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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.

Taylor-Teebles 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 Arabidopsis gene regulatory network for xylem specification and secondary wall biosynthesis. *Nature*, 517: 571-575.

Chang-Quan Wang, Cade Guthrie, Mostafa K. Sarmast, Katayoon Dehesh*. 2014. BBX19 interacts with CO to repress FT transcription, defining a flowering time checkpoint. *The Plant Cell*, 26: 3589-3602.

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. *Plant Physiology*, 164: 1151-1160.

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. *The Plant Journal*, 80: 82-92.