

# LI WANG

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## EDUCATION

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### **Wuhan University, China**

2006

BS Biology with biotechnology emphasis

Advisor: Dr. Shuangquan Huang

### **Institute of Botany, Chinese Academy of Sciences**

2011

PhD Biology

Thesis: Phylogeny, diversification and phylogeography of the derived fern genus *Lepisorus*

Advisor: Dr. Xianchun Zhang, Dr. Harald Schneider and Dr. Deyuan Hong

## WORK EXPERIENCE

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### **Institute of Hydrobiology, Chinese Academy of Sciences**

June 2005 - December 2005

*Undergraduate Research*

- Effect of construction of the three gorges dam on fish diversity in Yangtze River
- Research Advisor: D. Jianbo Chang

### **Institute of Botany, Chinese Academy of Sciences**

June 2007 - July 2011

*Research Assistant*

- Principal Investigator: Dr. Xianchun Zhang
- Investigating phylogeny, phylogeography, polyploidization and reticulate evolution in ferns
- Mentored multiple graduate students in experimental and analyses techniques

### **Goettingen University, Germany**

February 2009 - November 2010

*Research Assistant*

- Principal Investigator: Dr. Harald Schneider
- Investigating phylogeny, phylogeography, polyploidization and reticulate evolution in ferns

### **Natural History Museum, London, UK**

December 2009, April 2010

*Research Assistant*

- Principal Investigator: Dr. Harald Schneider
- Investigating phylogeny, phylogeography, polyploidization and reticulate evolution in ferns

### **Texas Tech University**

February 2012 - March 2014

*Postdoctoral Research Associate*

- Principal Investigator: Dr. Matt Olson
- Latitudinal adaptation leads to transcriptome differentiation among poplar populations
- Sex dimorphism and sex evolution in dioecious poplars
- Mentored graduate students Mitra Menon in molecular and bioinformatic techniques

### **Iowa State University**

April 2014 - December 2015

*Postdoctoral Research Associate*

- Principal Investigator: Dr. Andrew Severin
- Providing services at Genomic Informatics Center
- Detection of selection during soybean improvement

### **Iowa State University**

*Postdoctoral Research Associate*

April 2014 - present

- Principal Investigator: Dr. Matt Hufford
- Demography and its effect on mutation load in maize and teosinte
- Parallel adaptation to highland conditions in maize populations
- Comparative genomics of four de-novo assembled genomes of maize landraces
- Mentored graduate students Sarah Pederson and Garrett Janzen in molecular and bioinformatic techniques

## **ACCOMPLISHMENTS**

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### **Publicly available pipelines and scripts**

- [https://github.com/HuffordLab/Wang\\_et\\_al\\_Demography](https://github.com/HuffordLab/Wang_et_al_Demography) – computational pipeline for demography and its effect on mutation in maize
- <https://github.com/ISUgenomics/commonscripts> – Common genomic analyses

## **AWARDS AND HONORS**

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### **2011**

- DEAN Award in Chinese Academy of Sciences

### **2011**

- The excellent graduate student in Chinese Academy of Sciences

### **2010-2011**

- BHPB-GUCAS Scholarship for excellent Ph.D. candidates; RMB 12,000 yuan

### **2010**

- The second prize for giving talks at students' symposium in Natural History Museum, London

### **2008 - 2010**

- DAAD-CAS Joint Scholarship Program – *1,000 Euro per month for two years*

### **2009 - 2010**

- Merit Student by the Graduate University of Chinese Academy of Sciences (GUCAS)

## **SKILLS**

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### **Scripting languages**

- Proficient in Unix scripting/bash, python, perl, R, markdown and latex

### **Software proficiencies**

- **Assembly:** Trinity, Falcon, MaSuRCA, Platanus, GenomeScope, Redundans
- **Annotation:** GeneMark, Augustus, Busco, CEGMA, Repeatmasker, BLAST, Trinotate, Blobtools
- **Aligners:** Bowtie, BWA, Gmap, Gsnap, Hisat2

- **Expression:** Rsem, edgeR, WGCNA, mapMan
- **Comparative genomics:** GATK, Bedtools, vcftools, PLINK, TASSEL, MEGA,
- **Population genomics:** PopGenome, ANGSD, NGSadmix, MSMC, PSMC, fastSimcoal, ms
- **Phylogenetics:** Mafft, ClustalW, Muscle, RaxML, Phagon
- **Visualization:** Circos, Cytoscape, Photoshop
- **Other:** Seqtk, Aspera, Bamtools, Bioawk, Cdbfasta, Fastqc, Gawk, Jellyfish, Picard Tools, Samtools, SRA-Toolkit, Tabix, Trimmomatic, Sickle, Vcftools, BLAT, Emboss etc

### **Lab proficiencies**

- DNA and RNA extraction, bioNano, PCR, clone etc.

## **FIELD-TRIP EXPERIENCES**

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Nov 2015: Mexican Central Plateau

Jun-Jul 2012: Alaska, US

Jul 2010: Altai Mountains, Russia

Jun 2010: Swiss and French Alps

Aug 2009: Swiss Alps, Switzerland

Nov 2008: Hainan, Guangdong Province, Southeast of China

May 2008: Central Inner Mongolia

Dec 2007: Southeast of Yunnan, border of China and Vietnam

Oct 2007: The Himalayas, Qinghai-Tibetan Plateau, China

Aug 2007: Hengduan Mountains, China

Jun 2006: Shangri-La, China

May 2005: The three Gorges region, China

## **CONFERENCE PARTICIPATION**

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2017: 57th maize genetic conference, St. Luis, Missouri, USA

2016: 58th maize genetic conference, Jacksonville, Florida, USA

2015: 57th maize genetic conference, St. Charles, Illinois, USA

2015: Plant and Animal Genome Conference, San Diego, CA

2013: Evolution, Snowbird, Utah, US

2011: International Botany Conference, Melbourne, Australia

2010: The Fifth Asian Fern Symposium, Shenzhen, China

2010: The students' symposium at Natural History Museum, London, UK

2009: Systematics 2009, Leiden, Netherland

2009: Niche Evolution, Zurich, Switzerland

2008: Symposium on Academic study of Chinese ferns, Shenzhen, China

## PUBLICATIONS

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### Published

- Li Wang**, Timothy Mathes Beissinger, Anne Lorant, Claudia Ross-Ibarra, Jeffrey Ross-Ibarra, Matthew Hufford. 2017. The interplay of demography and selection during maize domestication and expansion. **bioRxiv**. doi: <https://doi.org/10.1101/114579>.
- Timothy Beissinger, **Li Wang**, Kate Crosby, Arun Durvasula, Matthew B Hufford, Jeffrey Ross-Ibarra. 2016. Recent demography drives changes in linked selection across the maize genome. **Nature plants** 2: 16084.
  - **Li Wang**, Peter Tiffin, Matthew Olson. 2014. Timing for success: expression phenotype and local adaptation related to latitude in the boreal forest tree, *Populus balsamifera*. **Tree Genetics and Genomes**. DOI: 10.1007/s11295-014-0731-3.
  - Harald Schneider, Lijuan He, Jeannine Marquardt, **Li Wang**, Jochen Heinrichs, Sabine Hennequin, Xianchun Zhang. 2013. Exploring the origin of the latitudinal diversity gradient: contrasting the sister fern genera *Phegopteris* and *Pseudophegopteris*. **Journal of Systematics and Evolution** 51: 61-70.
  - Xianchun Zhang, Ran Wei, Hongmei Liu, Lijuan He, **Li Wang**, Gangming Zhang. 2013. Phylogeny and classification of the extant lycophytes and ferns from China. **Chinese Bulletin of Botany** 48: 119-137.
  - **Li Wang**, Harald Schneider, Xianchun Zhang, Qiaoping Xiang. 2012. The rise of the Himalaya enforced the diversification of SE Asian ferns by altering the monsoon regimes. **BMC Plant Biology** 12:210. DOI: 10.1186/1471-2229-12-210.
  - **Li Wang**, Harald Schneider, Zhiqiang Wu, Lijuan He, Xianchun Zhang, Qiaoping Xiang. 2012. In-dehiscent sporangia enable the accumulation of local fern diversity at the Qinghai-Tibetan Plateau. **BMC Evolutionary Biology** 12:158. DOI:10.1186/1471-2148-12-158.
  - **Li Wang**, Zhiqiang Wu, Nadia Bystriakova, Stephen W. Ansell, Qiaoping Xiang, Jochen Heinrichs, Harald Schneider, Xianchun Zhang. 2011. Phylogeography of the alpine fern *Lepisorus clathratus* on “the roof of the world”. **PloS One** 6: e25896. DOI: 10.1371/journal.pone.0025896.
  - **Li Wang**, Xinping Qi, Qiaoping Xiang, Jochen Heinrichs, Harald Schneider, Xianchun Zhang. 2010. Phylogeny of the paleotropical fern genus *Lepisorus* (Polypodiaceae, Polypodiopsida) inferred from four chloroplast genome regions. **Molecular Phylogenetics and Evolution** 54: 211-225.
  - **Li Wang**, Zhiqiang Wu, Qiaoping Xiang, Jochen Heinrichs, Harald Schneider, Xianchun Zhang. 2010. A molecular phylogeny and a revised classification of tribe Lepisoreae (Polypodiaceae) based on an analysis of four plastid DNA regions. **Botanical Journal of the Linnean Society** 162: 28-38.
  - Hongmei Liu, **Li Wang**, Hui Zeng, Xianchun Zhang. 2008. Advances in the studies of lycophytes and monilophytes with reference to systematic arrangement of families distributed in China. **Journal of Systematics and Evolution** 46: 808-829.
  - Xianchun Zhang, **Li Wang**, Xinping Qi. 2008. Additions to the pteridophyte flora of Xizang (IV). **Newsletter of Himalayan Botany** 41: 20-27.
  - **Li Wang**, Xianchun Zhang. 2007. Pteridophyta. in Zhenyu Li, Lei Shi (editors), **Flora of Emei Mountain**. Beijing Science and Technology Press, Beijing, pp. 153-224.
  - **Li Wang**, Xianchun Zhang. 2007. Chinese aquatic ferns. **China Nature** 138: 54-55.

### In Preparation

- Purushottam R. Lomate, Veena Dewangan, Neha S. Mahajan, Yashwant Kumar, Abhijeet Kulkarni, **Li Wang**, Smita Saxena, Vidya S. Gupta, and Ashok P. Giri. 2017. Integrated transcriptomic and proteomic analyses revealed the participation of endogenous protease inhibitors in the regulation of protease gene expression in *Helicoverpa armigera* (**submitted**)
- Garrett M. Janzen, **Li Wang**, Matthew B. Hufford. Review: Adaptive Introgression Expanded the Genetic Base of Crops during post-Domestication Spread. (**Expected 2017**)

- Brian Sanderson, **Li Wang**, Peter Tiffin, Zhi-qiang Wu, Matthew S. Olson. Males and females of *Populus balsamifera* differ primarily in the expression of energy-related genes. (**Expected 2017**)

## REFERENCES

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### **Dr. Matt Hufford**

Assistant Professor of Biological Sciences  
Ecology, Evolution, & Organismal Biology  
Iowa State University  
Ames, Iowa 50011  
Tel: (515) 294-8511  
Email: mhufford@iastate.edu

### **Dr. Andrew Severin**

Scientist I/Facility Manager  
Genome Informatics Facility  
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### **Dr. Jeffrey Ross-Ibarra**

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Department of Plant Sciences  
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### **Dr. Matt Olson**

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Email: matt.olson@ttu.edu