Xiaomei Shu, PhD
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Education

Ph. D. Plant Pathology, North Carolina State University, Raleigh, NC 2009 – 2014
Advisor: Dr. Gary A. Payne
Dissertation: Pathogenesis and host response during infection of maize seeds by *Aspergillus flavus* and *Fusarium verticillioides*

M. S. Plant Science, Missouri State University, Mountain Grove, MO 2008 – 2009
Thesis: Characterization and functional analysis of *EDS6* promoters of Cabernet Sauvignon and Norton Grapevines

B. S. Biotechnology, Sichuan Agricultural University, Sichuan, China 2002 – 2006
Thesis: The influence of the maize callus differentiation by the kinetin and the proline

Professional Summary

A broad knowledge in genomics, plant pathology and microbiology. Excellent experience in Next Generation Sequencing data analysis and manuscript writing. Extremely passionate in research and teaching. Ability to manage challenging workload and drive results. A highly motivated researcher able to develop novel protocols and manage projects either independently or as part of a team.

Professional Experience

Postdoctoral Research Scientist, Texas Tech University, Lubbock, TX 2018 – current
- Develop novel Next Generation Sequencing data analysis platforms to analyze the transcriptional regulatory networks of *Escherichia coli* and *Listeria monocytogenes* in response to various abiotic interventions on tomato.
- Conduct genomics studies to discover the interactions between *E. coli* and their phages in nature.
- Establish a sustainable system to study transcriptional changes of *Staphylococcus aureus* and *Pseudomonas aeruginosa* treated by silver nanoparticles decorated titanium.

Associate Scientist, BASF Corporation, Research Triangle Park, NC 2014 – 2016
- Developed high-throughput bioassay to analyze the function of maize disease resistance genes.
- Established a novel sunflower tissue regeneration platform for chemical-mediated mutagenesis studies.

Research Assistant, North Carolina State University, Raleigh, NC 2009 – 2014
- Conducted four-year field studies to hand-pollinate maize plants and inoculate the kernels with *Aspergillus flavus* and *Fusarium verticillioides*.
- Developed histology, RNA-sequencing, RNA *in situ* hybridization, and fungal mutagenesis technologies to analyze the interaction between maize and its fungal pathogens *A. flavus* and *F. verticillioides*.
- Characterized the colonization patterns of *A. flavus* and *F. verticillioides* in maize kernels by performing histology studies.
- Identified novel maize genes and metabolic pathways that are associated with defense response to *A. flavus* and *F. verticillioides* by carrying out RNA-sequencing and pathway analysis.
- Determined two maize defense-related genes that were induced in the aleurone and scutellum by *A. flavus* and *F. verticillioides* before visible fungal colonization.
- Analyzed the function of a few novel pathogenesis genes from *A. flavus* and *F. verticillioides.*
- Served as a teaching assistant for two graduate courses. Conducted lectures and labs, graded exams and maintained a coursework management system.

Research Assistant, Missouri State University, Mountain Grove, MO 2008 – 2009

- Performed QTL studies to monitor inheritance of powdery mildew resistance in grapevine hybrids.
- Characterized the function of the grapevine defense-related gene *EDS1* using Arabidopsis and tobacco systems.

Research Assistant, Fruit Science, China Agricultural University, Beijing, China 2006 – 2008

- Established anther culture and plant regeneration platforms in grapevine.
- Determined the role of CLE peptides in grapevine embryogenesis and differentiation.

Research Assistant, Sichuan Agricultural University, Sichuan, China 2002 – 2006

- Developed young ear and tassel culture and regeneration technologies in maize.

University Teaching Experience

North Carolina State University, Raleigh, NC Aug. 2011 – Dec. 2011
Teaching Assistant – PP502 Plant Disease: Teaching Methods&Diagnosis (graduate course)

- Conducted lectures and labs, graded exams and responded to student questions.

North Carolina State University, Raleigh, NC Jan. 2012 – May 2012
Teaching Assistant – PP707 Plant Microbe Interactions (graduate course)

- Conducted lectures, graded exams and maintained a coursework management system.

Research Articles

Shu X, Singh M, Karampudi NBR, Kitazumi A, Bridges D, Wu V, De los Reye BG. (2019) Transcriptional regulatory networks determining the potential adaptation and acclimation of *Escherichia coli* O157:H7 to abiotic intervention mediated by gaseous chlorine dioxide on non-host tomato. In preparation.

Shu X, Livingston DP, Woloshuk CP and Payne GA. (2017) Comparative histological and transcriptional analysis of maize kernels infected with *Aspergillus flavus* and *Fusarium verticillioides* infection. Frontiers in Plant Science 8: 2075.

Shu X, Livingston DP, Franks RG, Boston RS, Woloshuk CP and Payne GA (2015) Tissue specific gene expression in maize seeds during colonization by *Aspergillus flavus* and *Fusarium verticillioides*. Molecular Plant Pathology 16:7.

Dolezal AL, **Shu X**, OBrian G, Nielsen D, Woloshuk CP, Boston RS and Payne GA (2014) *Aspergillus flavus* infection induces transcriptional and physical changes in developing maize kernels. Frontiers in Microbiology 5: 1-10.

Gao F, **Shu X**, Ali MB, Howard S, Li N, Winterhagen P, Qiu W and Gassmann W (2010) A functional *EDS1* ortholog is differentially regulated in powdery mildew resistant and susceptible grapevines and complements an Arabidopsis *eds1* mutant. Planta 231: 1037-1047.

Dai R, Ji M, **Shu X**, Chen S, Zhang W and Ma H (2009) 'Comparative study of total RNA extraction methods from the grape callus and a preliminary analysis of the genes' differential expression between the embryogenic callus and non-embryogenic callus. Journal of Yunnan University (Natural Sciences Edition) 31: 410-415.

Books and Book chapters

Ma H, Shao X, Chen S, Sun H, Dai R and **Shu X** (2008) "Making Good Wine Chinese version" Translation from "MAKING GOOD WINE, Revised Edition By Bryce Rankine". China Agricultural University Press, Beijing, China.

Presentations

Shu X, Livingston D, Franks RG and Payne GA. Histology and transcriptional changes of maize seed infected by *Aspergillus flavus* and *Fusarium verticillioides*. Aug. 2013. American Phytopathological Society-Mycological Society of America Joint Meeting, Austin, TX.

Shu X, Livingston D, Franks RG and Payne GA. Interaction between maize seed and its fungal pathogens *Aspergillus flavus* and *Fusarium verticillioides*. June 2013. Gordon Research Seminar, Easton, MA.

Shu X, Livingston D, Franks RG and Payne GA. Understanding the pathogenesis and host response during infection of maize seeds by *Aspergillus flavus* and *Fusarium verticillioides*. Apr. 2013. Plant Pathology PhD Symposium, North Carolina State University, Raleigh, NC.

Shu X, Livingston D, Franks RG and Payne GA. Pathogenesis and host response during infection of seeds by *Aspergillus flavus* and *Fusarium verticillioides*. July 2012. Mycological Society of America 2012 Meeting, Yale University, New Haven, CT.

Shu X and Qiu W. Characterization of promoters of defense-related *Enhanced Disease Susceptibility 1-Like Gene 6* (*EDL6*) of Cabernet Sauvignon and Norton. Apr. 2009. Graduate Interdisciplinary Forum, Missouri State University, Springfield, MO.

Conference Posters

Shu X, Livingston D, Franks RG and Payne GA. Molecular approaches to study temporal and spatial regulation of maize gene expression during fungal infection. Jan. 2014. International Plant & Animal Genome XXII, San Diego, CA.

Shu X and Payne GA. Host response of developing maize kernels during infection by *Aspergillus flavus* and *Fusarium verticillioides*. Nov. 2013. Sigma XI Student Research Conference, Research Triangle Park, NC.

Shu X, Livingston D, Franks RG and Payne GA. Integrated histology, molecular and functional genomic tools to control ear rots and mycotoxin contamination in developing maize seeds. Sept. 2013. BASF Open House, Durham, NC.

Shu X, Livingston D, Franks RG and Payne GA. Functional genomic tools to analyze pathogenesis of *Aspergillus flavus* and *Fusarium verticillioides* in developing maize seeds. June 2013. Gordon Research Seminar and Gordon Research Conference, Easton, MA.

Shu X, Livingston D, Franks RG and Payne GA. Tissue specific gene expression in maize seed in response to *Aspergillus flavus* infection. Mar. 2013. The 8th Annual NC State University Graduate Student Research Symposium**,** North Carolina State University, Raleigh, NC.

Shu X, Livingston D, Franks RG and Payne GA. *Aspergillus flavus* and *Fusarium verticillioides* induce tissue specific gene expression of *PRms* and *UGT* in maize seed before fungal colonization. Oct. 2011. 25th North Carolina Annual Plant Molecular Biology Retreat, Asheville, NC.

Shu X, Livingston D, Franks RG and Payne GA. Tissue specific gene expression of *PRms* and *UGT* in maize seed colonized by *Aspergillus flavus***.** Apr. 2011. Third Annual PhD Symposium, Department of Plant Pathology, North Carolina State University, Raleigh, NC.

Shu X, Livingston D, Franks RG and Payne GA. Tissue specific gene expression in maize seed colonized by *Aspergillus flavus.* Jan. 2011. Genetics of Maize Disease Workshop 2011, Raleigh, NC.

Awards

Plant Pathology Society of North Carolina Travel Award	2013
American Phytopathological Society Travel Award	2013

Professional Society Membership and Synergistic Activities

American Society for Microbiology, member	2019 – current
American Phytopathological Society, member	2013 – 2014
American Phytopathological Society, volunteer at the annual meeting	2013
The Mycological Society of America, member	2012 – 2013
Plant Pathology Society of North Carolina, member	2010 – 2014