Meng Wu

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EDUCATION

Indiana University, Bloomington, IN   Advisor: Leonie Moyle
Ph.D in Evolutionary Biology (Bioinformatics minor); GPA: 4.0   08/2014-07/2019

Miami University, Oxford, OH   Advisor: Richard Moore
M.S. in Biology; GPA: 3.9   08/2012-06/2014

Sichuan Agricultural University, China   Advisor: Dengcai Liu
B.S. in Plant Sciences; GPA: 3.5   09/2008-06/2012

PROFESSIONAL EXPERIENCE

Genentech, 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 bioinfomatic 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 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 some closely related plant species, 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**   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)

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, 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, RepeatMasker, LTRharvest, InterProScan, GFF utilities, JBrowse, IGV
6) Other analyses: PAML, RAxML, MrBayes, ASTRAL, CAFÉ, FastQC, Trimmomatic, Ontologizer, Jellyfish

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PUBILICATIONS

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, evy274.

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

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

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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