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教育经历

2000-2004华中农业大学植物科学技术学院 作物学 学士
2004-2009华中农业大学植物科学技术学院 遗传育种 博士

科研与学术工作经历

2009-2011国际玉米小麦改良中心 顾问
2011-2013华中农业大学 博士后
2013-2017马克斯普朗克分子植物生理所 博士后
2017-至今 华中农业大学 教授

主要研究方向

植物遗传与系统生物学(Plant genetics and systems biology)
种质资源与遗传改良(Genetic resources and crop improvement)

代表性论文

2021

33)Alseekh S, Scossa F, Wen W, Luo J, Yan J, Beleggia R, Klee HJ, Huang S, Papa R, Fernie AR. Domestication of crop metabolomes: Desired and unintended consequences. *Trends in Plant Science*, 2021, doi.org/10.1016/j.tplants.2021.02.005

32)Zhang W, Luo C, Scossa F, Zhang Q, Usadel B, Fernie AR, Mei H, Wen W. A phased genome based on single sperm sequencing reveals crossover pattern and complex relatedness in tea plants. *The Plant Journal* 2021, 105(1):197-208. (通讯作者)

31)Jia X, Zhang W, Fernie AR, Wen W. *Camellia sinensis* (Tea). *Trends in Genetics* 2021, 37(2): 201-202. (共同通讯)

30)Mou J, Zhang Z, Qiu H, Lu Y, Zhu X, Fan Z, Zhang Q, Ye J, Fernie AR, Cheng Y, Deng X, Wen W. Multiomics-based dissection of citrus flavonoid metabolism using a *Citrus reticulata* × *Poncirus trifoliata* population. *Horticulture Research* 2021, 8:56 (共同通讯)

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29)Zhang W, Zhang Y, Qiu H, Guo Y, Wan H, Zhang X, Scossa F, Alseekh S, Zhang Q, Wang P, Xu L, Schmidt M H W, Jia X, Li D, Zhu A, Guo F, Chen W, Ni D, Usadel B, Fernie AR, Wen W. Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties. *Nature Communications*. 2020. 11 (1) (通讯作者)

28)Zhang W, Alseekh S, Zhu X, Zhang Q, Fernie AR, Kuang H, Wen W. Dissection of the domestication-shaped genetic architecture of lettuce primary metabolism. *The Plant J*. 2020, https://doi.org/10.1111/tj.14950 (共同通讯)

27) Wen W, Alseekh S, Fernie AR. Conservation and diversification of flavonoid metabolism in the plant kingdom. *Curr Opin Plant Biol*. 2020. 55 100-108. (通讯作者)

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25)Zhu F, Luo T, Liu C, Wang Y, Zheng L, Xiao X, Zhang M, Yang H, Yang W, Xu R, Zeng Y, Ye J, Xu J, Xu J, Larkin R M, Wang P, Wen W, Deng X, Fernie AR, Cheng Y. A NAC transcription factor and its interaction protein hinder abscisic acid biosynthesis by synergistically repressing *NCED5* in *Citrus reticulata*. *J Exp Bot*. 2020. 71 (12) 3613-3625.

24)Qiu H, Zhu X, Wan H, Xu L, Zhang Q, Hou P, Fan Z, Lyu Y, Ni D, Usadel B, Fernie AR, Wen W. Parallel Metabolic and Transcriptomic Analysis Reveals Key Factors for Quality Improvement of Tea Plants. *J Agric Food Chem*. 2020. 68 (19) 5483-5495. (通讯作者)

23)Deng M, Zhang X, Luo J, Liu H, Wen W, Luo H, Yan J, Xiao Y. Metabolomics analysis reveals differences in evolution between maize and rice. *The Plant J*. 2020. https://doi.org/10.1111/tj.14856

22)Wan H, Liu H, Zhang J, Lyu Y, Li Z, He Y, Zhang X, Deng X, Brotman Y, Fernie AR, Cheng Y, Wen W. Lipidomic and transcriptomic analysis reveals reallocation of carbon flux from cuticular wax into plastid membrane lipids in a glossy "Newhall" navel orange mutant. *Hortic Res*. 2020, 7:41 (共同通讯).

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21)Li K, Wen W, Alseekh S, Yang X, Guo H, Li W, Wang L, Pan Q, Zhan W, Liu J, Li Y, Wu X, Brotman Y, Willmitzer L, Li J, Fernie AR, Yan J. Large-scale metabolite quantitative trait locus analysis provides new insights for high-quality maize improvement. *The Plant J*. 2019, 99(2):216-230 (并列第一作者).

20)Zhu F, Wen W, Fernie AR. Finding Noemi: The Transcription Factor Mutations Underlying Trait Differentiation Amongst Citrus. *Trends Plant Sci*. 2019, 24(5):384-386 (共同通讯).

19)He Y, Li Z, Tan F, Liu H, Zhu M, Yang H, Bi G, Wan H, Wang J, Xu R, Wen W, Zeng Y, Xu J, Guo W, Xue S, Cheng Y, Deng X. Fatty acid metabolic flux and lipid peroxidation homeostasis maintain the biomembrane stability to improve citrus fruit storage performance. *Food Chem*. 2019, 292:314-324.

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18)He Y, Han J, Liu R, Ding Y, Wang J, Sun L, Yang X, Zeng Y, Wen W, Xu J, Zhang H, Yan X, Chen Z, Gu Z, Chen H, Tang H, Deng X, Cheng Y. Integrated transcriptomic and metabolomic analyses of a wax deficient citrus mutant exhibiting jasmonic acid-mediated defense against fungal pathogens. *Hortic Res*. 2018, 5:43.

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16) Wen W, Jin M, Li K, Liu H, Xiao Y, Zhao M, Alseekh S, Li W, de Abreu E Lima F, Brotman Y, Willmitzer L, Fernie AR, Yan J. An integrated multi-layered analysis of the metabolic networks of different tissues uncovers key genetic components of primary metabolism in maize. *The Plant J*. 2018, 93(6):1116-1128.

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15)Jin M, Zhang X, Zhao M, Deng M, Du Y, Zhou Y, Wang S, Tohge T, Fernie AR, Willmitzer L, Brotman Y, Yan J, Wen W. Integrated genomics-based mapping reveals the genetics underlying maize flavonoid biosynthesis. *BMC Plant Biol*. 2017, 17(1):17 (通讯作者).

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13) Wen W, Liu H, Zhou Y, Jin M, Yang N, Li D, Luo J, Xiao Y, Pan Q, Tohge T, Fernie AR, Yan J. Combining Quantitative Genetics Approaches with Regulatory Network Analysis to Dissect the Complex Metabolism of the Maize Kernel. *Plant Physiol*. 2016, 170(1):136-46 (通讯作者).

12) Wen W, Brotman Y, Willmitzer L, Yan J, Fernie AR. Broadening Our Portfolio in the Genetic Improvement of Maize Chemical Composition. *Trends Genet*. 2016, 32(8):459-469.

11) Wen W, Li K, Alseekh S, Omranian N, Zhao L, Zhou Y, Xiao Y, Jin M, Yang N, Liu H, Florian A, Li W, Pan Q, Nikoloski Z, Yan J, Fernie AR. Genetic Determinants of the Network of Primary Metabolism and Their Relationships to Plant Performance in a Maize Recombinant Inbred Line Population. *Plant Cell*. 2015, 27(7):1839-56.

10)Liu H, Wang X, Warburton ML, Wen W, Jin M, Deng M, Liu J, Tong H, Pan Q, Yang X, Yan J. Genomic, Transcriptomic, and Phenomic Variation Reveals the Complex Adaptation of Modern Maize Breeding. *Mol Plant*. 2015, 8(6):871-84.

9)Yang N, Lu Y, Yang X, Huang J, Zhou Y, Ali F, Wen W, Liu J, Li J, Yan J. Genome wide association studies using a new nonparametric model reveal the genetic architecture of 17 agronomic traits in an enlarged maize association panel. *PLoS Genet*. 2014, 10(9):e1004573.

8) Wen W, Li D, Li X, Gao Y, Li W, Li H, Liu J, Liu H, Chen W, Luo J, Yan J. Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights. *Nat Commun*. 2014, 10.1038/ncomms4438.

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2) Wen W, Taba S, Shah T, et al. Detection of genetic integrity of conserved maize (*Zea mays* L.) germplasm in genebanks using SNP markers. *Genet Resour Crop Ev*. 2010, 58(2):189-207.

1) Wen W, Mei H, Feng F, Yu S, Huang Z, Wu J, Chen L, Xu X, Luo L. Population structure and association mapping on chromosome 7 using a diverse panel of Chinese germplasm of rice (*Oryza sativa* L.). *Theor Appl Genet*. 2009, 119(3):459-70.

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