

Meng Wu

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EDUCATION

Indiana University, Bloomington, IN

August 2014 - present

Ph.D. in Evolutionary Biology (Bioinformatics minor); GPA: 4.0; Advisor: Leonie Moyle

Miami University, Oxford, OH

August 2012 - June 2014

M.S. in Biology; GPA: 3.9; Advisor: Richard Moore

Sichuan Agricultural University, China

May 2008 - June 2012

B.S. in Plant Sciences; GPA: 3.5; Advisor: Dengcai Liu

PROFESSIONAL EXPERIENCE

Genentech, San Francisco, CA – Computational Biology Intern

May 2018 - August 2018

- Worked closely with the NGS bioinformatics team and got hands on experience exploring and managing a variety of NGS data from Oxford Nanopore, Illumina (RNA-Seq, PE & HI-C), 10X Genomics, and Bionano (optical mapping)
- Developed bioinformatic pipeline to automate genome assembly and annotation, and implemented quality control

Indiana University, Bloomington, IN – Associate Instructor

August 2014 - present

- Planned and conducted lab sections for the courses “Evolutionary Genetics” and “Biology Lab”

Miami University, Oxford, OH – Associate Instructor

August 2012 - December 2013

- Planned and conducted lab sections for the courses “Biotechnology” and “Evolution”

RESEARCH EXPERIENCE

Indiana University, Bloomington, IN - Research Projects in Evolutionary Genomics

August 2014 - present

- Infer sex-determination region(s) with sex-specific variants and sex-biased gene expression in two recently evolved dioecious species in *Solanum* using RNA-seq data and DNA-seq data from male or female populations
- *De novo* assembled and annotated the genomes of several plant (*Solanaceae*) and animal (snake and arthropod) species using PacBio and Illumina data, and conducted comparative genomic analyses
- Assembled transcriptomes of 14 species in the plant genus *Jaltomata*, generated phylogenetic relationship, inferred trait evolution, and identified candidate genes associated with novel trait evolution
- Quantified transcriptional activity of transposable elements in wild tomato species using RNA-seq data
- Identified copy number variation of retrogenes in Arabidopsis population using Illumina reads

Miami University, Oxford, OH - Research Projects in Population Genetics

June 2013 - August 2014

- Sequenced the lycopene beta cyclase locus and its flanking regions in wild populations of red/yellow-fleshed papaya and cultivars, and inferred the origin of allele in red-fleshed papaya using population genetic analyses
- Sequenced the coding sequences of sex-linked genes in wild populations of papayas, and performed population genetic analyses to investigate the degradation evolution of genes in the young Y chromosome

Sichuan Agricultural University, China - Research Projects in Genome Evolution

May 2010 - June 2012

- Investigated genome compositions of the synthetic wheat-rye allopolyploids through sequencing and cytogenetic approach (FISH and GISH)

TECHNICAL SKILLS

- Five-year experience in bioinformatic analyses with programming skills in Python, Bash, R, and the related packages such as Biopython, Bioconductor, Bioawk, SciPy, NumPy, Pandas, Skit-learn, Matplotlib, ggplot2, dplyr and SQLite
- Proficiency in shell scripting in Linux environment, pipeline development and version control using GitHub

- Understanding of algorithms in choosing efficient bioinformatics software and designing custom scripts
- Familiar with various bioinformatics software and pipelines used in different analyses, including:
 - 1) Variant calling: BWA, SAMtools, BEDtools, VCFtools, Picard, GATK, ANGSD, SnpEff, Beagle
 - 2) Gene expression: STAR, HISAT2, Trinity, StringTie, FeatureCounts, EdgeR, DESeq2, Ballgown, DEXSeq
 - 3) Sequence analyses: MCL, OrthoFinder, CD-HIT, PRANK, MAFFT, MUSCLE, BioEdit, BLAST, seqtk
 - 4) Genome assembly: MaSuRCA, CANU, Supernova, DBG2OLC, Jellyfish, PILON, ABySS, QUAST, BUSCO
 - 5) Genome annotation: MAKER2, AHRD, RepeatMasker, LTRharvest, InterProScan, GFF utilities, JBrowse, IGV
 - 6) Other analyses: PAML, RAxML, MrBayes, CAFÉ, MEGA, DnaSP, FastQC, Trimmomatic, Ontologizer

PUBLICATIONS

- Wu M**, Kostyun JL, Moyle LC. Genome sequence of *Jaltomata* addresses rapid reproductive trait evolution and enhances comparative genomics in the hyper-diverse Solanaceae. *Genome Biology and Evolution*, in press.
- Wu M**, Kostyun JL, Hahn MW, Moyle LC. 2018. Dissecting the basis of novel trait evolution in a radiation with widespread phylogenetic discordance. *Molecular Ecology*, 27:3301-3316.
- Wu M**, Lewis J, Moore RC. 2017. A wild origin of the loss-of-function lycopene beta cyclase (CYC-b) allele in cultivated, red-fleshed papaya (*Carica papaya*). *American Journal of Botany*, 104:1-11.
- Wu M** and Moore RC. 2015. The evolutionary tempo of sex chromosome degradation in *Carica papaya*. *Journal of Molecular Evolution*, 80:265-277.
- Lappin FM, Medert CM, Hawkins K, Mardonovich S, **Wu M**, Moore RC. 2015. A polymorphic pseudoautosomal boundary in the *Carica papaya* sex chromosomes. *Molecular Genetics and Genomics*, 290:1511-1522.
- Hao M, Luo J, Zhang L, Yuan Z, Yang Y, **Wu M**, Chen W, Zheng Y, Zhang H, Liu D. 2013. Production of hexaploid triticale by a synthetic hexaploid wheat-rye hybrid method. *Euphytica*, 193:347-357.
- Tang Z*, **Wu M***, Zhang H, Yan B, Tan F, Zhang H, Fu S, Ren Z. 2012. Loss of parental coding sequences in early generation of wheat-rye allopolyploid. *International Journal of Plant Sciences*, 173:1-6 (*co-1st authorship).

CONFERENCE PRESENTATIONS

- Identifying sex determination region from a dioecious *Solanum* species by using whole-genome sequencing and transcriptomic data. **[Poster]**. The Plant and Animal Genome XXVII Conference, Jan 2019, San Diego
- Sequencing and *de novo* assembly of the genome of *Jaltomata sinuosa*, a species in the sister clade to *Solanum* and *Capsicum*. **[Poster]**. The Plant and Animal Genome XXVI Conference, Jan 2018, San Diego
- Inferring phenotypic trait evolution and contributing loci in a recent radiation with widespread phylogenetic discordance. **[Poster]**. The Annual Meeting of the Society for Molecular Biology and Evolution, July 2017, Austin
- The evolutionary tempo of sex chromosome degradation in *Carica papaya*. **[Talk]**. The Midwest Ecology and Evolution Conference, March 2014, Dayton
- The investigation on protein evolution of Y chromosome in *Carica papaya*. **[Poster]**. The Annual Meeting of the Botanical Society of America, July 2013, New Orleans

AWARDS AND HONORS

- “Genetics Section Student Poster Award”, Botanical Society of America, 2013
- “Academic Challenge Research Grant”, \$2000, Miami University, 2013
- “Heimsch Award”, Outstanding Graduate Student, \$900, Miami University, 2012