

Li Ji



Areas of Research

Fruit development, Resistance gene, Plant architecture, Genetic Engineering Breeding

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Research Interests

1. Fruit development

Fruits are essential part of human diet. In most fruit crops, fruit set normally occurs after pollination and fertilization. Fruit yield is often reduced by suppression of pollination or fertilization when crops grow in sub-optimum conditions such as low or high temperature, low light and high humidity either in open field or in greenhouses. Parthenocarpy is an alternative pathway to normal fruit-set and development, in which ovary grows into seedless fruit in the absence of pollination and/ or fertilization, thus it is recognized as an attractive agronomic trait for growers to overcome the problems of low fruit yield under unfavorable condition for pollination. Our group focused on the genetic and molecular mechanism of parthenocarpy.

2. Resistance gene

Cucumber (*Cucumis sativus* L.) is an economically important vegetable crop and is widely cultivated in the world with total harvest of more than two million hectares in 2016, globally ranking 4th in quantity of world vegetable production (FAO). Downy mildew (DM), Powdery mildew (PM) and Gummy stem blight(GSB) are three most common and destructive foliar diseases of cucumber that cause significant losses in yield and quality in cucumber production. The cucumber Introgression lines such as IL52 and IL77 derived from interspecific hybridization between cucumber and the wild relative species *Cucumis hystrix* Chakr. were originally identified that have high resistances to DM, PM and GSB. The main objective of our research is to clone these excellent resistance

genes, and reveal the resistant mechanism.

3. Plant architecture

Plant architecture originates from the organization and activity of the shoot apical meristem (SAM) and is determined by the development of stem, leaves, inflorescences and shoot branches, it has a profound impact on key agronomical aspects such as crop management, yield and yield stability. Determinate and indeterminate growth habits of cucumber can affect plant architecture and crop yield. Identification and characterization of the determinate-growth genes in cucumber could provide a new insight in plant architecture modification and development of cucumber cultivars suited to mechanized production system.

4. Genetic Engineering Breeding

Marker assisted selection (MAS) is the process by which traits are followed through DNA markers. DM, PM and GBS resistance traits of cucumber can be followed in a breeding scheme by DNA analysis rather than assessing resistance phenotypically.

Genome editing technologies is highly desirable for molecular engineering and breeding in many crops. The CRISPR/Cas9 system is a simple, inexpensive and versatile tool for genome engineering. It is a challenge to cucumber breeding and improvement by using the CRISPR/Cas9 technique.

Education Background

Bachelor: Wuhan University

Master: Chongqing University

Doctor: Chongqing University

Work experience

Visiting students, Genomique et Biotechnologie des Fruits, INRA, France, 2008-2009

Lecturer/Associate Professor, Nanjing agricultural University, 2012-

Honors and Awards

Fellow(4/7), Chinese Agricultural Science and Technology Award(2017)

Fellow(4/7), Science and Technology Award of Jiangsu Province(2015)

Selected Publication

Njogu Martin Kagiki+, Yang Fan+, Li Ji+, Wang xueyan, Joshua Otieno Ogwen and Chen Jinfeng. A novel mutation in TFL1 homolog sustaining determinate growth in cucumber (*Cucumis sativus* L.). Theoretical and Applied Genetics, 2020, 133(1).

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Wu Zhe, Zhang Ting, Li Lei, Xu Jian, Qin Xiaodong, Zhang Tinglin, Cui Li, Lou Qunfeng, Li Ji *and Chen Jinfeng *. Identification of a stable major-effect QTL (Parth 2.1) controlling parthenocarpy in cucumber and associated candidate gene analysis via whole genome re-sequencing. *BMC plant biology*, 2016, 16, 182

Li Ji+, Wu Zhe+, Cui Li+, Zhang Tingling, Guo Qinwei, Xu Jian, Jia Li, Lou Qunfeng, Huang Sanwen, Li Zhengguo and Chen Jinfeng. Transcriptome comparison of global distinctive features between pollination and parthenocarpic fruit set reveals transcriptional phytohormone cross-talk in cucumber (*Cucumis sativus* L.). *Plant and Cell Physiology*. 2014, 55(7): 1325-1342

