

The University of British Columbia



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June 3, 2021

BSA Council

Dear Council Members,

It is with great pleasure that I nominate Professor Jianquan Liu to be a Corresponding Member of the Botanical Society of America. I view Professor Liu as an international leader in the areas of plant hybridization and phylogeography. His work is notable for its high quality, thoroughness, and careful and nuanced interpretations of results. Also, included in this nomination package are letters of support from Corresponding Members Professor Richard Abbott (University of St. Andrews), Professor Bao-Rong Lu (Fudan University), and Professor Suhua Shi (Sun Yat Sen University) along with Prof. Liu's CV.

As mentioned in Prof. Abbot's letter, Prof. Liu is the son of a peasant farmer from the foothills of the Tibetan Plateau, and he has become the world's foremost authority on the phylogeography and evolution of its flora. After graduating from the Chinese Academy of Sciences in 1999 (and receiving the National 100 Excellent PhD Thesis Award), he moved through the academic ranks at the Northwest Plateau Institute of Biology in the Chinese Academy of Science in Qinghai, China. Since 2012 he has been a Professor at Sichuan University in Chengdu, China.

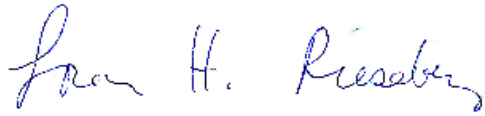
Prof. Liu has an impressive academic record, with >150 publications, many of which are in leading general science journals (e.g., *Nature Communications* and *PNAS*) or top disciplinary journals (e.g., *Nature Plants*, *Evolution*, *Molecular Biology and Evolution*, *Molecular Ecology*, *Molecular Plant*, and *New Phytologist*). His work is well-cited (> 12,000 citations; h = 59), which provides a further indication of its quality.

As pointed out by in the letters of support, Prof. Liu is especially well known for his work on homoploid hybrid speciation, molecular biogeography, and plant adaptation to arid conditions. For example, Prof. Abbott writes that "His recent paper in *Molecular Plant* (2021) demonstrating that HHS [homoploid hybrid speciation] can occur through the inheritance of alternate alleles of parental premating isolating genes is a *tour de force*." Prof. Shi notes that Prof. Liu's work on the molecular biogeography of the Cupressaceae (*PNAS* 2012) is included in the textbook "*Evolution*" as a case study of modern biogeography. Lastly, Prof. Bao-Rong Lu highlights Prof. Liu's application of genomic approaches to identify the genetic architecture of adaptation of desert poplars to arid environments.

In addition to his research prowess, Prof. Liu has shown himself to be an excellent mentor, supervising more than 50 graduates, 20 of whom have already obtained tenure track academic positions.

In conclusion, Prof. Liu has been a highly influential figure in the development of our understanding of plant phylogeography and hybridization. In the absence of his efforts, we would know much less about the evolutionary consequences of hybridization or the origins of world's floras. He is highly deserving of this honor.

Sincerely,

A handwritten signature in blue ink that reads "Loren H. Rieseberg". The signature is written in a cursive style with a large initial 'L'.

Loren H. Rieseberg FRS, FRSC
Director, Biodiversity Research Centre
University Killam Professor of Botany
Member, National Academy of Sciences



School of Life Science
Fudan University



June 3, 2021

To whom it may concern,

Ref: Nomination of Prof. Jianquan Liu as a corresponding member of the Botanical Society of America (BSA)

It is my great pleasure and honor to nominate Prof. Jianquan Liu, who is currently a full Professor of Sichuan University, as a corresponding member of the Botanical Society of America (BSA). I fully support my nomination of Prof. Liu to be a BSA corresponding member because of his outstanding contribution to the research and teaching in botany. Here, I would focus mainly on his scientific research merits.

I knew Prof. Liu many years ago when we shared our research interests in phylogeny and biosystematics of plant species. I gradually recognized that he had a broad knowledge and deep understanding on biology, genetics, evolution, conservation, and ecology. As an excellent team leader, he and his team members have made great progresses and contributed significantly to the botanic research fields. Owing to these contributions, Prof. Liu received the Awards of Top 10 Progresses of Science and Technology of Ministry of Education, China in 2012.

Prof. Liu and his team members had the following major contributions to the botanic studies. First, they unveiled the genetic mechanism of homoploid hybrid speciation by integrating genomic data, field experiments, and functional tests of allelic divergence and recombination. They pointed out that most species are 'on the speciation way' without incomplete reproductive isolations, resulting in widespread interspecific hybridizations and introgression. Second, they uncovered adaption of the desert poplars to arid habitat at the genomic level, in addition to their diversification/speciation with frequent gene flow between closely related species. Third, they pioneered molecular phylogeographic studies in China and revealed numerous refugia during the Last Glacial Maximum across regions, particularly in the Qinghai-Tibet Plateau.

Your kind consideration of my nomination will be highly appreciated. I shall be glad to answer your further questions concerning this nomination. Thank you very much.

Yours Sincerely,

Bao-Rong Lu Ph. D. (brlu@fudan.edu.cn)

Professor of Biology

Corresponding member of the BSA

School of Life Sciences, Fudan University, 220 Handan Road, Shanghai 200433, China



中山大學
SUN YAT-SEN UNIVERSITY

Department of Ecology
School of Life Sciences
Sun Yat-Sen University
Guangzhou, 510275, China

April 8, 2021

BSA Council

Dear Council Members,

It is my great pleasure to nominate Professor Jianquan Liu to be a Corresponding Member of the Botanical Society of America. I regard Professor Liu as an excellent biologist in the fields of plant hybridization, speciation and biogeography. He has made many remarkable advancements in the issues of homoploid hybrid speciation and plant diversity evolution on the Qinghai-Tibet plateau. His work is admirable for the high quality, novelty, and comprehensiveness. Below I highlight some of Prof. Liu's most important contributions to plant sciences.

The most significant contribution of Prof. Liu is probably the new molecular model for homoploid hybrid speciation (HHS). He pioneered in integrating multi-layered methods of genomes, transgenics, allelic biochemicals, common garden field planting and pollination experiments to study hybridization and speciation. He revealed that reproductive isolation of the hybrid species in the genus *Ostryopsis* was formed by alternative inheritance of alleles of two genes determining high iron tolerance and two genes controlling early flowering time from the parental species (Wang et al. 2021, *Molecular Plant*). That is the first time of the development of a method to pinpoint HHS to individual genes. Inspired by the findings in *Ostryopsis*, he proposed a molecular model, i.e. HHS 'via inheritance of alternate alleles of parental isolating genes.' This model resolved the problem of how genetic combinations from two distinct species produce one third species at the same ploidy.

More generally, I have appreciated Prof. Liu's outstanding works in examining historical hybridizations in diverse plant groups through phylogenetic analyses (Liu et al. 2006, *Molecular Phylogenetics and Evolution*; Yang et al. 2020, *Nature Plants*) and species delimitation (Ma et al. 2018, *PNAS*). Through most thorough and far-reaching studies of more than 30 groups in China (mainly in the Qinghai-Tibet Plateau (QTP) and adjacent regions), he and his colleagues identified frequent gene flow during speciation and high phylogenetic inconsistency in deeply diverged lineages at different loci. The evidence convincingly demonstrated widespread hybridizations during diversification of plants. He suggested that numerous species should have been 'on the way' to speciation with incomplete reproductive isolation (Liu, 2016, *Biodiversity Science*), and more interspecific hybridizations should have occurred than previously expected.

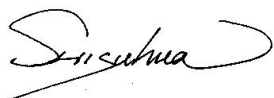
Prof. Liu also stands out in the studies of biogeography, especially on the alpine plants in the QTP and adjacent regions. The most prominent contributions are his elucidations of the migration and evolutionary diversifications of the QTP plants in response to

historical climatic and geological changes. He and his colleagues performed systematic investigation on the phylogeographic patterns of QTP plant species in response to climatic oscillations. They uncovered that the climate-sensitive species (for example, trees) retreated to the plateau edge during glaciations and recolonized the plateau platform after the last glacial maximum (LGM) (Meng et al. 2007, *Molecular Ecology*), whereas some cold- or arid-tolerant species persisted on the high-altitude platform throughout the glacial periods and LGM despite deep intraspecific divergence (Wang et al. 2009, *Molecular Ecology*; Opgenoorth et al. 2010, *New Phytologist*). They further tested the hypotheses that temperate plants now distributed across Eurasia may have originated and migrated from the QTP (Jia et al. 2012, *New Phytologist*). They revealed rapid diversification of QTP plant species in response to the recent extensive mountainous uplifts since Oligocene (Liu et al. 2002, *Molecular Phylogenetics and Evolution*; Liu et al. 2006, *Molecular Phylogenetics and Evolution*; Mao et al. 2010, *New Phytologist*). His findings convincingly rejected the large LGM ice-shield hypothesis in the plateau, which has been deputed for a long time for the total scientific community, thus deepening our understanding of the natural history of the QTP.

Basing on the robustly dated phylogenies, ancient climates, widely recorded fossils and phylogeography, they comprehensively depicted the pattern of diversification dynamics of the family Cupressaceae, which consists of >170 species and occurs worldwide, including the QTP. They illuminated how the common ancestor of Cupressaceae diverged in response to the breakup of Pangea and diversified and/or died out in both Northern and Southern Hemispheres because of geological and climatic oscillations (Mao et al. 2010, *New Phytologist* and Mao et al. *PNAS*). This study has been included in the textbook 'Evolution' as a case of molecular biogeography. They also revealed several glacial refugia for plants in northern and southeastern China, and they demonstrated that local conditions had determined the range expansion of these refugia (Chen et al. 2008, *Molecular Ecology*; Zhou et al. 2010, *Evolution*). Genomic analyses they performed further invalidated population shrinks and expansions (Yang et al, 2018, *Nature Communications*), and adaptations (Ma et al. 2013; *Nature Communications*) in response to Quaternary climatic oscillations in plants of China.

In my opinion, Prof. Liu has made important contributions to our knowledge in plant hybridization, speciation and biogeography. He has been a distinguished biologist with broad influence both in and outside China. He is highly deserving of this honor.

Sincerely,



Suhua Shi

Ph.D, Professor
Sun Yat-Sen University
Tel: 86-20-84113677, 86-13922729336
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<http://evolution.sysu.edu.cn>

Jianquan Liu: Letter of support for Nomination as a Corresponding Member of the Botanical Society of America

Jianquan Liu (Sichuan University) has made outstanding research advances over the past two decades to diverse areas of plant ecology, systematics and evolution, including the evolutionary history of the Tibetan Plateau flora, the genomic basis of adaptation to high altitude and desert environments, and the evolutionary consequences of hybridization. Son of a peasant farmer who grew up in the foothills of the Tibetan Plateau, Jianquan pioneered plant phylogeographic studies in China, becoming a leader in the field and influencing a generation of younger researchers, many of whom have obtained professorships at universities and research institutes in China and elsewhere. His work in this area has been published in *Nature Communications*, *PNAS*, *Molecular Ecology*, *New Phytologist*, *Molecular Biology & Evolution*, *Evolution*, *Journal of Biogeography* etc., with major reviews appearing in the *Journal of Systematics & Evolution* (2012, 2014).

His genomic analyses of the desert poplar, *Populus euphratica*, and related species have led to the detection of candidate genes for salt tolerance (*Nature Communications*, 2013) and sex determination (*MBE*, 2020), and shown that genomic islands of divergence result partly from divergent sorting of ancient polymorphisms and divergence hitchhiking (*PNAS*, 2018). Particularly notable is his research on hybridization leading to allopolyploid speciation, adaptive introgression and homoploid hybrid speciation (HHS). His recent paper in *Molecular Plant* (2021) demonstrating that HHS can occur through the inheritance of alternate alleles of parental pre-mating isolating genes is a *tour de force*. It reports transplant analysis, genome sequencing and assembly, population genomics and transgenic analysis, to show that the hybrid species (*Ostryopsis intermedia*, Betulaceae) inherited alleles of parental isolating genes related to flowering time from one parent and alleles of major genes conferring iron tolerance from the other parent. In this way, the hybrid became reproductively isolated from one parent by a difference in flowering time and from the other by habitat adaptation (iron tolerance). Computer simulations indicate that HHS can occur relatively easily in this way.

In addition to his outstanding research contributions, Jianquan is a great ambassador for plant science. He has reached out to the community in both China and elsewhere, making connections and forging links between his group and a large number of plant scientists in North America and Europe. His research interests are not limited to plants, however. He also has a long-term interest in yak domestication and adaptation to high altitude, heading the group who first sequenced the yak genome. Moreover, by dating yak domestication and subsequent increases in yak population size, he linked these events to early human population expansions on the Tibetan Plateau during the early-Neolithic and late-Holocene periods.

In summary, Jianquan Liu is a special scientist who has undertaken ground-breaking research over the last 20 years or so and had a massive influence on our current understanding of plant phylogeography in central and eastern Asia. I strongly support his nomination to be elected a Corresponding Member of the Botanical Society of America and the recognition it will bring him in China and the wider plant community for his outstanding contributions to plant evolution and systematics research.



Sincerely

Date: 14 April 2021

Richard Abbott, Emeritus Professor, University of St Andrews (UK); Corresponding Member of BSA.

Curriculum Vitae – Jianquan Liu

Date and place of birth: 12 March 1969, Sichuan, China

Address: College of Life Sciences
Sichuan University
Chengdu, 610064, China

Email: liujq@nwipb.ac.cn or liujq@lzu.edu.cn
Tel: +8618011455756
<http://life.scu.edu.cn/info/1048/3243.htm>

Current post: Professor (since 2002)

Education & Career

1987-1991	B.S., Botany, Sichuan University, China
1991-1994	Msc, University of Chinese Academy of Science, China (at Northwest Plateau Institute of Biology by advisers: Profs. Tingnong He, Shangwu Liu and Jingtang Pan; Master Thesis, Systematics and Taxonomy of <i>Comastoma</i> and related genera (Gentianaceae)
1996-1999	PhD., University of Chinese Academy of Science, China (at Institute of Botany by advisers: Profs. Anmin Lu and Tingnong Ho; PhD Thesis, Systematics of the subtribe Tussilaginatae (Asteraceae: Senecioneae) in eastern Asia
1994-1996	Assistant scientist, Northwest Plateau Institute of Biology, Chinese Academy of Science, Xining 81001, Qinghai, China
1999-2001	Associate Professor, Northwest Plateau Institute of Biology, Chinese Academy of Science, Xining 81001, Qinghai, China
2001-2002	STA fellow, Forestry and Forest Product Research Plateau Institute, Japan
2002-2004	Professor, Northwest Plateau Institute of Biology, Chinese Academy of Science, Xining 81001, Qinghai, China
2004-2012	Professor, Lanzhou University, Lanzhou 730000, China
2012-	Professor, Sichuan University, Chengdu 610064, China

Honors and Awards

- 2001 National 100 Excellent PhD Thesis Award, China
- 2004 National Natural Science Second Award, China (3/5)
- 2007 National Prize for the Young Scientists, China
- 2007 National Science Fund for Distinguished Young Scholars, China
- 2008 Chang Jiang Scholar of Ministry of Education, China
- 2012 Top 10 Progresses of Science and Technology of Ministry of Education, China

Research Summary

I am an ecologist and evolutionary biologist. I am particularly interested in integrating molecular evidence from genomic data to gene (especially allele) functions and ecology to examine adaptation, speciation, diversification and distribution of plants. My research is at the interface of ecology, genetics and evolution. I and my group mainly aim to:

- Understand genetic changes underlying environmental adaptation, phenotypic divergence and species diversification;
- Explore demographic and evolutionary histories of the current species and predict their future adaptations and distributions in response to global climate change.

- **Published >150 research papers as the corresponding author or the first author** in a wide range of journals, including *Nature Plants*, *Nature Communications*, *Nature Climate Change*, *PNAS*, *Molecular Ecology*, *Molecular Biology and Evolution*, *New Phytologist*, *Evolution*, *Journal of Biogeography* etc.

Major contributions: (1) We integrated genomic data, field experiments and functional tests of allele divergence and recombination to unravel genetic mechanism of homoploid hybrid speciation (HHS). We proposed a genetic model without genomic rearrangement and new mutation for HHS and firstly linked genes to HHS. In addition, through species delimitation, speciation and phylogenetic studies of more than 30 groups mainly distributed in China, we suggest that most species are ‘on the speciation way’ without incomplete reproductive isolations, which might have resulted in widespread interspecific hybridizations and introgressions-numerous hybrids in the nature and more frequent hybrid speciation than previously expected. (2) We uncover genomic adaption of the desert poplar to arid habitat and speciation with high gene flow with the closely related species. We also revealed genetic drives for repeated turnovers of sex determination during poplar diversification. (3) We pioneered molecular phylogeographic studies in China and revealed numerous refugia during the Last Glacial Maximum (LGM) across this region despite distinct postglacial range expansions, particularly in the high-altitude Qinghai-Tibet Plateau, which rejected the large LGM ice-shield hypothesis in the plateau. (4) We finely illuminated distribution and diversification dynamics of Cupressaceae in response to Pangea breakup and further to geological and climatic oscillations in Northern Hemisphere based on the robustly dated molecular biogeography, which has been taken as an example by the textbook ‘Evolution’.

- **Citations:** Total citations > 11800. H-index=58; Citations: per paper: >500 (2), >300 (2), >200 (6) and >100 (20) (Google Scholar, <https://scholar.google.com/citations?hl=zh-CN&user=>)
- **Supervised >50 PhD and Msc students; and >20 graduates obtained professor posts in China and other countries.**

Research Periods Abroad

2005 3 months at University of St. Andrews, UK – Diversification of *Ligularia* and related genera.

2006 2 months at Marburg University, Germany- Glacial survival of alpine plants.

2009 2 months at University of St. Andrews, UK – Plant speciation in western China.

2010 1 months at University of St. Andrews, UK – Plant speciation in western China.

2018 1 months at Texas Tech University, USA- Sex chromosomes and dioecy in plants.

Research Grants

- 1) 2020-2024 ¥2980K-NSFC (National Science foundation of China) - Adaptive evolution of the Tibet ecotype of *Arabidopsis thaliana*.
- 2) 2016-2020 ¥3000K-NSFC-Dimensions US-China: Collaborative Research: Sex chromosomes and dioecy in plants as drivers of multi-level biodiversity
- 3) 2016-2020 ¥4680K-NSFC Evolutionary history of new species and their adaptive survivals in the Sino-Himalaya flora.
- 4) 2014-2016 ¥1200K-Genetic bases of speciation between two *Pugium* sister species under the arid and sub-arid habitats
- 5) 2015-2018 ¥950K0-NSFC-Distributional changes and origin of new species of *Ostryopsis* (Betulaceae) in response to Quaternary climate changes.

- 6) 2011-2014 ¥5680K-Ministry of Science and Technology-Genomic insights into wood formation and stress tolerance of the desert poplar and relates species
- 7) 2010-2012 ¥500K-NSFC-The evidence of Quaternary climate oscillation in Qinghai-Tibet Plateau from extant plant population genetic variation
- 8) 2010-2013 ¥1800K-Genetic diversity of Chinese spruces and conservation of genetic resources
- 9) 2010-2012 ¥110K-NSFC- Plant speciation in western China.
- 10) 2008-2011 ¥2000K-NSFC-Phylogeny and Evolution.
- 11) 2007-2009 ¥350K-NSFC-Distribution, origin and dispersals of tetraploids in *Allium przewalskii*
- 12) 2005-2008 ¥1450K-NSFC- Population genetics, eco-physiological characteristics and conservation and restoration strategies of the key tree species in the natural forests in west China
- 13) 2003-2005 ¥210K-NSFC- A comparison on reproducing systems of *Gentiana straminea* at different-altitude populations
- 14) 2001-2003 ¥150K-NSFC-Comparison on the speciation mechanism of *Ligularia* and *Cremanthodium*

Teaching

Molecular Ecology (Since 2004-, for both Msc and PhD candidate students, more than 500 students in total)

Speciation (Since 2013, for undergraduates, more than 200 students in total)

Evolutionary Advances (Since 2015, for PhD candidate students, more than 200 students in total)

Selected PhD and Msc students supervised and their current posts

1. Yuanwen Duan, Pollination adaptation of five plants in the Qinghai-Tibet Plateau (PhD, 2001-2006). The current post: Professor, Kunming Institute of Botany, Chinese Academy of Sciences, email: duanyw@mail.kib.ac.cn; <http://people.ucas.edu.cn/~duanyw>
2. Yujing Wang, Rapid diversification of *Saussurea* (Asteraceae) in the Qinghai-Tibet Plateau (PhD, 2002-2006). The current post: Professor, Lanzhou University, email: wangyujin@lzu.edu.cn; http://lifesc.lzu.edu.cn/t/wangyujin_391.html
3. Lihua Meng, Phylogeography of *Picea crassifolia* (PhD, 2003-2008). The current position: Professor, Yunnan Normal University, email: menglihua@mails.ucas.ac.cn; <https://life.ynnu.edu.cn/info/1026/1547.htm>
4. Qiushi Yu, Interspecific delimitation and phylogenetic origin of *Pugionium* (Brassicaceae) (PhD, 2006-2009). The current position: Professor, Gansu Desert Control Research Institute, email: yqs528@126.com; <http://www.scholarmate.com/P/eY3qym>
5. Liuyang Wang, Phylogeographic structure of *Potentilla glabra* L. (Rosaceae) on the Qinghai-Tibet Plateau (PhD, 2004-2009). The current post: Assistant Research Professor, Duke University, email: wallacewly@gmail.com; <https://scholars.duke.edu/person/liuyang.wang>
6. Dongshi Wan, Duplication and adaptive evolution of the CHS-like genes within the genus *Rheum* (Polygonaceae) (PhD, 2006-2010). The current position: Professor, Lanzhou University, email: wandsh@lzu.edu.cn; http://lifesc.lzu.edu.cn/t/wandongshi_375.html

7. Kangshan Mao, Biogeography of Cupressaceae sensu lato: from plate tectonics to glacial refugia (PhD, 2004-2010). The current post: Professor, Sichuan University, email: maokangshan@scu.edu.cn; <https://www.x-mol.com/university/faculty/67839>
8. Fei Ma, Ecophysiological differences in adaptive mechanisms between diploid hybrid species and its parental species (PhD, 2005-2010). The current post: Professor, Ningxia University, email: mafei05@163.com; <https://www.x-mol.com/university/faculty/199501>
9. Zhonghu Li, Population genetics and speciation of *Juniperus tibetica* complex (PhD, 2007-2010). The current post: Professor, Northwest University (China), email: lizhonghu@nwu.edu.cn; <https://biology.nwu.edu.cn/zsxx/yjs1.htm>
10. Fang Du, Gene flow-dependent introgression and species delimitation: evidence from mtDNA & cpDNA variation in spruce (PhD: 2005-2010) (Co-supervised with RÉMY J. PETIT). The current post: Professor, Beijing Forestry University, email: dufang325@bjfu.edu.cn; <http://styzrbh.bjfu.edu.cn/szdw/zrjs/slstxjs/342334.html>
11. Qinzhen Hou, Pollination adaptation of three alpine plants in the Qinghai-Tibet Plateau (PhD, 2005-2010). The current post: Professor, Northwest Normal University, email: hou_qzh@nwnu.edu.cn; <https://www.x-mol.com/university/faculty/149618>
12. Yongfeng Zhou, Local adaptation to climate in *Pinus densata* complex (PhD, 2007-2010) (Co-supervised with OUTI SAVOLAINEN) The current post: Professor, Shenzhen agricultural Genome Research Institute, Chinese Academy of Agricultural Sciences, email: zhouyongfeng@caas.cn; <http://www.agis.org.cn/kydw/z/261655.htm>
13. Qiang Qiu, Genome sequence and adaptive evolution of the yak (PhD, 2004-2011). The current post: Professor, Northwestern Polytechnical University, email: qiuqiang@lzu.edu.cn; <http://renshi.nwpu.edu.cn/info/1376/4647.htm>
14. Xinming Tian, Biogeographical studies of the Qinghai-Tibet Plateau endemic genus *Parapteropyrum* (Polygonaceae) (PhD: 2006-2011). The current post: Professor, Xinjiang University, email: tianxm06@lzu.edu.cn; <http://sky.xju.edu.cn/info/1151/1956.htm>
15. Guangpeng Ren, Phylogeography and speciation of four pine species in northeast China (Msc, 2009-2011). The current post: Yong Research Professor, Lanzhou University, email: reng@lzu.edu.cn; <http://lifesc.lzu.edu.cn/fh/201803/2094.html>
16. Tao Ma, Genomic basis for salt adaptation in a desert poplar (PhD, 2009-2014). The current post: Professor, Sichuan University, email: 13519669951@139.com; <http://life.scu.edu.cn/info/1048/1868.htm>
17. Jing Wang, Species differentiation and phylogeography of *Abies chensiensis* and *A. fargesii* (Msc, 2008-2012). The current post: Professor, Sichuan University, email: wangjing2019@scu.edu.cn; <http://life.scu.edu.cn/info/1048/1868.htm>

18. Yongshuai Sun, Diploid hybrid origin of *Picea purpurea* (PhD: 2008-2012). The current position: Professor, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, email: sunyongshuai@xtbg.ac.cn; http://sourcedb.xtbg.cas.cn/zw/zjrck/yjy/202101/t20210120_5873303.html
19. Yongzhi Yang, Phylogenomics of *Carpinus* and *Ostrya* (Betulaceae) (PhD, 2015-2018). The current position: Yong Research Professor, Lanzhou University, email: yangyz@lzu.edu.cn; <http://lifesc.lzu.edu.cn/fh/201909/5783.html>
20. Kun Wang, Genome-wide genetic variation and high-altitude adaptation of gene expression in yak (PhD, 2010-2015). The current post: Associate Professor, Northwestern Polytechnical University, email: wk8910@gmail.com; <http://renshi.nwpu.edu.cn/info/1164/3723.htm>

Media Coverage

Our works on the desert poplar, yak and cypress have received extensive media coverage, including poplar journals (e.g. Readers), radio, various newspapers (e.g. Chinese Science Daily) and more than 100 online news (e.g. Science daily).

<https://www.sciencedaily.com/releases/2012/07/120705144619.htm>

<http://news.sciencenet.cn/sbhtmlnews/2012/5/257978.shtm>

<https://www.fx361.com/page/2015/1230/286272.shtml>

https://tieba.baidu.com/p/5221287312?red_tag=3456645791

<http://news.sciencenet.cn/sbhtmlnews/2021/2/360944.shtm>

Invited lectures

More than 50 invited lectures/keynotes/plenaries since 2003 (China, Germany, UK and USA) and a few of them are listed as below:

- 2020 -Genomic studies of resource plants (Nanjing Agriculture University, China; Online meeting)
- 2020 -Molecular genetic mechanism of hybrid speciation: inheritance of alternate alleles of parental isolating genes (Institute of Botany, Chinese Academy of Sciences, Beijing, China)
- 2020 -Species concept, barcode and species delimitation (Yangzhou University, Yangzhou, China)
- 2019 -Species concept and the total number of plant species in China (Kunming Institute of Botany, Kunming, China)
- 2019 -A systematic study of *Eutrema* (Zunyi Medical University, Zunyi, China)
- 2018 -*Ostrya* genomes and evolutionary history (Chinese Forest Symposium, Changsha, China)
- 2018 -Yak high-altitude adaptation and domestication (Texas Tech University, Texas, USA)

2017 -How to delimitate plant species? (Shangxi Normal University, Xian, China)
 2017 - Evolutionary history of *Populus euphratica* (Chinese Plant Symposium, Taian, China)
 2016 -Where will we go? Phylogeographic studies of plants in the Qinghai-Tibet Plateau (Systematics and Evolutionary Symposium in China, Beijing)
 2016 -Adaptation and evolution of alpine plants in the Qinghai-Tibet Plateau (Peking University, Beijing, China)

Committee membership/advisory

Member of the second round of NSFC *Founding Panel* (2008-); Associate editor of *Journal of Systematics and Evolution* (2004-); Editor of *Plant Ecology & Diversity* (2014-); Editorial review board of *Molecular Ecology* (2014-)

Publications (* corresponding authors)

2021

- Wang ZF, Jiang YZ, Bi H, Lu ZQ, Ma YZ, Yang XY, Chen NN, Tian B, Liu BB, Mao XX, Ma T, DiFazio SP, Hu QJ*, Abbott RJ*, Liu JQ* (2021). Hybrid speciation via inheritance of alternate alleles of parental isolating genes. **Molecular Plant**, 14(2), 208-222 (Cover Story and heighted comments).
<https://doi.org/10.1016/j.molp.2020.11.008>
- Lu ZQ, Sun YS, Li Y, Yang YZ, Wang GN, Liu JQ* (2021). Species delimitation and hybridisation history of a hazel species complex. **Annals of Botany**, online: <https://doi.org/10.1093/aob/mcab015>
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