Jingjie Hao

E238 Beadle Center, Dept. of Agronomy and Horticulture, University of Nebraska-Lincoln, NE 68503

(515)-509-1309 | jingjie.hao@unl.edu

Education

Iowa State University, Ames, IA
Ph.D. of Genetics, Department of Horticulture — 2009-2014
Minor of Business Administration, College of Business — 2011-2012

China Agricultural University, Beijing, China
Master of Agriculture, Department of Vegetable Science — 2007-2009

China Agricultural University, Beijing, China
Bachelor of Agriculture, Department of Horticulture — 2003-2007

Employment

University of Nebraska-Lincoln, Lincoln, NE
Research Assistant Professor — 2022-Present
Post-Doctoral Research Associate — 2018-2022

Viosimos Agriculture LLC
Research Scientist — 2022-Present

University of California, Davis, CA
Laboratory Manager (Research Associate) (50% fixed) — 2015-2017

Forage Genetics International, Davis, CA
Research Associate (50% fixed) — 2015-2017
Acting Laboratory Manager — 2017

Research Experience & Activities

University of Nebraska-Lincoln, Lincoln, NE
Post-Doctoral Research Associate *2018-2022*

- Optimized 16S rRNA sequencing library preparation protocol to generate high-quality MiSeq data of the microbial communities for soil, rhizosphere and plants
- Conducted microbiome analysis investigating the functions and changes in bacterial and fungal communities in diverse environments
- Characterized the functions of *CCD* genes in strigolactones biosynthesis and plant-microbe interactions through CRISPR/Cas9 in sorghum
- Studying on how microbes alter root function through characterization of the changes occur in the maize root transcriptome
- Analyzed high-throughput phenotyping data generated from an automated plant phenotyping platform to quantify plant traits non-destructively in soybean

Undergraduate Creative Activities and Research Experiences (UCARE) selection committee *2022-Present*

- Review research project proposals from undergraduate students

University of California, Davis, CA
Research Associate *2015-2017*

- Generated high-quality genotyping data for studying plant fall dormancy using optimized Genotyping-by-Sequencing (GBS) protocol on alfalfa
- Optimized spiked GBS (sGBS) protocol for alfalfa, generated high-quality data for QTL mapping studies

Forage Genetics International, Davis, CA

Research Associate *2015-2017*

- Performed large-scale production genotyping assays to identify alfalfa plants that conform standard quality criteria for forage production
- Maintained the routine genotyping and screening procedure for alfalfa to keep the operations running smoothly

Iowa State University, Ames, IA

Graduate Research Assistant *2009-2014*

- Developed stable *Agro*-mediated plant transformation systems for both *Brachypodium* and bentgrass
- Differential expression analysis of cold-responsive genes in *BdCBF3* mutants by RNA-seq
- Constructed a salt stress-specific RNAi library from a cDNA library in creeping bentgrass

Service Learning Chair of MBA Association *2011-2012*

- Coordinated on community service projects and social activities for the MBA Association

China Agricultural University, Beijing, China

General Affairs Chair of Graduate Student Association *2007-2009*

- Hosted cultural and recreational activities, involved in class discipline construction procedures

Academic Exchange to Japan Hirosaki University *Aug 2007*

- Intercommunicated with the university students and professors scientifically and culturally

Professional Skills

Sequencing Library Construction and Genotyping

- Genotyping-by-Sequencing (GBS) library and Restriction site Associated DNA (RAD) library construction for Illumina HiSeq
- TaqMan large-scale SNP genotyping and copy number assays
- 16S rRNA library preparation for Illumina MiSeq
- RNAi library and cDNA library construction

Wet Laboratory Experience

- DNA and RNA isolation, reverse transcription, PCR, quantitative real-time PCR, Southern blot
- CRISPR and RNAi vector construction including primer design, digestion, ligation, and cloning
- Culture of bacteria, plasmid isolation and transformation
- RNAi mutagenesis and gene expression profiling
- Plant transformation and tissue culture for several plant species, such as *Brachypodium* and bentgrass
- Operation and programming of liquid handling robotics platforms (Beckman, Agilent)
- Plant hydroponic culturing and collection of root exudates
- Plant maintenance in greenhouse and growth chamber
- Operation of automated phenotyping system for plant phenotype data collection

Computational Skills

- Sequencing data management and statistical analysis
- Basic bioinformatics and data processing
- Image processing, analysis, and time-series modeling of plant phenotype imaging data using LabVIEW, MATLAB, and DIRT
- 16S rRNA/ITS sequencing data analysis using the QIIME pipeline and R programming language

Publications

1. **Hao J**, Chai YN, Lopes LD, Ordóñez R, Wright E, Archontoulis S, Schachtman D. The effects of soil depth on the structure of microbial communities in agricultural soils in Iowa, USA. *Applied and Environmental Microbiology*. (2021)

2. Lopes LD, **Hao J**, Schachtman DP. Alkaline soil pH affects bulk soil, rhizosphere and root endosphere microbiomes of plants growing in a Sandhills ecosystem. *FEMS Microbiology Ecology*. (2021)

3. **Hao J**, Ma C, Yin Y, Fei SZ. A novel method of generating RNAi library for high throughput gene function analysis in creeping bentgrass (*Agrostis stolonifera* L.). *International Turfgrass Society Research Journal*. (2021)

4. Munjal G, **Hao J**, Teuber LR, Brummer EC. Selection mapping identifies loci underpinning autumn dormancy in alfalfa (*Medicago sativa*). *G3: Genes, Genomes, Genetics*. (2018)

5. **Hao J**, Yang J, Dong J, Fei SZ. Characterization of the *BdCBF* gene family and genome-wide analyses on *BdCBF3*-dependent and -independent cold-responsive genes in *Brachypodium distachyon*. *Plant Science*. (2017)

6. Li Y, Han L, **Hao J**, Fei SZ. *Agrobacterium tumefaciens*-mediated transformation of big bluestem (*Andropogon gerardii* Vitman). *Plant Cell, Tissue and Organ Culture*. (2015)

7. **Hao J**. Genomic studies of abiotic stresses in grasses. Ph.D. dissertation. (2014)

8. **Hao J**, Yin Y, Fei SZ. Brassinosteroid signaling network: implications on yield and stress tolerance. *Plant Cell Reports*. (2013)

Manuscripts in Preparation

1. **Hao J**, Zhang C, Yu B, Schachtman DP. Elucidating the molecular influence of soil microbes on the maize root transcriptome.

2. **Hao J**, Yang Y, Kelly L, Lasky JR, Schachtman DP. Characterization of the CRISPR/Cas9 targeted mutations of *SbCCD* genes in sorghum

3. **Hao J**, Yin Y, Fei SZ. Knockdown of the *AsBri1* gene enhances drought tolerance in creeping bentgrass (*Agrostis stolonifera* L.).

Posters & Presentations

1. **Hao J**, Ma C, Fei SZ. Construction of a high throughput salt-specific RNAi library for creeping bentgrass (*Agrostis stolonifera* L.). Poster: The Plant & Animal Genome XXII Conference, January 11-15, 2014

2. **Hao J**, Dong J, Fei SZ. Knockdown of *CBF1* and *CBF3* genes reduces the capacity for cold acclimation and freezing tolerance in *Brachypodium distachyon*. Poster: The Plant & Animal Genome XXII Conference, January 11-15, 2014

3. **Hao J**, Yang J, Dong J, Fei SZ. Transcriptome analysis of a *cbf3* mutant by RNA-seq in *Brachypodium distachyon*. Poster: The Plant & Animal Genome XXIII Conference, January 10-14, 2015

4. Munjal G, **Hao J**, Teuber LR, Brummer EC. Using selection mapping to assess the genetic control of fall dormancy in cultivated Alfalfa (*Medicago sativa*). Poster: The Plant & Animal Genome XXIV Conference, January 9-13, 2016

5. **Hao J**, Yu B, Zhang C, Schachtman DP. Elucidating the molecular influence of soil microbes on the maize root transcriptome. Poster: The American Society of Plant Biologists (ASPB) Conference, August 3-7, 2019