

# Curriculum Vitae

## Miao Sun

### Contact Information

*Plant Evolution and Biodiversity (PEB) Group  
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### Positions

- **Postdoctoral Research Fellow (2019.10 ~ present)**  
Department of Bioscience, Aarhus University  
Advisor: Dr. Wolf L. Eiserhardt
- **Postdoctoral Research Fellow (2016 ~ 2019.8)**  
Florida Museum of Natural History, University of Florida  
Advisor: Dr. Pamela S. Soltis
- **Postdoctoral Research Fellow (2015 ~ 2016)**  
Department of Biology, University of Florida  
Advisor: Dr. Douglas E. Soltis
- **Research Assistant (2014.07 ~ 2015.01)**  
State Key Laboratory of Systematic and Evolutionary Botany  
Institute of Botany, Chinese Academy of Sciences  
Advisor: Dr. Zhiduan Chen

### Research Interests

A phylogenetic tree is a pivotal framework for solving fundamental issues in biology. My long-term research goal is to use a robust phylogeny to elucidate patterns of evolutionary radiations in angiosperms and to address the causes of plant diversification using the tools of comparative biology.

### Education

- 2009 ~ 2014, PhD in Botany, Institute of Botany, Chinese Academy of Sciences
- 2006 ~ 2009, Master of Botany, Institute of Botany, Chinese Academy of Sciences
- 2002 ~ 2006, Bachelor of Environmental Science, College of Resources and Environment, Beijing Forestry University

## Research Skills

- **Taxonomic skills:**

Able to identify most seed plants at genera level or at least family level and expert in *Elaeagnus* (Elaeagnaceae), familiar with International Code of Botanical Nomenclature and mastering the process of compressing specimens

- **Molecular biology skills:**

DNA extraction, clone, PCR, sequencing, genome assembling, and genome size measurement  
*Experienced in Target Enrichment data analyses using aTRAM and HybPiper, and gene tree congruence visualization using Phyparts and Pycharts.*

- **Bioinformatical skills:**

- Experienced with standard biological software and genome dataset analysis (e.g., probe design, genome assembly)
- Proficient in Shell, R, git, Perl, and Python programming languages, familiar with SQL, version control (git), experienced in applied programming for biological data analysis and reproducible data science.

- **Language skills:**

Fluent spoken and written Chinese and English

## Honors & Awards

- 2017: Certified Instructor of Software Carpentry, and qualified to teach Software Carpentry's core curriculum.
- 2006 ~ 2014: First-class Scholarship for Graduate Student of Chinese Academy of Sciences
- 2008: Honored as a science popularization volunteer
- 2004 ~ 2005: Second Scholarships for Excellent Academic Score BFU and National Grants.
- 2003: Third Scholarships for Excellent Academic Score and National second-class scholarship.
- 2002: Chinese scholarship.

## Publications

\*equally contributing author; 23 publications, h-index 8; **336** total citations according to Google Scholar

### Papers:

1. Shimai H, Setoguchi P, Roberts D, **Sun M**. (In prep.) Phylogeny and biogeography of the genus *Pinguicula* L. (Lentibulariaceae) based on nuclear ribosomal DNA and chloroplast DNA.
2. **Sun M**, Folk FA, Gitzendanner MA, Guralnick RP, Soltis PS, Chen ZD, Soltis DE. Estimating rates and patterns of diversification with incomplete sampling: A case study in the rosids. *bioRxiv* 749325. doi: <https://www.biorxiv.org/content/10.1101/749325v1>.
3. **Sun M**, Folk FA, Gitzendanner MA, Smith SA, Germain-Aubrey C, Guralnick RP, Soltis PS, Chen ZD, Soltis DE. Exploring the phylogeny and diversification of rosids with a five-locus supermatrix. *bioRxiv* 694950. doi: 10.1101/694950.
4. Xue B, Guo X, Landis JB, **Sun M**, Tang CC, Soltis PS, Soltis DE, R.M.K. Saunders RMK. (2019). Accelerated diversification correlated with functional traits shapes extant diversity of the early divergent angiosperm family Annonaceae. *Molecular Phylogenetics and Evolution* 142: 106659. doi: 10.1016/j.ympev.2019.106659

5. Li DJ, Lauren Trotta L, Marx HE, Allen JM, **Sun M**, Soltis DE, Soltis PS, Guralnick RP, Baiser BH. (2019). For comparing phylogenetic diversity among communities, go ahead and use synthesis phylogenies. *Ecology*. doi: 10.1002/ecy.2788.
6. Yang T, Tedersoo L, Soltis PS, Soltis DE, Gilbert JA, **Sun M**, Shi Y, Wang HF, Li YT, Zhang J, Chen ZD, Lin HY, Zhao YP, Fu CX, Chu HY. (2018). Phylogenetic imprint of woody plants on the soil mycobiome in natural mountain forests of eastern China. *The ISME Journal* 13: 686–697.
7. Marodiev EV, **Sun M**, Schroder L, Steadman DW, Ebach MC. (2018). Moving from modern toward post-modern science: comment on “An integrated assessment of the vascular plants of the Americas.” *Phytotaxa* 351: 96–98.
8. Folk RA, **Sun M**, Soltis PS, Smith SA, Soltis DE, and Robert P. Guralnick. (2018). Challenges of comprehensive taxon sampling in comparative biology: Wrestling with Rosids. *American Journal of Botany* 105(3): 433–445.
9. Lu LM, Mao L, Yang T, Ye JF, Liu B, Li HL, **Sun M\***, Miller JT, Mathews S, Hu HH, Niu YT, Peng DX, Chen YH, Smith SA, Chen M, Xiang KL, Le CT, Dang VC, Lu AM, Soltis PS, Soltis DE, Li JH, Chen ZD. (2018). Evolutionary history of the angiosperm flora of China. *Nature* 554: 234–238. doi: 10.1038/nature25485.
10. Mu XY, **Sun M**, Yang PF, Lin QW. (2017). Unveiling the identity of Wenwan walnuts and phylogenetic relationships of Asian Juglans species using restriction site-associated DNA-sequencing. *Frontiers in Plant Science* (8): 1708. doi: 10.3389/fpls.2017.01708
11. Hodel RG, Gitzendanner MA, Germain-Aubrey CC, Liu X, Crowl AA, **Sun M**, Landis JB, Segovia-Salcedo MC, Douglas NA, Chen SC, Soltis DE, Soltis PS. (2016). A new resource for the development of SSR markers: Millions of loci from a thousand plant transcriptomes. *Applications in Plant Sciences* 4(6): 1600024.
12. Hodel RG, Segovia-Salcedo MC, Landis JB, Crowl AA, **Sun M**, Liu XX, Gitzendanner MA, Douglas NA, Germain-Aubrey CC, Chen SC, Soltis DE, Soltis PS. (2016). The report of my death was an exaggeration: A review for researchers using microsatellites in the 21st century. *Applications in Plant Sciences* 4(6): 1600025.
13. Chen ZD, Yang T, Li Lin, Lu LM, Li HL, **Sun M**, Liu B, Chen M, Niu YT, Ye JF, Cao ZY, Liu HM, Wang XM, Wang W, Zhang JB, Meng Z, Cao W, Li JH, Wu SD, Zhao HL, Liu ZJ, Du ZY, Wang QF, Guo J, Tan XX, Su JX, Zhang LJ, Yang LL, Liao YY, Li MH, Zhang GQ, Chung SW, Zhang J, Xiang KL, Li RQ, Soltis DE, Soltis PS, Zhou SL, Ran JH, Wang XQ, Jin XH, Chen YS, Gao TG, Li JH, Zhang SZ, Lu AM. (2016). Tree of life for the genera of Chinese vascular plants. *Journal of Systematics and Evolution* 54(4): 227–306.
14. Li HL, Wang W, Li RQ, Zhang JB, **Sun M**, Naeem R, Su JX, Xiang XG, Mortimer PE, Li DZ, Hyde KD, Xu JC, Soltis DE, Soltis PS, Li JH, Zhang SZ, Wu H, Chen ZD, Lu AM. (2016). Global versus Chinese perspectives on the phylogeny of the N-fixing clade. *Journal of Systematics and Evolution* 54(4): 392–399.
15. **Sun M**, Naeem R, Su JX, Burleigh GJ, Solits DE, Soltis PS, Chen ZD. (2016). Phylogeny of the Rosidae: A dense taxon sampling analysis. *Journal of Systematics and Evolution* 54(4): 363–391.
16. **Sun M**, Solits DE, Soltis PS, Zhu XY, Burleigh GJ, Chen ZD. (2015). Deep phylogenetic incongruence in the angiosperm clade Rosidae. *Molecular Phylogenetics and Evolution* 83: 156–166.
17. Wang B, Zhang Y, Wei P, **Sun M**, Ma X, Zhu X. (2015). Identification of nuclear low-copy genes and their phylogenetic utility in rosids. *Genome* 57(10): 150203143525007.
18. Lu LM, **Sun M**, Zhang JB, Li HL, Lin L, Yang T, Chen M, Chen ZD. (2014). Tree of life and its applications. *Biodiversity Science* 22: 3–20.
19. **Sun M**, Lin Q. (2010). A revision of *Elaeagnus* L. (Elaeagnaceae) in mainland China. *Journal of Systematics and Evolution* 48(5): 356–390.
20. **Sun M**, Lin Q, Sun Q, Bei SQ, Li HL, Yang ZR. (2008). Validation of eight names of Chinese taxa in Ranunculaceae, Rosaceae and Scrophulariaceae. *Kew Bulletin* 64: 573–575.
21. **Sun M**, Lin Q. (2008). Lectotypification of five scientific names in Rosaceae. *Guihaia* 28: 295–297. (In Chinese)
22. Lin Q, Bei SQ, Li HL, Cao ZY, Sun Q, **Sun M**, Yang ZR. (2008). Lectotypification of twenty names of Chinese taxa in Angiospermae. *Bulletin of Botanical Research* 5: 534–539.
23. Lin Q, Sun Q, **Sun M**, Bei SQ, Li HL. (2007). Lectotypification of twenty-eight names of Chinese

taxa in Angiospermae. *Acta Botanica Boreali-occidentalia Sinica*, 27: 1247-1255.

#### Book chapters:

1. **Sun M** et al. (2018). Malvaceae, Malpighiaceae, Celastraceae. In: Li DZ, Chen ZD, Wnag H, Lu AM eds. *Flora of Genera and Families of China Vascular Plants*, Science Press, Beijing
2. **Sun M** et al. (2018). Malvaceae, Malpighiaceae, Celastraceae. In: Li DZ, Chen ZD, Wnag H, Lu AM eds. *Dictionary of Genera and Families of China Vascular Plants*, Science Press, Beijing
3. **Sun M**, Peng H. (2016). Elaeagnaceae. In: Liu B, Lin QW eds. *Higher Plants of China in Color*, Volume 5, Angiosperms: Euphorbiaceae — Cornaceae, Science Press, Beijing, China
4. **Sun M** et al. (2015). In: Lin Q, Yang ZR eds. *Types Specimens in China National Herbarium (PE)*, Volume 6, Angiospermae, Henan Science and Technology Press, Henan, China
5. **Sun M** et al. (2015). In: Lin Q, Yang Y, Yang ZR eds. *Types Specimens in China National Herbarium (PE)*, Volume 7, Angiospermae, Henan Science and Technology Press, Henan, China
6. **Sun M** et al. (2015). In: Lin Q, Yang ZR, Lin Y eds. *Types Specimens in China National Herbarium (PE)*, Volume 10, Angiospermae, Henan Science and Technology Press, Henan, China
7. **Sun M**. (2014). Exploring deep phylogenetic incongruence of the COM clade in Rosidae: Phylogenomics approach. [PhD dissertation], Institute of Botany, the Chinese Academy of Sciences, Beijing, China
8. Simpson M. (2012). *Plant Systematics* (2nd Edition) (Chen ZD, Lu AM, **Sun M** Trans.), Science Press, Beijing, China (Original publisher Academic Press)
9. **Sun M**. (2009). Primary Taxonomic Study of Elaeagnus (Elaeagnaceae) in Mainland China. [Master thesis], Institute of Botany, the Chinese Academy of Sciences, Beijing, China

#### Conference Presentations/Posters:

1. **Sun M**. (2019). Build and use large-scale phylogenetic trees. *IBCAS Youth Forum*. (Presentation)
2. **Sun M**. (2018). Building, Using, and Tending the Tree of Life. *Chinese Genomics Meet-up*. (Presentation)
3. **Sun M**, Germain-Aubrey CC, Smith SA, Soltis PS, Chen ZD, Soltis DE. (2018). Exploring the phylogeny and diversification of rosids with a five-locus supermatrix. *The 1st AsiaEvo Conference 2018 (Shenzhen, China)*. Abstract ID: S38. (Poster)
4. Millar J, Collins M, Picardi S, Riemer K, Stucky B, **Sun M**, Ye H. (2018). A Carpentries Culture at the University of Florida. *CarpentryCon 2018* (Dublin, Ireland), Abstract ID: 13. (Poster)
5. **Sun M**, Whitten WM, Gitzendanner MA, Soltis DE, Soltis PS. (2017). Exploring the Applicability of Fluidigm Amplification and NGS Sequencing Using Samples From Multiple Families. *The XIX International Botanical Congress 2017 (Shenzhen, China)*, Abstract ID: T2-12-19. (Poster)
6. **Sun M**, Germain-Aubrey CC, Smith SA, Soltis PS, Chen ZD, Soltis DE. (2017). Exploring the phylogeny and diversification of rosids through a five-gene supermatrix approach. *The XIX International Botanical Congress 2017 (Shenzhen, China)*, Abstract ID: T2-44-15. (Poster)
7. Zhang T, Lichstein JW, **Sun M**. (2017). Functional traits and population dynamics of North American tree species in a phylogenetic and biogeographic context. Annual Meeting of Ecological Society of America (ESA), August 10, 2017 (Portland, USA). Abstract ID: COS135-5. (Poster)
8. Lichstein J, Zhang T, **Sun M**, Mack M, Graves S, Whitten M, Jantzen J, Park J, Bohlman S, Gitzendanner M, Soltis D, Soltis P. (2017). Ecological traits and recent population dynamics of eastern Asian-eastern North American disjunct tree species in North America. *The XIX International Botanical Congress 2017 (Shenzhen, China)*, Abstract ID: T2-12-05. (Presentation)
9. **Sun M**, Germain-Aubrey CC, Gitzendanner MA, Smith SA, Soltis PS, Chen ZD, Soltis DE. (2016). Wrestling with the Rosids I: progress and challenges for phylogenetics of a large, hyper-diverse angiosperm clade. *Botany Conference 2016 (Savannah, Georgia)*, Abstract ID: 404. (Presentation)

#### Classes Audited

- 2018

- RSSIG - R Social Sciences Interest Group
- Phylogenetics Systematics ( *BOT6935/ZOO6927* )
- Computational Tools for Research ( *ZOO6927/ZOO4926* )
- the Origin of Species Reading Group ( *BOT6935/ZOO6927* )
- **2017**
  - Grant Writing Seminar ( *ZOO6927/BOT6935* )
  - Principles of Systematic Biology ( *BOT6726/ZOO6927* )
  - Niche Modelling ( *ZOO6927* )
- **2016**
  - Data & Analysis in Natural Sciences ( *ZOO6927/ZOO4926//GLY6932/GLY4930* )
  - Phylogenomics ( *BOT6935/ZOO6927* )
  - Practical Computational Biology ( *ZOO4926/ZOO6927* )
- **2015**
  - Taxonomy of Vascular Plants ( *BOT5725C* )
  - Principles of Systematic Biology ( *BOT6726/ZOO6927* )

## Fieldwork Experience

- **2015**
  - Worked in Mountain Lake Biological Station (Virginia State) with Jeremy Lichstein (Department of Biology, University of Florida) and other ecologists collecting DNA, metabolites, RNA materials from canopy trees and understory communities, soil samples, and other microbial materials for **Dimensions US-China Project** ( *Collaborative Research: How historical constraints, local adaptation, and species interactions shape biodiversity across an ancient floristic disjunction Dimensions* ).
  - Participated in Talladega National Forest (Alabama State) with Doug Soltis and Pam Soltis (Florida Museum of Natural History, University of Florida) and other ecologists for material collection and first hand data generation for **Dimensions US-China Project**.
  - Worked in Ordway Biological Station (Florida State) with Mark Whitten, Eric Triplets, and other ecologists for material collection and first hand data generation for **Dimensions US-China Project**.
- **2012**
  - Trip to southern Yunnan along Myanmar border with Pam S. Soltis and Doug E. Soltis, collecting materials for Tree of life — China Project.
  - Trip to Hainan tropical rain forest with Doug E. Soltis, collecting materials of Tree for life — China Project.
- **2006 ~ 2011**
  - Joined in the expedition team of national herbarium (PE) for collection many times, successively visited a series of biodiversity hotspots, such as Hubei, Chongqing, Guangxi, Sichuan, Xizang, etc.

## Academic Activities

- **2019**
  - Plantae Seminar: How to Be an Effective Mentor organized by Plantae Community
  - Biodiversity Research Coordinate Networking
  - UF Biodiversity Institute and IFAS Geospatial Workshop
  - 3rd Annual Collaborations in Biodiversity Symposium
  - Data Carpentry Workshop: Genomics
  - Data Science and Informatics (DSI) Spring Symposium 2019 at UF
  - Participated in Writing Workshop at UF Biodiversity Institute  
Instructed by Dr. Nancy DeJoy, Associate Professor *Michigan State University*

- Research Lightning Talks at Florida Museum of Natural History
- **2018**
  - Co-organizer and co-translator of The Great Tree of Life
  - Co-organizer of Research Bazaar event
  - Instructor and Helper of a serial of “Software and Data Carpentry Workshops” events
  - Instructor for Precollegiate Education and Training event
  - co-translated TreeTender movie into Chinese language for public education
  - Digital outreach with 4th and 5th graders from Bunker Hill Elementary School in D.C
- **2017**
  - Board member of UF Carpentries Club
  - Organizer of several Tree of Life pop-up tent events (UF campus, FLMNH public museum, local brew-pub)
  - Helper of Research Computing Training at UF Information Technology, Research Computing (University of Florida)
  - Coordinated with the 100-year anniversary exhibit celebration of FLMNH
  - Organizer of One Tree one Planet Encore
  - Judge for Graduate Student Research Day
  - Instructor and Helper in several “Software Carpentry Workshop” events
  - Instructor for the 54th Florida Regional Junior Science, Engineering, and Humanities Symposium
- **2016**
  - Volunteer Tree of Life Pop-Up Science! Florida Museum of Natural History
  - Member of Botanical Society of America
  - Oral Talk “Wrestling with the Rosids I: progress and challenges for phylogenetics of a large, hyper-diverse angiosperm clade.” in the annual Botany Conference (Savannah, Georgia)
  - Table volunteer for iDigBio at BSA meeting
  - Organizing volunteer, iDigBio workshop: Using Digitized Herbarium Data in Research: A Crash Course
- **2015 ~ 2010**
  - Training college students for taxonomic skills
  - Speaker of the conference about dioecious plants in Angiosperm in Peking University
  - Participate in the evaluation of “Red List of China Higher Plants” as a taxonomy expert
  - Contributed to develop a “Molecular Data and Application Environment” website and a winner for the best of website name and domain name, “Darwin Tree” and “<http://www.darwintree.cn/>”, respectively

## Service

- Peer reviews for: *South African Journal of Botany*, *Evolutionary Bioinformatics*, *Journal of Systematics and Evolution*, *International Journal of Tropical Biology and Conservation*, *Plant Physiology and Biochemistry*, *Taxon*, *Scientific Reports*, *Botany*, *PeerJ*, and *Phytotaxa*.
- Certified Instructor of Software Carpentry (The Carpentries; taught classes of >400 students)
- Board member of UF Carpentries Club (a workshop series to teach informatics skills)
- Judge for Graduate Student Research Day at University of Florida
- Judge Graduate Student Research Grant proposals for American Society of Plant Taxonomists
- Educator Summer Science Institute Tree of Life for high school teacher
- Volunteer Tree of Life Pop-Up Science
- Member of Botanical Society of America
- Table volunteer for iDigBio events

- Taxonomic instructor for training college students
- Board member of “*Red List of China Higher Plants*” evaluation committee

## References contact information

### **Matthew A. Gitzendanner** (Bioinformatics Mentor)

Scientist, Department of Biology

Collection Manager, Florida Museum of Natural History

Training Coordinator and Bioinformatics Specialist, UF Research Computing

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### **Douglas E. Soltis** (Postdoc advisor)

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### **Pamela S. Soltis** (Postdoc advisor)

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### **Zhiduan Chen** (PhD advisor)

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