

Ruijuan Li

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<https://leejimmy93.github.io/>

Education

08/2009 – 12/2014	Auburn University, Auburn, AL, U.S.A Ph.D. in Plant Genomics and Bioinformatics
09/2005 – 07/2009	Hebei Normal University, Hebei, China B.S. in Biotechnology

Research Experience

<u>01/2016 – Present</u>	<u>Postdoctoral Scholar, University of California, Davis</u>
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- Constructed an ultra-high density genetic map using genotypic information obtained from RNA-seq data of 166 canola lines
- Identified candidate causative genes for various phenotypes using integrated QTL and eQTL approach
- Identified phenotypic associated genes from GWAS analysis on genotypic information obtained from RNA-seq data of 130 canola lines
- Trained machine learning model using genotypic and phenotypic data from canola lines, achieving 80% prediction accuracy on test data
- Examined napa cabbage tissue specific responses to shade using expression and machine learning enabled co-expression analyses

<u>04/2015 – 12/2015</u>	<u>Research Associate, USDA-ARS</u>
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- Identified nematode resistance associated genes from GWAS analysis on GBS data for 250 diploid cotton lines
- Examined population structure and genetic diversity of diploid cotton germplasm collection

<u>01/2010 – 04/2015</u>	<u>Research Assistant, Auburn University</u>
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- Found a list of candidate R genes for nematode resistance from RNA-seq expression analysis of three different genotypes of polyploid cotton, combined with prior QTL information
- Examined nematode responsive small RNA-target gene network through small RNA expression analysis of polyploid cotton

<u>05/2013 – 12/2013</u>	<u>Research Assistant, Auburn University</u>
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- Genotyped 200 polyploid cotton lines using SSR marker

Bioinformatics and/or Statistics Related Training

Summer Institute in Statistical Genetics (regression and ANOVA; quantitative genetics; association Mapping: GWAS and Sequencing Data; network and pathway analysis of omics data), University of Washington. 2016

Bioinformatics and Statistical Data Analysis Skills

Proficient with R scripting, Linux/Unix operating system, shell scripting, and Git

Knowledge and experience in high performance computing (slurm scheduler), Python scripting, and machine learning methods

Years of research experience on sequence alignment/mapping (STAR, BWA, bowtie, bowtie2, TopHat, BLAST, blat), expression and co-expression analysis (edgeR, SOM, WGCNA), SNP calling (Freebayes, GATK), genome-wide association analysis (GAPIT, Tassel), transcriptome assembly (Trinity, Cufflinks), gene annotation and gene ontology annotation (BLAST, Blast2Go, Interproscan), QTL and eQTL mapping (r/qtI package), genetic map construction (onemap, r/qtI package), genomic prediction (bigRR), population structure analysis (STRUCTURE, GENEPOP), phylogenetic analysis (PhyIip), miRNA identification (Mireap, CentroidFold), and phasiRNA identification (UEA sRNA workbench).

Statistical modeling using mixed linear model (lme4) and Bayesian statistics (brms)

Publications

Li R, Davis J, Jeong K, S Kim, Lee S, Kim S, Micheltmore R, Maloof JN. “integrated QTL and eQTL mapping provides insights and promising candidates for fatty acid composition, flowering time, and growth traits in a F2 population of synthetic allopolyploid *Brassica napus*” (in preparation)

Li R, Nozue K, Devisetty UK, Maloof JN. “An atlas of gene expression changes in response to shade in two *Brassica rapa* genotypes” (in preparation)

Li R, Erpelding JE. “Genome-wide association study of *Gossypium arboreum* resistance to reniform nematode” (under review in BMC genetics)

Li R, Erpelding JE. “Genetic diversity analysis of *Gossypium arboreum* using genotyping-by-sequencing” *Genetica*. 2016; doi:10.1007/s10709-016-9921-2

Li R, Rashotte AM, Singh NK, Weaver DB, Lawrence KS, Locy RD. “Transcriptome Analysis of Cotton (*Gossypium hirsutum* L.) Genotypes That Are Susceptible, Resistant, and Hypersensitive to Reniform Nematode (*Rotylenchulus reniformis*)” *PLoS One*. 2015; 10(11): e0143261. doi: 10.1371/journal.pone.0143261.

Li R, Rashotte AM, Singh NK, Weaver DB, Lawrence KS, Locy RD. “Integrated Signaling Networks In Plant Responses to Sedentary Endoparasitic Nematodes - A Perspective.” *Plant Cell Reports*. 2015; 34(1): 5–22.

Proceedings (non-peer reviewed)

Wang H, Weaver DB, Sikkens RB, Lawrence KS, and **Li R**. 2015. Field Performance of BARBREN-713 Derived Cotton Lines. Proc. Beltwide Cotton Conf., San Antonio, TX.

Li R, Pant S, Hu H, Sikkens RB, Weaver DB, Singh NK, and Locy RD. 2012. Changes in gene expression during reniform nematode infestation of cotton seedlings as determined by deep sequencing of cDNA libraries. p. 779 – 784 In S. Boyd, M. Huffman, B. Robertson (ed.). Proc. Beltwide Cotton Conf. Orlando, FL.

Posters and Talks

Li R., John Davis, Kwang-Ju Jeong, Sunboun Lee, Shinje Kim, Richard Michelmore, Julin N. Maloof. eQTL regulating transcript levels associated with oil composition and growth traits in *Brassica napus*. PAG (Plant & Animal Genome Conference), 2018. San Diego, CA. (Poster)

Li R. “From QTL analysis to genomic prediction using RNA-seq data in *Brassica napus*” UC Davis Plant Cell Biology Retreat, 2017 (Talk)

Li R., Kwang-Ju Jeong, John Davis, Richrad Michelmore, Shinje Kim, Julin Maloof. SNP calling between two genotypes of *Brassica napus*. PAG (Plant & Animal Genome Conference), 2017. San Diego, CA. (Poster)

Li R. “Dissection of *Brassica rapa* Shade Responses Using RNA-seq” UC Davis Plant Cell Biology Retreat, 2016. (Talk)

Li R., Erpelding JE. “Genome-wide association study of *Gossypium arboreum* resistance to reniform nematode”. PAG (Plant & Animal Genome Conference), 2016. San Diego, CA. (Poster)

Li R., Erpelding JE. “Genetic diversity analysis of *Gossypium arboreum* using Genotyping-by-Sequencing”. ASPB (American Society of Plant Biologists), 2015. Minneapolis, MN. (Poster)

Li R., Hu H, Singh NK, Lawrence KS, Weaver DB, Locy RD. “Small RNA Expression in Cotton (*Gossypium hirsutum*) During Reniform Nematode (*Rotylenchulus reniformis*) Infestation & small RNA Regulated Networks”. PGRP (Post-transcriptional Gene Regulation in Plants) workshop, 2013. Providence, RI. (Poster)

Li R., Locy RD, Hu H, Singh NK, Lawrence KS, Weaver DB. “Small RNA Regulatory Networks in Susceptible, Hypersensitive, and Resistant Genotypes of Cotton (*Gossypium hirsutum*) During Reniform Nematode (*Rotylenchulus reniformis*) Infestation”. (Plant & Animal Genome Conference), 2013. San Diego, CA. (Poster)

Li R., Hu H, Weaver DB, Singh NK, Locy RD. “Changes in Small RNAs During Infestation of Cotton (*Gossypium hirsutum*) Roots by Reniform Nematodes (*Rotylenchulus reniformis*)”. ASPB (American Society of Plant Biologists), 2012. Austin, TX. (Poster)

Li R., Pant S, Hu H, Sikkens R, Weaver DB, Singh NK, Locy RD. “Changes in Gene Expression During Reniform Nematode Infestation of Cotton Seedling as Determined by Deep Sequencing of cDNA Libraries” Beltwide Cotton Conferences, 2012. Orlando, FL. (Talk)

Research Recognition and Awards

ASPB travel grant award, American Society of Plant Biologists (2015)

Graduate student dissertation research grant award, Auburn University (2014)

Outstanding international student, Auburn University (2014)

PGRP workshop travel award, American Society of Plant Biologists (2013)

Cellular and Molecular Biosciences fellowship, Auburn University (2009-2010; 2013)