



陈飞

职称：讲师

邮箱：[feichen@njau.edu.cn](mailto:feichen@njau.edu.cn)

办公地址：南京农业大学行政北楼 102

## 研究方向：

1. 花卉遗传、育种、园林应用

使用多组学技术、分子生物学技术，利用睡莲为模式材料，解析花的起源、花器官形态建成、花香、花色、性别决定、开花时间、花的节律钟、抗逆性等的分子基础和进化特征；

基于杂交育种、多倍体育种、分子育种等手段选育新品种花卉。

花卉种质资源圃建设，花卉的园林景观应用

2. 大数据和数据可视化

建立了 eplant 植物多组学数据库 <http://eplant.njau.edu.cn>。

建立了园艺植物大数据数据库。

组学大数据相关工具的开发。

## 教育经历：

2014.09-2016.05，美国田纳西大学，联合培养博士，导师：Feng Chen 教授

2011.09-2016.06, 南京农业大学, 果树学, 博士, 导师: 程宗明教授

2007.09-2011.06, 南京农业大学, 生物技术, 本科

## 工作经历:

2019.05-至今, 南京农业大学, 园艺学院, 程宗明教授团队

2016-2019.04, 福建农林大学海峡联合研究院, 科研助理, 张亮生教授团队

## 执教课程:

- ◆ 本科生黄山实习

## 承担课题:

- ◆ 2020-2021, 作物遗传与种质创新国家重点实验室开放基金, 主持, 在研
- ◆ 2020-2021, 中央高校基本业务费-南京农业大学联合项目, 主持, 在研
- ◆ 2019-2020, 南京农业大学新进博士科研经费, 主持, 在研
- ◆ 2019-2021, 国家自然科学基金青年基金项目, 主持, 在研
- ◆ 2018-2020, 福建省自然科学基金, 面上项目, 主持, 已结题
- ◆ 2017-2018, 省部共建闽台作物有害生物生态防控国家重点实验室, 开放基金, 主持, 已结题

## 代表性成果:

### 2020

- (33) Chen, Xuequn; Tong, Chaobo ; Zhang, XIngtan; Dong, Wei; Hu, Ming; Song, Aixia; **Chen, Fei**; Wang, Youping; Tu, Jinxing; Liu, Shengyi; Tang, Haibao; Zhang, Liangsheng [A high-quality Brassica napus genome reveals expansion of transposable elements, subgenome evolution and disease resistance.](#) *Plant Biotechnology Journal* 2020.

- (32) Zhang L#\*, Wu S#, Chang X, Wang X, Zhao Y, Xia Y, Trigiano RN, Jiao Y\*, **Chen F\***. The ancient wave of polyploidization events in flowering plants and their facilitated adaptation to environmental stress. *Plant, Cell & Environment* 2020.
- (31) Tang H, Zhang L, **Chen F**, Zhang X, Chen F, Ma H, Van de Peer Y. *Nymphaea colorata* (Blue-Petal Water lily). *Trends in Genetics* 2020.
- (30) Cover story: Lan Mo, Junhao Chen, **Chen F**, Qiangwei Xu, Zaikang Tong, Huahong Huang, Renhui Dong, Xiongzen Lou, Erpei Lin\***Induction and characterization of polyploids from seeds of Rhododendron fortunei Lindl.** . *Journal of Integrative Agriculture* 2020, 19(2-12).
- (29) Zhang L.\*, Shen F, **Chen F**, Lin Z. **Origin and evolution of the 2019 novel coronavirus.** *Clinical Infectious Diseases* ciaa112(2020).

## 2019

- (28) Zhang L.#\*, **Chen F#**, Zhang X#, et al. **The water lily genome and the early evolution of flowering plants.** *Nature* 577, 79-84(2020).
- #####This article is highlighted by: Lyu, J. **Encoding beauty.** *Nature Plants* (2020). <https://doi.org/10.1038/s41477-019-0587-5>
- (27) **Chen F\***, Song Y, Li X, Chen J, Mo L, Zhang X, Lin Z, Zhang L\*. **Genome sequences of horticultural plants: past, present, and future.** *Horticulture Research* 2019, 6:112.
- (26) **Chen F**, Chen J, Wang Z, Zhang J, Lin M, Song Y, Zhang L. **Genomics: cracking the mysteries of walnuts.** *Journal of Genetics* 2019, 98:33.

## 2018

- (25) Yang X, Yue Y, Li H, Ding W, Chen G, Shi T, Chen J, Park MS\*, **Chen F\***, Wang L\*. **The chromosome-level quality genome provides insights into the evolution of the biosynthesis genes for aroma compounds of *Osmanthus fragrans*.** *Horticulture Research* 2018, 5:72
- (24) Chen J, Zhang J, Lin M, Wang Z, Zhang L, **Chen F\***. **MGH: a genome hub for the medicinal plant maca (*Lepidium meyenii*).** *Database*, 2018, bay113.
- (23) Yu C, Qiao G, Qiu W, Yu D, Zhou S, Shen Y, Yu G, Jiang J, Han X, Liu M, Zhang L, **Chen F\***, Chen Y\*, Zhuo R\*. **Molecular breeding of water lily: engineering cold stress tolerance into tropical water lily.** *Horticulture Research* 2018, 5:73

- (22) Dong S, Zhao C, **Chen F**, Liu Y, Zhang S, Wu H, Zhang L\*, Liu Y\*. The complete mitochondrial genome of the early flowering plant *Nymphaea colorata* is highly repetitive with low recombination. *BMC Genomics* 19: 614.
- (21) Xu M#(Co-first), **Chen F#(Co-first)**, Qi S, Zhang L, Wu S. Loss or duplication of key regulatory genes coincides with environmental adaptation of stomatal complex in *Nymphaea colorata* and *Kalanchoe laxiflora*. *Horticulture Research* 2018, 5: 42.
- (20) Dong W, Vannozzi A, **Chen F**, Liangsheng Zhang. MORC Domain Definition and Evolutionary Analysis of the MORC Gene Family in Green Plants. *Genome Biology and Evolution* 2018, 10:1730-1744
- (19) **Chen F\***, Zhang J, Chen J, Li X, Dong W, Hu J, Lin M, Liu Y, Wang Z, Zhang L\*. realDB: a genome and transcriptome resource for the red algae (phylum Rhodophyta). *Database* doi:10.1093/database/bay072
- (18) **Chen F**, Hu Y, Vannozzi A, Wu K, Cai H, Qin Y, Mullis A, Lin Z, Zhang L\*. The WRKY transcription factor family in model plants and crops. *Critical Reviews in Plant Sciences* 2018. DOI: 10.1080/07352689.2018.1441103.
- (17) **Chen F**, Zhang L, Lin Z, Cheng Z. Identification of a novel fused gene family implicates convergent evolution in eukaryotic calcium signaling. *BMC Genomics*. 2018. 19:306
- (16) **Chen F**, Dong W, Zhang J, Guo X, Chen J, Wang Z, Lin Z, Tang H, Zhang L. The sequenced angiosperm genomes and genome databases. *Frontiers in Plant Sciences*. 2018. 9: 418.

## 2017

- (15) **Chen F**, Liu X, Yu C, Chen Y, Tang H, Zhang L. Water lilies as emerging models for Darwin's abominable mystery. *Horticulture Research*. 4,17051(2017)
- (14) **Chen F**, Zhang X, Liu X, Zhang L, Evolutionary analysis of MIKCC-type MADS-box genes in gymnosperms and angiosperms. *Frontiers in Plant Sciences*. 2017, 8: 895
- (13) **Chen F**, Zhang L, Cheng Z, The calmodulin fused kinase novel gene family is the major system in plants converting Ca<sup>2+</sup> signals to protein phosphorylation responses. *Scientific Reports*. 2017, 7: 4127

## 2016

- (12) Zhu K, **Chen F**, Chen X, Hewezi T, Cheng Z. Evolution of an intron-poor cluster of the CIPK gene family and expression in response to drought stress in soybean. *Scientific Reports*, 2016, 6:28225

- (11) Liangsheng Zhang (Co-first), **Chen F (Co-first)**, Guo-Qiang Zhang, Yong-Qiang Zhang, Shance Niu, Jin-Song Xiong, Zhenguo Lin, Zong-Ming (Max) Cheng, Zhong-Jian Liu. [Origin and mechanism of crassulacean acid metabolism in orchids as implied by comparative transcriptomics and genomics of the carbon fixation pathway](#). *The Plant Journal* 2016, 86: 175-185.
- (10) GQ Zhang, ... **Chen F**,... et al. [The Dendrobium catenatum Lindl. genome sequence provides insights into polysaccharide synthase, floral development and adaptive evolution](#). *Scientific Reports* 6, 19029. **ESI highly cited paper**

## 2014

- (9) Wang G, Lovato A, Liang Y, Wang M, **Chen F**, Tornielli GB, Polverari A, [Validation by isolation and expression analyses of the mitogen-activated protein kinase gene family in the grapevine \(Vitis vinifera L.\)](#) *Australian Journal of Grape and Wine Research*, 2014
- (8) Yinghai Liang, Bin Cai, **Chen F**, Gang Wang, Min Wang, Yan Zhong, Zong-Ming (Max) Cheng. (2014) [Construction and validation of a gene co-expression network in grapevine \(Vitis vinifera. L.\)](#) *Horticulture Research* 1:14040
- (7) Liu J, Chen N, **Chen F**, Cai B, Dal Santo S, Tornielli G, Pezzotti M, and Cheng Z. (2014) [Genome-wide analysis and expression profile of the bZIP transcription factor gene family in grapevine \(Vitis vinifera\)](#). *BMC Genomics*, 15:281

## 2013

- (6) Cai T, Ye X, Ma Y, Wang X, **Chen F**, Cheng Z. [Over-expression of 1-aminocyclopropane-1carboxylic acid oxidase genes \(ACO\) from Vitis vinifera in tomato \(Solanum lycopersicum\) and its effects on ethylene release rates](#) *Journal of Agricultural Biotechnology* 21(9):1037-1044 (2013)
- (5) Liang Y, **Chen F**, Wang G, Wang M, Feng G, Cheng Z. [Bioinformatics identification, analysis of gene structure and expression characters on lineage-specific genes of grapevine](#). *Journal of Nanjing Agricultural University* 36 (6): 19-24 (2013)
- (4) **Chen F**, Yin H, Liang Y, Cai B. [Evolution of Calcium-dependent Protein Kinase Gene Family in Apple \(Malus domestica\)](#) *Acta Agriculturae Jiangxi* 2013, 25(9): 15-20.
- (3) Yin H, Cai B, Li C, **Chen F**. [Genome-wide analysis of bHLH transcription factor family in grape](#). *Acta Agriculturae Jiangxi* 2013, 25(9): 1-6

- (2)[Meeting abstract] Zong-Ming Cheng, **Chen F**, Fasoli M, Tornielli GB, Dal Santo S, Pezzotti M, et al. (2013) [The evolutionary history and diverse physiological roles of the grapevine calcium-dependent protein kinase gene family](#). *HortScience*, 48(9): S172-S172.
- (1) **Chen F**, Fasoli M, Tornielli GB, Dal Santo S, Pezzotti M, et al. (2013) [The evolutionary history and diverse physiological roles of the grapevine calcium-dependent protein kinase gene family](#). *PLoS ONE* 8(12): e80818.

## 社会服务工作:

- ◆ 《Horticulture Research》 副主编
- ◆ 《Horticulture Research》 专刊"horticultural Plant Genome"的客座编辑
- ◆ 《Plant Biotechnology Journal》, 《Horticulture Research》, 《Plant, Cell & Environment》, 《Peer Journal》, 《Scientific Reports》, 《Horticultural Plant Journal》, 《Plant Cell Reports》, 《Gene》, 《Frontiers in Plant Science》等杂志的审稿人。

## 荣誉奖励:

- ◆ 南京农业大学 2019 年考核优秀
- ◆ 参与获得浙江省林业局林学会第十九届科技兴林奖, 二等, 荷花和睡莲新品种选育及园林应用技术, 证书编号: 2019 (II) 08-R06

## 其他:

- ◆ 2017-7 中国深圳 第 17 届国际植物学大会, 大会报告