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Areas of Research

Rose, floral development, continuous flowering

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Research Interests

Rose plants are economically important ornamental plants all over the world, and can be classified into three different flowering modes, including once flowering (OF), continuous flowering (CF) and occasionally re-blooming (OB). Wang's lab mainly focuses on dissecting the molecular mechanism of CF trait from three dimensions: photoperiod, vernalization and gibberellin.

1. Photoperiod

Photoperiodic flowering responses are classified into three major types: long day (LD), short day (SD), and day neutral (DN). Modern roses are economically important ornamental plants with CF features, and are generally regarded as DN plants. Because of the conserved role of the CO/FT pathway in *Arabidopsis thaliana*, rice and other crops, we aimed to investigate the function of the B-box (BBX) family members in rose photoperiod responses. We propose a schematic model of the regulation of the flowering time by RccCOL4-RccCO in *R. chinensis* according to the day length. Under LD condition, RccCO promotes flowering via direct binding to *RcFT* promoter to activate its expression while under SD condition, RccCO is downregulated and RccCOL4 accelerates flowering via physically interacting with RccCO to enhance its binding to *RcFT*. Consequently, the *R. chinensis* CF 'Old Blush' variety could flower under both LD and SD.

2. Vernalization

At present, researches about the vernalizations in perennial woody plants are rare. *FLC* (*FLOWERING LOCUS C*) subgroup genes, which act as the key components in the vernalization responses of cruciferous plants, are extensively losing in rosaceous plants. While another branch in the same MADS-Box gene family, *SVPs* (*SHORT VEGETATIVE PHASE*) are expanded significantly. Our results showed OF rose *Rosa multiflora* ‘Qizimei’ must experience low temperature induced vernalization before flower bud differentiation, in contrast, CF rose *Rosa chinensis* ‘Old blush’ can flower at any favorable conditions without low temperature induction. Furthermore, the expressions of *SVPs* in *R. multiflora* were tightly regulated by low temperature and that in *R. chinensis* didn’t response to low temperature anymore, so the functional differentiation of *SVPs* in the two species with opposite flowering phenotype implied the crucial roles of *SVPs* in vernalization. Thus, the comprehensive techniques including VIGS (Virus-induced Gene Silencing), RNA-seq, DNA methylation sequencing, lncRNA (Long Noncoding RNA) sequencing, histone modification examination, co-expression network analysis and gene function identification were used to determine the function of *SVPs* in vernalization.

3. Gibberellin

The function of GA on flowering regulation varies from species to species, it has been shown exogenous application of GA inhibits floral bud formation in OF rose, whereas it has no effect on flowering in CF rose. Considering apical dominance existed in bush-grown roses, which may subject to the axillary bud do not respond to flower initiation conditions. Furthermore, in addition to being genetically determined, axillary bud burst and flower initiation may also be influenced by the topophysis, cyclophysis and periphysis. Thus, it is high relevant to further careful analyze the rose flowering response to GA in controlled conditions with high-resolution. Our lab developed self-rooted single-stemmed plants from single-node cuttings of CF rose *Rosa chinensis* to study the GA responses in details.

Education Background

Bachelor: Shandong Agricultural University, China

Master: Shandong Agricultural University, China

Doctor: Shandong Normal University, China

Work experience

Assistant/Associate Professor, Shandong University of Technology, 1996.7-2011.2

Postdoc/Research Associate, University of California, Davis, 2011.3-2015.9

Selected Publication

- Liu Jinyi, Ren Min, Chen Hui, Wu Silin, Yan Huijun, Abdul Jalal, **Wang Changquan***. 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. *The Plant Genome*, 1-19.
- Ren Haoran, Bai Mengjuan, Sun Jingjing, Liu Jinyi, Ren Min, Dong Yuwei, Wang Na, Ning Guogui, **Wang Changquan***. 2020. *RcMYB84* and *RcMYB123* mediate JA induced defenses against *Botrytis cinerea* in *Rosa chinensis*. *The Plant Journal* 103: 1839-1849.
- Lu Jun, Sun Jingjing, Jiang Anqi, Bai Mengjuan, Fan Chunguo, Liu Jinyi, Ning Guogui, **Wang Changquan***. 2020. Alternate expressions of *CONSTANS-LIKE 4* in short days and *CONSTANS* in long days facilitate day-neutral response in *Rosa chinensis*. *Journal of Experimental Botany*, 71: 4057-4068.
- Dong Yuwei, Lu Jun, Liu Jinyi, Abdul Jalal, **Wang Changquan***. 2020. Genome-wide identification and functional analysis of JmjC domain-containing genes in flower development of *Rosa chinensis*. *Plant Molecular Biology*, 102: 417-430.
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- Liu Jinyi, Fu Xiaodong, Dong Yuwei, Lu Jun, Ren Min, Zhou Ningning, **Wang Changquan***. 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
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Reference

<http://yyxy.njau.edu.cn/szdw/gsyxk.htm>