# Ruijuan Li

University of California, Davis
Email: rzl0007@gmail.com  Cell:334-332-9887
https://leejimmy93.github.io/

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## Education

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

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## Bioinformatics and Statistical Data Analysis Skills

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| **Basic programming** | Proficient with R, Linux/Unix, shell scripting, and git<br>experience in Python and high-performance computing (slurm) |
| **Statistics** | Mixed linear model (lme4); Bayesian statistics (brms)<br>Machine learning models (lasso, ridge, tree-based methods, SVM, PCA) |
| **Bioinformatics** | sequence alignment/mapping (STAR, TopHat, bowtie2; BWA; bowtie; blat)<br>expression and Co-expression (edgeR, SOM, WGCNA)<br>SNP calling (Freebayes, GATK)<br>genome-wide association analysis (GAPIT, Tassel)<br>transcriptome assembly (Trinity, Cufflinks)<br>gene annotation and gene ontology annotation (BLAST, Blast2Go, Interproscan)<br>QTL and eQTL mapping (r/qtl package)<br>genetic map construction (onemap, r/qtl package)<br>genomic prediction (bigRR)<br>population structure analysis (STRUCTURE, GENEPOP),<br>phylogenetic analysis (Phylip)<br>miRNA identification (Mireap, CentroidFold) and phasiRNA identification |

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## 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

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## Research Experience

**Postdoctoral Scholar, University of California, Davis**                **01/2016 – Present**
**(Maloof lab and Michelmore lab)**
- Constructed an ultra-high density genetic map using RNA-seq data of 166 canola F2 plants
- Identified candidate causative genes for various phenotypes using integrated QTL and eQTL approach
- Identified phenotypic associated genes from GWAS analysis using RNA-seq data of 130 canola lines
- Trained machine learning models using genotypic and phenotypic data from canola lines, achieving 80% prediction accuracy on test data
- Examined napa cabbage tissue, genotype, and environmental specific responses to shade using expression and machine learning enabled co-expression analyses

**Research Associate, USDA-ARS**                                    **04/2015 – 12/2015**

- Identified nematode resistance associated genes from GWAS on GBS data of diploid cotton lines
- Examined population structure and genetic diversity of diploid cotton germplasm collection

**Research Assistant, Auburn University**                           **01/2010 – 04/2015**

- 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

**Research Assistant, Auburn University**                           **05/2013 – 12/2013**

- Genotyped 200 polyploid cotton lines using SSR marker

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## Publication

**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,** Jeong K, Davis J, S Kim, Lee S, Michelmore R, Kim S, Maloof JN. "integrated QTL and eQTL mapping provides insights and candidate genes for fatty acid composition, flowering time, and growth traits in a $F_2$ population of a novel synthetic allopolyploid *Brassica napus*" (under review in Frontiers in Plant Science)

**Li R,** Erpelding JE, Stetina SR. "Genome-wide association study of *Gossypium arboreum* resistance to reniform nematode" BMC Genetics 2018; doi:10.1186/s12863-018-0662-3

**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.

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## 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.

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## Teaching and Mentoring Experience

Mentored one high school student, three undergraduates, and multiple graduate students for RNA-seq pipeline, SNP calling, transcriptome assembly and annotation, QTL mapping, and allelic specific expression related analysis, UC Davis (2016-present)
Genomic Biology lab instructor, Auburn University (2013-2014)
Human Anatomy and Physiology I&II lab instructor, Auburn University (2010-2013)