



Insights into the evolution and fruit color change related genes of chromosome doubled sweet cherry from an updated complete T2T genome assembly

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² Cherry Engineering and Technical Research Center of the State Forestry and Grassland Administration

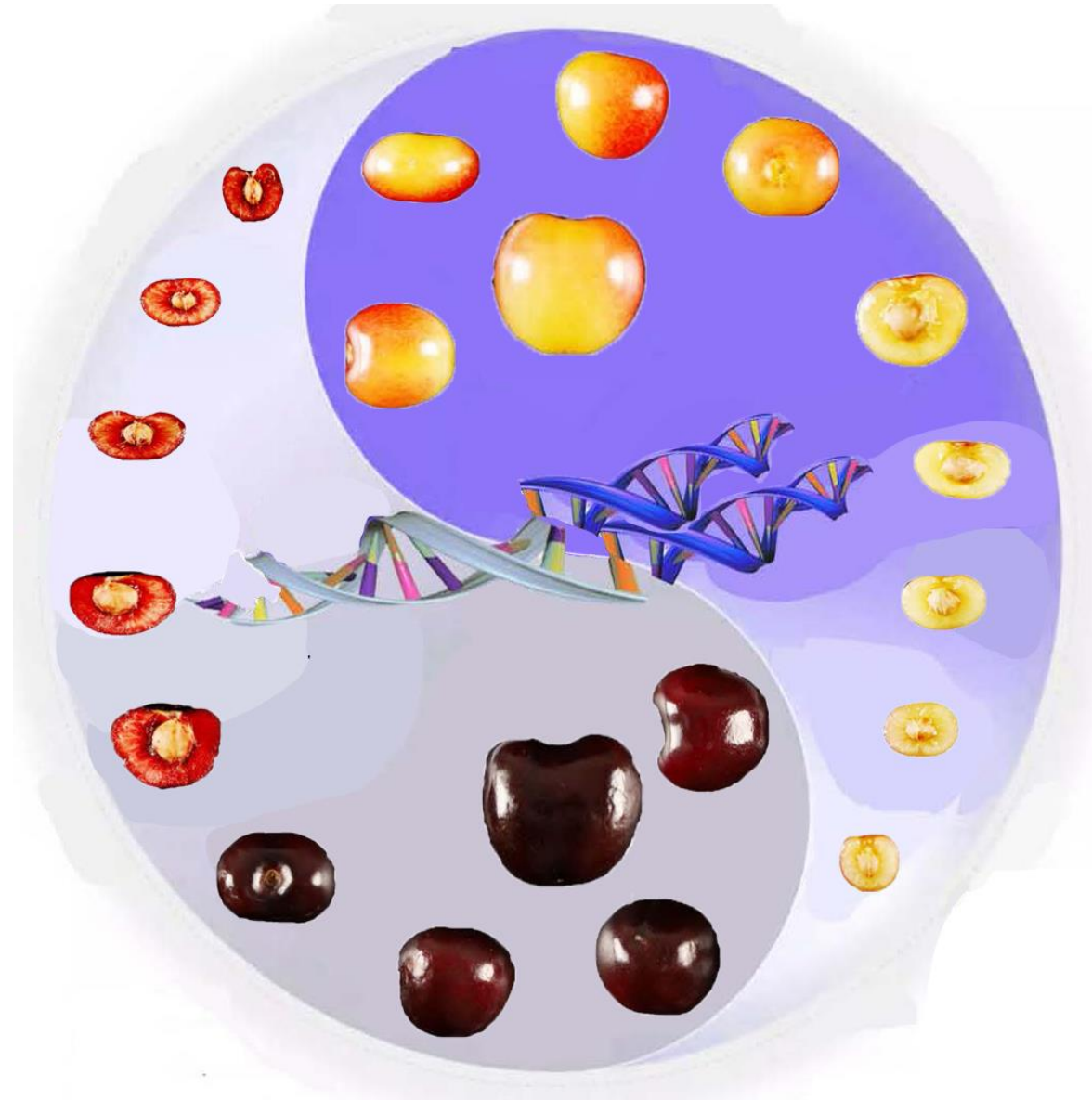
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Introduction

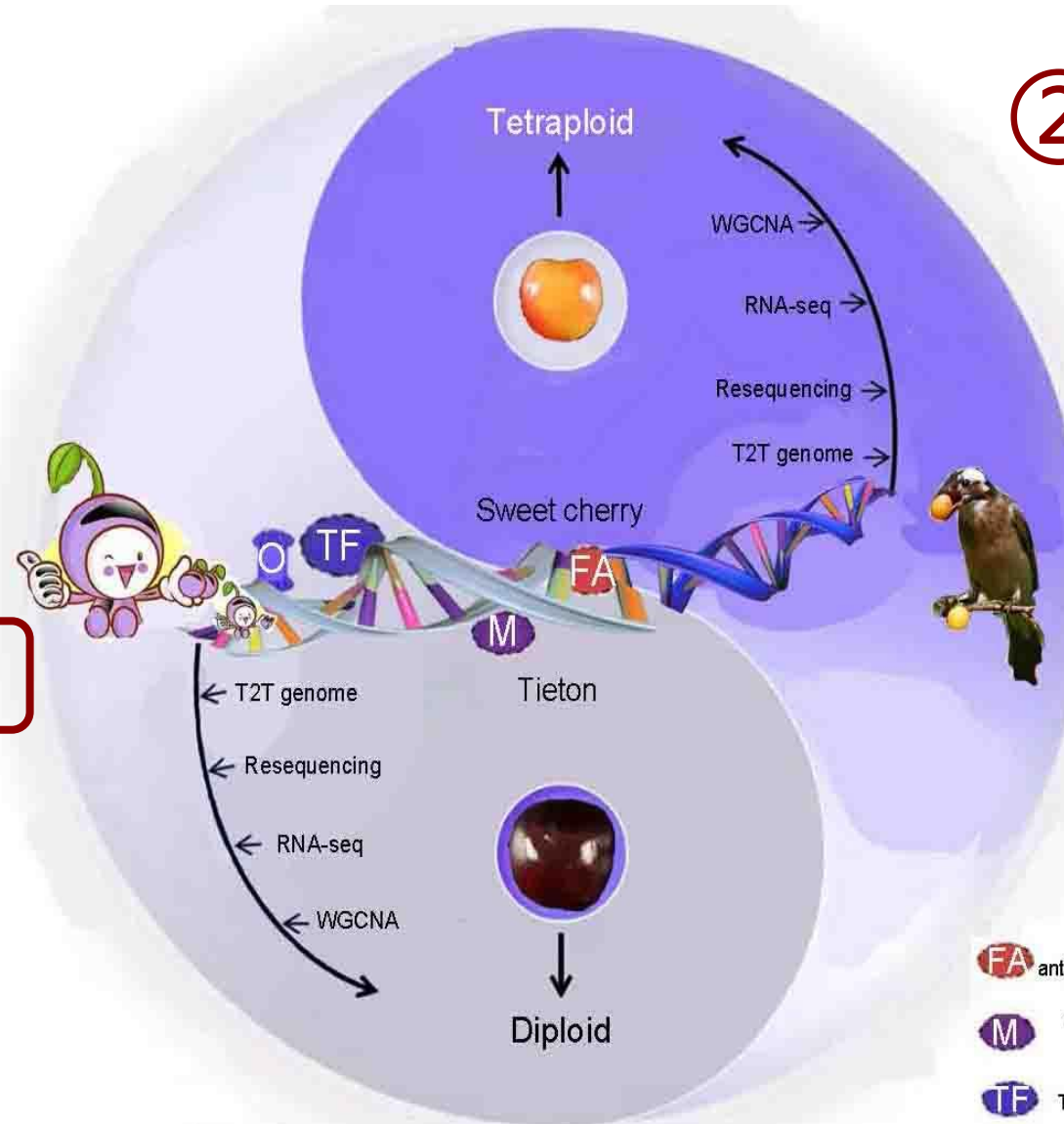




Highlights

1

Complete T2T genome assembly of sweet cherry;



2

Chromosome doubled sweet cherry;

3

Mutations that affecting fruit color related genes.

- FA** Flavonoids and anthocyanin related genes
- M** Mutations affecting functional genes
- TF** Transcription factors
- O** Mutations affecting TFs

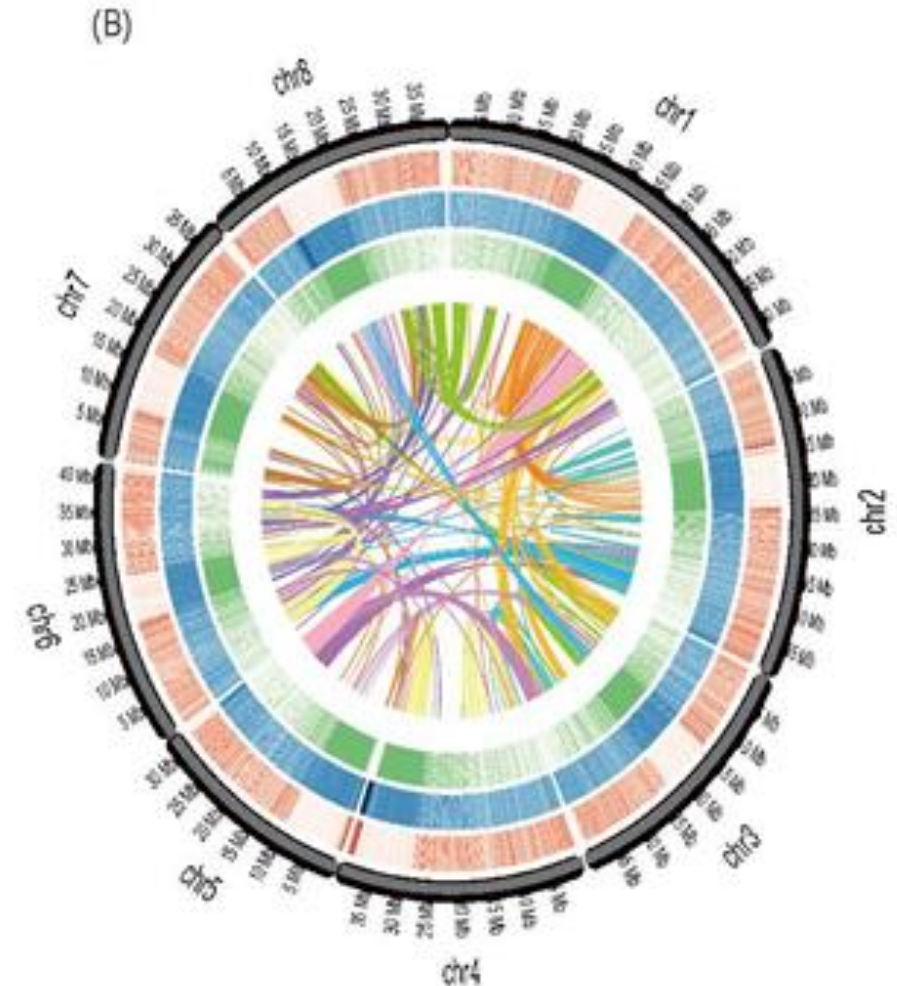


Genome assembly and annotation

This study assembled the complete genome of Tieton. The assembly, annotation, and application metrics have all significantly improved.

(A)

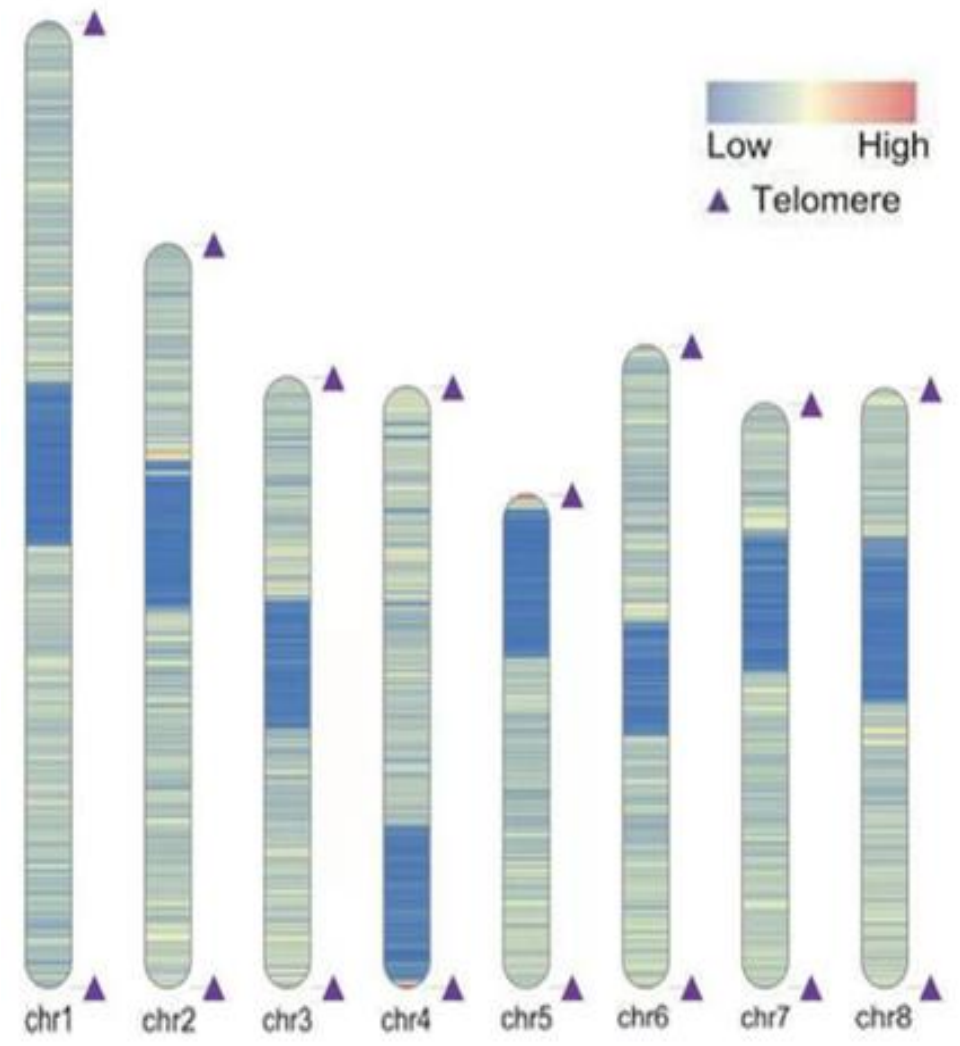
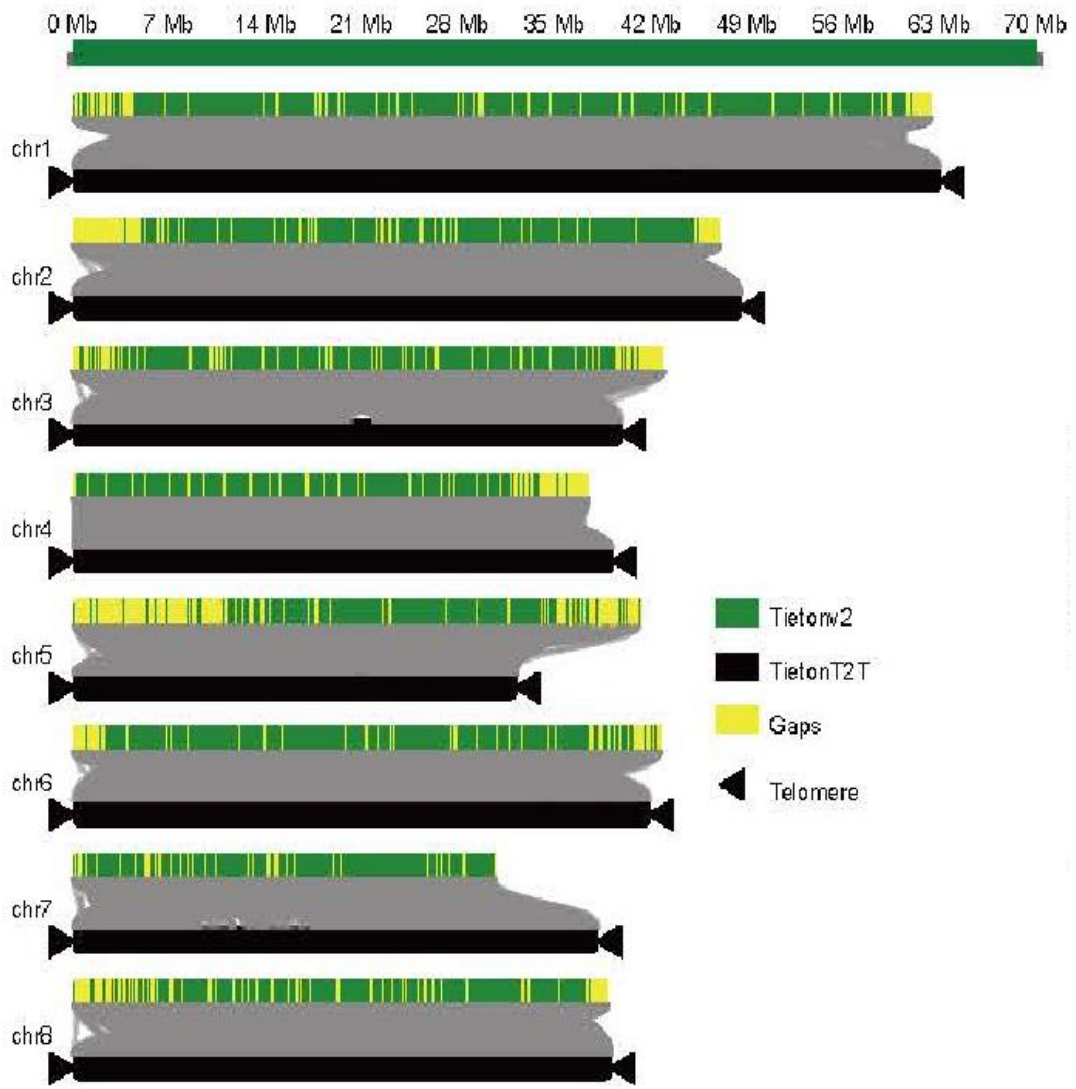
	Indexes	Tieton (v2.0)	Tieton (T2T)
Genome	Total sequence length (bp)	342,881,614	341,620,392
	GC content (%)	38.43%	38.62%
	Repeat content (%)	59.38%	59.29%
	Cortig N50	3,247,195	39,808,788
	Cortigs number	610	8
	BUSCOs (%)	97.20%	98.4%
Annotation	LTR assembly index (LAI)	15.60	25.45
	Gene_number	39,984	58,204
	Total_CDS_length (bp)	41,779,462	88,964,838
	CDS_Number	173,294	366,035
Application	BUSCOs (%)	93.50%	98.4%
	RNAseq mapped rate (%)	95.65%	96.23%
	RNAseq unique mapped rate (%)	87.83%	90.55%
	RNAseq multi mapped rate (%)	7.81%	5.68%
	DEGs found	2,841	3,046
	Resequencing mapped rate (%)	88.64%	97.31%
	Resequencing mapped coverage (%)	99.98%	99.99%
	SNPs call rate	98.50%	98.92%
	INDELs call rate	92.28%	94.50%
	SVs call rate	95.98%	96.09%
	SNPs found	1,143,107	1,121,762
INDELs found	305,891	250,919	
SVs found	6,436	6,948	





Genome assembly and annotation

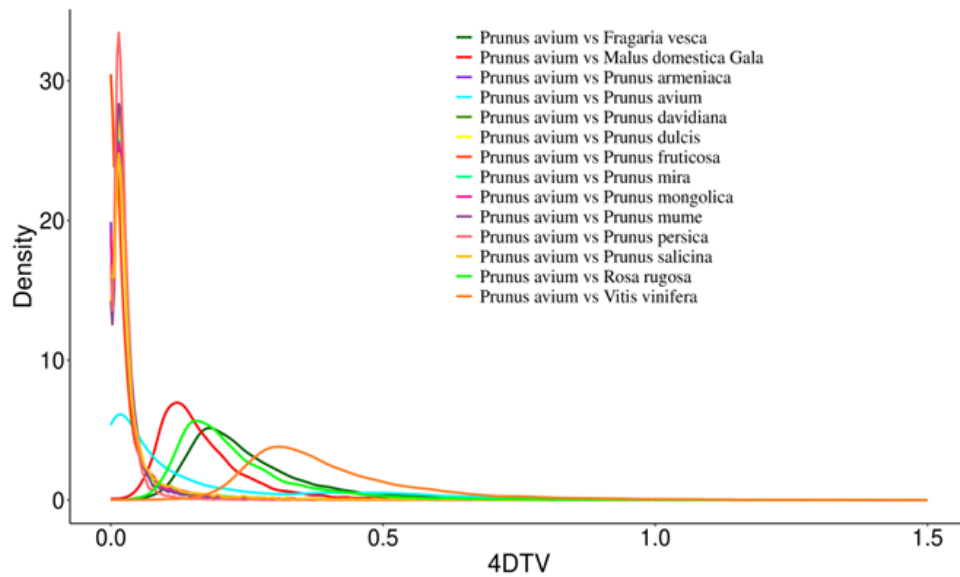
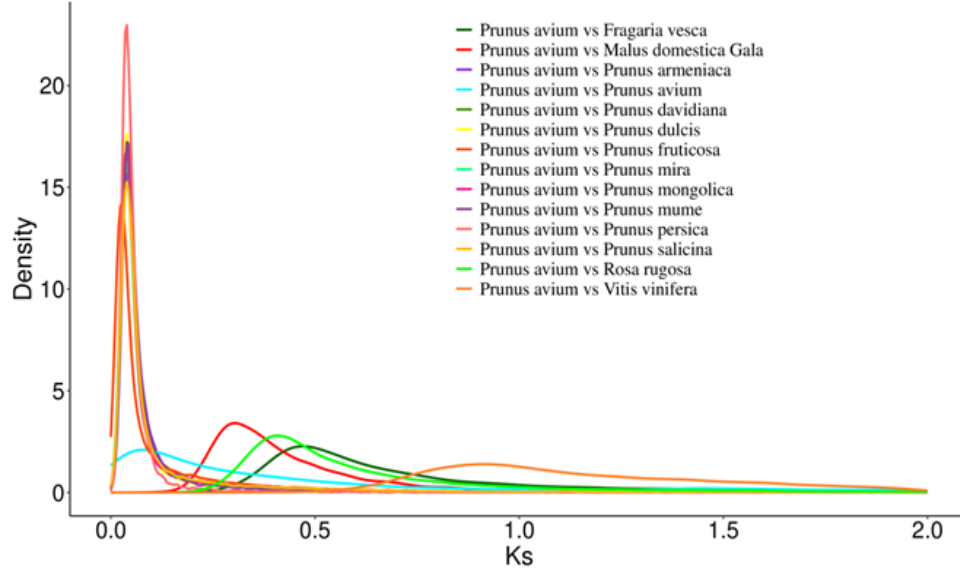
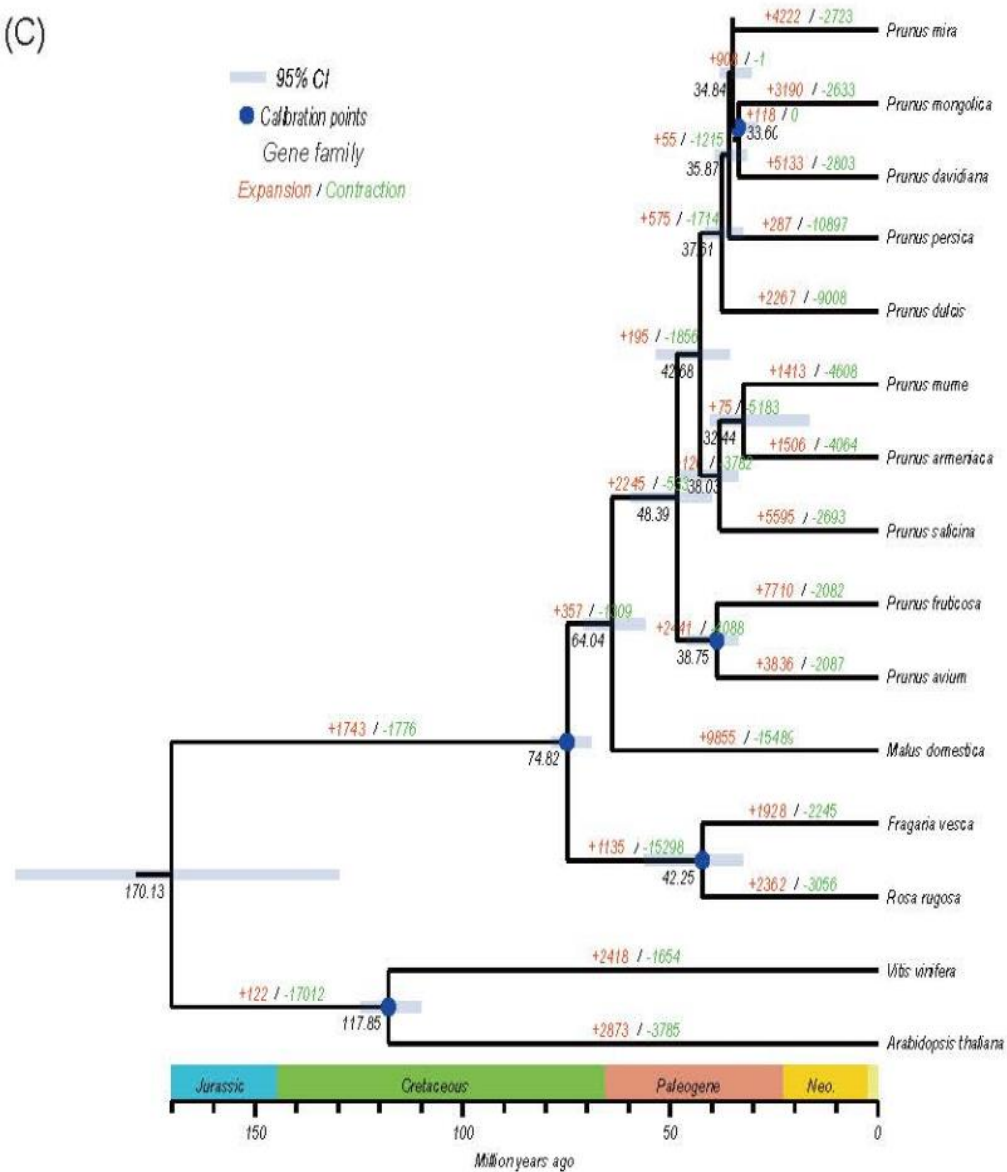
Complete T2T genome testing of Tieton: gap, centromere, and telomere.





Comparative genomic analysis

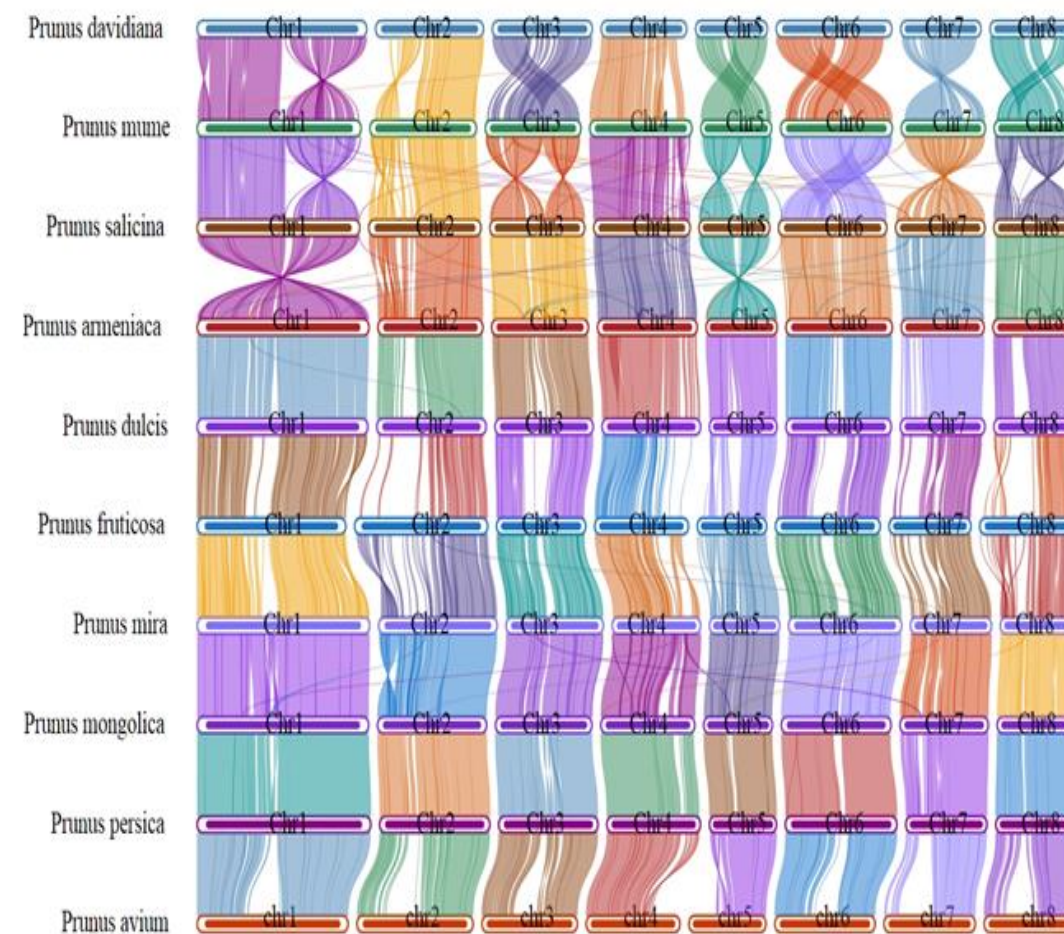
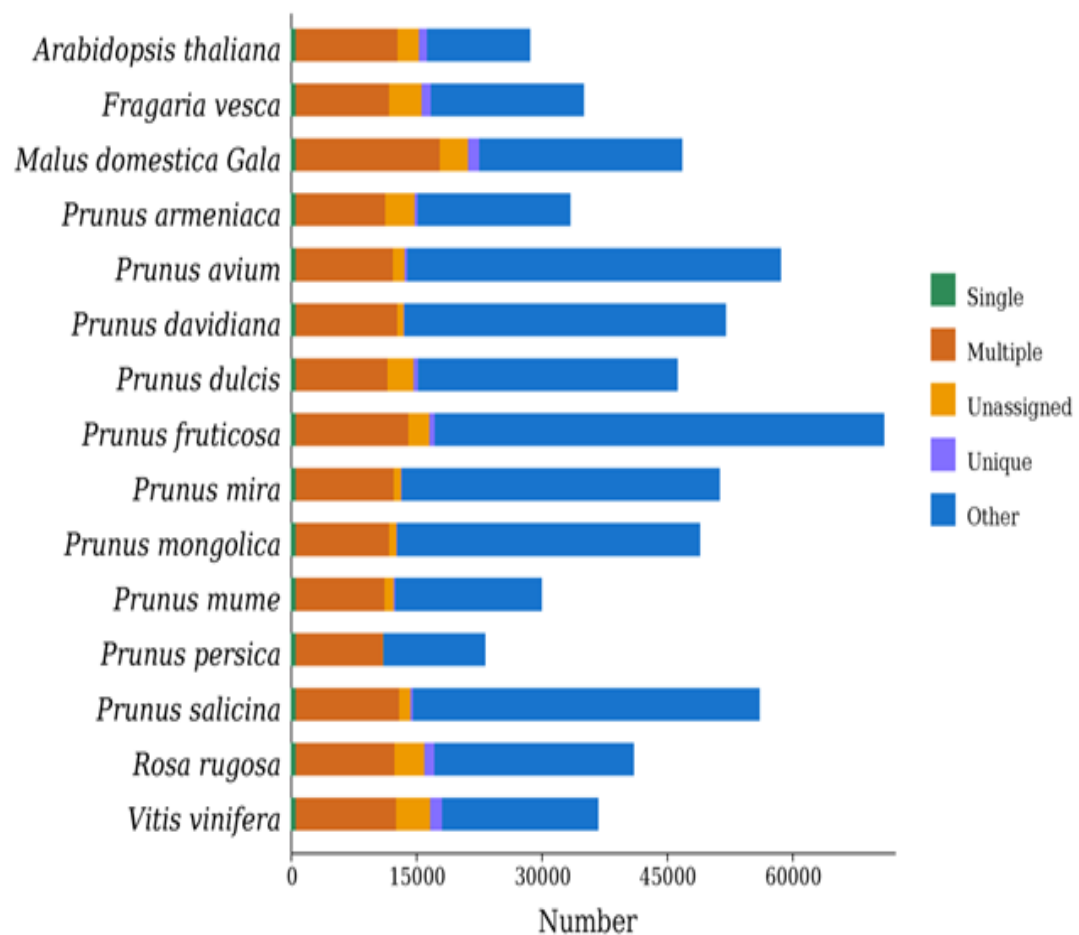
(C)



Analysis of evolutionary relationship and WGD events



Comparative genomics analysis



Gene family analysis and collinearity analysis



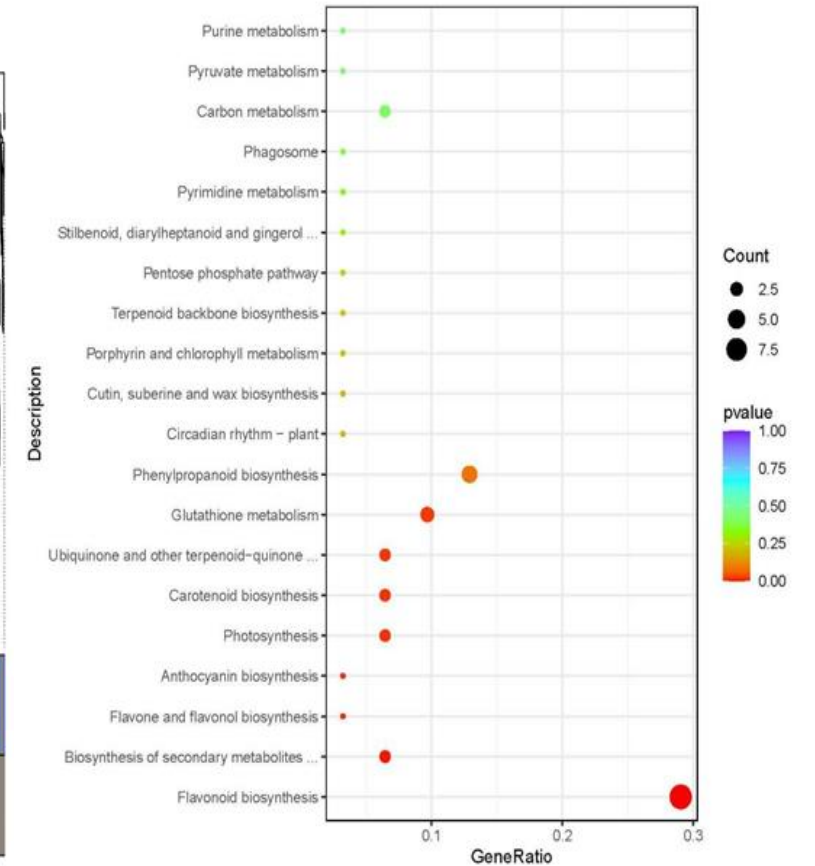
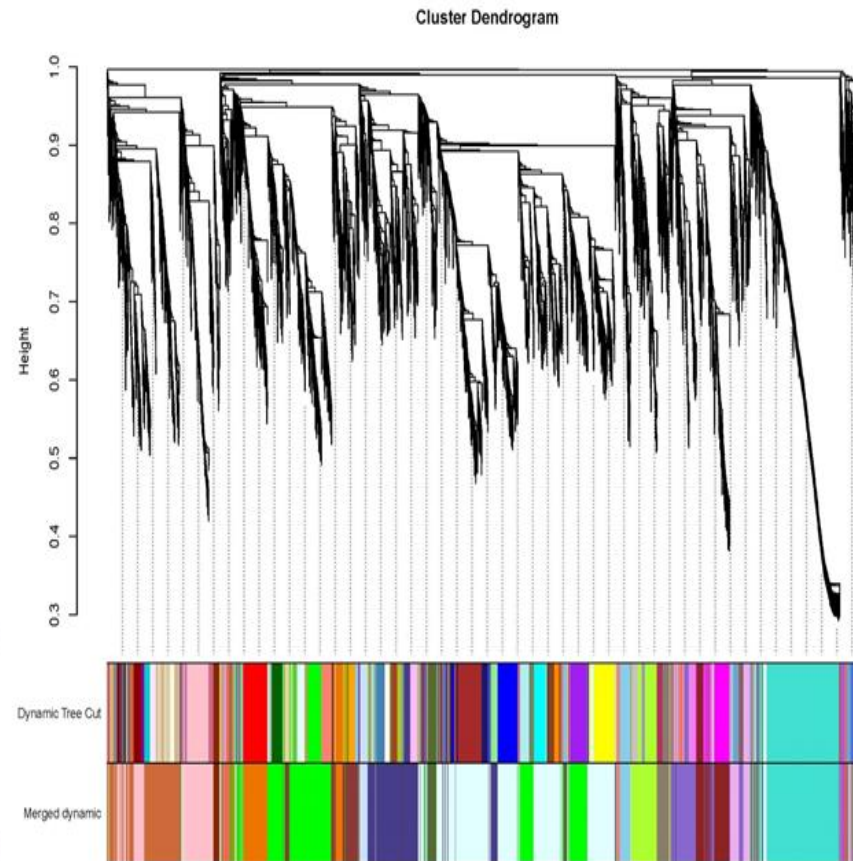
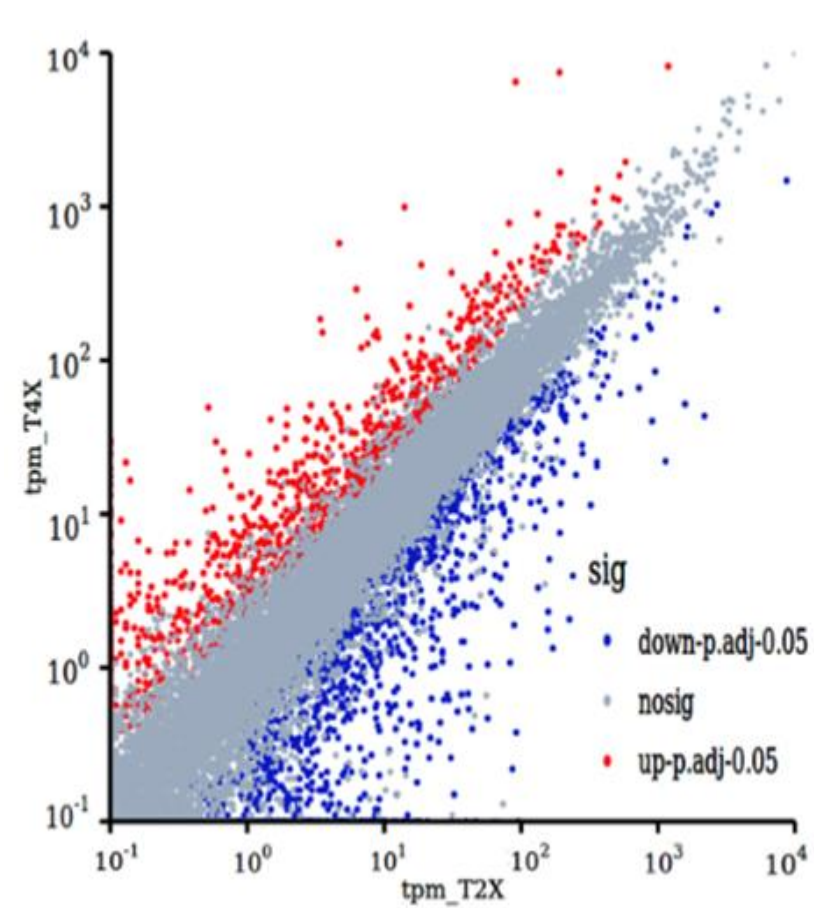
Chromosome doubling



Sweet cherry fruits of Tieton (before and after doubling)



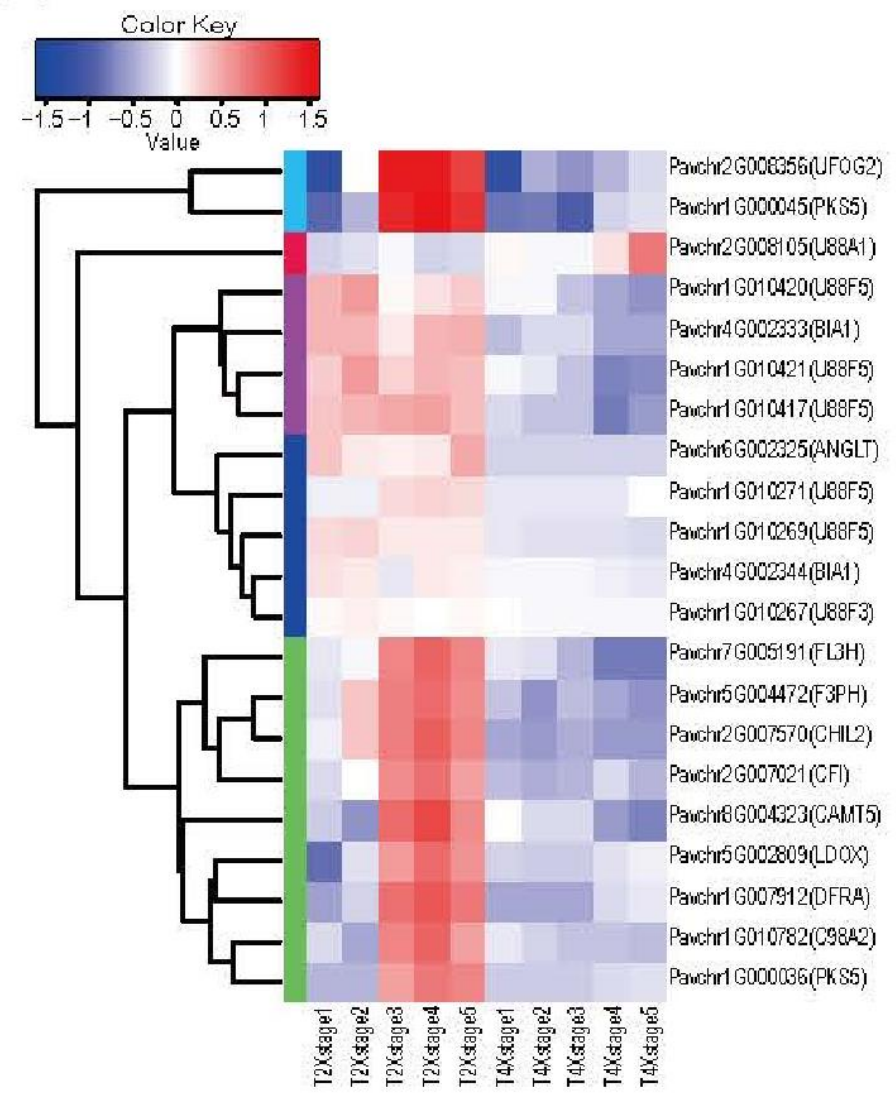
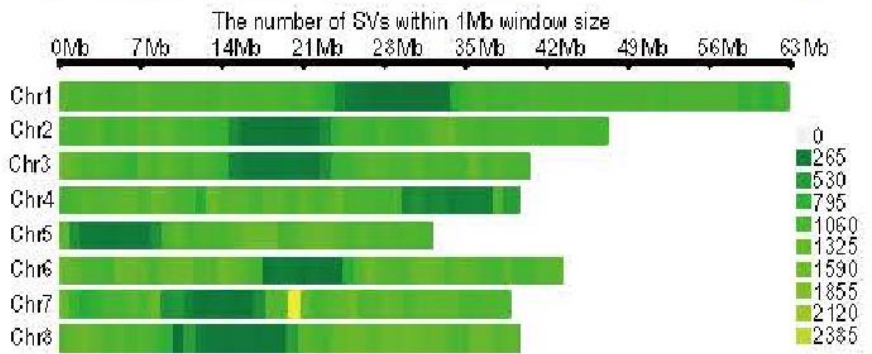
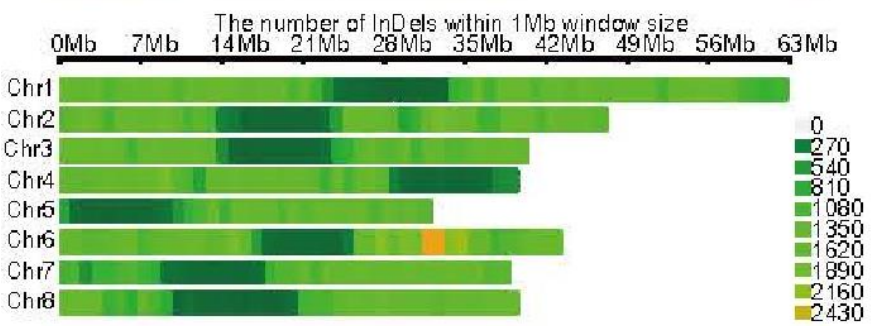
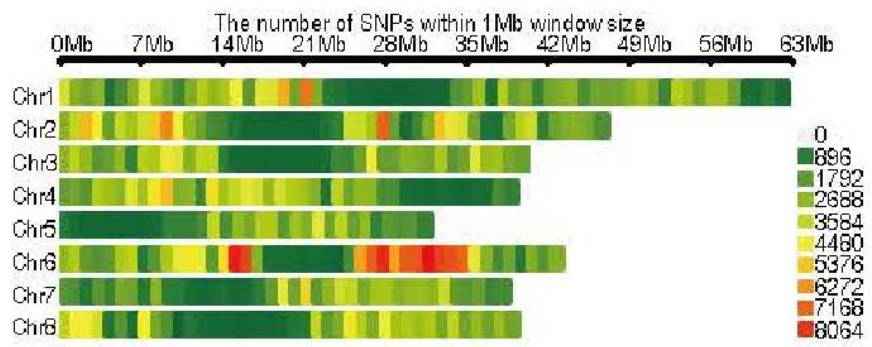
Transcriptome and mutation analysis



Transcriptome and WGCNA analysis



Transcriptome and mutation analysis





Summary

- ❑ In this study, we assembled a complete genome of the main sweet cherry variety Tieton - the T2T genome;
- ❑ Comparative genomics and evolutionary studies were conducted on sweet cherries represented by newly assembled genomes in the *Rosaceae* family;
- ❑ Based on the above data and research, multiple omics analyses were conducted on candidate genes and mutations for fruit color changes in Tieton tetraploid after chromosome doubling;
- ❑ Data and method acquisition:
<https://db.cngb.org/search/project/CNP0004619/>
<http://www.imeta.science/imetaomics/>

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Team Introduction



Kaichun Zhang Professor

- The chairperson of ISHS Working Group Cherry Production
- The president of China Society for Horticultural Science, Cherry Section

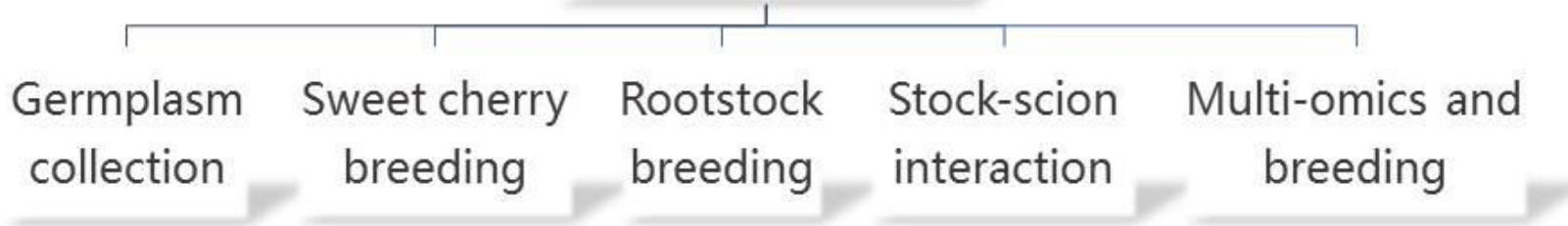


Xuwei Duan

Associate Professor

The leader of cherry group

Research area



Guohua Yan



Xiaoming Zhang



Yu Zhou



Jing Wang



Chuanbao Wu



Xin Zhang

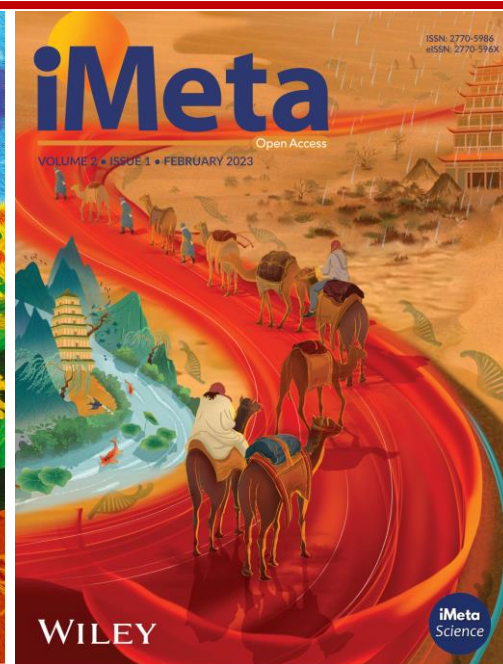
Associate Professor

Assistant Professor

Post Doctor

iMeta: Integrated meta-omics to change the understanding of the biology and environment


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