

Meng Wu

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EDUCATION

Indiana University, Bloomington, IN

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

Advisor: Leonie Moyle

08/2014-07/2019

Miami University, Oxford, OH

M.S. in Biology; GPA: 3.9

Advisor: Richard Moore

08/2012-06/2014

Sichuan Agricultural University, China

B.S. in Plant Sciences; GPA: 3.5

Advisor: Dengcai Liu

09/2008-06/2012

PROFESSIONAL EXPERIENCE

Genentech, South San Francisco, CA | **Computational Biology Intern**

05/2018-08/2018

- 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 a bioinformatic pipeline to automate genome assembly and annotation, and implemented quality control

Indiana University, Bloomington, IN | **Associate Instructor**

08/2014-05/2019

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

Miami University, Oxford, OH | **Associate Instructor**

08/2012-12/2013

- Planned and conducted lab sections for the courses "Biotechnology" and "Evolution"

RESEARCH EXPERIENCE

Indiana University, Bloomington, IN | **Research Projects in Evolutionary Genomics** 08/2014-Present

- Investigated the genetics basis of sexual differentiation in two recently evolved dioecious plant species, through identification of sex-biased genes and sex-determination region using RNA-seq and population resequencing data
- 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 some closely related plant species, generated phylogenetic relationship, inferred trait evolution, examined gene tree discordance, 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**

08/2012-06/2014

- 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**

05/2010-06/2012

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

PEER REVIEW EXPERIENCE

Journal: *Molecular Ecology*

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, Scikit-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, Beagle, Minimap2, Sniffles
 - 2) Gene expression: STAR, HISAT2, Trinity, StringTie, FeatureCounts, EdgeR, DESeq2, Ballgown, DEXSeq, DiffCorr
 - 3) Sequence analyses: MCL, OrthoFinder, CD-HIT, PRANK, MAFFT, MUSCLE, BioEdit, BLAST, seqtk, MEGA, DnaSP
 - 4) Genome assembly: MaSuRCA, CANU, Supernova, DBG2OLC, PILON, ABySS, QUASt, BUSCO, GenomeScope
 - 5) Genome annotation: MAKER2, AHRD, TransDecoder, RepeatMasker, InterProScan, GFF utilities, JBrowse, IGV
 - 6) Other analyses: PAML, RAxML, MrBayes, ASTRAL, CAFÉ, FastQC, Trimmomatic, Ontologizer, Jellyfish, SnpEff

PUBLICATIONS

Suryamohan K, ..., **Wu M**, ..., Seshagiri S (7th out of 32 co-authors). The indian cobra reference genome and transcriptome enable comprehensive identification of venom gland-specific genes. Under review.

Wu M, Kostyun JL, Moyle LC. 2019. Genome sequence of *Jaltomata* addresses rapid reproductive trait evolution and enhances comparative genomics in the hyper-diverse Solanaceae. *Genome Biology and Evolution*, 11:335-349.

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 triticales 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

The genomic basis of sexual differentiation in a recently evolved dioecious species (*Solanum appendiculatum*). [**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

"College of Arts and Sciences Travel Award", \$500, Indiana University, 2014

"Heimsch Award", Outstanding Graduate Student, \$900, Miami University, 2014

"Academic Challenge Research Grant", \$2000, Miami University, 2013

"Genetics Section Student Poster Award", Botanical Society of America, 2013