

Chunyan Cheng



Areas of Research

Plant breeding and germplasm enhancement in cucumber crop

Contact Information

Office location: Room B6005 Life Science Building (Lab room B6001) (Mailing Address: B6005 Life Science Building, No.1 University Blvd. Vancouver, BC. V6T 1Z4)

Office phone: 025-84396279

Lab location : Room B6001 Life Science Building

Lab phone: 025-84396279

Email address: chunyancheng@njau.edu.cn

Research Interests

Quantitative genetics and genomics; Cytogenetics; Organelle inheritance

The overall theme of my program is focus on cucumber breeding enhancement, the genetics of the resistance genes and organelle inheritance, and the cytogenetics in different *Cucumis* species. Some of the problems we are currently working on are described below:

1. Quantitative genetics and genomics

The occurrence of southern root-knot nematode (RKN, *Meloidogyne incognita*) result in huge losses to cucumber (*C. sativus* L., 2n=14) production. As there is no resistance available in cucumber resources and varieties, it is of great significance to explore and utilize the RKN resistance genes for cucumber genetic improvement. In previous studies, an RKN-resistant introgression lines (ILs), which can be used directly in breed improvement, was created, derived from the successful hybridization between cucumber and the wild cucumber (*Cucumis hystrix* Chakr., 2n=24).

Our primary research interest concerns is the molecular mechanism in the *Cucumis-hystrix* IL10-1, which the resistant gene was gained from the excellent wild relative *C. hystrix*, combining transcriptome sequencing analysis with omics joint analyzing based on iTRAQ and phosphorylated proteomic sequencing.

2. Cytogenetics

Differentiation and copy number of repetitive sequences affect directly chromosome structure, which contributes to reproductive isolation and speciation. Comparative cytogenetic mapping has been verified an efficient tool to elucidate the differentiation and distribution of repetitive sequences in genome. So, I am also working on the distinct chromosomal structures of different *Cucumis* species applying cytogenetic techniques, including fluorescence *in situ* hybridization (FISH), genomic *in situ* hybridization (GISH), single-copy gene chromosome painting (ScgCP).

3. Organelle inheritance

Plants predominantly show maternal transmission of mitochondrial DNA (mtDNA). One known exception is cucumber, in which the mtDNA is paternally inherited. However, the mechanisms regulating this unique mode of transmission are unclear. Previous work in our lab, we characterized the cucumber homolog (*CsDPD1*) of the Arabidopsis gene defective in pollen organelle DNA degradation 1 (*AtDPD1*), which plays a direct role in mtDNA degradation. All the cytological and molecular analyses suggested that protection of mtDNA in the generative cell may be the critical factor for paternal mtDNA transmission, rather than mtDNA degradation mediated by *CsDPD1*. So now what we are working on this mechanism which may protect paternal mtDNA from degradation and is likely to be the genetic basis of paternal mtDNA transmission.

Education Background

Bachelor: Nanjing Agricultural University

Doctor: Nanjing Agricultural University

Work experience

Postdoc, School of Integrative Plant Science, Cornell University, 2017.01-2018.01

Assistant Professor, College of Horticulture, Nanjing Agricultural University, 2018.02-

Selected Publication

Cheng Chunyan, Li Qingrong, Wang Xing, Li Ying, Qian Chuntao, Li Ji, Lou Qunfeng, Chen Jinfeng and John Molly. 2020. Identification and expression analysis of the *CsMYB* gene family in Root Knot Nematode-resistant and susceptible cucumbers. *Frontier in Genetics*, doi: 10.3389/fgene.2020.550677

Cheng Chunyan, Wang Xing, Liu Xuejiao, Yang Shuqiong, Qian Chuntao, Li Ji, Lou Qunfeng, Chen Jinfeng. 2019. Candidate genes underlying the quantitative trait loci for

root-knot nematode resistance in *Cucumis-hystrix* introgression line based on population sequencing. *Journal of Plant Research*, 132 (6): 813-823.

Wang Xing[†], **Cheng Chunyan**[†], Li Qingrong, Zhang Kaijing, Lou Qunfeng, Li Ji *, Chen Jinfeng*. 2020. Multi-omics analysis revealed that MAPK signaling and flavonoid metabolic pathway contributed to resistance against *Meloidogyne incognita* in the introgression line cucumber. *Journal of Proteomics*, 220
<https://doi.org/10.1016/j.jprot.2020.103675>

Yang Shuqiong, **Cheng Chunyan**, Qin Xiaodong, Yu Xiaqing, Lou Qunfeng, Li Ji, Chen Jinfeng. 2019. Comparative cyto-molecular analysis of repetitive DNA provides insights into the differential genome structure and evolution of five *Cucumis* species. *Horticultural Plant Journal*, 5 (5): 192-204.

Wang Xing, **Cheng Chunyan**, Zhang Kaijing, Tian Zhen, Xu Jian, Yang Shuqiong, Lou Qunfeng, Li Ji, and Chen Jinfeng. 2018. Comparative transcriptomics reveals suppressed expression of genes related to auxin and the cell cycle contributes to the resistance of cucumber against *Meloidogyne incognita*. *BMC Genomics*. 19, 583.

Wang Xing, Li Qingrong, **Cheng Chunyan**, Zhang Kaijing, Lou Qunfeng, Li Ji, Chen Jinfeng. 2020. Genome-wide analysis of a putative lipid transfer protein *LTP_2* gene family reveals *CsLTP_2* genes involved in response of cucumber against root-knot nematode (*Meloidogyne incognita*). *Genome*, 63: 225-238.

Ngure Joyce W[†], **Cheng Chunyan**[†], Yang Shuqiong, Lou Qunfeng, Li Ji, Qian Chuntao, Chen Jie and Chen Jinfeng. 2015. Cultivar and seasonal effects on seed oil content and fatty acid composition of cucumber as a potential industrial crop. *Journal of the American Society for Horticultural Science*, 140(4):362-372.

Zhang Yunxia[†], **Cheng Chunyan**[†], Li Ji, Yang Shuqiong, Wang Yunzhu, Li Ziang, Chen Jinfeng* and Lou Qunfeng*. 2015. Chromosomal structures and repetitive sequences divergence in *Cucumis* species revealed by comparative cytogenetic mapping *BMC Genomics*, 16:730 DOI 10.1186/s12864-015-1877-6

Yang Shuqiong, Qin Xiaodong, **Cheng Chunyan**, Li Ziang, Lou Qunfeng, Li Ji, and Chen Jinfeng. 2017. Organization and evolution of four differentially amplified tandem repeats in the *Cucumis hystrix* genome. *Planta*, 2017, 246(4):749-761.
