

Education

- University of Illinois at Urbana-Champaign** 2017.09 - 2021.05
- PhD in Crop Sciences; GPA: 4.0/4.0; Concentrations: *Crop genetics and molecular biology*
Anticipated graduation date: May 2021
 - Specialized courses: Advanced Bioinformatics, Programming for Genomics, Applied Statistics for Experimental Design
- University of Illinois at Urbana-Champaign** 2014.08 - 2017.08
- Master of Science in Crop Sciences; GPA: 3.97/4.0; Concentrations: *Crop genetics and Bioinformatics*
 - Specialized courses: Molecular Biology of Microbe-Plant Interactions, Plant Pathogenic Fungi, Advanced Plant Genetics, Genomics for Plant Improvement, Perl & Unix for Bioinformatics
- Zhejiang University, P.R. China** 2010.09 - 2014.06
- Bachelor of Science in Agronomy; GPA: 3.96/4.0(1st in class); Major: *Plant Protection*

Research

- Postdoctoral research scholar** 2022.06 - present
- University of California at Berkeley, Department of Plant & Microbial biology
Advisor: Ksenia Krasileva (kseniak@berkeley.edu)
NLR engineering for enhanced crop disease resistance
- Postdoctoral research scholar** 2021.07 - 2022.05
- University of Illinois at Urbana-Champaign, Carl R. Woese Institute for Genomic Biology
Advisor: Stephen Long (slong@illinois.edu)
Improvement of crop transformation pipeline
- Developed a copy number measurement assay using duplex droplet digital PCR in transgenic soybean and tobacco
 - Evaluation of carbon nanotube-mediated transient gene expression in cowpea and soybean
- Graduate Research Assistant (PhD)** 2017.08 - 2021.05
- University of Illinois at Urbana-Champaign, Department of Crop Science
Advisor: Steven Clough (sjclough@illinois.edu) & Matthew Hudson (mhudson@illinois.edu)
Genetic characterization of a susceptible allele inverting the dominance of *Rpp1*-mediated rust resistance in soybean
- Constructed DNA fosmid libraries for three soybean genotypes and screened the libraries for the targeted *Rpp1* regions
 - Assembled and annotated the *Rpp1* regions with Oxford Nanopore and Illumina Miseq sequence data
 - Evaluated the RNA and small RNA expressions of candidate genes with both read alignments and qRT-PCR
 - Silenced the dominant susceptible candidate gene with a virus-induced gene silencing tool (VIGS)
 - Conducted protein interaction assays with yeast-two-hybrid assay and co-immunoprecipitation in *Nicotiana benthamiana* using *Agrobacterium tumefaciens*-mediated transient gene expression
- A genome-wide association study (GWAS) to identify genetic loci for soybean resistance to Asian soybean rust (ASR)**
- Explored the genetic architecture of soybean quantitative resistance to ASR by GWAS using a published phenotypic data of leaf disease severity and SoySNP50K genotypic data
 - Applied a logistic regression model to identify qualitative ASR resistance loci using a published phenotypic data of leaf lesion type and SoySNP50K genotypic data
- Graduate Research Assistant (Master)** 2014.08 - 2017.08
- University of Illinois at Urbana-Champaign, Department of Crop Science
Advisor: Steven Clough & Frank Zhao (zhao888@illinois.edu)
RNA sequencing analysis of an oxalate-degrading transgenic soybean infected with *S. sclerotiorum* during early infection
- Conducted *de novo* assembly of soybean transcriptome using RNA-seq data from Illumina HiSeq2500

- Identified differentially expressed genes and pathways by *S. sclerotiorum* infection or in response to degradation of oxalic acid
- Conducted real-time qRT-PCRs through a high-throughput Fluidigm system to validate candidate resistance gene responses

Comparative transcriptomic analysis of S. sclerotiorum to identify potential fungal virulence factors

- Applied reference genome-based RNA-Seq analysis to *S. sclerotiorum* in soybean leaves vs. in culture
- Performed GO enrichment analysis and gene functional annotations to identify potential novel virulence factors

A genome-wide association study of soybean resistance to Sclerotinia sclerotiorum

- Constructed Genotyping-by-Sequencing library of 384 soybean genotypes
- Identified significant QTLs with statistical analyses using a mixed linear model and a FARMCPU model
- Analyzed haplotypes and LD blocks for candidate gene identifications

Research Internship

2013.07 - 2013.08

University of Illinois at Urbana-Champaign, Department of Crop Science

Advisor: Glen L. Hartman (Glen.Hartman@ars.usda.gov)

- Measured the viability of infected soybean vascular system by fluorescent staining
- Utilized real-time qPCR to quantify the DNA of *F. virguliforme* in stem tissues at different elevations

Undergrad Research Assistant

2012.09 - 2014.05

Department of Plant Protection, Zhejiang University, China

Advisor: Fengming Song (fmsong@zju.edu.cn)

Identification and characterization of a pathogenicity-related gene BTF3a in Fusarium oxysporum

- Screened for non-pathogenic *F. oxysporum* mutants through *Agrobacterium tumefaciens*-mediated transformation
- Applied TAIL-PCR to clone the flanking region of T-DNA inserted sites and identified the *BTF3a* gene
- Generated knock-out and complemented mutants with PEG-mediated transformation in *F. oxysporum*

Publications

Wei, W., Wu, X., Garcia A., Hudson, M. and Clough, S.J. (2021) An NBS-LRR protein in the Rpp1 locus negates the dominance of Rpp1-mediated resistance against *Phakopsora pachyrhizi* in soybean. *Under review*. The Plant Journal.

Wei, W., Wu, X., Blahut-Beatty, L., Simmonds, D.H. and Clough, S.J. (2021) Transcriptome profiling reveals molecular players in early soybean-*Sclerotinia sclerotiorum* interaction. *In press*. Phytopathology.

Moro, S.M., Wu, X., **Wei, W.**, Mendes, L.W., Allen, K.C., Pinheiro, J.B., Clough, S.J. and Zucchi, M.I. (2020) Characterization and comparison of intestinal bacterial microbiomes of *Euschistus heros* and *Piezodorus guildinii* collected in Brazil and the United States. *Frontiers in Microbiology*, 12.

Wei, W., Mesquita, A.C.O., Figueiró, A. de A., Wu, X., Manjunatha, S., Wickland, D.P., Hudson, M.E., Juliatti, F.C. and Clough, S.J. (2017) Genome-wide association mapping of resistance to a Brazilian isolate of *Sclerotinia sclerotiorum* in soybean genotypes mostly from Brazil. *BMC Genomics*, 18: 1–16.

Wei W. and Clough, S.J. (2016) *Sclerotinia sclerotiorum*: molecular aspects in plant-pathogenic interactions. *Revisão Anual de Patologia de Plantas*, 24:174-189 (a comprehensive review).

Grando, C., Amon, N. D., Clough, S. J., Guo, N., **Wei, W.**, Azevedo, P., López-Urbe, M. M, Zucchi, M. I. (2018). Two colors, one species: The case of *melissodes nigroaenea* (Apidae: Eucerini), an important pollinator of cotton fields in Brazil. *Sociobiology*, 65:645–653.

Awards

Richard Bernard Award, UIUC

2020

In recognition of outstanding graduate students doing soybean research

Crop Sciences Department Travel Award, UIUC

2016

Crop Sciences Department Fellowship; Provost Match Fellowship, UIUC

2014

In recognition of outstanding applicants

Hengyi Fellowship of China, ZJU

2013

National Fellowship of China

2011,2012

In recognition of outstanding undergrad (top ~2%)

Teaching

Teaching assistance

University of Illinois at Urbana-Champaign, Department of Crop Sciences

Course: PLPA204 Introductory Plant Pathology

2020.01-2020.05

Course instructor: Nathan Schroeder (nes@illinois.edu)

- Instructed the lab session every week for basic plant pathology observations and experiments
- Prepared lab materials and graded students' lab report

Courses: PLPA509 Molecular Biology of Microbe-Plant Interaction

2018.04, 2020.04

Course instructor: Frank Zhao

- Invited presentations on "Soybean-*Sclerotinia sclerotiorum* Interaction"

Co-instructor and co-organizer

2017.08

Universidade Federal de Uberlândia, Brazil

Workshop on "Genome Analysis of Plants"

- Assisted my advisor and a fellow student in the organization of talks to give a 3-day workshop
- Gave 2 lectures on methods used in plant genome wide association study
- Organized and instructed a hands-on lab session about GWAS using the softwares TASSEL and GAPIT
- Assisted in the hands-on lab session about analysis of transcriptome data and genome sequencing

Conference Experience

The Plant Genomes, Systems Biology, and Engineering Meeting, Cold Spring Harbor Laboratory

2019.12

*Poster: In search of genetic introgression by intersubgeneric hybridization between *Glycine max* and *Glycine tomentella**

The Plant and Animal Genome XXVII Conference, San Diego, CA

2019.01

Poster: Genetics characterization of a dominant susceptible phenotype to Asian Soybean Rust disease

The 17th Biennial Conference on the Molecular and Cellular Biology of the Soybean, Athens, GA

2018.08

Poster: Genetic characterization of a dominant susceptible phenotype to Asian soybean rust

The 16th International *Sclerotinia* Workshop, Uberlândia, Brazil

2017.08

*Poster: Transcript responses in leaves to very early infection by *Sclerotinia sclerotiorum**

The 9th Brazilian Congress of Plant Breeding, Foz do Iguaçu, Brazil

2017.08

*Poster: Genome-wide association mapping of resistance to a Brazilian isolate of *Sclerotinia sclerotiorum* in soybean genotypes mostly from Brazil*

The 14th Annual National *Sclerotinia* Initiative Meeting, Bloomington, MN

2016.01

*Presentation: Identifying and verifying genes for defense to *Sclerotinia sclerotiorum**

The Joint Fall Symposium at Donald Danforth Plant Center, St. Louis, MO

2015.09

*Poster: Transcript responses in leaves to very early infection by *Sclerotinia sclerotiorum**