Loren Rieseberg

Areas of Research

Brassica species, Quantitative genetic, Heterosis, growth and development.

Contact Information

Office location: Office room D108, North Executive Building (Mailing Address: Nanjing Agricultural University, Weigang 1#, Xuanwu district, 210095, Nanjing city, Jiangsu, China)

Office phone：+86 84395296

Lab location：Room B6008 Biological Sciences Building

Lab phone：+86 84395332

Email address： Dong.xiao@njau.edu.cn

Research Interests

Plant genetical genomics; quantitative trait locus; real-time quantitative PCR; photoperiodic; association mapping;

The main aim of my research is to understand the genetic basis of the enormous variation present within Brassica rapa. We follow quantitative genetic approaches to unravel the genetic regulation of nutritional, developmental (heading, turnip formation, flowering) and heterosis traits in Brassica's. In recent years, we built up genetic resources to exploit this variation, and recently we invested into resequencing and transcriptome strategies. We have built up a strong position in *B. rapa* research, as this is in the China an economically important species, and several Plant Breeding companies based in the China, play a leading role in Brassica rapa vegetable breeding. The Research invested in genetic dissection of (nutritional-) quality and developmental traits (flowering time and leaf traits) in *Brassica rapa* using quantitative genetic approaches and genomic tools. For this goal, segregating populations and core collections are developed, genetic maps are constructed, and many trait QTL are identified using QTL and association mapping. Studies effect of ambient temperature fluctuations on flowering time regulation in cauliflower and *Arabidopsis*. In addition to that a research program for breeding *Brassica's* heterosis.

1. Genetical genomics

We present data that indeed Flowering time genes are preferentially retained, so the next intriguing question is whether these different orthologues of *Arabidopsis* flowering time genes play similar roles compared to *Arabidopsis*, and what is the role of these different orthologues

in *B. rapa*. Using a genetical-genomics approach, colocation of flowering time QTL (fQTL) and expression QTL (eQTL) resulted in identification of candidate genes for fQTL and visualization of co-expression networks of flowering time genes and flowering time.

2. Quantitative trait locus

We phenotyped the flowering time of a doubled haploid population, established from a cross between Yellow sarson and Pak choi under diverse environmental conditions. We identified flowering-time QTL (fQTL) in different photoperiod and temperature regimes in the greenhouse, and studied their colocation with known flowering time genes. As several fQTL colocalized with FLC paralogues, we studied the expression patterns of four FLC paralogues during the course of vernalization in parental lines. Under all environmental conditions tested the major fQTL that mapped to the BrFLC2_A02 locus was detected, however its effect decreased when plants were grown at low temperatures. Another fQTL that mapped to the FLC paralogue, BrFLC5_A03 was also identified under all tested environments, while no fQTL colocated with BrFLC1_A10 or BrFLC3_A03. Furthermore, the vernalization treatment decreased expression of all BrFLC paralogues in the parental lines, and showed the lowest transcript level after 28 days of vernalization.

3. Real-time quantitative PCR

We assessed the expression of 13 candidate reference genes for their stability. Their expression stabilities were analyzed using two programs, geNorm and NormFinder, in 20 different samples that represent four strategic groups.

4. Photoperiodic

The variations in photoperiod responses were obtained in the 11 morphotypes of B. rapa. We selected three key genes(GI-CO-FT) components of circadian clock in the photoperiod pathway(every four hour). Using a 300K gene B. rapa array, three hundred and twelve flowering time genes in Chinese cabbage were found differentially expressed under short(8 h light)or long(16 h light)daylengths at 9 and at 21 h after dawn, suggesting that the complexity of the photoperiodic for controlling the flowering time mechanism.

5. Association mapping

A diverse collection of 250 *B. rapa* accessions based on two core collections representing different morphotypes from different geographical origins were used by 55 simple sequence repeats(SSR) markers closely to the Ft candidate genes and 22 candidate FT genes for association mapping in *B. rapa*. Flowering time was scored with in several years.

Education Background

Bachelor：Shanxi Agricultural University

Master：Nanjing Agricultural University

Doctor：Nanjing Agricultural University, China and Wageningen University and Research Centre, Wageningen (WUR), The Netherlands

---

Work experience

Postdoc, Wageningen University and Research Centre, Wageningen (WUR), The Netherlands, 2012-2013

Teacher, Nanjing Agricultural University, 2014-

Selected Publication

Xiao Dong, Shen Haoran, Zhao Jianjun, Wei Yanping, Hou Xilin *, Bonnema Guusje*. 2019. QTL analysis of flowering time in response to temperature and photoperiods in a *Brassica rapa* doubled haploid population. Plant science **280**: 110-119.

Xiao Dong, Liu Shituo, Wei Yanping, Zhou Daoyun, Hou Xilin, Li Ying, Hu Chunmei*. 2016. cDNA-AFLP analysis reveals differential gene expressionin incompatible interaction between infected non-headingChinese cabbage and *Hyaloperonosporaparasitica*. Horticulture Research **3**, 16034.

Xiao Dong, Wang Huange, Basnet Ramkumar, Zhao Jianjun, Lin Ke, HouXilin*, and Bonnema Guusje*. 2014. Genetic dissection of leaf development *in Brassica rapa* using a genetical genomics approach. Plant physiology **164**: 1309-1325.

Xiao Dong #, Zhao Jianjun #, Hou Xilin, Basnet Ram K., Carpio dunia P.D., Zhang Ningwen, Bucher Johan, Lin Ke, Cheng Feng, Wang Xiaowu and Bonnema Guusje*. 2013. The *Brassica rapa FLC* homolog *BrFLC2* is a key regulator of flowering time, identified through transcriptional co-expression networks. Journal of Experimental Botany **64**: 4503-4516.

Xiao Dong, Zhang Ningwn, Zhao Jianjun, Bonnema Guusje and Hou Xilin*. 2012. Validation of reference genes for quantitative PCR normalization in Non-heading Chinese cabbage. Functional Plant Biology **39**: 342-350.