427-019-1618-7