Meng Wu | PhD Candidate

639 E Alpine Trail, Bloomington, IN, 47401
(513) 593-4686, wum5@indiana.edu

EDUCATION

Ph.D. in Evolutionary Genetics (minor: Bioinformatics), 2014~, Indiana Univ., USA (GPA 4.0)
M.S. in Biology, 2012.8~2014.8, Miami University, USA (GPA 3.9)
B.S. in Plant Sciences, 2008.9~2012.6, Sichuan Agricultural University, China (GPA 3.5)

RESEARCH PROJECTS

- Assembled transcriptomes of 14 *Jaltomata* species (closely related plant taxon of tomato species), generated phylogenetic relationship, inferred trait evolution, and identify candidate genes or SNPs associated with morphological trait diversification [Project Scripts]
- Assembled the genome of *Jaltomata sinuosa* using PacBio and Illumina reads, annotated repeats and gene models, conducted comparative genomic analyses (gene family dynamics and gene molecular evolution) with other sequenced Solanaceae species [Project Scripts]
- Quantified the transcriptional activity of transposable elements in wild tomatoes using RNA-seq data, and investigated their expression relationship with surrounding genes
- Sequenced the lycopene beta cyclase locus and its up/down-stream flanking regions in wild populations of red/yellow-fleshed papaya and cultivars, performed population genetic analyses to reveal the origin of allele in red-fleshed papaya
- Compared the coding sequences of X/Y-linked genes in papaya sex chromosomes, and performed population genetic analyses on several sequenced X-Y genes pairs to suggest the degradation evolution of Y-linked gens on papaya's young sex chromosome
- Study genome evolution in the synthetic wheat-rye allopolyploids using molecular (PCR and sequencing) and cytogenetic approach (FISH and GISH)

COMPUTATIONAL SKILLS

- Four-year experience in Python and R, including using related packages or libraries such as biopython, bioconductor, SciPy, NumPy, pandas, skit-learn, Matplotlib
- Proficiency in shell scripting in Linux environment and pipeline development
- Ability to use relational database management system, such as SQLite
- Familiar with various bioinformatics software and pipelines, including:
    1) Reads processing: Trimmomatic, Scythe, FastQC
    2) Reads mapping: BWA, STAR, SAMtools, featureCounts, BEDtools, VCFtools
    3) Sequence clustering and alignment: MCL, CD-HIT, PRANK, MAFFT, MUSCLE
    4) Genome/transcriptome assembly: Trinity, MaSuRCA, DBG2OLC
    5) Functional annotations: MAKER, AHRD, RepeatMasker, LTR_harvest
    6) Phylogeny analyses: PAML, RAxML, FastTree, ASTRAL, BUCKy
    7) Evolutionary analyses: CAFÉ, MEGA, DnaSP

PUBLICATIONS

Wu M, Kostyun JL, Hahn MW, Moyle LC. Dissecting the basis of novel trait evolution in a radiation with widespread phylogenetic discordance. BioRxiv 201376.

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 (***equal contribution**).

CONFERENCES/WORKSHOPS

"The Plant and Animal Genome XXVI Conference", San Diego, 01/2018
Sequencing and *de novo* assembly of the genome of *Jaltomata sinuosa*, a species in the sister clade to *Solanum* and *Capsicum*. [Poster]

"The Annual Meeting of the Society for Molecular Biology and Evolution", Austin, 07/2017
Inferring phenotypic trait evolution and contributing loci in a recent radiation with widespread phylogenetic discordance. [Poster]

"The Midwest Ecology and Evolution Conference", Dayton, 03/2014
The evolutionary tempo of sex chromosome degradation in *Carica papaya*. [Talk]

"The Annual Meeting of the Botanical Society of America", New Orleans, 07/2013
The investigation on protein evolution of Y chromosome in *Carica papaya*. [Poster]

AWARDS AND HONORS

"Heimsch Award", Outstanding Graduate Student, $900, Dept. of Biology, Miami Univ., 2012
"Genetics Section Student Poster Award", Botanical Society of America, 2013
"Academic Challenge Research Grant", $2000, Dept. of Biology, Miami University, 2013

GRADUATE ASSISTANTSHIPS

Teaching "Evolutionary Genetics" and "Biology Lab", Indiana University, 01/2015~05/2018
Teaching "Biotechnology" and "Evolution", Miami University 01/2013~05/2014
Research assistant, Herbarium of Miami University, 08/2012~12/2012