Curriculum Vitae

Li Zhang
Department of Plant Biology **email: zhangl25@msu.edu**
DOE Plant Research Laboratory

EDUCATION:

2011-present: PhD candidate in Department of Plant Biology, DOE Plant Research Laboratory, Michigan State University
2008-2011: M. Sc. in Botany, State Key Laboratory of Pharmaceutical Biotechnology, Department of Biology, Nanjing University.
2004-2008: B. Sc. in Biotechnology, Department of Biology, Nanjing University.

THESIS PROJECT (2012-present)

Project 1: Host target modification as a strategy to counter pathogen hijacking of the jasmonate hormone receptor

My results show that host target modification could be a promising new approach to "correct" the disease-vulnerable components of plant. In particular, recent studies have identified the plant hormone jasmonate (JA) receptor as one of the common targets of virulence factors from highly evolved biotrophic/hemi-biotrophic pathogens. Strains of the bacterial pathogen Pseudomonas syringae, for example, produce proteinaceous effectors as well as a JA-mimicking toxin, coronatine (COR), to activate JA signalling as a mechanism of promoting disease susceptibility. Guided by the crystal structure of the JA receptor and evolutionary clues, we succeeded in modifying the JA receptor that allows for sufficient endogenous JA signaling, but has greatly reduced sensitivity to COR. Transgenic Arabidopsis expressing the modified JA receptor not only are fertile and maintained a high level of insect defense, but also gained the ability to resist COR-producing pathogens Pseudomonas syringae pv. tomato and P. s. pv. maculicola. Our results provide a proof-of-concept demonstration that host target modification can be a promising new approach to prevent the virulence action of highly evolved pathogens.

Project 2: identify how activation of JA signaling promotes *Pseudomonas syringae* pv. *tomato* (*Pst*) DC3000 infection

Coronatine, a phytotoxin from *P. syringae* and analogs of JA-Ile, would also bind to COI1 and JAZ proteins with a higher affinity, and triggers stomata re-opening and increased bacteria entry. In 2011, Zeng et al., screened T-DNA insertion mutated Arabidopsis lines using coronatine deficient *Pst* DC3118, and 8 mutants showed susceptibility to coronatine-deficient *Pst* DC3118. Among them, *scord2* and *scord4* were defective in apoplast/mesophyll defense and *scord7* was affected in ABA response or a general step in stomatal closure. Through second generation sequencing, rough map based cloning and functional analysis, we will be able to identify the mutated genes and analyze their function in stomata and/or apoplast defense.

RESEARCH EXPERIENCE IN CHINA

2007-2011: I mainly focused on evolution study of plant resistance related genes using both genetic and bioinformatic methods.

Highly-adaptable R-genes in closely-related Arabidopsis species

Plant resistance genes (R-genes) evolve rapidly in response to changing environments. Sequence polymorphism and divergence were analyzed in five R-genes within two closely-related Arabidopsis species (*A. thaliana* and *A. lyrata*). Comparisons of evolutionary patterns among R-genes suggested that the same R-gene homolog can be quickly shaped by different evolutionary processes, which indicated that R-genes harbor highly adaptable alleles to cope with different pathogens, permitting rapid recognition of molecules presented by rapidly-evolving pathogens in the co-evolution context.

Co-variation of LRR-encoding genes among pairs of plant species

In this study, plant LRR-encoding genes were divided into three subclasses: NB-LRR, LRR-RLK and LRR-only. Using bioinformatics methods, the evolutionary patterns of three classes of LRR-encoding genes were studied through pair-wised comparison in 6 pairs of closely related plant genomes. Co-variation of LRRs was detected and genes with similar functions perform parallel evolutionary rates.

PUBLICATIONS:

Li Zhang, J. Withers, J. Yao, XF Xin, R. Banerjee, Q. Fariduddin, G. Howe, H. Yan, SY He. (2015) Host target modification as a strategy to counter pathogen hijacking of the jasmonate hormone receptor. (*PNAS*, under review)

F. Zhang*, J. Yao*, J. Ke*, **Li Zhang**, VQ Lam, XF Xin, XE Zhou, J. Chen, J. Brunzelle, PR Griffin, M. Zhou, HE Xu, K. Melcher, SY He. (2015) Structural basis of JAZ repression of MYC transcription factors in jasmonate signaling. *Nature, in press*.

J. Wang, **Li Zhang**, J. Li , A. Lawton-Rauh and D. Tian. (2011) Unusual signatures of highly adaptable R-loci in closely-related Arabidopsis species. *Gene* 482: 24-33. (co-first author)

J. Wang, S. Tan, **Li Zhang**, P. Li and D. Tian. (2011) Co-variation among major classes of LRR-encoding genes in two pairs of plant species. *JME* 72:498-509.

POSTERS:

Li Zhang, J. Withers, J. Yao, XF Xin, R. Banerjee, Q. Fariduddin, G. Howe, H. Yan, SY He. (2015) Abstract Title: Structure-guided design of a jasmonate receptor that uncouples endogenous hormone perception from pathogen toxin hijacking. *26th International Conference on Arabidopsis Research*.

Li Zhang, W. Zeng and SY He. (2014) Abstract Title: Arabidopsis stomatal defense against pathogen infection. *American Society of Plant Biologists*.