Ji Huang

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Research Interests

 My primary research interest is gene and transposon element (TE) regulation in plants. More specifically on two questions, can we infer gene regulation through genome-wide expression assays, and what's the role of epigenetic marks in gene and TE regulation. I have constructed an optimized gene co-expression network in maize. I have studies several mutants in maize RNA-directed DNA methylation pathway to reveal small RNA and cytosine methylation functions in gene regulation. My long-term goal is to incorporate epigenetic and expression information together to decipher gene regulatory network.

Education

- **Ph.D. candidate, Cellular and Molecular Biology (08/2012 – Present)**
  Department of Biological Science, Florida State University (FSU)

- **B.S., Biological Science (09/2008 - 06/2012)**
  College of Life Science&Technology, Huazhong Agricultural University (HZAU)

Awards and Honors

Dean's Scholarship (FSU) 2012
"Monsanto" Scholarship (HZAU), 2nd prize for 2010 & 2011
Straight-A Student Scholarship (HZAU), 2009-2011
Outstanding League Member Scholarship (HZAU), 2010 & 2011
Academic Record Outstanding (HZAU)

Publications

- Huang J, Vendramin S, Shi L, McGinnis K (2017) Construction and Optimization of Large Gene Co-expression Network in Maize Using RNA-Seq Data. Plant Physiology 175: pp.00825.2017
- Huang J[*], Lynn JS[*], Schulte L[*], Vendramin S[*], McGinnis K (2017) Chapter Two-Epigenetic Control of Gene Expression in Maize. Int Rev Cell Mol Biol 328: 25–48
- Li Q, Eichten SR, Hermanson PJ, Zaunbrecher VM, Song J, Wendt J, Rosenbaum H, Madzima TF, Sloan AE, Huang J, et al (2014) Genetic Perturbation of the Maize Methylome. Plant Cell 26(12): 4602-4616
- Madzima TF, Huang J, McGinnis KM (2014) Chromatin structure and gene expression changes associated with loss of MOP1 activity in Zea mays. Epigenetics 9: 1047–59

Abstracts and Presentations

- Madzima T, McGinnis K, Huang J, Vendramin S. (presentation) ABA-induced epigenetic changes in maize. 2017 Plant Biology Conference.
- Huang J**.** (**presentation**) Construction and Comparison of Large Gene Co-expression

Network in Maize Using RNA-Seq Data. 2017 Meeting of the Sounthern Section of the American Society of Plant Biologists
- Huang J, McGinnis K. (poster) Optimizing a transient gene expression system using *Zea mays* protoplasts. 2016. 58th Annual Maize Genetics Conference
- Huang J, McGinnis K. (poster) Characterizing and mapping of *Transgene reactivated* 9 in maize. 2015. 57th Annuall Maize Genetics Conference

Core courses taken in Plant Biology and Bioinformatics

Bioinformatics, Intro to Python, Statistic in Applications, Applied Logistic Regression, Machine Learning, Calculus, Linear Algebra, Probability and Statistics, Field Experiment Designs and Statistics, Visual Basic Net Programming, Plant Biology (two semesters with labs), Biochemistry, Genetics, Plant Physiology, Molecular Biology, Cell Biology, Cell Engineering, Gene Engineering.

Research Skills and Techniques

- **Molecular Biology**
  - Proficient in standard molecular biology techniques: molecular cloning and plasmid construction, PCR, qRT-PCR etc
  - High-throughput nucleic acid (DNA and RNA) isolation and genotyping
  - Small RNA extraction
  - Maize protoplast preparation and transient expression
  - Genetic mapping
  - Sample preparation and analysis for illumina HiSeq sequencing
  - Bisulfate sequencing

- **Bioinformatics**
  - Differential expressed gene analysis for NimbleGen maize expression microarray
  - Differential expressed gene analysis for illumina NGS platform
  - ChIP-Seq data analysis for illumina NGS platform
  - Small RNA data analysis for illumina NGS platform
  - Analysis of Whole-genome Bisulfite Sequencing and Sequence Capture Bisulfate sequencing for Roche NimbleGen SeqCap platform
  - Processing large quantity of NGS data using Snakemake workflow management system
  - Programming in R, Python, shell and SAS
  - Large amount of sequence BLAST using NCBI standalone BLAST
  - Submitting High Performance Computing (HPC) jobs using Slurm

- **Other skills**
  - Application of machine learning algorithm on various data type in R environment
  - Git version control and Github hosting
  - Markdown and R markdown document writing
  - Static web development

- **Field Research**
  - Maize growth in field and greenhouse settings ranging from seed preparation, tissue collection, conducting large-scale genetic crosses and hand pollinations

◦ Mutant screens, isolation, characterization and genotype-phenotype analysis

Research Experience

- **08/2012 – Present Dr. Karen McGinnis Lab, Florida State University**
  - ◦ **Project 1:** Optimization of large Gene Co-expression Network (GCN) in maize using RNA-Seq Data
    I conducted a comprehensive evaluation of expression normalization, network inference on GCN performance and first applied ranked aggregation strategies on maize GCN using RNA-Seq libraries from 1266 maize samples. Three normalization methods (VST, CPM, RPKM) and ten inference methods, including six correlation and four mutual information (MI) methods, were tested. A robust, optimized maize GCN was constructed and shared with the community (http://www.bio.fsu.edu/mcginnislab/mcn).

  - ◦ **Project 2:** Genetic mapping of *Transgene reactivated 9* in maize
    Previously our lab found a mutant, *transgene reactivated 9* (*tgr9*), based on a screen for release of transcriptional gene silencing. SeqCap genome methylation analysis showed that *Tgr9* may have a locus-specific effect on methylation making this an interesting mutant for further analysis. I used B-A translocation lines and IDP marker mapping to localize *Tgr9* to the long arm of chromosome 3. To further locate *Tgr9*, I took advantage of next generation sequencing (NGS) combined with bulk segregant analysis. I also found the total 24nt small RNAs were decreased in *tgr9* mutants. Combined with the fact that B1-transgene was activated and methylation at promoter region was lost in mutant, it's likely *Tgr9* is involved in RdDM pathway. Identification of this gene will help us understand the diversity of transcriptional silencing pathways in maize.

  - ◦ **Project 3:** ABA-induced epigenetic changes in maize
    Mediator of paramutation 1 (MOP1) has been shown to play a very important role in maize development. It's also required for RdDM. To elucidate the mechanism of MOP1-mediated RdDM with abiotic stress response induced by abscisic acid (ABA), we used a sequence-capture(SeqCap) bisulfate sequencing approach to identify ABA-induced differentially methylated regions (DMRs) in wildtype and *mop1-1* mutant. I participated in this project by analyzing SeqCap bisulfate sequencing data.

  - ◦ **Project 4:** Effect of losing MOP1 in chromatin organization and gene expression
    We used a microarray based micrococcal nuclease sensitivity assay to identify chromatin structure changes in *mop1-1* mutant. We found that *mop1-1* mutant had an increase in chromatin accessibility at chromosome arm regions. Together with transcriptome data and small RNA sequencing data, we discovered a subset targets that likely to be silenced by Pol IV-RdDM pathway. Our results suggested that MOP1 may control a small set of genes that cause a larger effect on chromatin structure and transcription. In collaboration with Dr. Madzima, I analyzed expression microarray, RNA-Seq and small RNA sequencing dataset.

- **02/2011 – 06/2012 Dr. Jie Luo Lab, National Key Laboratory of Crop Genetic Improvement (HZAU)**
  - ◦ **Project**: Cloning, expression analysis and characterization of plant cell wall related gene *CslF6* in rice

- **11/2009 – 02/2011 Dr. Daohong Jiang Lab, State Key Laboratory of Agricultural Microbiology (HZAU)**
  - ◦ **Project**: The interaction analysis between a newly discovered pathogenic gene (SS1G_02486) and proteins of *Sclerotinia sclerotirum* (Independent Research, supported by Students Research Funding of HZAU)

Teaching Experience

- **08/2012 – Present (Florida State University)** Teaching Assistant
  - BOT3015L - Plant Biology Lab
  - BCS2010 - Biological Science I Lab
  - BCS2011 - Biological Science II Lab
  - PCB3063 - General Genetics
  - PCB4024 – Molecular Biology

Mentoring and Outreach Experience

- I have extensive experience in teaching several biology laboratory courses, especially plant biology lab.
- As a teaching assistant for General Genetics and Molecular Biology, I have a tutoring session for undergraduates one hour per week.
- In the lab, I mentored undergraduate Eleni Jaecklein and Jacquelyn Kennedy in the *Tgr9* mapping project. I taught them DNA extraction, PCR and gel electrophoresis. I also worked with Jacquelyn in the maize field.
- Lastly, as the treasurer of Badminton Club at Florida State University I manage club funding and help to organize regular practice for the people who enjoy playing badminton.