

CURRICULUM VITAE ABREVIADO (CVA)

IMPORTANT – The Curriculum Vitae cannot exceed 4 pages. Instructions to fill this document are available in the website.

Part A. PERSONAL INFORMATION

First name	Chunlin		
Family name	Chen		
Gender (*)	Male	Birth date (dd/mm/yyyy)	02/03/1995
Social Security, Passport, ID number	EK0585457		
e-mail	chencl424@nenu.edu.cn	URL Web	
Open Researcher and Contributor ID (ORCID) (*)	0000-0003-4292-0553		

(*) *Mandatory*

A.1. Current position

Position	Research Assistant		
Initial date	01/07/023		
Institution	Sichuan University		
Department/Center	Life Science College		
Country	China	Teleph. Number	+86 18583622752
Key words	Plant evolution; Comparative genomics; Phylotranscriptomics; Population genomics; Hybridization		

A.2. Previous positions (research activity interruptions, indicate total months)

Period	Position/Institution/Country/Interruption cause
01/09/2020-20/06/2023	PhD contract/Life Sciences College, Sichuan University/China
01/07/2023-present	Research Assistant/Life Sciences College, Sichuan University/China

A.3. Education

PhD, Licensed, Graduate	University/Country	Year
PhD in Ecology	Sichuan Univerisity/China	2023

(Include all the necessary rows)

Part B. CV SUMMARY (max. 5000 characters, including spaces)

Total Publications: 9 peer reviewed SCI papers, including 5 first author papers. 1 doctoral thesis.

I conduct my research on the phylotranscriptomics of tribe Gentianeae (Gentianaceae) from September 1st, 2017 to 20th, June 2023 under the guidance of Prof. Jianquan Liu. During the 6 years of researching this group, I have sampled over 150 species, which covered all the 21 genera for this tribe, with my steps covering over 10 provinces of China. I sequenced the transcriptomic data of these collected species and focused on the phylogenetic reconstruction of this tribe. I resolved the backbone phylogeny of this group with strong support. In addition, I uncovered complex evolutionary process including hybridization, large scale gene duplication and whole genome duplications during the species radiation of tribe Gentianeae.

I then assembled the chromosome level genome of *Megacodon stylophrus* based on PacBio HiFi data and HiC data. I annotated this genome and uncovered two rounds of whole genome duplications for tribe Gentianeae based on comparative genomic analysis. I also identified the mechanisms underlying adaptation to high-altitude Qinghai-Tibet Plateau.

I assisted Prof. Liu and other teachers of the Liu Lab in guiding over 10 master students. I mainly helped them with phylogeny construction, hybridization detection and genome assembly and annotation. I graduated as a PhD in Science on July 20th, 2023. My PhD thesis



was entitled “Genomic phylogeny and evolution of Gentianeae”. I also gave an oral presentation at a conference and attended three other conferences during my school years in Sichuan University

Part C. RELEVANT MERITS (sorted by typology)

C.1. Publications (see instructions)

- Chen Chunlin** Zhang Lei, Li Jialiang,, Liu Jianquan and Xi Zhenxiang, 2021. Phylotranscriptomics reveals extensive gene duplication in the subtribe Gentianinae. *Journal of Systematics and Evolution* 59: 1198-1208. **IF=3.7, Q1 Plant Sciences (WoS).**
- Chen Chunlin** et al., 2023. Phylotranscriptomics of Swertiinae (Gentianaceae) reveals that key floral traits are not phylogenetically correlated. *Journal of Integrative Plant Biology*. 00: 1-15. **IF=11.4, D1 Plant Sciences (WoS).**
- Chen Chunlin** Liu Jianquan, 2021. Population Transcriptomics Reveals Gene Flow and Introgression Between Two Non-sister Alpine Gentians. *Frontiers in Ecology and Evolution*. 9: 638230. **IF=4.49, Q1 Ecology (WoS).**
- Chen Chunlin** and Liu Jianquan, 2023. Hybridization and polyploidization generate evolutionary diversification of the genus *Buddleja* in the Sino-Himalayan region. A commentary on ‘Deciphering complex reticulate evolution of Asian *Buddleja* (Scrophulariaceae): insights into the taxonomy and speciation of polyploid taxa in the Sino-Himalayan region’. *Annals of Botany*. Online. Available at, <https://doi.org/10.1093/aob/mcad074>. **IF=5.04, Q1 Plant Sciences (WoS).**
- Chen Chunlin**, Gong Yihua and Hao Guoqian. 2019. Characterization of the complete chloroplast genome of *Saussurea integrifolia* (Compositae). *Mitochondrial DNA Part B*. 4: 3502-3503. **IF=0.5, Q4 Genetics (WoS).**
- Zhang Lushui, **Chen Chunlin**, Mao Xingxing and Liu Jianquan, 2023. Phylogenomics and evolutionary diversification of the subfamily Polygonoideae. *Journal of Systematics and Evolution*. 61: 587-593. **IF=3.7, Q1 Plant Sciences (WoS).**
- Hu Qianjun, Ma Yazhen, Mandakova Terezie, Shi Sheng, **Chen Chunlin**,, Liu Jianquan. 2021. Genome evolution of the psammophyte *Pugionium* for desert adaptation and further speciation. *Proceedings in the National Academy of Sciences USA*. 118: e2025711118. **IF=12.77, D1 Multidisciplinary (WoS).**
- Wang Zefu, Kang Minghui, Li Jialiang, Zhang Zhiyang, Wang Yufei, **Chen Chunlin**, Yang Yongzhi, Liu Jianquan. 2022. Genomic evidence for homoploid hybrid speciation between ancestors of two different genera. *Nature Communications*. 13: 1987. **IF=16.6, D1 Biochemistry, Genetics and Molecular Biology (WoS).**
- Minghui Kang, Haolin Wu, Huanhuan Liu, Wenyu Liu, Mingjia Zhu, Yu Han, Wei Liu, **Chunlin Chen**,, Liu Jianquan. 2023. The pan-genome and local adaptation of *Arabidopsis thaliana*. *Nature Communications*. 14: 6259. **IF=16.6, D1 Biochemistry, Genetics and Molecular Biology (WoS).**

C.2. Congress, indicating the modality of their participation (invited conference, oral presentation, poster)

Chen Chunlin “Phylotranscriptomics reveals extensive gene duplication in the subtribe Gentianinae (Gentianaceae)”. Students’ Seminar of International Symposium on Mountain Ecology and Evolution, online conference 09-10 December, 2022, Chengdu, China. Oral presentation.

C.3. Research projects, indicating your personal contribution. In the case of young researchers, indicate lines of research for which they have been responsible.

Research on the mechanisms underlying plant lineage formations among the China Himalayan Region. Funded by National Science Foundation of China. Grant NO. 3 1590821 PI: Liu Jianquan. Grant funding: 3 900 ,000, RMB. Duration: Jan. 2016-Dec. 2020. Responsible for: taxon sampling, genomic data analysis.



Research on the adaptive evolution of *Arabidopsis thaliana* among Tibet and Sichuan. Funded by National Science Foundation of China. Grant NO. 32030006 PI: Liu Jianquan. Grant funding: 2 950,000, RMB. Duration: Jan. 2021-Dec. 2025.

Population investigation on the endangered plant species among the Sichuan Chongqing region Funded by Ministry of Science and Technology of China. PI: Hu Quanjun. Grant NO. 2017FY100100. Grant funding: 1,400,000 RMB. Duration: Jan. 2017 Dec. 2022. Responsible for: taxon sampling, genomic data analysis, population status assessment.

C.4. Contracts, technological or transfer merits, Including patents and other industrial or intellectual property activities (contracts, licenses, agreements, etc.) in which you have collaborated. Indicate: a) the order of signature of authors; b) reference; c) title; d) priority countries; e) date; f) Entity and companies that exploit the patent or similar information, if any

10 Master students under my training guidance graduated:

Landi Feng, supervised by Prof. Zhenxiang, Xi. Genomics analysis of an alpine plant *Crucihimalaya lasiocarpa*. Defense time: May 15th, 2022.

Zhanpeng Xu, supervised by Prof. Zhenxiang XI. Genomics analysis of the Halophytes plant: *Eutrema salsugineum*. Defense time: May 15th, 2022.

Shuo Wang, supervised by Prof. Zhenxiang, Xi. Study on the formation of geographical distribution patterns of species diversity in Subtribe Swertiinae. Defense time: May 20th, 2023.

Xi Yu, supervised by Prof. Zhenxiang, Xi. Conservation genetics of *Davidia involucrate*. Defense time: May 20th, 2023.

Yumeng Ren, supervised by Prof. Zhenxiang, Xi. Population Genetic analysis of *Camptotheca acuminata* based on whole genome resequencing. Defense time: May 20th, 2023.

Ting Li, supervised by Prof. Jianquan Liu. Genomics analysis of *Gentiana dahurica* provides insights into the synthesis of gentiopicroside. Defense time: May 15th, 2022.

Heng Yang, supervised by Prof. Kangshan Mao. Conservation genetics of *Cupressus gigantea*. 15 th May, 2022.

Hongying Zhang, supervised by Prof. Kangshan Mao. Phylogeographic studies of *Populus koreana*. Defense time: May 15th, 2022.

Yufei Wang, supervised by Prof. Kangshan Mao. The landscape genomics of *Cupressus duclouxiana* (Cupressaceae). Defense time: May 15th, 2022

Dayu Wu, supervised by Prof. Kangshan Mao. Phylogenomics and spatio temporal evolutionary history of the genus *Cupressus* L. (Cupressaceae). Defense time: May 21st, 2023.