



Mu Li

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Education Background

2014-2016 **Northwest A&F University** (NWAUFU, Project 211 and Project 985 University)

M.S. in Mycology, College of Plant Protection

GPA: 87.2/100 (Overall), 88 /100 (Major), Rank: 5/44

2010-2014 **Northwest A&F University** (NWAUFU, Project 211 and Project 985 University)

B.S. in Biotechnology, National Biological Science Base, College of Innovative Experiment

GPA: 88.91/100 (3.62/4.0 converted), Rank: 11/215

Research Experiences

Jan 2015-present Transcriptomics of *Brachypodium*-pathogen interactions

Supervisor: Associate Professor Huiquan Liu

Co-supervisor: Professor Jin-Rong Xu

(1) *Brachypodium distachyon* is used as a model for studies on host-pathogen interactions and fungal pathogenicity, especially for the rice blast fungus *Magnaporthe oryzae* and the wheat scab fungus *Fusarium graminearum*.

(2) Profiled the transcriptomes of *Brachypodium* and the two pathogens during their peculiar interactions by RNA-seq.

(3) Identified transcriptional alterations in infected *Brachypodium*. Infections with both pathogens triggered massive metabolic reprogramming in the diseased tissues.

(4) Analyzed the temporal gene expression profiles of infected *Brachypodium*. Numerous defense-related genes and pathways showed distinct temporal dynamics of expression across the infection time course.

(5) Identified transcriptional alterations in pathogens during invasive plant infection. The two pathogens employed different nutritional acquisition and infection strategies.

(6) Identified the putative effectors that pathogens secreted to inhibit the immune system of *B. distachyon*.

(7) Identified the specific expression patterns of various plant cell wall degrading enzymes from the two pathogens.

In summary, the results contribute to a comprehensive understanding of fungal pathogenicity and development of host-pathogen interactions.

Sep 2013-Dec 2014 Comparative genomics of chitin synthase (CHS) gene family

Supervisor: Associate Professor Huiquan Liu

Co-supervisor: Professor Jin-Rong Xu

(1) CHSs are key enzymes in the biosynthesis of chitin, an important structural component of fungal cell wall that can trigger innate immune responses in host plants and animals.

(2) Systematically identified and compared members of CHS gene family from 109 fungal species.

(3) Phylogenetic analysis revealed that fungal ancestral orthologous clades underwent multiple



independent duplications and losses in different fungal lineages during evolution.

(4) Genes in some clades were specifically expanded in pathogenic fungi of animals and plants.

(5) Identified a novel clade which mainly occurred in plant pathogenic fungi and members of this clade were specifically up-regulated during plant infection.

(6) Identified specificity-determining sites potentially responsible for functional divergence of different CHS clades.

In summary, the results provide new insights to the evolution and function of the fungal CHS genes.

Apr 2011-Sep 2013 Functional genomics in the cereal pathogen *F. graminearum*

Supervisor: Professor Jin-Rong Xu

Co-supervisor: Associate Professor. Chenfang Wang

(1) *F. graminearum* is an important pathogen that can cause devastating yield loss and produce a variety of mycotoxins. It is essential to study genes that are important for *F. graminearum* biology and pathogenesis.

(2) Cooperating with others, generated approximately 300 knockout mutants.

(3) Analyzed phenotypes of mutants, including colony morphology, growth rate and asexual reproduction.

(4) Performed the infection assays with corn stalks and corn silks.

In summary, we constructed a mutant database and screened candidate genes for the further functional analysis.

Jul 2012-Aug 2012 Rice genetics and map-based cloning

Supervisor: Professor Xiangdong Fu

(1) Rice is one of the most important staple food crops. It is valuable to investigate the genetic and molecular bases of complicated traits in rice.

(2) Participated in constructing a high-density SSR genetic map from F₂ population of rice.

(3) Participated in identifying a new gene related to grain number located on the chromosome 8.

Honors and Awards

- 2015 First-class professional scholarship for graduate student
- 2015 Outstanding graduate student (**Top 10 Percent**)
- 2014 Scholarship for outstanding prospective graduate student of NWAUFU (**Top 5 Percent**)
- 2013 First prize in the undergraduate innovative experiment program of NWAUFU (**Top 10 Percent**)
- 2013 Professional scholarship for undergraduate student
- 2012 First prize in academic poster competition of NWAUFU (**Rank: 2/45**)
- 2012 "Triple-A" student (**Top 10 Percent**)
- 2012 Outstanding student leader
- 2012 Professional scholarship for undergraduate student
- 2011 Professional scholarship for undergraduate student
- 2010 Best debater in freshmen debate

Additional Experiences

- Sep 2012-Sep 2013 College of Innovative Experiment, Assistant Instructor.
Helped instructor to deal with college business and collated data.
- Sep 2011-Sep 2012 College of Innovative Experiment, Deputy Division Chief of Student Association.
Organized student activities and provided students with academic support.



Tests

GRE: 312 (V: 147, Q: 165)

TOEFL: 90 (R: 28, W: 24, S: 20, L: 18)

Publications

1. Li, M, Jiang, C, Wang, Q, Zhao, Z, Jin, Q, Xu, JR, and Liu, H. Evolution and functional insights of different ancestral orthologous clades of chitin synthase gene family in the fungal tree of life. **Front. Plant Sci.** (In revision)
2. Li, M, Liang, Y, Xu, JR, and Liu, H. Global transcriptome profiling of the hemibiotrophic interactions between *Brachypodium distachyon* and the fungal cereal pathogens *Magnaporthe oryzae* and *Fusarium graminearum*. (In preparation)
3. Liu, H, Zhang, Y, Zhang, S, Li, M, Zhang, Q, Sun, M, Wang, Q, Wu, Z, and Xu, JR. Novel rapidly evolving superfamilies of modular effectors drive divergent adaptation and speciation in basal ascomycete *Taphrina*. **New Phytologist**. (Submitted)

Conferences

- Jul 2015 Chinese Society for Plant Pathology annual conference, Haikou, China.
Title: Global transcriptome profiling of the hemibiotrophic interactions between *Brachypodium distachyon* and the fungal cereal pathogens *Magnaporthe oryzae* and *Fusarium graminearum*. (Submitted a poster and an abstract)
- Jul 2014 Chinese Society for Plant Pathology annual conference, Shenyang, China.
Title: Evolutionary genomics analysis of fungal chitin synthase gene family. (Submitted a poster and an abstract)

Referees

Dr. Huiquan Liu

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Dr. Jin-Rong Xu

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