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| 姓名 | 王长泉 | 性别 | 男 |  | |
| 出生日期 | 1970.6 | 职称 | 教授 | | |
| 学历 | 研究生 | 学位 | 博士 | | |
| 毕业院校 | 山东师范大学 | 学科专业 | 植物学 | | |
| 任课名称 | 《花卉栽培学》、《园艺学总论》、《智慧园艺概论》、《园艺生产实习与调研》等。 | | | | |
| 电话 | 18651852517 | EMAIL | cqwang@njau.edu.cn | | |
| 个人情况 | <p>2015年9月作为海外高层次人才加盟南京农业大学，承担了国家重点研发项目、国家自然科学基金、新疆联合基金、中央高校基本业务费、江苏省重点研发项目、江苏省农业自主创新、地方政府委托项目等10余项。在国内外学术期刊发表论文50余篇，出版专著一部，申请国家发明专利6项，已经授权2项。</p> <p>主要研究领域为花卉发育生物学。以蔷薇属植物为主要对象，充分利用野生蔷薇、古老月季和现代月季的遗传多样性，实施优良种质资源的收集保护、精准评价和种质创新。综合运用传统分离群体和QTL定位、现代分子生物学及多组学技术，发掘控制月季成花以及花器官发育的关键基因及调控网路，重点从光周期响应、低温春化和激素途径三个维度解析月季多次开花的分子机制，为月季定向分子育种及生产实践提供理论指导及物质基础。</p> | | | | |
| 学习和工作简历 | <p>学习经历：</p> <p>2004/09—2007/07， 山东师范大学生命科学学院，博士学位；</p> <p>1993/09—1996/07， 山东农业大学园艺系，硕士学位；</p> <p>1988/09—1992/07， 山东农业大学林学系，学士学位。</p> <p>工作经历：</p> <p>2015/09—至今， 南京农业大学园艺学院教授；</p> <p>2011/03—2015/08， 美国加州大学戴维斯分校博士后；</p> <p>1996/07—2011/02， 山东理工大学生命科学学院讲师、副教授。</p> | | | | |
| 科研项目 (2014-) | <p>国家自然科学基金面上项目，转录因子RmSVPs调控野蔷薇低温春化的分子机制，31972449，：2020/01-2023/12，57万，在研，主持。</p> <p>国家重点研发计划（子课题），基于多组学的优良种质资源精准评价，2019YFD1000402，2019/05-2022/12，580万，在研，主持。</p> <p>NSFC-新疆联合基金，转录因子调控单叶蔷薇耐旱的作用机制解析，U1803102，2019/01-2021/12，56万，在研，主持。</p> <p>南京农业大学海外高层次人才启动基金，130/804113，蔷薇属植物多次开花的分子机制研究，150万，在研，主持。</p> | | | | |

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| | <p>盐城市盐都区台湾农民创业园委托项目，玫瑰引种、驯化及新品种研发，2019/05-2024/04, 500 万, 在研, 主持。</p> <p>江苏省重点研发项目（现代农业），BE2016377, 多次开花玫瑰的分子育种和种质创新, 2016/07-2019/06, 50 万, 结题, 主持。</p> <p>江苏省农业科技自主创新项目, CX(16)1056, 微型月季盆花冬季调控栽培关键技术, 2016/07-2019/06, 50 万, 结题, 共主持。</p> |
| 发表论文 (2014-) | <p>Jingjing Sun, Jun Lu, Mengjuan Bai, Yeqing Chen, Weinan Wang, Chunguo Fan, Jinyi Liu, Guogui Ning, Changquan Wang*. 2021. Phytochrome-interacting factors interact with transcription factor CONSTANS to suppress flowering in rose. <i>Plant Physiology</i> (online preview).</p> <p>Mengjuan Bai, Jinyi Liu, Chunguo Fan, Yeqing Chen, Hui Chen, Jun Lu, Jingjing Sun, Guogui Ning, Changquan Wang*. 2021. KSN heterozygosity is associated with continuous flowering of <i>Rosa rugosa</i> Purple branch. <i>Horticulture Research</i>, 8: 26.</p> <p>Jinyi Liu, Min Ren, Hui Chen, Silin Wu, Huijun Yan, Abdul Jalal, Changquan Wang*. 2020. Evolution of SHORT VEGETATIVE PHASE (SVP) genes in Rosaceae: Implications of lineage-specific gene duplication events and function diversifications with respect to their roles in processes other than bud dormancy. <i>The Plant Genome</i>, 13: e20053.</p> <p>Haoran Ren, Mengjuan Bai, Jingjing Sun, Jinyi Liu, Min Ren, Yuwei Dong, Na Wang, Guogui Ning, Changquan Wang*. 2020. RcMYB84 and RcMYB123 mediate jasmonate-induced defense responses against <i>Botrytis cinerea</i> in rose (<i>Rosa chinensis</i>). <i>The Plant Journal</i>, 103: 1839-1849.</p> <p>Jun Lu, Jingjing Sun, Anqi Jiang, Mengjuan Bai, Chunguo Fan, Jinyi Liu, Guogui Ning, Changquan Wang*. 2020. Alternate expressions of CONSTANS-LIKE 4 in short days and CONSTANS in long days facilitate day-neutral response in <i>Rosa chinensis</i>. <i>Journal of Experimental Botany</i>, 71: 4057-4068.</p> <p>Yuwei Dong, Jun Lu, Jinyi Liu, Abdul Jalal, Changquan Wang*. 2020. Genome-wide identification and functional analysis of JmjC</p> |

domain-containing genes in flower development of *Rosa chinensis*. ***Plant Molecular Biology***, 102: 417-430.

Mengjuan Bai, Jingjing Sun, Jinyi Liu, Haoran Ren, Kang Wang, Yanling Wang, **Changquan Wang***, Katayoon Dehesh*. 2019. The B-box protein BBX19 suppresses seed germination via induction of ABI5. ***The Plant Journal***, 99: 1192–1202.

Yuxiao Shen, Tingting Sun, Qi Pan, Nachaisin Anupol, Hai Chen, Jiewei Shi, Fang Liu, Duanmu Deqiang, **Changquan Wang**, Jian Zhao, Shuhua Yang, Caiyun Wang, Jihong Liu, Manzhu Bao, Guogui Ning*. 2019. RrMYB5- and RrMYB10-regulated flavonoid biosynthesis plays a pivotal role in feedback loop responding to wounding and oxidation in *Rosa rugosa*. ***Plant Biotechnology Journal***, 17: 2078–2095.

Jinyi Liu, Xiaodong Fu, Yuwei Dong, Jun Lu, Min Ren, Ningning Zhou, **Changquan Wang***. 2018. MIKCC-type MADS-box genes in *Rosa chinensis*: the remarkable expansion of ABCDE model genes and their roles in floral organogenesis. ***Horticulture Research***, 5: 25.

Jun Lu, Mengjuan Bai, Haoran Ren, Jinyi Liu, **Changquan Wang***. 2017. An efficient transient expression system for gene function analysis in rose. ***Plant Methods***, 13: 116.

Xiang He, Jishan Jiang, **Chang-Quan Wang**, Katayoon Dehesh*. 2017. ORA59 and EIN3 interaction couples jasmonate-ethylene synergistic action to antagonistic salicylic acid regulation of PDF expression. ***Journal of Integrative Plant Biology***, 59: 275-287.

Mark Lemos, Yanmei Xiao, Marta Bjornson, Jin-Zheng Wang, Derrick Hicks, Amancio de Souza, **Chang-Quan Wang**, Panyu Yang, Shisong Ma, Savithramma Dinesh-Kumar, Katayoon Dehesh*. 2016. The plastidial retrograde signal methyl erythritol cyclopyrophosphate is a regulator of salicylic acid and jasmonic acid crosstalk. ***Journal of Experimental Botany***, 67: 1557-66.

Chang-Quan Wang, Mostafa Khoshhal Sarmast, Jishan Jiang, Katayoon Dehesh*. 2015. The transcriptional regulator BBX19 promotes hypocotyl growth by facilitating COP1-mediated EARLY FLOWERING3 degradation in Arabidopsis. ***The Plant Cell***, 27: 1128-1139.

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| | <p>Taylor-Teeples M, Lin L, de Lucas M, Turco G, Toal TW, Gaudinier A, Young NF, Trabucco GM, Veling MT, Lamothe R, Handakumbura PP, Xiong G, Wang C, Corwin J, Tsoukalas A, Zhang L, Ware D, Pauly M, Kliebenstein DJ, Dehesh K, Tagkopoulos I, Breton G, Pruneda-Paz JL, Ahnert SE, Kay SA, Hazen SP, Brady SM*. 2015. An <i>Arabidopsis</i> gene regulatory network for xylem specification and secondary wall biosynthesis. <i>Nature</i>, 517: 571-575.</p> <p>Chang-Quan Wang, Cade Guthrie, Mostafa K. Sarmast, Katayoon Dehesh*. 2014. BBX19 interacts with CO to repress FT transcription, defining a flowering time checkpoint. <i>The Plant Cell</i>, 26: 3589-3602.</p> <p>Tatyana Savchenko, Venkat Kolla, Chang-Quan Wang, Zainab Nasafi, Derrick Hicks, Bpantamars Phadungchob, Wassim Chehab, Federica Brandizzi, John Froehlich, Katayoon Dehesh*. 2014. Functional convergence of oxylipin and ABA pathways controls stomatal closure in response to drought. <i>Plant Physiology</i>, 164: 1151-1160.</p> <p>Geoffrey Benn, Chang-Quan Wang, Derrick R. Hicks, Jeffrey Stein, Cade Guthrie, Katayoon Dehesh*. 2014. A key general stress response motif is regulated non-uniformly by CAMTA transcription factors. <i>The Plant Journal</i>, 80: 82-92.</p> |
| 申请专利 (2014-) | <p>一种月季扦插生根能力的评价方法 (CN2020100480502)；</p> <p>一种提高月季扦插生根的方法 (CN2020100122803)；</p> <p>一种用病毒诱导的基因沉默体系鉴定月季开花基因功能的方法 (CN201810437844)；</p> <p>一种诱导金樱子叶片直接产生不定芽及植株再生的方法 (CN201810438916)；</p> <p>月季不定芽真空渗透转基因方法 (CN201710263493) (已授权)；</p> <p>一种利用月季瞬时表达系统鉴定蛋白互作的方法 (CN201710259815) (已授权)。</p> |