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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 of 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]

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 programming or statistical languages (Python and R), including packages or libraries such as biopython, bioconductor, numpy, pandas, skit-learn, matplotlib
- Proficiency in shell scripting in Linux environment and pipeline development
- 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, FigTree, ASTRAL, BUCKy
 - 5) Genome/transcriptome assembly: Trinity, MaSuRCA, DBG2OLC
 - 6) Functional annotations: MAKER, AHRD, RepeatMasker, LTR_harvest
 - 7) Evolutionary analyses: CAFÉ, MEGA, DnaSP, ms