

Jingjie Hao

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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 Vegetable Science, Department of Agriculture 2007-2009
Bachelor of Horticulture, Department of Horticulture 2003-2007

Professional Positions

University of Nebraska-Lincoln, Lincoln, NE

Director of the Biomedical and Obesity Research Core 2023-Present
Research Assistant Professor 2022-Present
Post-Doctoral Research Associate 2018-2022

Viosimos Agriculture LLC, Lincoln, NE

Research Scientist (0.5 FTE) 2022-Present

University of California, Davis, CA

Laboratory Manager (Research Associate) (0.5 FTE) 2015-2017

Forage Genetics International, Davis, CA

Research Associate (0.5 FTE) 2015-2017
Acting Laboratory Manager 2017

Research Experience & Activities

University of Nebraska-Lincoln, Lincoln, NE

Director of the Biomedical and Obesity Research Core 2023-Present

- Oversee the core's day-to-day operations, serving as the primary contact for biostatistics coordinators and the Holland Computing Center to ensure seamless core support
- Conduct user satisfaction surveys; Coordinate equipment upgrades along with maintenance and repairs
- Ensure the core's compliance with federal, state, and university policies and regulations
- General management of the core budget

Research Assistant Professor

2022-Present

- Coordinated and led a collaborative soil microbiome project for a maize diversity panel. Managed all aspects of the project, including experimental planning, personnel and timeline coordination, sample collection, processing, and data analysis
- Generated high-quality MiSeq data of microbial communities by creating a large number of 16S rRNA sequencing libraries with samples from the aforementioned project
- Characterized the functions of *CCD* genes in strigolactones biosynthesis and plant-microbe interactions through CRISPR/Cas9 in sorghum

Undergraduate Creative Activities and Research Experiences (UCARE) selection committee

2022-Present

- Assess and evaluate research project proposals submitted by undergraduate students

Viosimos Agriculture LLC, Lincoln, NE

Research Scientist

2022-Present

- Identify potential target pathogens, modes of action, and strategies for fungal disease control in leafy green
- Design and implement research protocols to identify approaches for the development of biofungicide
- Establish connections and collaborations with external research institutions and consultants. Monitor and stay informed about industry trends and advancements in the field of biofungicides
- Ensure compliance with relevant regulatory guidelines and accommodate regulations related to the development, testing, and commercialization of biofungicides

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
- Investigated the effects of microbial interactions on maize root functions through transcriptomic analysis
- Performed data analysis on high-throughput phenotyping data generated from an automated plant phenotyping platform in soybean to quantify plant traits non-destructively

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 ensure smooth operations

Iowa State University, Ames, IA

Graduate Research Assistant

2009-2014

- Established stable *Agro*-mediated plant transformation systems for *Brachypodium* and bentgrass
- Conducted differential expression analysis of cold-responsive genes in *BdCBF3* mutants using 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

- Organized cultural and recreational activities, and contributed to class discipline construction procedures

Academic Exchange to Japan Hirosaki University

Aug 2007

- Engaged in scientific and cultural exchange with university students and professors

Professional Skills

Sequencing Library Construction and Genotyping

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

Wet Laboratory Experience

- DNA and RNA isolation, reverse transcription, PCR, quantitative real-time PCR, Southern blot
- Construction of CRISPR and RNAi vector, including primer design, digestion, ligation, and cloning
- Bacterial and fungal culture, plasmid isolation and transformation
- RNAi mutagenesis and gene expression profiling
- Plant transformation and tissue culture for various plant species (eg., *Brachypodium* and bentgrass)
- Operation and programming of liquid handling robotics platforms (eg., 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
- Analysis of 16S rRNA/ITS sequencing data using the QIIME pipeline and R programming language

Managerial Skills

- Efficient project planning, organizing, and execution with clear goals, timelines, and deliverables
- Laboratory resource allocation including equipment, supplies, budgets, and personnel
- Excellent verbal and written communication skills for effective collaboration and conveying information
- Strong supervision and mentoring skills in providing guidance, support, and mentorship to lab members
- Knowledge of regulatory requirements and ethical guidelines in biological research activities

Publications

1. **Hao J**, Yang Y, Futrell S, Kelly EA, Lorts CM, Nebie B, Runo S, Yang J, Alvarez S, Lasky JR, Schachtman DP. CRISPR/Cas9-mediated mutagenesis of *carotenoid cleavage dioxygenase (CCD)* genes in sorghum alters strigolactone biosynthesis and plant biotic interactions. *Phytobiomes Journal*. (2023)
2. Lopes LD, Futrell SL, Bergmeyer E, **Hao, J**, Schachtman DP. Root exudate concentrations of indole-3-acetic acid (IAA) and abscisic acid (ABA) affect maize rhizobacterial communities at specific developmental stages. *FEMS Microbiology Ecology*. (2023)
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. *International Turfgrass Society Research Journal*. (2022)
4. **Hao J**, Chai YN, Lopes LD, Ordóñez R, Wright E, Archontoulis S, Schachtman DP. The effects of soil depth on the structure of microbial communities in agricultural soils in Iowa, USA. *Applied and Environmental Microbiology*. (2021)
5. 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)
6. Munjal G, **Hao J**, Teuber LR, Brummer EC. Selection mapping identifies loci underpinning autumn dormancy in alfalfa (*Medicago sativa*). *G3: Genes, Genomes, Genetics*. (2018)

7. **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)
8. 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)
9. **Hao J**. Genomic studies of abiotic stresses in grasses. Ph.D. dissertation. (2014)
10. **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**, Shi Y, Zhang C, Yu B, Schachtman DP. Elucidating the molecular influence of soil microbes on the maize root transcriptome.
2. **Hao J**, Xu G, Ulutas M, Jin H, Schachtman DP, Yang J. Root-associated microbiomes contribute to phenotypic heterosis in a maize diversity population under varying nitrogen conditions.
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**, 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
2. 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
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. **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
5. **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