

## Ruijuan Li

University of California, Davis  
Department of Plant Biology  
Email: rzl0007@gmail.com  
Cell: 334-332-9887

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### Education

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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

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### Research Experience

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<u>01/2016 – Present</u>	<u>Postdoctoral Scholar, University of California, Davis</u> Development of novel plant prediction pipeline integrating genomic, transcriptomic, and phenotypic data for <i>Brassica napus</i> breeding Supervisor: Julin Maloof & Richard Michelmore
<u>04/2015 – 12/2015</u>	<u>Research Associate, USDA-ARS</u> Analysis of genotyping-by-sequencing data with the aim of identifying population structure and associating QTL/SNPs with reniform nematode resistance trait of <i>Gossypium arboreum</i> Supervisor: John E. Erpelding
<u>01/2010 – 04/2015</u>	<u>Research Assistant, Auburn University</u> Small RNA and transcriptome analysis of <i>Gossypium hirsutum</i> susceptibility, resistance, and hypersensitivity to reniform nematode using molecular, genomic, and bioinformatics tools Supervisor: Robert D. Locy
<u>05/2013 – 12/2013</u>	<u>Research Assistant, Auburn University</u> SSR marker assisted genotyping of <i>Gossypium hirsutum</i> Supervisor: David B. Weaver

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### Bioinformatics and/or Statistics Related Training

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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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## Bioinformatics and Statistical Data Analysis Skills

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- 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 (Phylip), miRNA identification (Mireap, CentroidFold), and phasiRNA identification (UEA sRNA workbench).
- Statistical modeling using mixed linear model (lme4) and Bayesian statistics (brms)

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## Publications

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**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.

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## Proceedings (non-peer reviewed)

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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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## Posters and Talks

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**Li R.** John Davis, Kwang-Ju Jeong, Sunboun Lee, Shinje Kim, Richrad 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)

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## Research Recognition and Awards

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- 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)