

# Chen Fadi

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## Areas of Research

Ornamental plants, Abiotic and biotic stresses, Flower color, Flower development, *Chrysanthemum* genome

## Contact Information

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## Research Interests

**Abiotic and biotic stresses; Flower color; Flower development; *Chrysanthemum* genome**

Our lab integrates transcriptome methods, bioinformatics, reverse genetic methods to study the molecular mechanisms involved in flower color, flower development, and *Chrysanthemum* genome. Some of the topics we are currently working on are described below:

### 1. Abiotic stresses

Waterlogging causes the death and loss of chrysanthemum to a great extent. Ethylene is a key plant hormone involved in the response of chrysanthemum to waterlogging. We are focusing on regulatory roles of key transcription factors modulating the production of ethylene and ethylene signaling upon waterlogging.

### 2. Flower color

Flower color is one of the most important traits in ornamental plants, and it has also been an important breeding goal in the long history of chrysanthemum breeding. Flavonoids confer a wide range of colors to chrysanthemum flowers. We are interested in molecular networks regulating flavonoid synthesis, mechanisms involved in flower color bud sport mutation in chrysanthemum, and how environmental factors influence flower color formation in chrysanthemum.

### 3. Flower development

Chrysanthemum is well-known for showy highly compressed capitulum which is composed of both female ray florets and bisexual disc florets. Chrysanthemum is rich in inflorescence form and petal type, which are the significant embodiment of its ornamental value. However, the molecular mechanism underlying flower and petal shape is still largely unexplored. The weighted gene coexpression network analysis (WGCNA) revealed important networks and hub genes including ray floret petals-specific coexpression network, disc floret petals-specific network, B and E class genes involved network and *CYC2* genes network. We are going to focus on these

networks in determining petal morphogenesis and ray and disc flowers.

#### **4. Chrysanthemum genome**

The lack of genomic data from chrysanthemum species has hampered dissection of the evolutionary mechanisms involved in their diversification. Therefore, we used Oxford Nanopore long-read technology to sequence the diploid *Chrysanthemum nankingense* genome which is probably one of the progenitors of domesticated chrysanthemums. Our analysis revealed that the evolution of the *C. nankingense* genome was driven by bursts of repetitive element expansion and WGD events including a recent WGD that distinguishes chrysanthemum from sunflower. Variations of ornamental and medicinal traits in chrysanthemums are linked to the expansion of candidate gene families by duplication events including paralogous gene duplication. Our study of the assembled reference genome will be aid to disclose the history and pattern of evolution and diversification of chrysanthemum plants, and also to accelerate the breeding and improvement of chrysanthemum. Now, we are focusing on analyzing the genome of hexaploid chrysanthemum, which will give us a clue to discipline the origin of cultivated chrysanthemum.

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## **Education Background**

**Bachelor:** Nanjing Agricultural University

**Master:** Nanjing Agricultural University

**Doctor:** Nanjing Agricultural University

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## **Work experience**

Assistant Professor, Nanjing Agricultural University, 1994-1996

Lecturer, Nanjing Agricultural University, 1997-1999

Associate Professor, Nanjing Agricultural University, 2000-2004

Professor, Nanjing Agricultural University, 2004-

Visiting Scholar, Chiba University, 2004-2005

Vice Dean, College of Horticulture, Nanjing Agricultural University, 2009-2013

Dean, College of Horticulture, Nanjing Agricultural University, 2014-2015

Vice President, Nanjing Agricultural University, 2016-2019

President, Nanjing Agricultural University, 2019-

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## **Honors and Awards**

The second class national technology award for invention prize (1<sup>st</sup> contributor)

The second class national award for S&T Progress prize (3<sup>rd</sup> contributor)

The first class Jiangsu Provincial S&T Progress Award (1<sup>st</sup> contributor)

The first class Jiangsu Provincial Agricultural Technology Extension Award (1<sup>st</sup> contributor)

Distinguished professor of the Ministry of Education

Outstanding Young Scholars of National Science Fund

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## **Selected Publication**

- (1) Song Chi<sup>#</sup>, Liu Yifei<sup>#</sup>, Song Aiping<sup>#</sup>, Dong Gangqiang<sup>#</sup>, Zhao Hongbo<sup>#</sup>, Sun Wei, Ramakrishnan Shyam, Wang Ying, Wang Shuaibin, Li Tingzhao, Niu Yan, Jiang Jiafu, Dong Bin, Xia Ye, Chen Sumei, Hu Zhigang, **Chen Fadi\***, Chen Shilin\*. The Chrysanthemum nankingense Genome Provides Insights into the Evolution and Diversification of Chrysanthemum Flowers and Medicinal Traits. *Molecular Plant*. 2018, 11: 482-1491.
  - (2) Zhang Zixin, Hu Qian, Liu Yanan, Cheng Peilei, Cheng Hua, Liu Weixin, Xing Xiaojuan, Guan Zhiyong, Fang Weimin, Chen Sumei, Jiang Jiafu\*, **Chen Fadi\***. Strigolactone represses the synthesis of melatonin, thereby inducing floral transition in Arabidopsis thaliana in an FLC-dependent manner. *Journal of Pineal Research*. 2019, 67(2): e12582.
  - (3) Ding Lian, Zhao Kunkun, Zhang Xue, Song Aiping, Su Jiangshuo, Hu Yueheng, Zhao Wenqian, Jiang Jiafu, **Chen Fadi\***. Comprehensive characterization of a floral mutant reveals the mechanism of hooked petal morphogenesis in Chrysanthemum morifolium. *Plant Biotechnology Journal*. 2019, 17(12): 2325-2340.
  - (4) Chen Yu, Jiang Jiafu, Song Aiping, Chen Sumei, Shan Hong, Luo Huolin, Gu Chunsun, Sun Jing, Zhu Lu, Fang Weimin, **Chen Fadi\***. Ambient temperature enhanced freezing tolerance of Chrysanthemum dichrum *CdICE1* Arabidopsis via miR398. *BMC Biology*. 2013, 11: 121.
  - (5) Qi Xiangyu, Wang Haibin, Song Aiping, Jiang Jiafu, Chen Sumei, **Chen Fadi\***. Genomic and transcriptomic alterations following intergeneric hybridization and polyploidization in the Chrysanthemum nankingense × Tanacetum vulgare hybrid and allopolyploid (Asteraceae). *Horticulture Research*. 2018, 5: 5.
  - (6) Liu Peng, Chen Sumei, Song Aiping, Zhao Shuang, Fang Weimin, Guan Zhiyong, Liao Yuan, Jiang Jiafu\*, **Chen Fadi\***. A putative high affinity phosphate transporter, CmPT1, enhances tolerance to Pi deficiency of chrysanthemum. *BMC Plant Biology*. 2014, 14: 18.
  - (7) Wang Jingjing<sup>#</sup>, Guan Yunxiao<sup>#</sup>, Ding Lian, Li Pirui, Zhao Wenqian, Jiang Jiafu, Chen Sumei, **Chen Fadi\***. The CmTCP20 gene regulates petal elongation growth in Chrysanthemum morifolium. *Plant Science*. 2019, 280: 248-257.
  - (8) Li Huiyun, Chen Sumei, Song Aiping, Wang Haibin, Fang Weimin, Guan Zhiyong, Jiang Jiafu\*, **Chen Fadi\***. RNA-Seq derived identification of differential transcription in the chrysanthemum leaf following inoculation with Alternaria tenuissima. *BMC Genomics*. 2014, 15: 9.
  - (9) Wang Jingjing, Wang Haibin, Ding Lian, Song Aiping, Shen Feng, Jiang Jiafu, Chen Sumei, **Chen Fadi\***. Transcriptomic and hormone analyses reveal mechanisms underlying petal elongation in *Chrysanthemum morifolium* 'Jinba'. *Plant Molecular Biology*. 2017, 93: 593-606.
  - (10) Chong Xinran<sup>#</sup>, Zhang Fei<sup>#</sup>, Wu Yangyang, Yang Xiaodong, Zhao Nan, Wang Haibin, Guan Zhiyong, Fang Weimin, **Chen Fadi\***. A SNP-enabled assessment of genetic diversity, evolutionary relationships and the identification of candidate genes in chrysanthemum. *Genome Biology and Evolution*. 2016, 8 (12): 3661-3671.
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