

Rongkui Han

Summary

- Deep understanding of frequentist and Bayesian statistics
- Proficient in sequestering genomic and high-throughput phenotyping data for a large variety of analytical purposes
- Strong in making and delivering engaging scientific presentations for interdisciplinary and non-expert audiences
- Creative and curious, yet pragmatic and prudent

Techniques & Software

Statistics

Analysis of variance (ANOVA)
Linear regression
General linear models
Experimental Design
Principle component analysis (PCA)
Time Series Analysis
Bayesian inference
Machine learning
 K-nearest neighbors
 Ridge regression
 LASSO
 Support vector machine
 Deep neural network
 Random forest

Bioinformatics

Sequence alignment: BWA; STAR; BLAST
SNP calling: FreeBayes; samtools
Genetic map construction: MSTMap; LepMap
QTL mapping: R/qtl
GWAS: Plink, Tassel
Co-expression analysis: edgeR; WGCNA
Transcriptome assembly: Trinity
Promoter analysis: MEME suite
Gene orthology: OrthoFinder
Genome Prediction: sommer; synbreed
Population structure: FastSTRUCTURE
Visualization: Geneious; CLC

Programming

Proficiency with R
Experience with Unix
Experience with Python
 for machine learning using
 numpy, pandas, sklearn,
 TensorFlow and keras
Experience with Perl
Experience with high-performance
 computing using slurm
Experience with git

Experience

September 2016 – Present

Ph.D. Candidate *University of California, Davis*

High-throughput drone phenotyping and genetic mapping of floral opening time

- Synthesized an innovative solution to a challenging phenotyping problem
- Built partnership with expert collaborators to simplify the process, reduce costs and amplify the impact of the project
- Developed a machine-learning- and Bayesian-statistics-based pipeline for high throughput analysis
- Made new discoveries regarding the genetic control of floral opening time

Genetic mapping of photoperiod sensitivity in lettuce

- Designed and implemented a series of experiments across multiple years, locations and conditions to comprehensively investigate the trait
- Performed QTL mapping for genetic-by-environment variations using custom R scripts
- Discovered major loci underlying in photoperiod sensitivity

Bioinformatic prediction of transcription factor binding sites in lettuce

- Integrated information from multiple independent sources for robust conclusion
- Annotated lettuce genomic promoter sequences with regulatory motifs using MEME suite
- Performed interspecific orthology analysis of seven eudicot species
- Will build lettuce gene co-expression network using RNAseq data
- Will create publicly available genomic resources for the plant genetic community

July 2015 – July 2016

Technician *Cornell University, Sorrells Lab*

- Took initiative to optimize lab equipment operations and record-keeping protocols
- Built ridge regression models to predict protein, β -glucan and lipid contents in wheat and oat grains from near-infra-red spectrum data
- Managed germplasm records on T3 Wheat database

May 2014 – August 2014

Summer Intern, Research & Development *Dow AgroSciences, IN*

- Performed intensive, deliverable-oriented horticultural research
- Demonstrated teamwork-centered work ethics
- Developed professional network within the agricultural industry

August 2013 – May 2015

Undergraduate Researcher *Cornell University, McCouch Lab*

- Conducted independent research with extensive self-teaching and self-motivation
- Performed population structure analyses on historical US rice varieties using Genotyping-by-Sequencing data and software PLINK, FastStructure, TASSEL and Geneious

Publication

- Han, R.**, Wong, A. J. Y., Tang, Z., Truco M. J., Lavelle, D. O., Kozik A., Jin, Y., Michelmore R. Drone phenotyping and machine learning enable discovery of loci regulating daily floral opening in lettuce. In Review. doi:10.1101/2020.07.16.206953
- Yu, C., Yan, C., Liu, Y., Liu, Y., Jia, Y., Lavelle, D., An, G., Zhang, W., Zhang, L., **Han, R.**, Larkin, R., Chen, J., Michelmore, R.W., Kuang, H. Upregulation of a KN1 homolog by transposon insertion promotes leafy head development in lettuce. In Review.
- Zhang, Y., Fletcher, K., **Han, R.**, Michelmore, R., & Yang, R. (2019). Genome-Wide Analysis of Cyclophilin Proteins in 21 Oomycetes. *Pathogens*, 9(1), 24. doi: 10.3390/pathogens9010024
- Montilla-Bascón, G., Paul, A. R., **Han, R.**, & Sorrells, M. (2017). Quantification of betaglucans, lipid and protein contents in whole oat groats (*Avena sativa* L.) using near infrared reflectance spectroscopy. *Journal of Near Infrared Spectroscopy*, 25(3), 172-179. doi:10.1177/0967033517709615
- Wang, D. R., **Han, R.**, Wolfrum, E. J., & McCouch, S. R. (2017). The buffering capacity of stems: Genetic architecture of nonstructural carbohydrates in cultivated Asian rice, *Oryza sativa*. *New Phytologist*, 215(2), 658-671. doi:10.1111/nph.14614

Education

September 2016 - Present

Ph.D. Candidate

PLANT BIOLOGY

M.S. Student

STATISTICS

University of California, Davis

GPA: 3.89/4.00

August 2011 – May 2015

Bachelor of Science

AGRICULTURAL SCIENCES

Cornell University

GPA: 4.00/4.00

Languages

- Mandarin Chinese
- English

Awards

2016-2021 NSF Graduate Research Fellow

Interests

- Botanical Illustration
- Calligraphy
- Baking
- Audiobooks

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