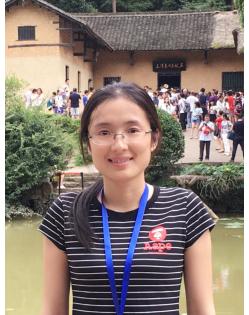


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科研项目	1. 国家自然科学基金面上项目, 32171855, 2022/1-2025/12, 在研, 主持 2. 国家重点研发计划(子任务), 2020YFD1000405, 2020/07-2022/12, 在研, 主持 3. 国家自然科学基金青年科学基金项目, 31701959, 结题, 主持 4. 江苏省自然科学基金-青年基金, BK20170717, 结题, 主持 5. 中央高校基本业务费, KJQN201815 6. 中国博士后科学基金会面上资助项目, 2017M611843, 结题, 主持 7. 江苏省博士后科研资助计划(B类) 1701154B, 结题, 主持				
发表论文	1. Ding Lian [#] , Zhao Kunkun [#] , Zhang Xue [#] , Song Aiping, Su Jiangshuo, Hu Yueheng, Zhao Wenqian, Jiang Jiafu, Chen Fadi*. (2019) Comprehensive characterization of a floral mutant reveals the mechanism of hooked petal morphogenesis in <i>Chrysanthemum morifolium</i> . <i>Plant biotechnology journal</i> 17 (12): 2325-2340. IF _{5years} = 7.658 2. Ding Lian [#] , Song Aiping [#] , Zhang Xue, Li Song, Su Jiangshuo, Xia Weikang, Zhao Kunkun, Zhao Wenqian, Guan Yunxiao, Fang Weimin, Chen Sumei, Jiang Jiafu, Chen Fadi* (2020) The core regulatory networks and hub genes				

	<p>regulating flower development in <i>Chrysanthemum morifolium</i>. <i>Plant Molecular Biology</i>. 103 (6):669-688. IF_{5years} = 4.065</p> <p>3. Zhao Kunkun[#], Ding Lian[#], Xia Weikang, Zhao Wenqian, Zhang Xue, Jiang Jiafu, Chen Sumei, Chen Fadi* (2020) Characterization of an APETALA1 and a FRUITFUL-like homolog in chrysanthemum. <i>Scientia Horticulturae</i> 272:109518. IF_{5years} = 2.844</p> <p>4. Wang Jingjing[#], Guan Yunxiao[#], Ding Lian, Li Peiling, Zhao Wenqian, Jiang Jiafu, Chen Sumei, Chen Fadi* (2019) The CmTCP20 gene regulates petal elongation growth in <i>Chrysanthemum morifolium</i>. <i>Plant Science</i> 280:248-257. IF_{5years} = 4.253</p> <p>5. Wang J, Wang H, Ding L, Song A, Shen F, Jiang J, Chen S, Chen F* (2017) Transcriptomic and hormone analyses reveal mechanisms underlying petal elongation in <i>Chrysanthemum morifolium</i> ‘Jinba’. <i>Plant Molecular Biology</i> 93 (6):593-606. IF_{5years} = 4.065</p> <p>6. Ding Lian; Yan Shuangshuang; Jiang Li; Liu Meiling; Zhang Juan; Zhao Jianyu; Zhao Wensheng; Han Yingyan; Wang Qian.; Zhang Xiaolan*; HANABA TARANU (HAN) bridges meristem and organ primordia boundaries through PINHEAD, JAGGED, BLADE-ON-PETIOLE2 and CYTOKININ OXIDASE 3 during flower development in <i>Arabidopsis</i>, <i>PLoS Genetics</i>, 2015, 11(9): e1005479. IF_{5years} = 5.857</p> <p>7. Ding Lian[#]; Yan Shuangshuang[#]; Jiang Li[#]; Zhao Wensheng; Ning Kang; Zhao Jianyu; Liu Xiaofeng; Zhang Juan; Wang Qian; Zhang Xiaolan*; HANABA TARANU (HAN) bridges meristem and organ primordia boundaries through PINHEAD, JAGGED, BLADE-ON-PETIOLE2 and CYTOKININ OXIDASE 3 during flower development in <i>Arabidopsis</i>, <i>PLoS Genetics</i>, 2015, 11(9): e1005479. IF_{5years} = 5.857</p> <p>8. Zhao Jianyu[#]; Li Yanqiang[#]; Ding Lian[#]; Yan Shuangshuang; Liu Meiling; Jiang Li; Zhao Wensheng; Wang Qian; Yan Liqiang; Liu Renyi; Zhang Xiaolan*; Phloem transcriptome signatures underpin the physiological differentiation of the pedicel, stalk and fruit of cucumber (<i>Cucumis sativus L.</i>), <i>Plant and Cell Physiology</i>, 2015, 57: 19-34. IF_{5years} = 4.799</p>