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## CURRICULUM VITAE

Mr. Meng Wu

### EDUCATION

Ph.D. in Evolutionary Biology (minor: Bioinformatics), 2014.8~, Indiana University, USA  
*Committee: Leonie C. Moyle (advisor), Matthew W. Hahn, Haixu Tang, Volker Brendel*  
M.S. in Biology, 2012.8~2014.8, Miami University, USA  
*Committee: Richard C. Moore (advisor), James R. Hickey, Chun Liang*  
B.S. in Plant Science & Technology, 2008.9~2012.6, Sichuan Agricultural University, China  
*Thesis advisor: Dengcai Liu, Zongxiang Tang*

### RESEARCH PROJECTS

- Assembly of the plant (*Jaltomata sinuosa*) genome using PacBio and Illumina NGS data
- Phylogenomic study of 14 *Jaltomata* species using whole-transcriptome data
- Investigation of the activity of transcriptional elements in wild tomatoes using RNA-seq data
- Investigation of the origin of the allele at *CYC-b* locus contributing to red-fleshed papaya
- Population genetic study on sex chromosome degradation evolution in papaya
- Study genome evolution in the synthetic wheat-rye allopolyploids

### 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

Wu M, Kostyun JL, Moyle LC. Sequencing and *de novo* assembly of the genome of *Jaltomata sinuosa*, a species in the sister clade to *Solanum* and *Capsicum*, allows new comparative genomic analyses in the *Solanaceae*. [Poster Presentation]

“The Annual Meeting of the Society for Molecular Biology and Evolution”, Austin, 07/2017

Wu M, Kostyun JL, Moyle LC. Inferring phenotypic trait evolution and contributing loci in a recent radiation with widespread phylogenetic discordance. [Poster Presentation]

“The Midwest Ecology and Evolution Conference”, Dayton, 03/2014

Wu M and Moore RC. The evolutionary tempo of sex chromosome degradation in *Carica papaya*. [Oral Presentation]

“The Annual Meeting of the Botanical Society of America”, New Orleans, 07/2013

Wu M and Moore RC. The investigation on protein evolution of Y chromosome in *Carica papaya*. [Poster Presentation]

## 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 assistant in course “Evolution”, Indiana University, 08/2016~05/2017

Teaching assistant in course “Biology Laboratory”, Indiana University, 01/2015~05/2016

Teaching assistant in course: “Biotechnology”, Miami University, 08/2013-12/2013

Teaching assistant in course: “Evolution”, Miami University, 01/2013~05/2013

Research assistant, Herbarium of Miami University, 08/2012~12/2012

## 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, GATK
  - 3) Sequence clustering and alignment: MCL, CD-HIT, PRANK, MAFFT, MUSCLE
  - 4) Phylogeny analyses: PAML, RAxML, FastTree, ASTRAL, BUCKy
  - 5) Genome/transcriptome assembly: Trinity, MaSuRCA, DBG2OLC
  - 6) Functional annotations: MAKER, AHRD, RepeatMasker, LTR\_harvest
  - 7) Evolutionary analyses: CAFÉ, MEGA, DnaSP, ms