The 24th Pacific Science Congress

Pan-genome Analysis Reveals the Contribution of Interspecific Hybridization to Genetic Variation and Local Adaptation in Quercus (Oak)

Boasheng Wang

South China Botanical Garden, CAS

Shantou
2025-11-23

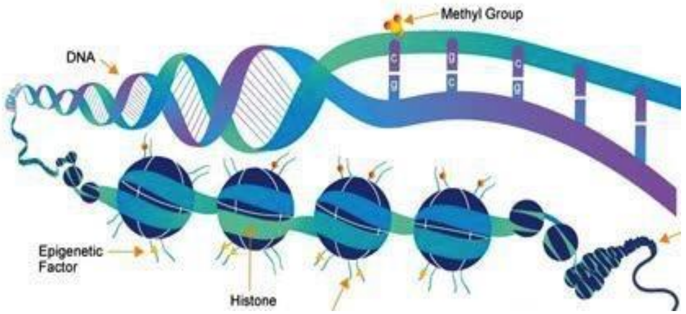
The loss of biodiversity due to climate change

Genetic diversity is a cornerstone of biodiversity

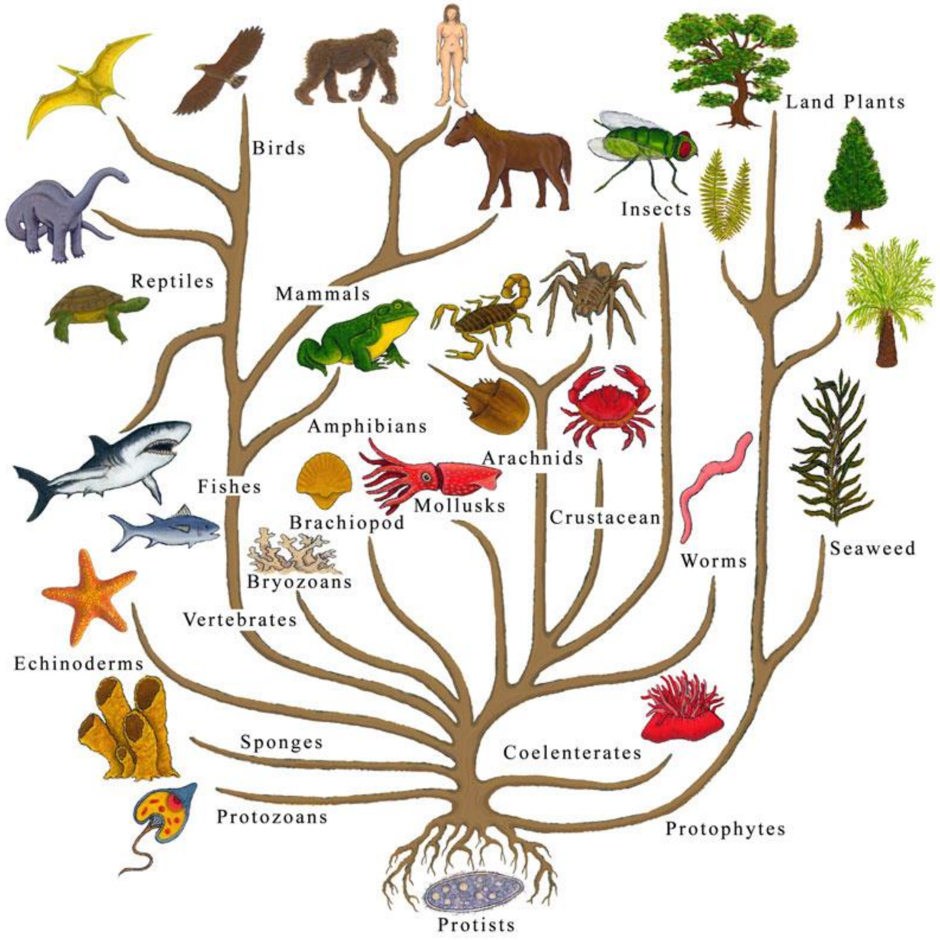
Genetic diversity

Species diversity

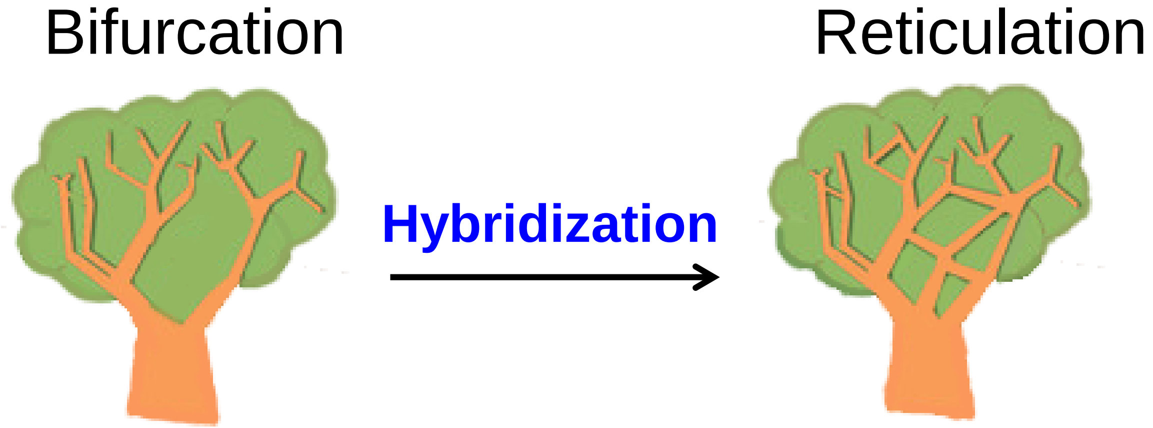
Ecosystem diversity



Hybridization contributes to genetic diversity



Tree of Life



Plant

25%

Animal

10%

Hybridization

Mallet, 2005

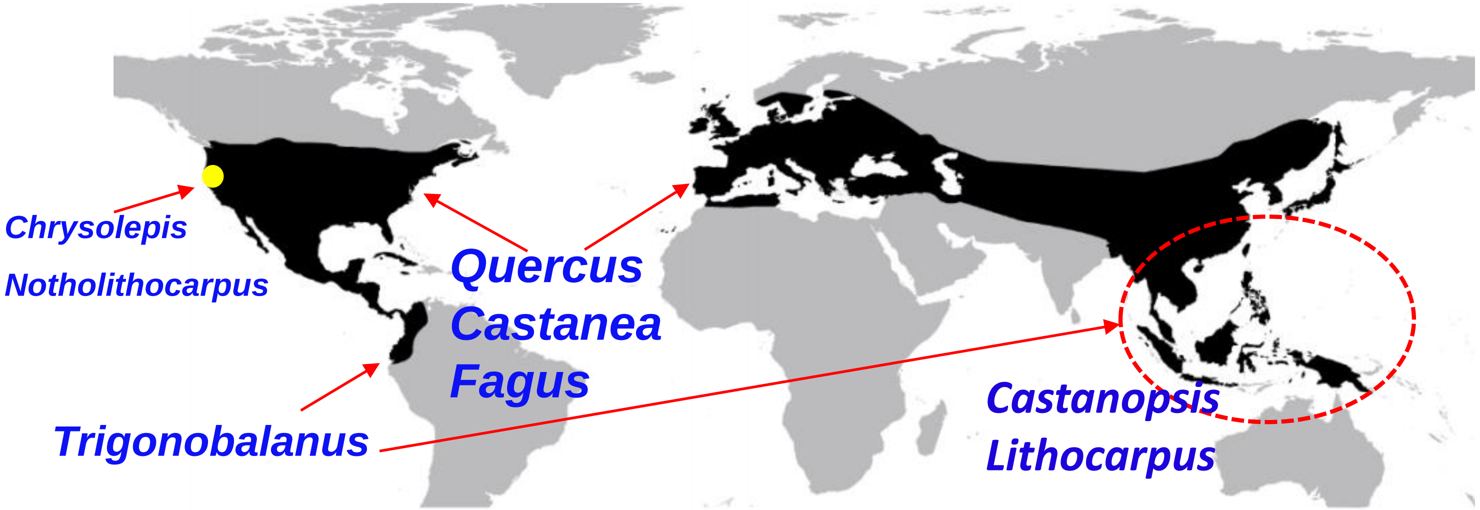
What is an oak? **Woody plants, shrubs or trees**

***Quercus pseudosetulosa*, Zhuhai, China, May 2023**

***Quercus robur*, Stockholm, Sweden, July 2025**

What is an oak? **Acorns**

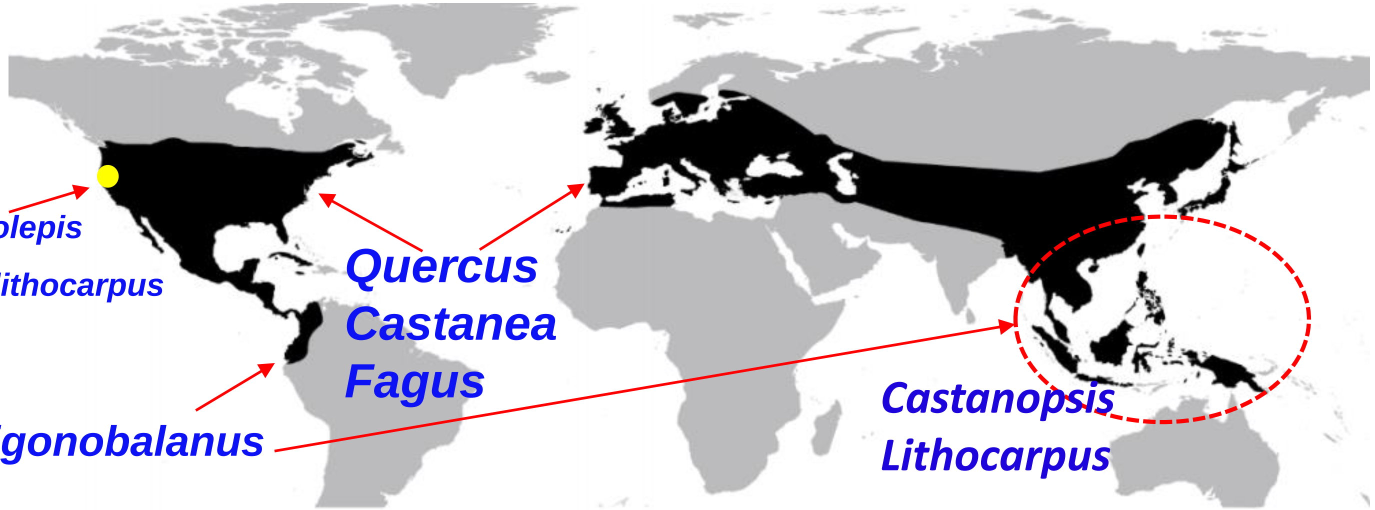
Global distribution of Fagaceae species



- ~ 900 species
- 8 genera
- Dominated trees in northern hemisphere forests

Oh & Manos 2008
Manso et al. 2001

Questions



Chrysolepis

Notholithocarpus

Quercus

Castanea

Fagus

Trigonobalanus

Castanopsis

Lithocarpus

- ~ 900 species
- 8 genera
- Dominated trees in northern hemisphere forests

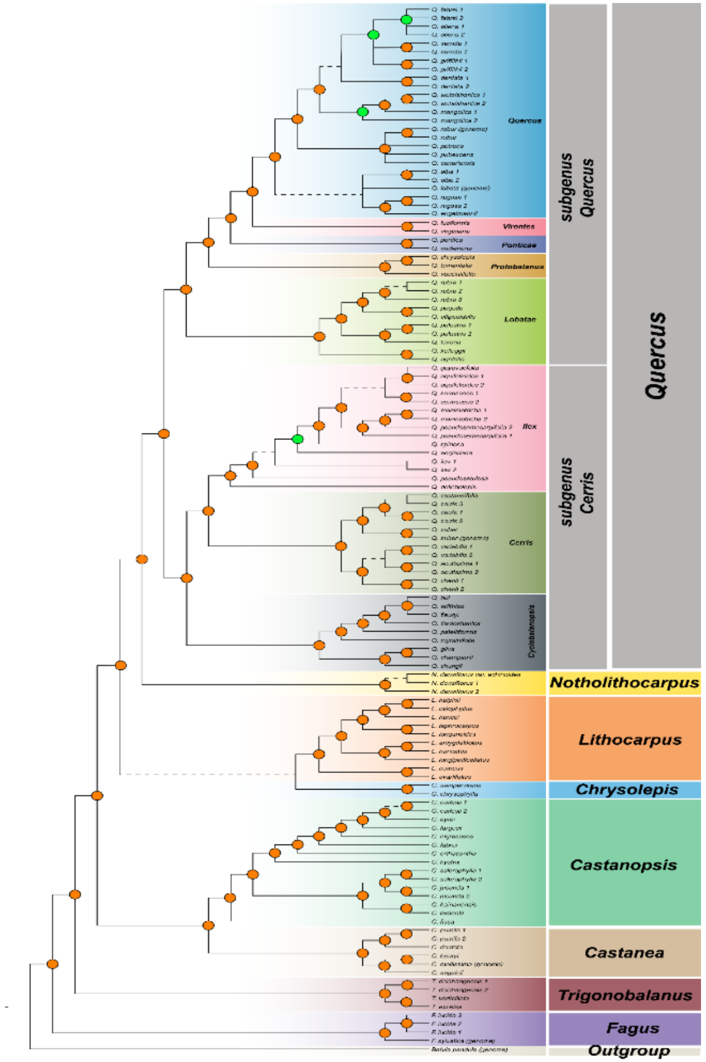
- What is the process of diversification in Fagaceae?
- What role does hybridization play in these events?

Oh & Manos 2008

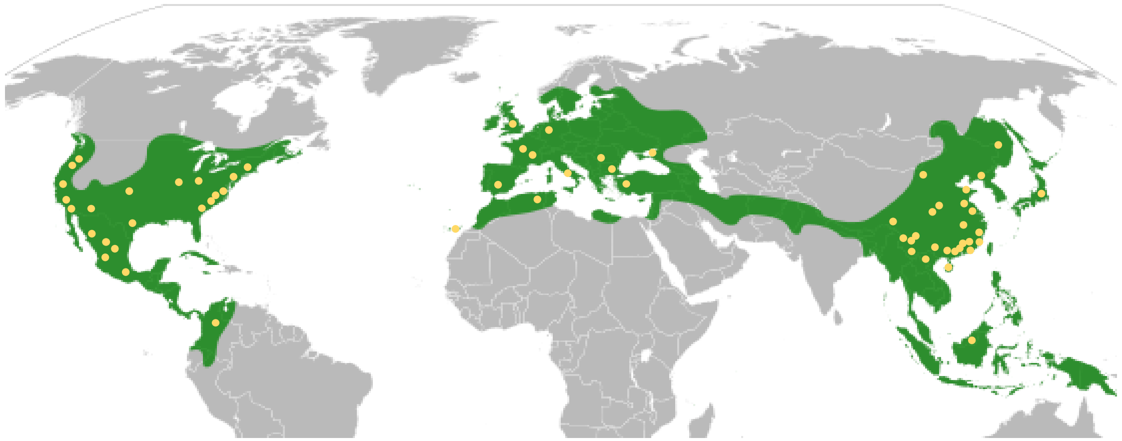
Manso et al. 2001

Phylogenetic relationship of Fagaceae species

Maximum likelihood tree



Sampling sites

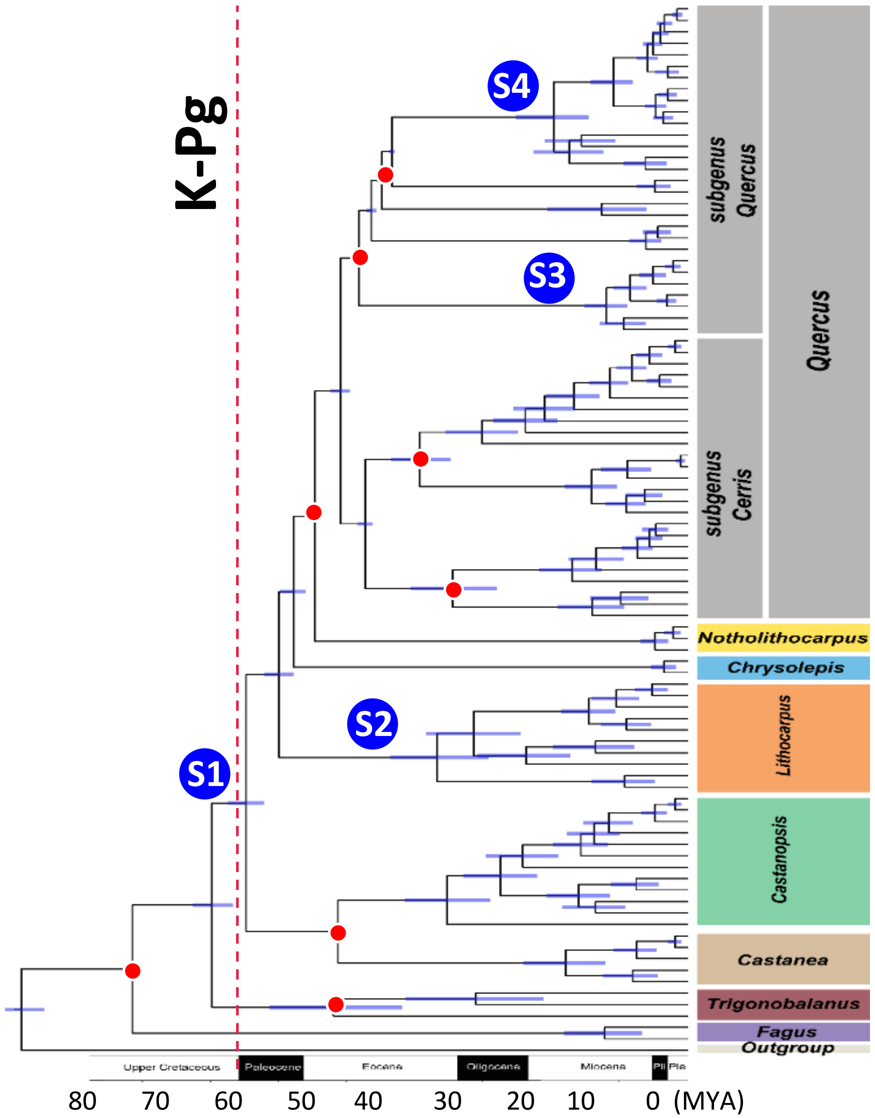


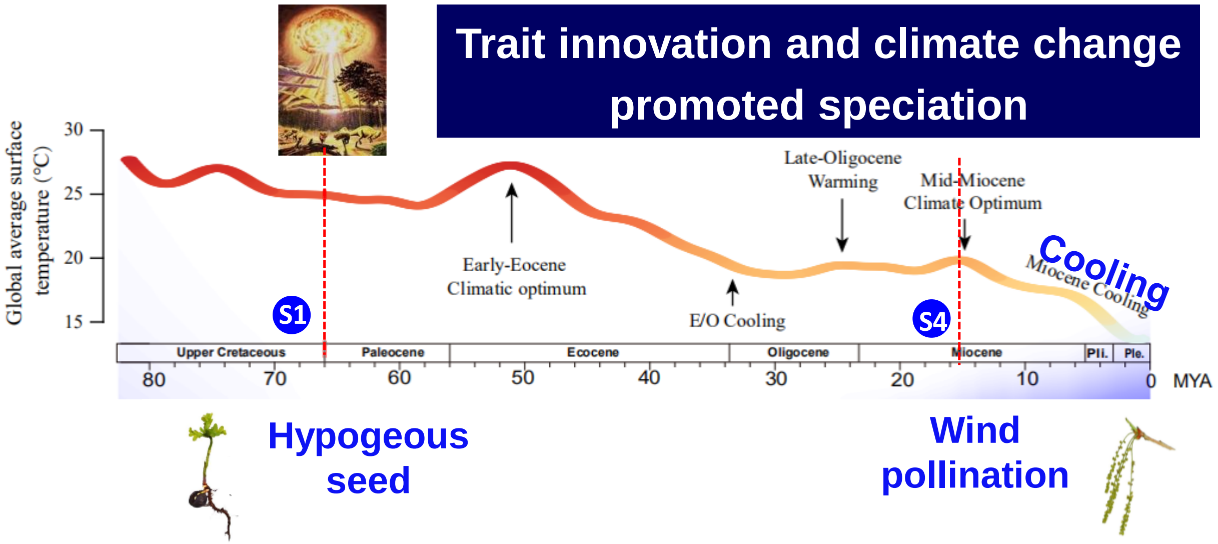
- ➢ **91 species from all 8 recognized genera**
- ➢ **2124 nuclear loci and full plastomes**
- ➢ **The relationship among eight genera of Fagaceae and eight sections of the genus *Quercus* were highly supported**

Zhou et al. 2022

Divergence time and diversification rate

Dated tree based on 8 fossil records





Trait innovation and climate change promoted speciation

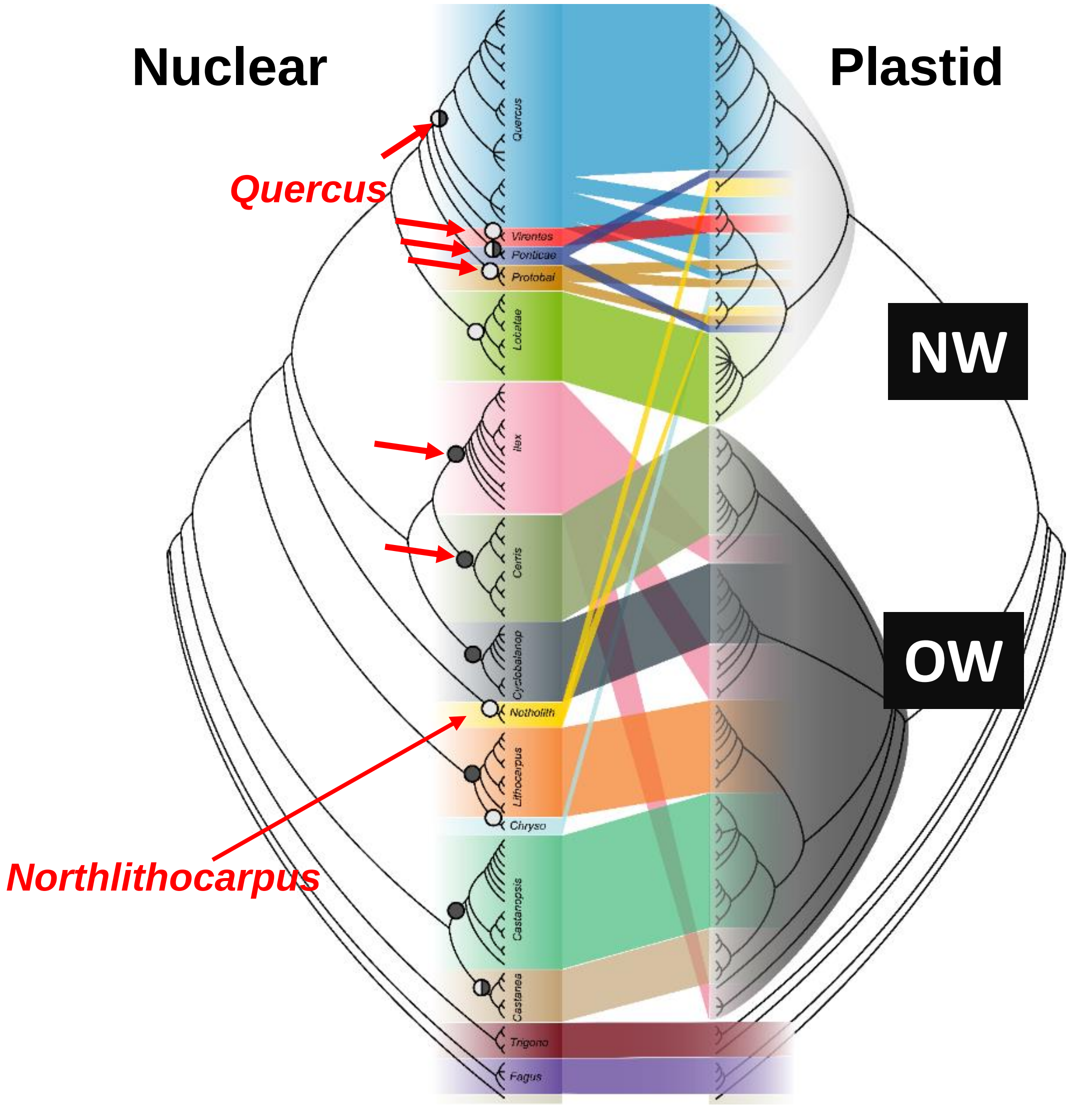
Hypogeous seed

Wind pollination

- ➢ Divergence in Fagaceae initiated at the late Cretaceous
- ➢ Rapid radiation after K-Pg boundary generated the six genera that comprise 99% of the modern species.
- ➢ Recent radiation is coincident with global temperature cooling during Miocence.

Zhou et al. 2022

Conflicts between nuclear and plastid gene trees



Three major conflicts

Topology	Nuclear	Plastid
Monophyly of genera *Quercus* and *Notholithocarpus*	✓	✗
Monophyly of 6 sections of the genus *Quercus*	✓	✗
Two geographical clade New World (NW) and Old World (OW)	✗	✓

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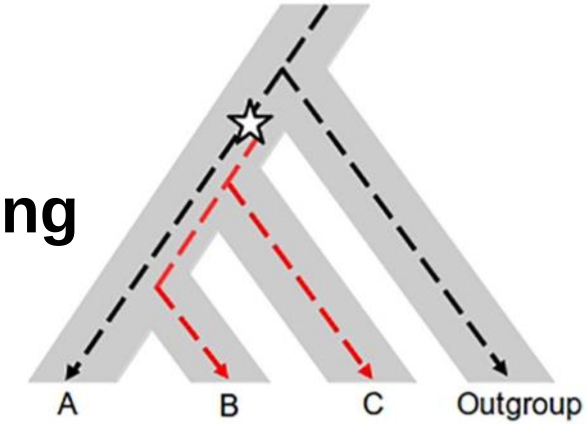
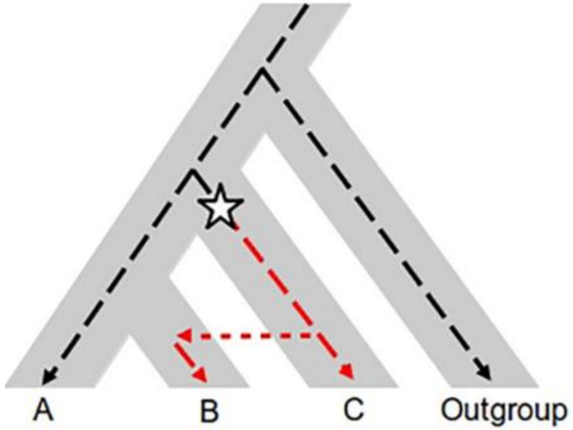
Hypothesis of Plastid-Nuclear discordance

- **Incomplete lineage sorting**

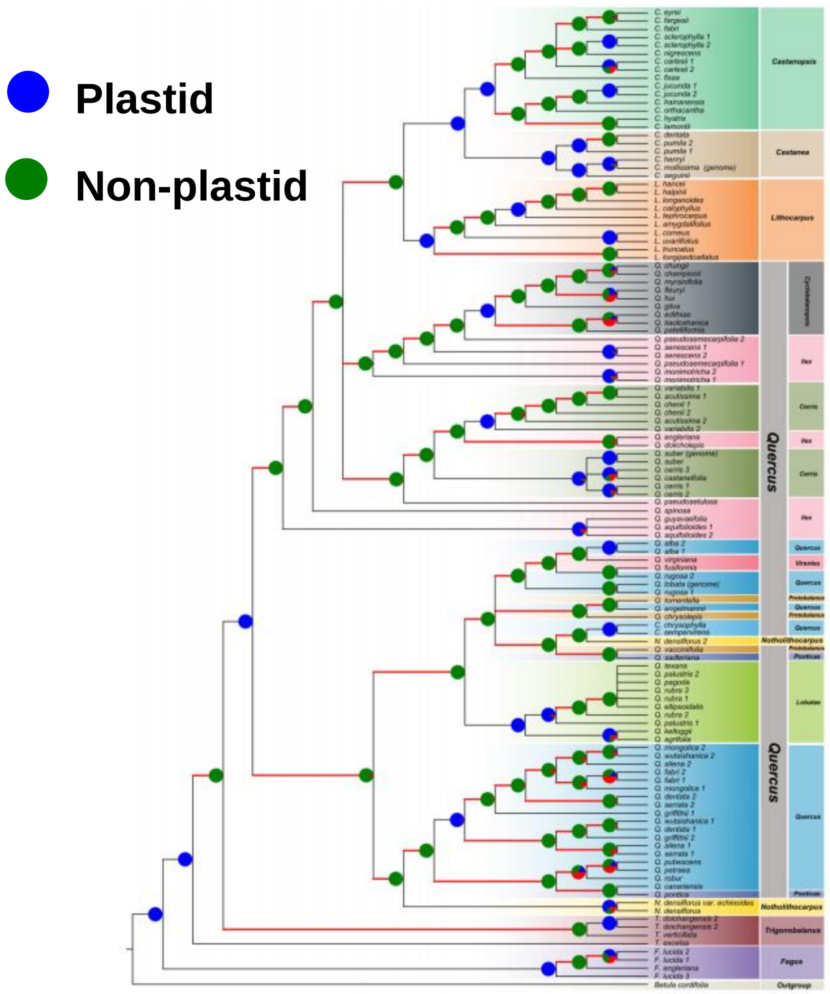


- **Hybridization**

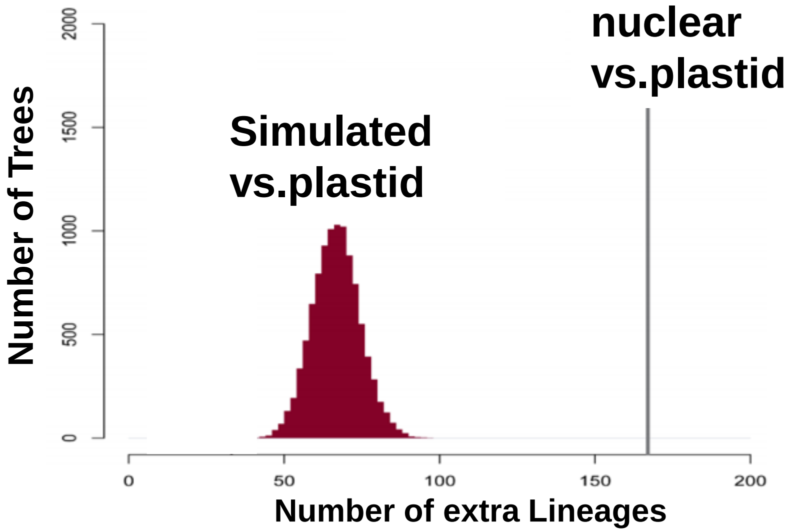


Testing hypothesis

10000 simulated tree vs. plastid tree



Simulated vs. plastid < nuclear vs. plastid



- ➢ **Simulated trees do not support the topology of plastid tree**
- ➢ **Observed plastid-nuclear discordance is higher than expectation**
- ➢ **Plastid-nuclear conflicts due to hybridization**

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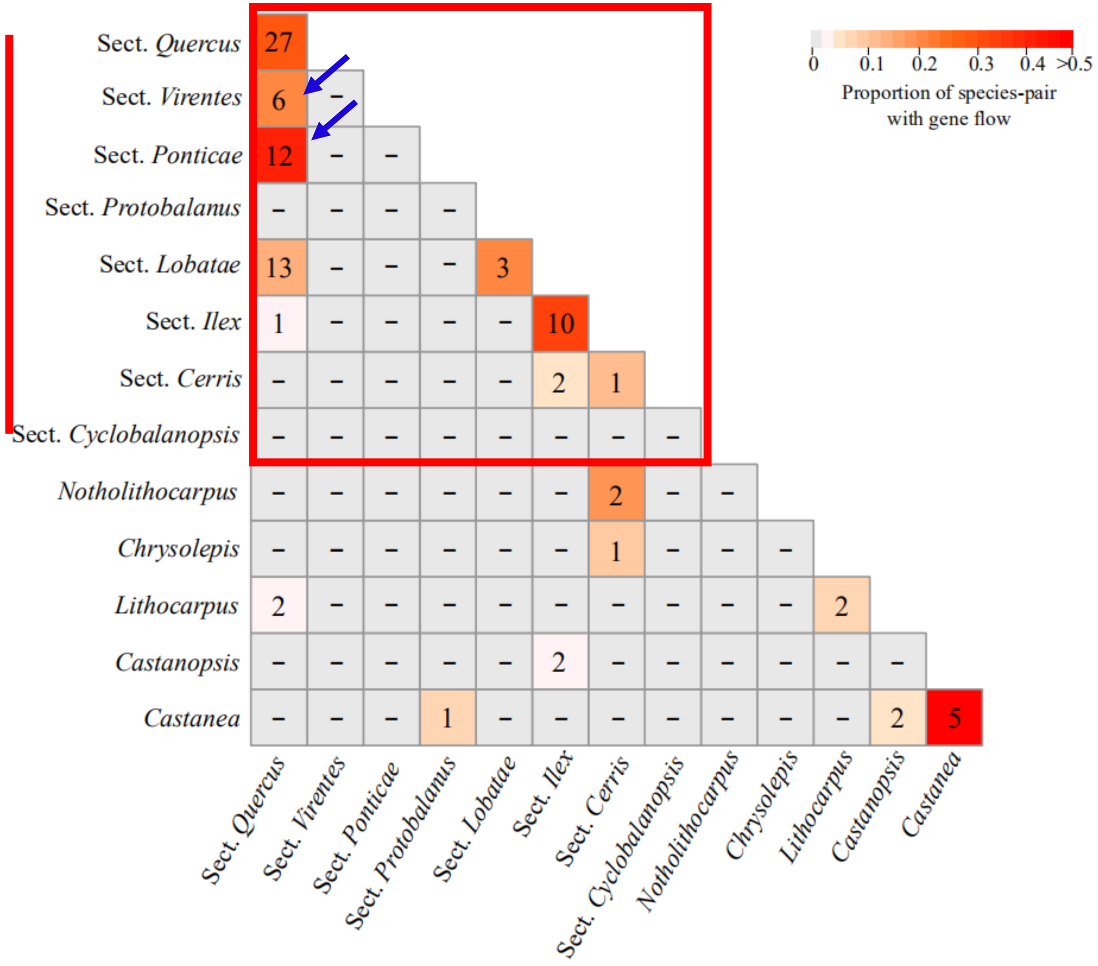
Patterns of gene flow among Fagaceae species

D-statistic test



	Sect. *Quercus*	Sect. *Virentes*	Sect. *Ponticae*	Sect. *Protobalanus*	Sect. *Lobatae*	Sect. *Ilex*	Sect. *Cerris*	Sect. *Cyclobalanopsis*	*Notholithocarpus*	*Chrysolepis*	*Lithocarpus*	*Castanopsis*	*Castanea*
Sect. *Quercus*	27												
Sect. *Virentes*	6	–											
Sect. *Ponticae*	12	–	–										
Sect. *Protobalanus*	–	–	–	–									
Sect. *Lobatae*	13	–	–	–	3								
Sect. *Ilex*	1	–	–	–	–	10							
Sect. *Cerris*	–	–	–	–	–	2	1						
Sect. *Cyclobalanopsis*	–	–	–	–	–	–	–	–					
Notholithocarpus	–	–	–	–	–	–	2	–	–				
Chrysolepis	–	–	–	–	–	–	1	–	–	–			
Lithocarpus	2	–	–	–	–	–	–	–	–	–	2		
Castanopsis	–	–	–	–	–	2	–	–	–	–	–	–	
Castanea	–	–	–	1	–	–	–	–	–	–	–	2	5

Genus *Quercus*

- **Gene flow was detected on 236 (0.911%) of 25882 trios**
- **Hybridization is recent and between closely related species**
- **Ancient gene flow between three sections of *Quercus***

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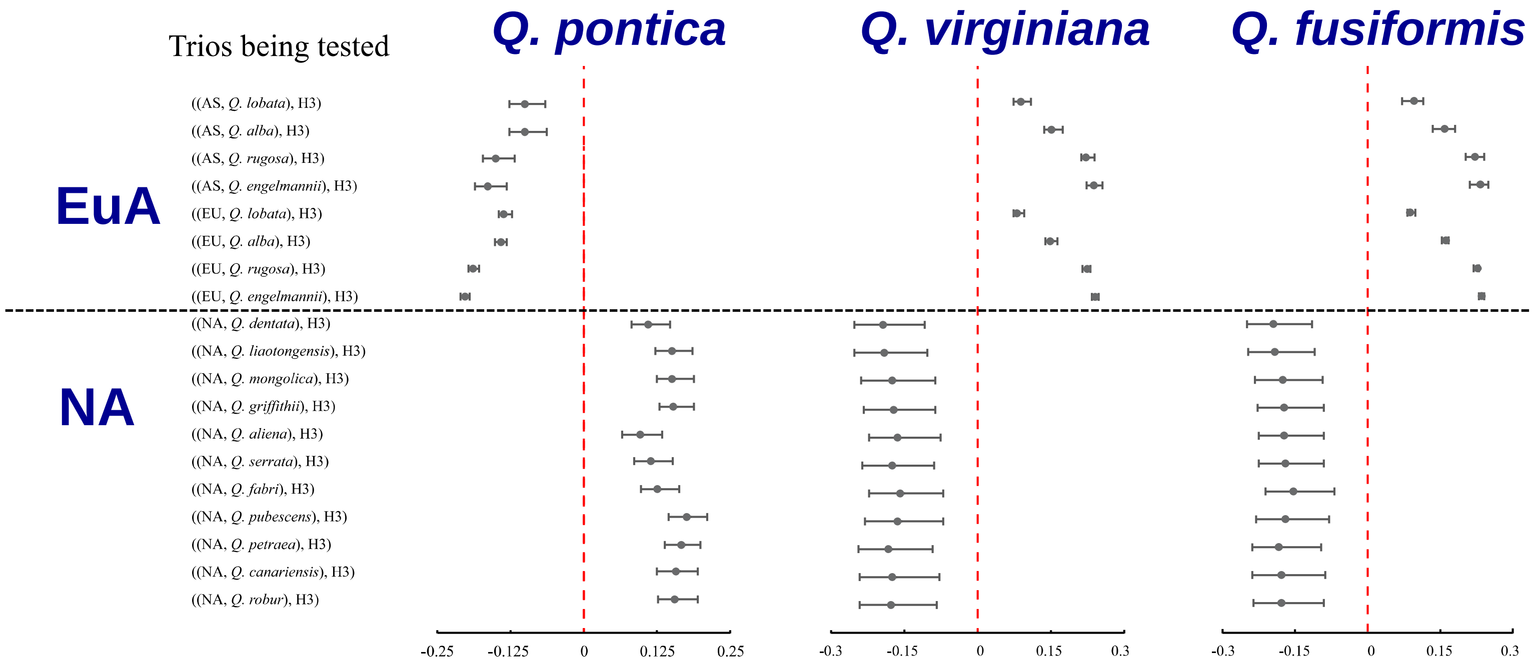
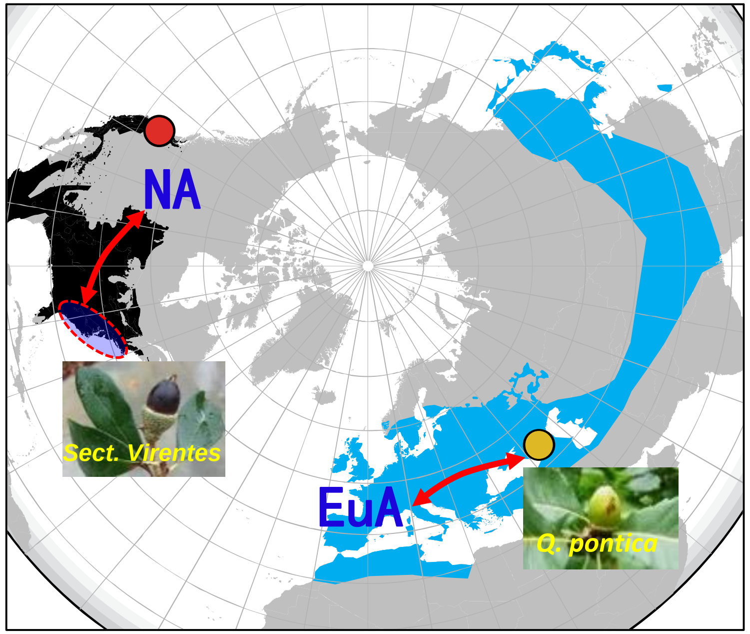
Gene flow between sections of *Quercus*


Q. pontica Q. virginiana Q. fusiformis



- ➢ **Eurasian white oaks （set. *Quercus*）vs. *Q. pontica***
- ➢ **North American white vs. sect. *Virentes* (*Q. virginiana & Q. fusiformis*)**

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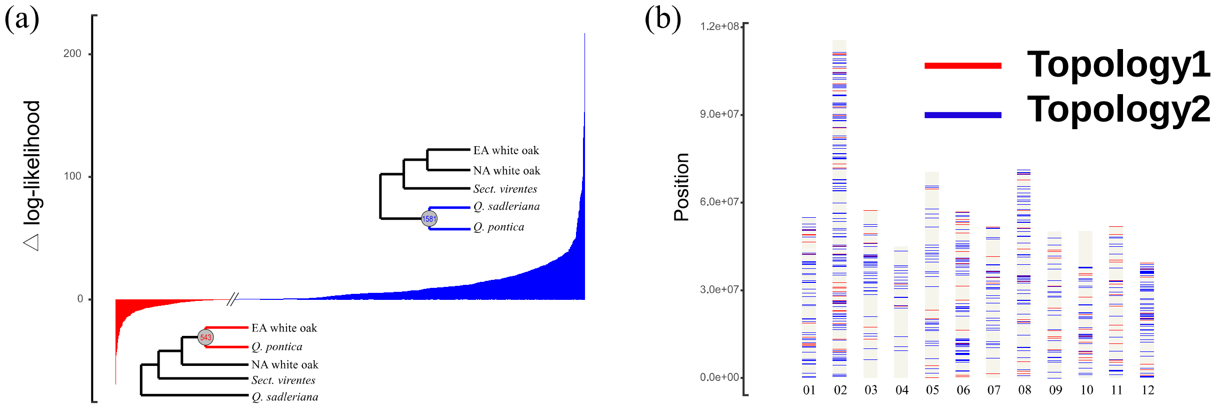
Distribution of alternative topologies

Sect. *Quercus*

vs.

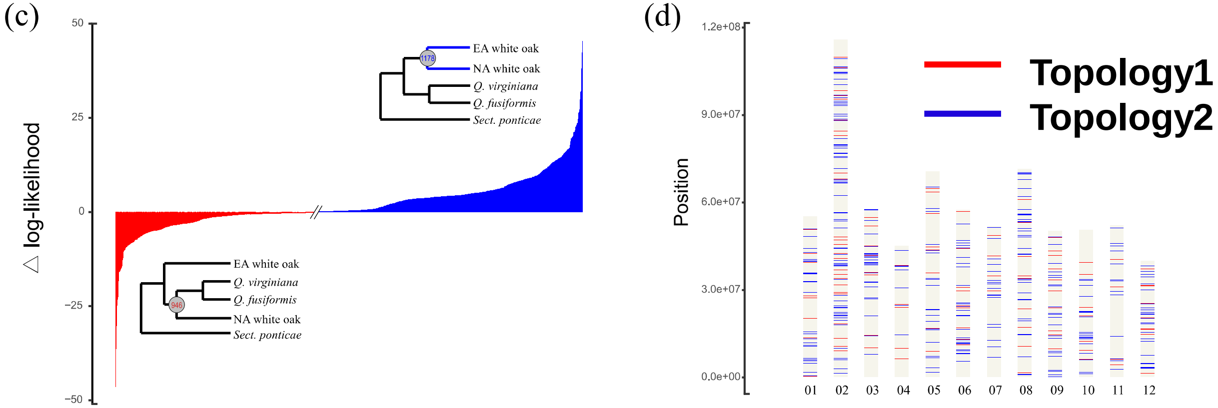
Sect. Ponticae



Sect. *Quercus*

vs.

Sect. Virentes



Introgression were widely scattered across the genome

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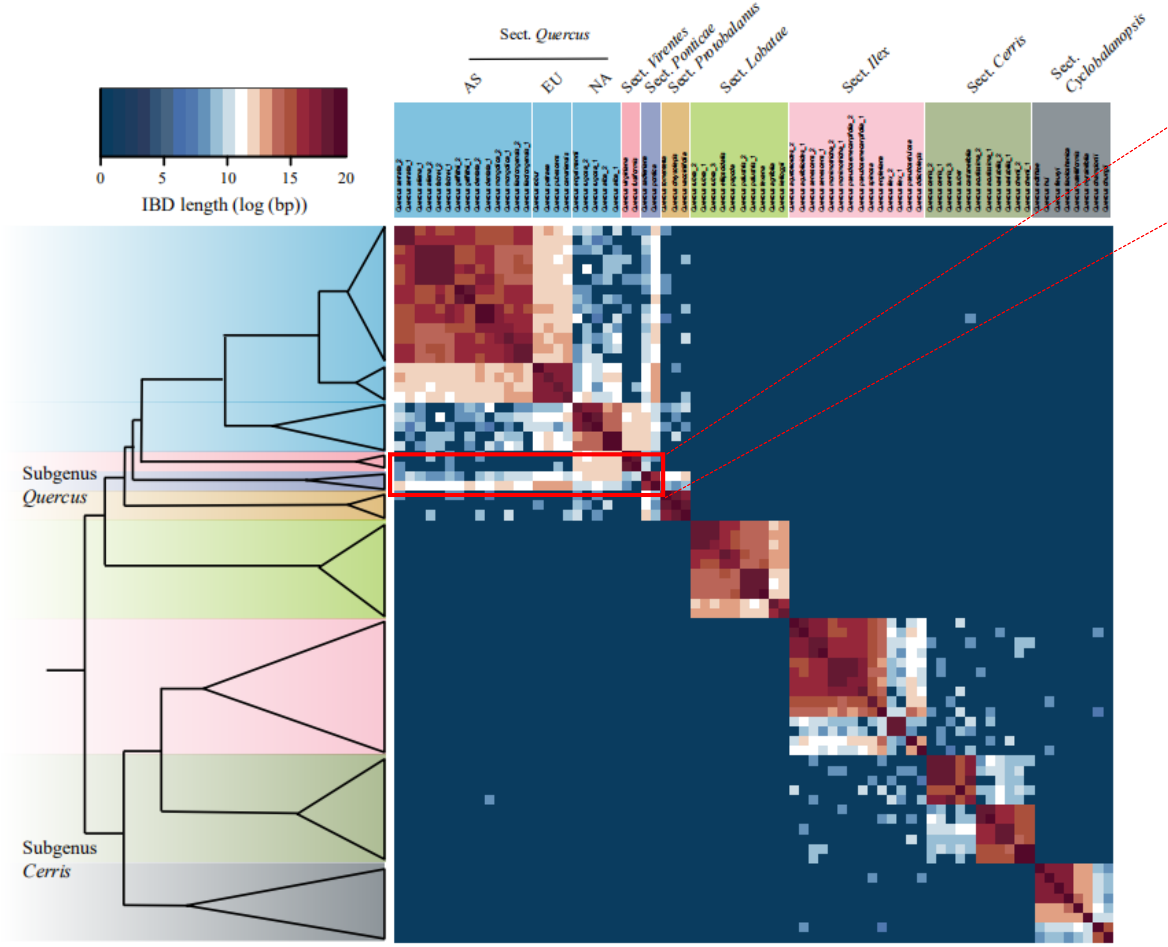
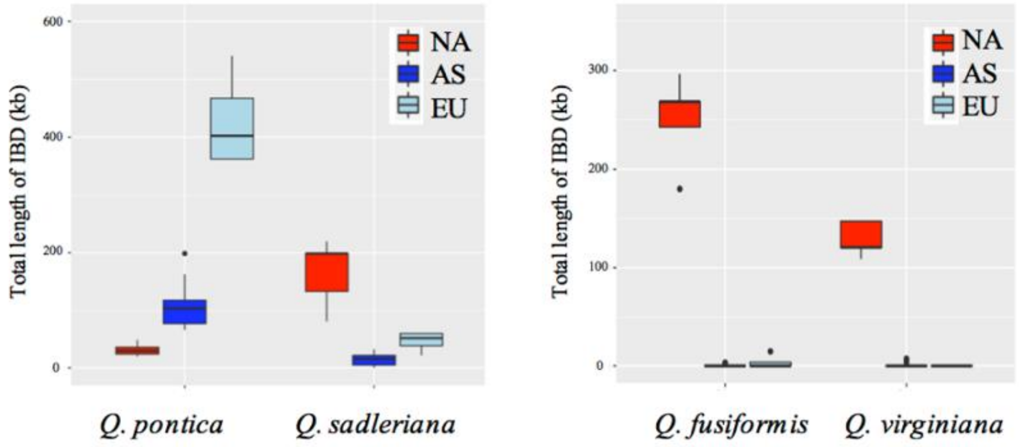
Identity by descent (IBD) analyses

Shared IBD between species





- **EuA white oak vs. *Q. pontica***
- **NA white oak vs. Sect. *Virentes***

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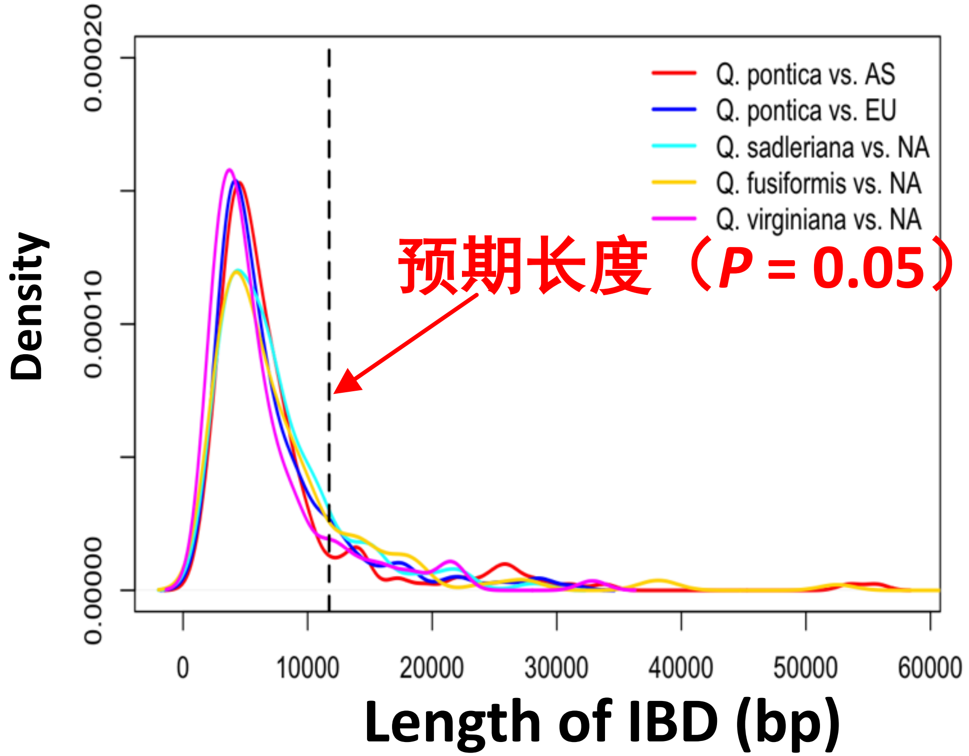
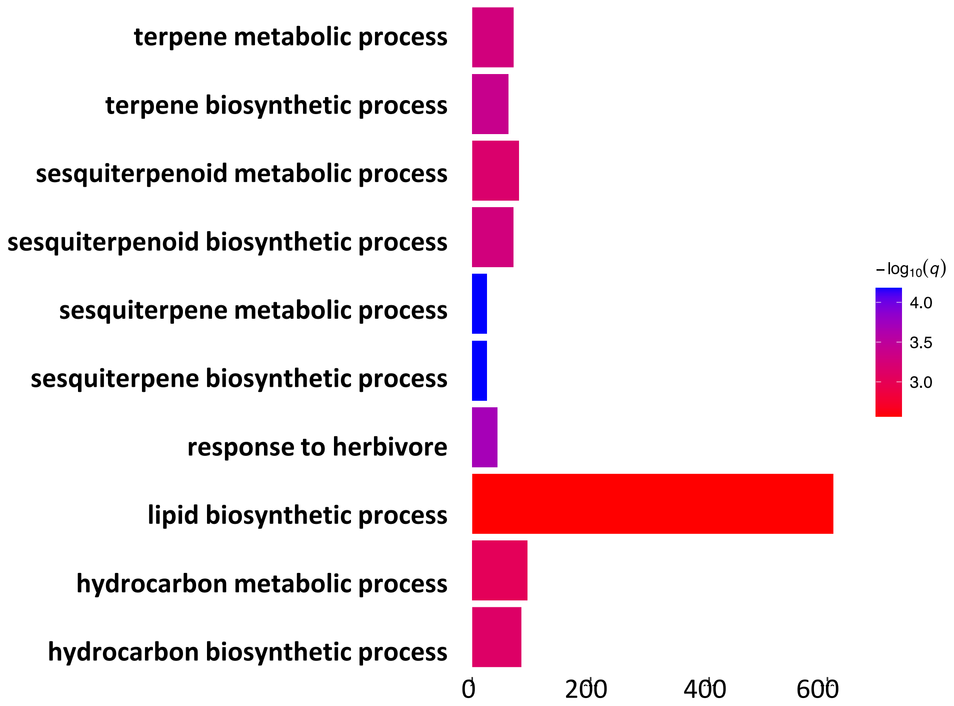
Adaptive introgression between oaks

Length distribution of IBD



Gene Ontology (GO) enrichment



- 166 IBD blocks were longer than expected under selectively neutral
- Multiple GO categories were overrepresented for genes in these IBD regions

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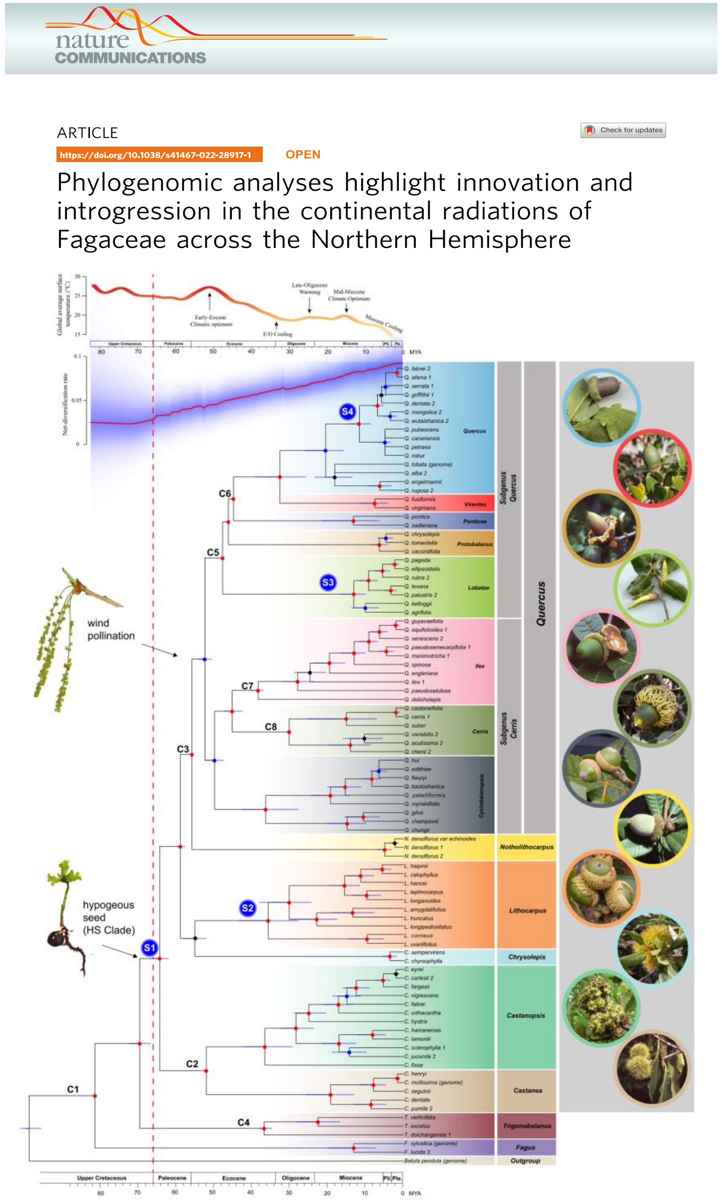
Conclusion 1



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ARTICLE

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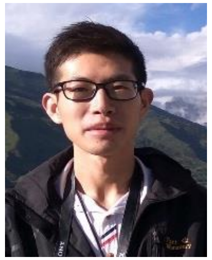
Phylogenomic analyses highlight innovation and introgression in the continental radiations of Fagaceae across the Northern Hemisphere

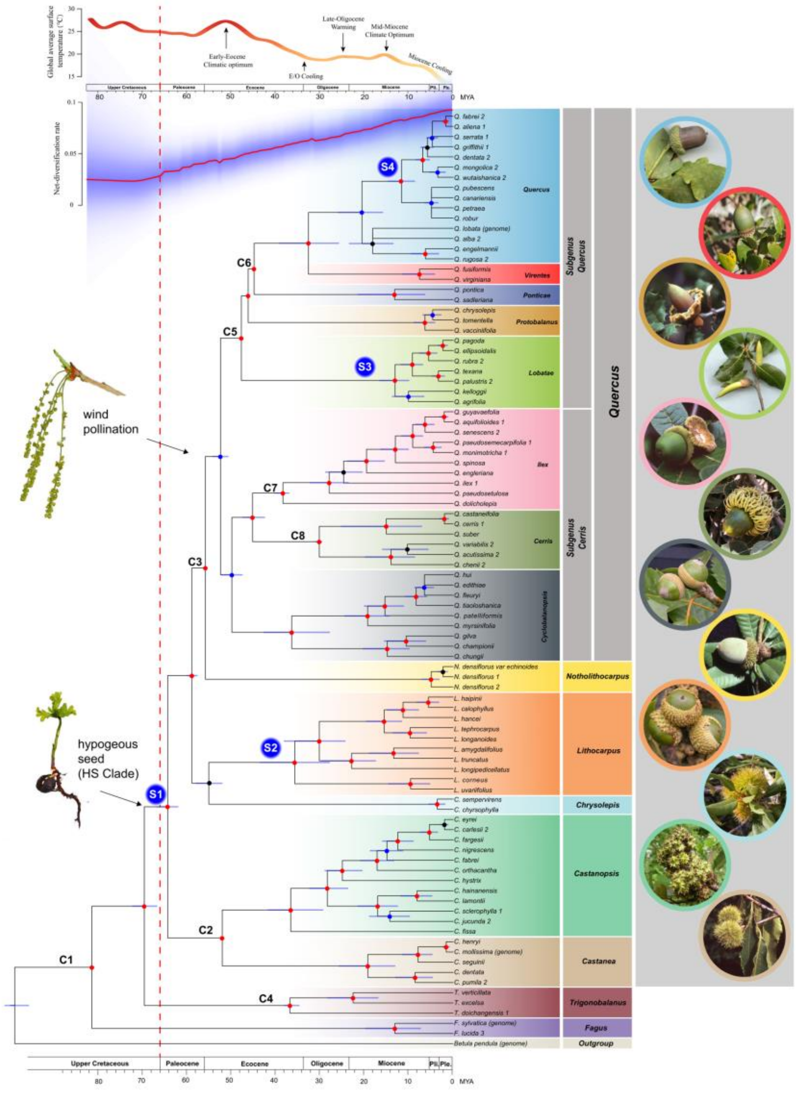


Main contributor:

Dr. Biao-Feng Zhou

- **Ecological opportunities, climate change and trait innovation promoted the differentiation and expansion of Fagaceae species**
- **Chloroplast genome capture due to ancient hybridization leads to conflicts between plastid and nuclear gene trees**
- **Interspecific hybridization serves as an important source of adaptive variation**

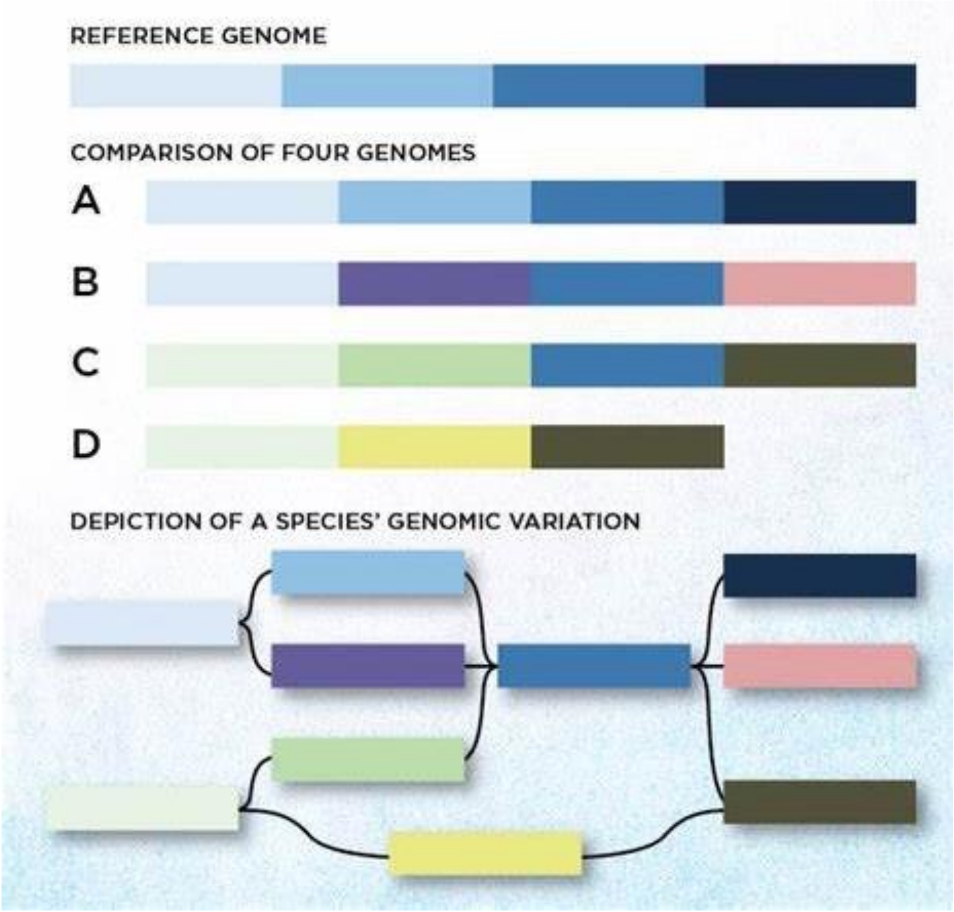
Part 2



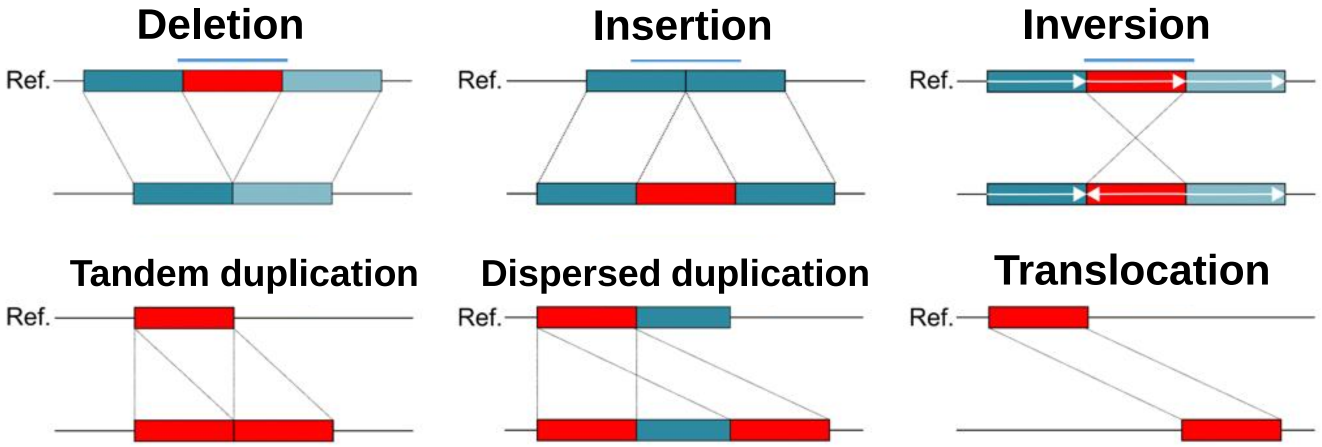
How does current hybridization contribute to local adaptation?

Why use pan-genome?

Graph-based pan-genome



Structural variants (SVs)

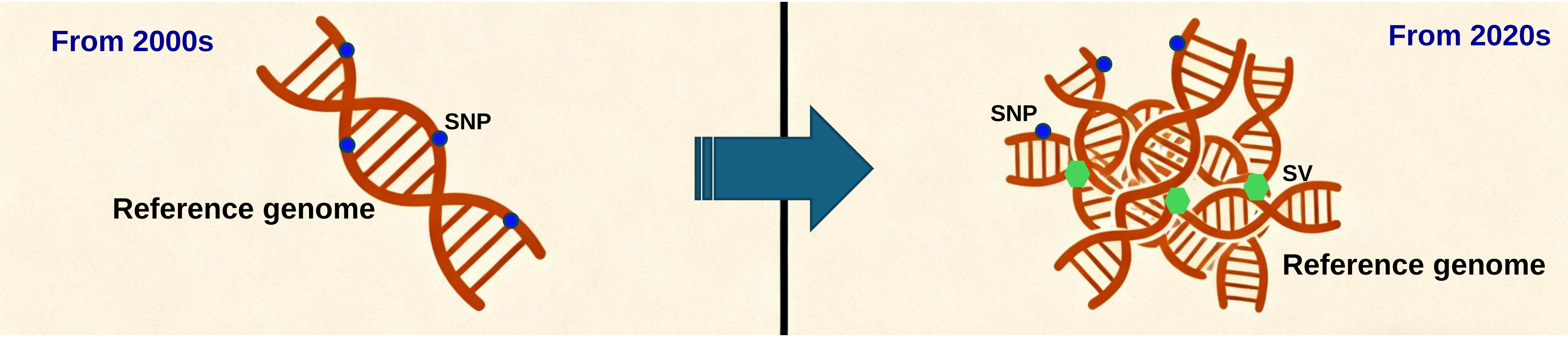


- **Single reference genome cannot capture the full genetic variation within a species, particular structural variants (SVs)**
- **Graph-based pan-genome has been developed to identify SVs based on multiple high-quality assemblies**

From genomic era to pan-genomic era

Genomic Era

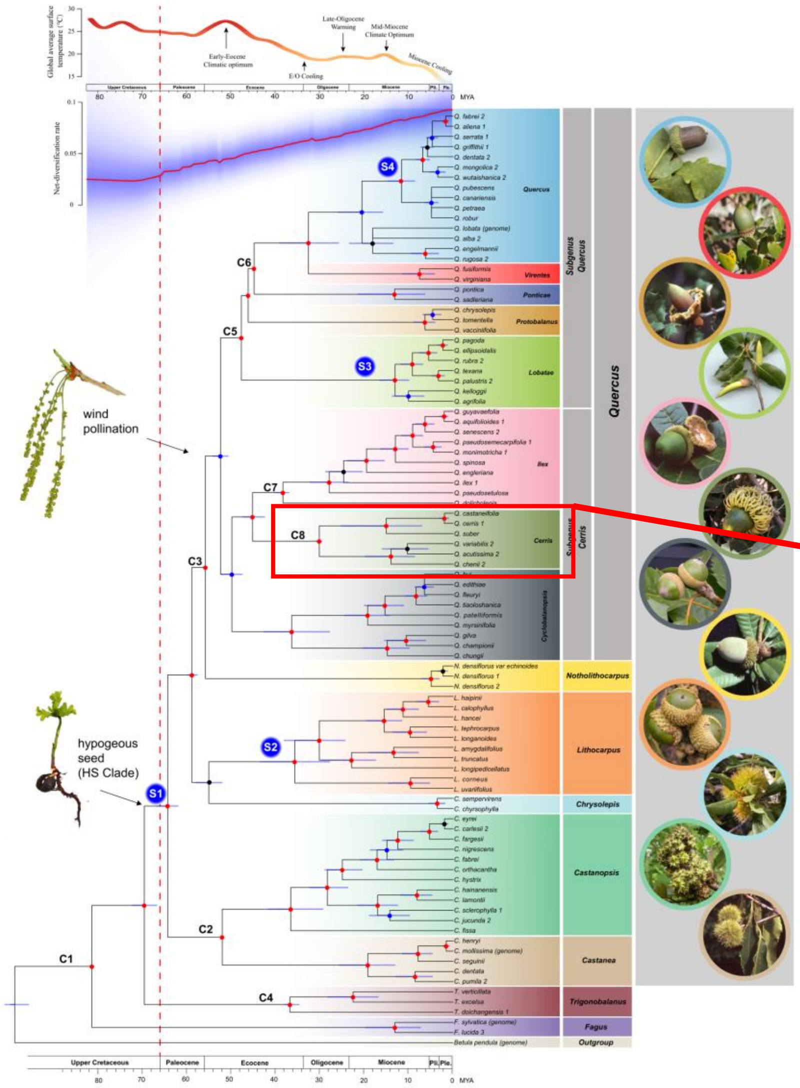
Pan-genomic Era



- **Single** reference genome
- Detecting Single Nucleotide Polymorphisms (**SNPs**)

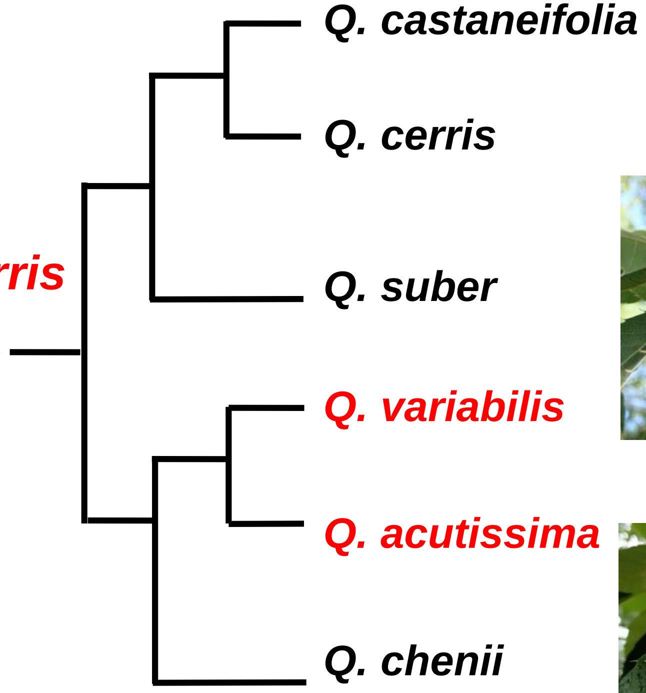
- **Multiple** reference genomes
- Detecting both **SNPs** and structural variations (**SVs**)

Focused on a pair of sister oak species



How does current hybridization contribute to local adaptation?

Sect. *Cerris*



Q. castaneifolia

Q. cerris

Q. suber

Q. variabilis

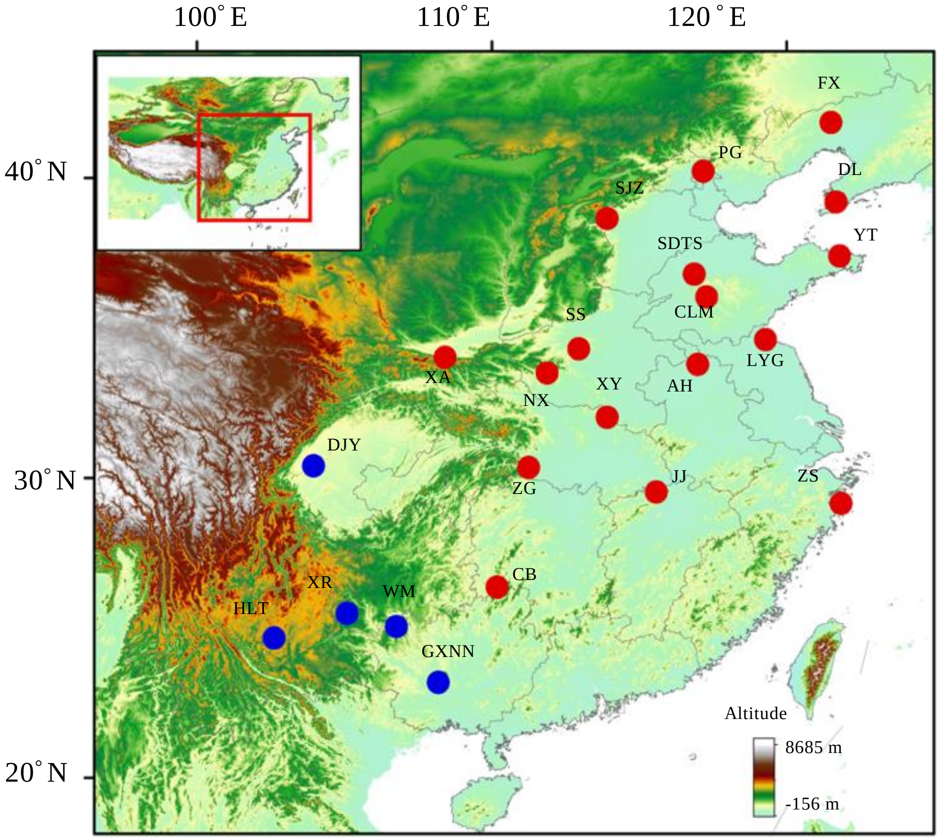
Q. acutissima

Q. chenii

Pan-genome analyses in *Q. variabilis*

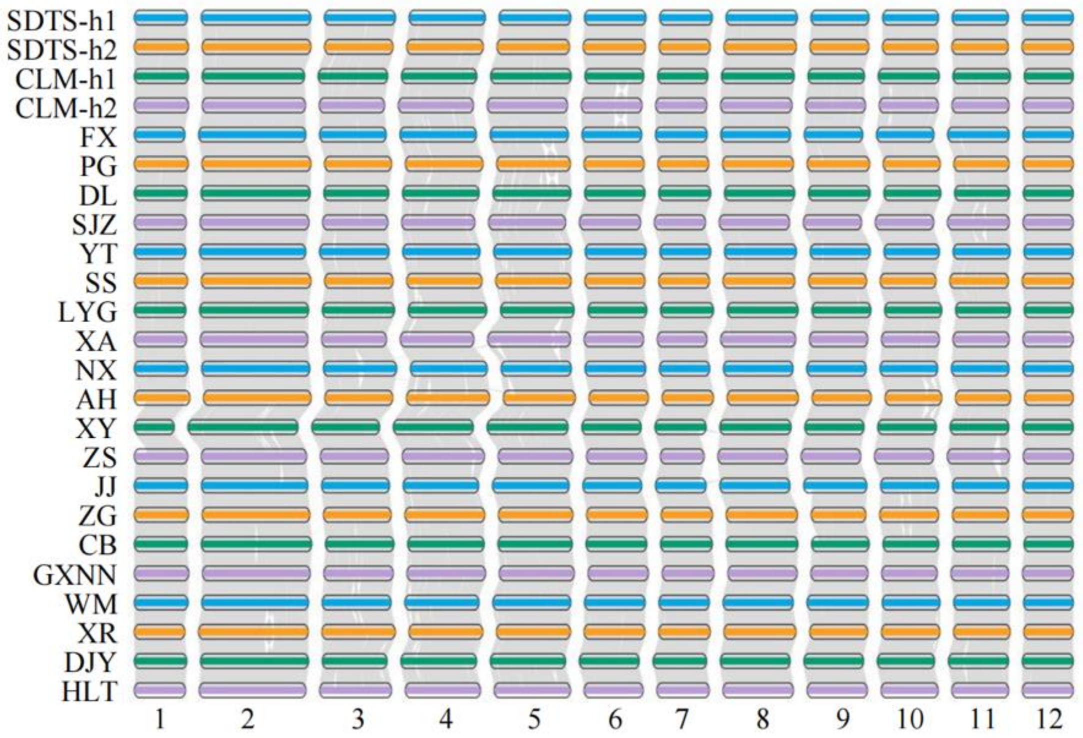
Quercus variabilis

22 sampled individuals

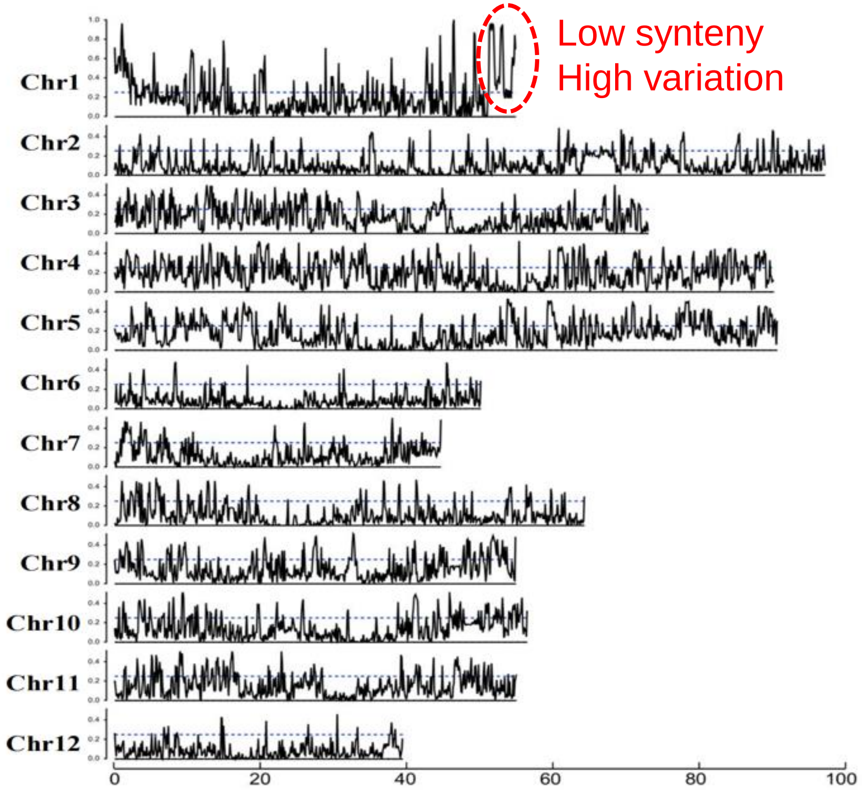


High Global Synteny and Significant Genomic Variation

Collinearity among 22 *Q. variabilis* genomes



Variation in synteny diversity



Low synteny
High variation

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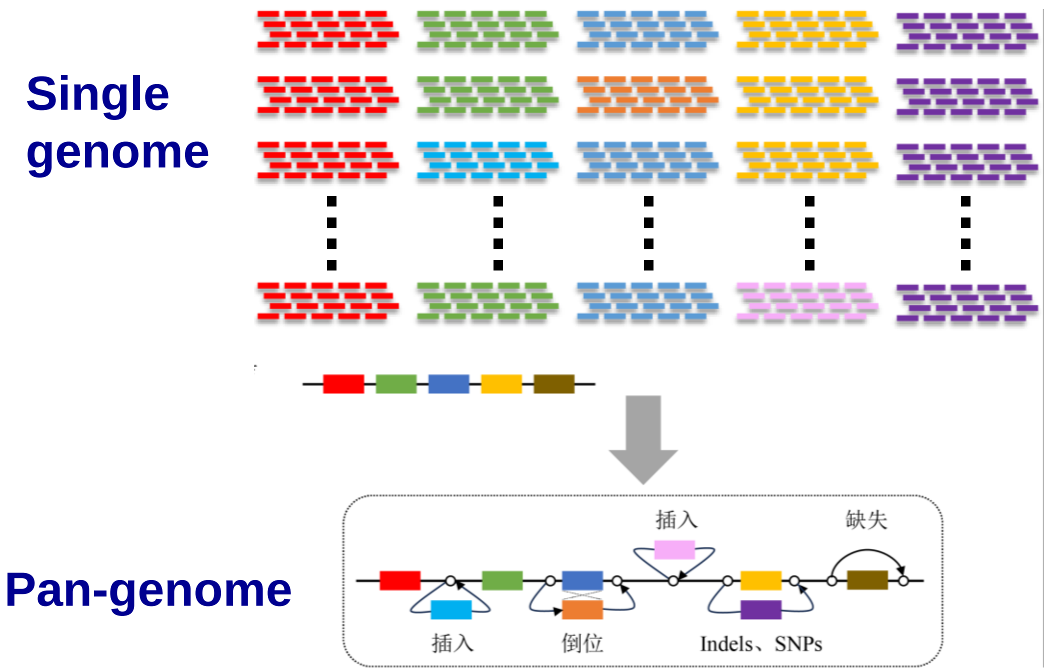
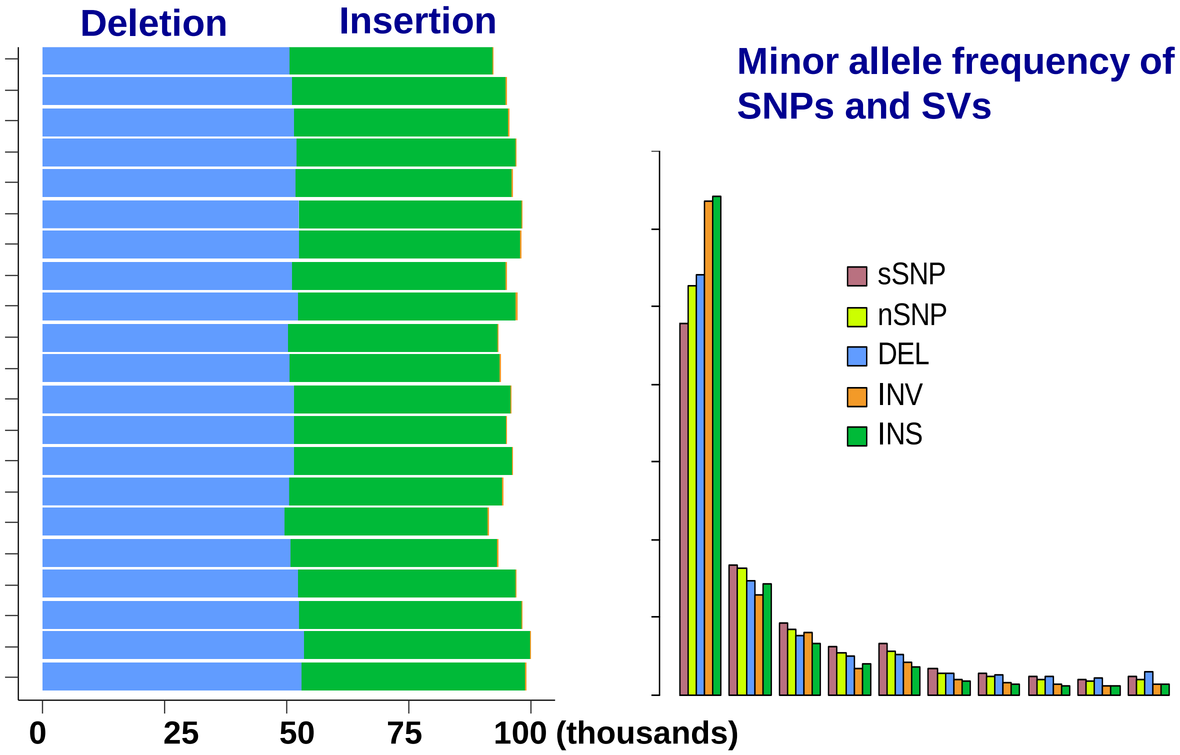
Pan-genome construction

Pan-genome construction



259 thousands SVs and 21.7 million SNPs



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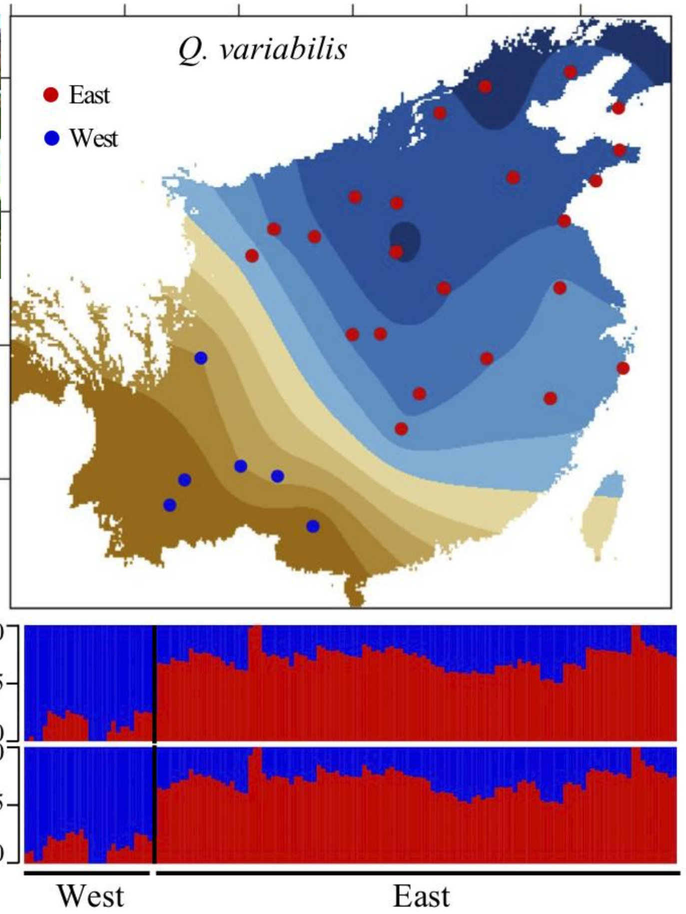
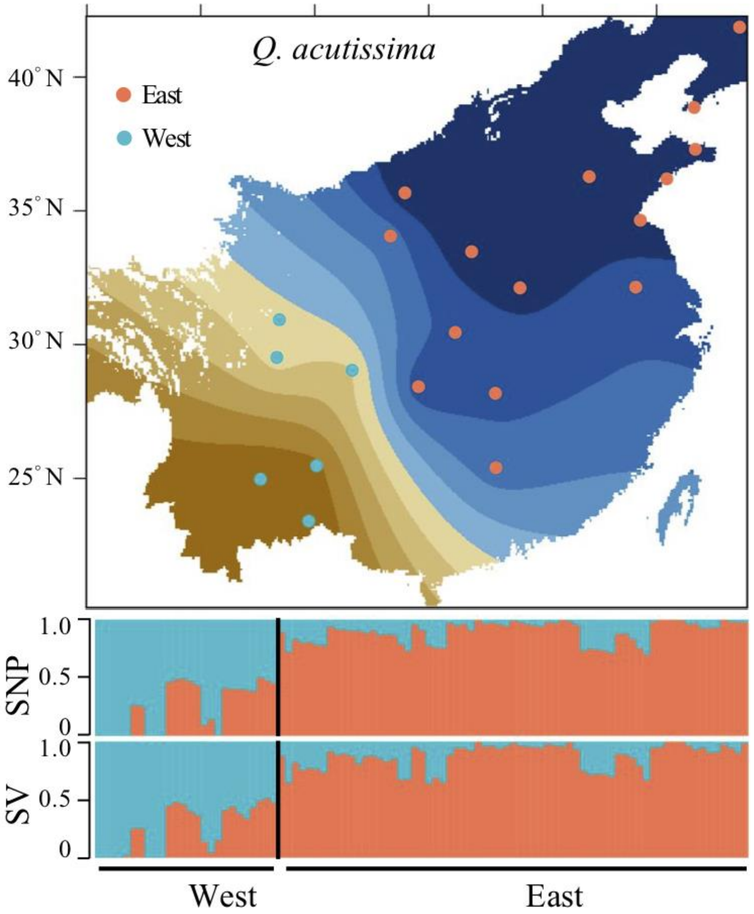
Parallel east–west divergence

Quercus variabilis





Quercus acutissima

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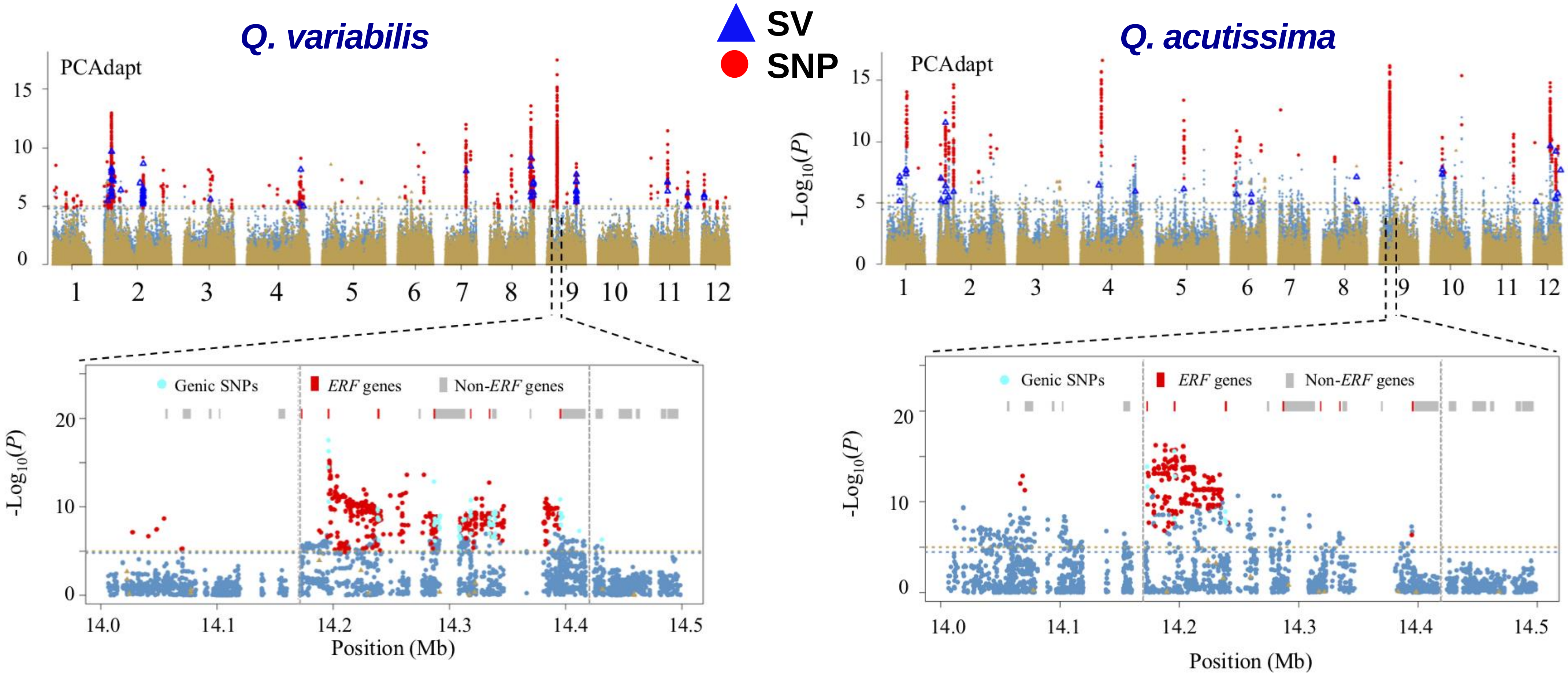
Genomic signatures of local adaptation


Q. variabilis

Q. acutissima

Strong signal of selection in a *Chr9-ERF* region

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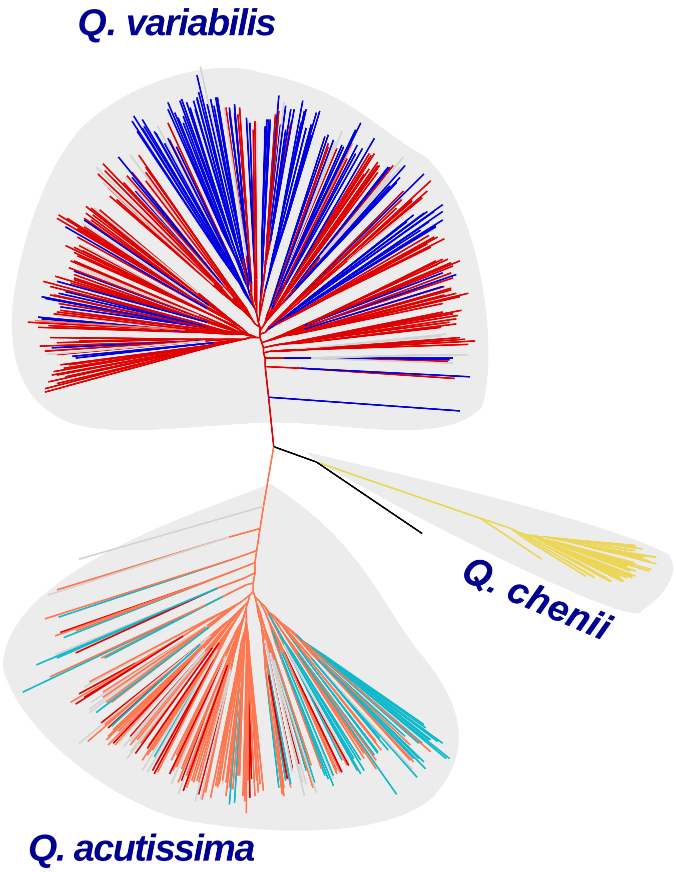
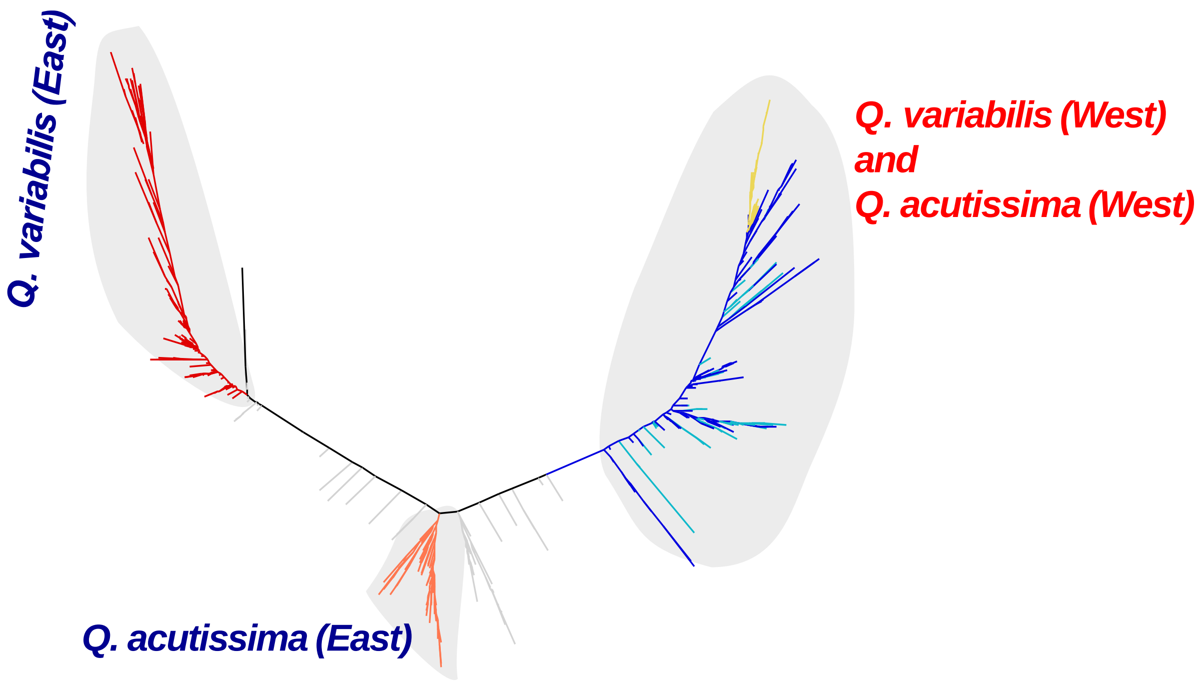
Phylogentic analyses

Genome–wide SNPs



Chr9-ERF region



West populations of *Q. variabilis and Q. acutissima grouped together, suggesting introgression or shared ancestral polymorphisms*

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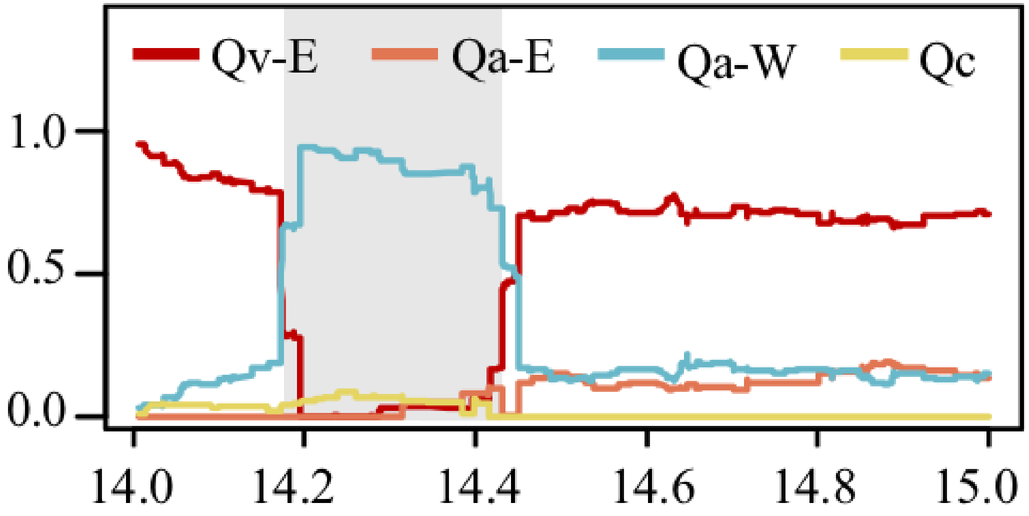
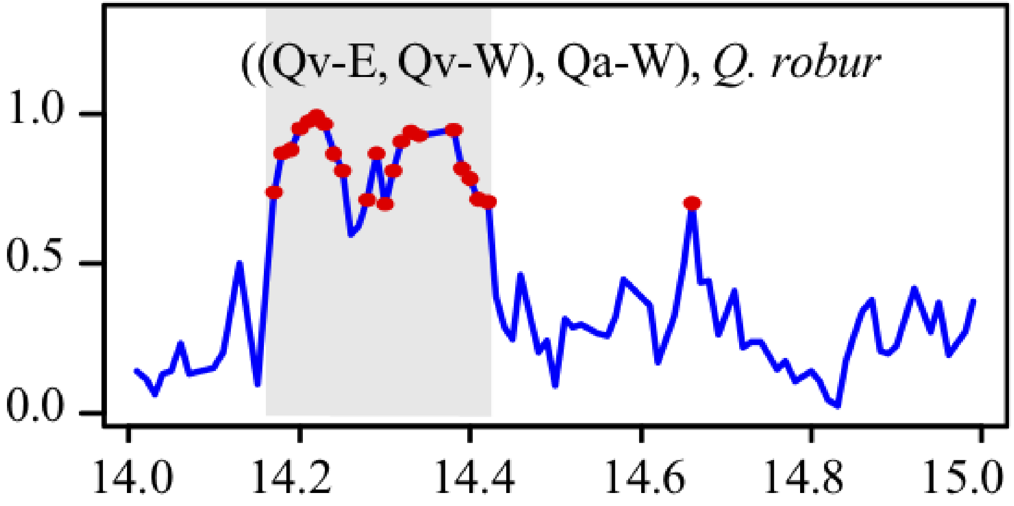
Signals of introgression in *Chr9-ERF* region

Allele dosage of *Q. variabilis* (West)



Ancestry of Qv-W haplotypes was from Qa-W haplotypes

Testing gene flow between species



Qa-W and Qv-W haplotype had an excess of shared derived variants

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Conclusion 2

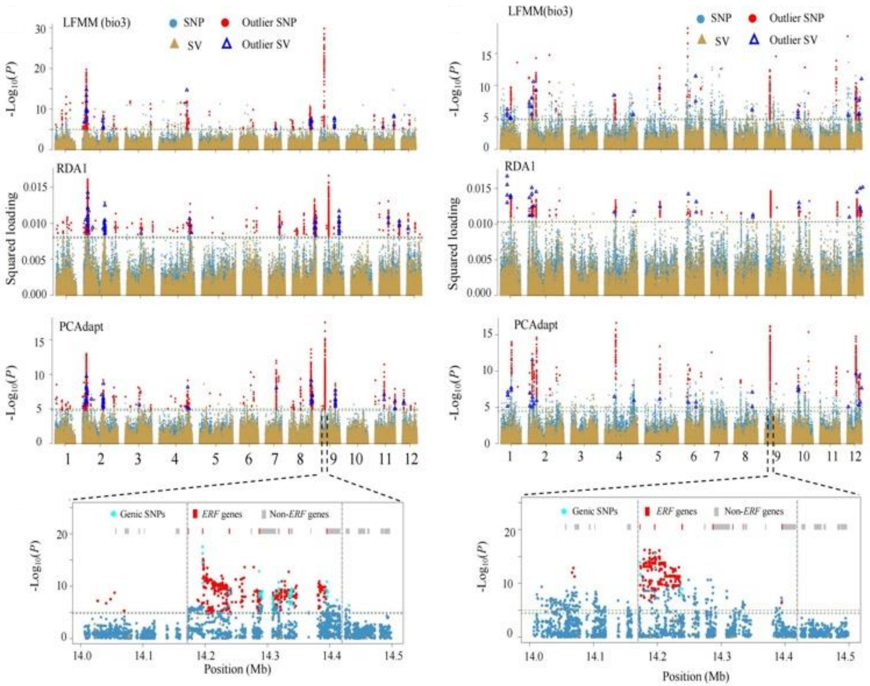
Society for Molecular Biology & Evolution

Pan-genome analysis reveals local adaptation to climate driven by introgression in oak species

Yi-Ye Liang , Hui Liu , Qiong-Qiong Lin , Yong Shi , Biao-Feng Zhou , Jing-Shu Wang , Xue-Yan Chen , Zhao Shen , Liang-Jing Qiao , Jing-Wei Niu , Shao-Jun Ling , Wen-Ji Luo , Wei Zhao , Jian-Feng Liu , Yuan-Wen Kuang , Pär K Ingvarsson , Ya-Long Guo , Baosheng Wang ✉

Author Notes

Molecular Biology and Evolution, msaf088, https://doi.org/10.1093/molbev/msaf088



Main contributor:
Dr. Yi-Ye Liang

- **SNPs and SVs contributed to local adpatation**
- **A Chr9-ERF region show parallel signal of selection in both *Q. variabilis* and *Q. acutissima***
- **Beneficial alleles in this region originated through introgression between these two species.**

Liang et al. *Mol Biol Evol* 2025

Acknowledgement

Prof. Paul Manos
(Duke Univ., USA)

Prof. P. Ingvarsson
(SLU, Sweden)

国家自然科学基金委员会 NSFC

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