



# 甜樱桃T2T基因组及多组学方法揭示其进化和加倍后果色变化的候选基因

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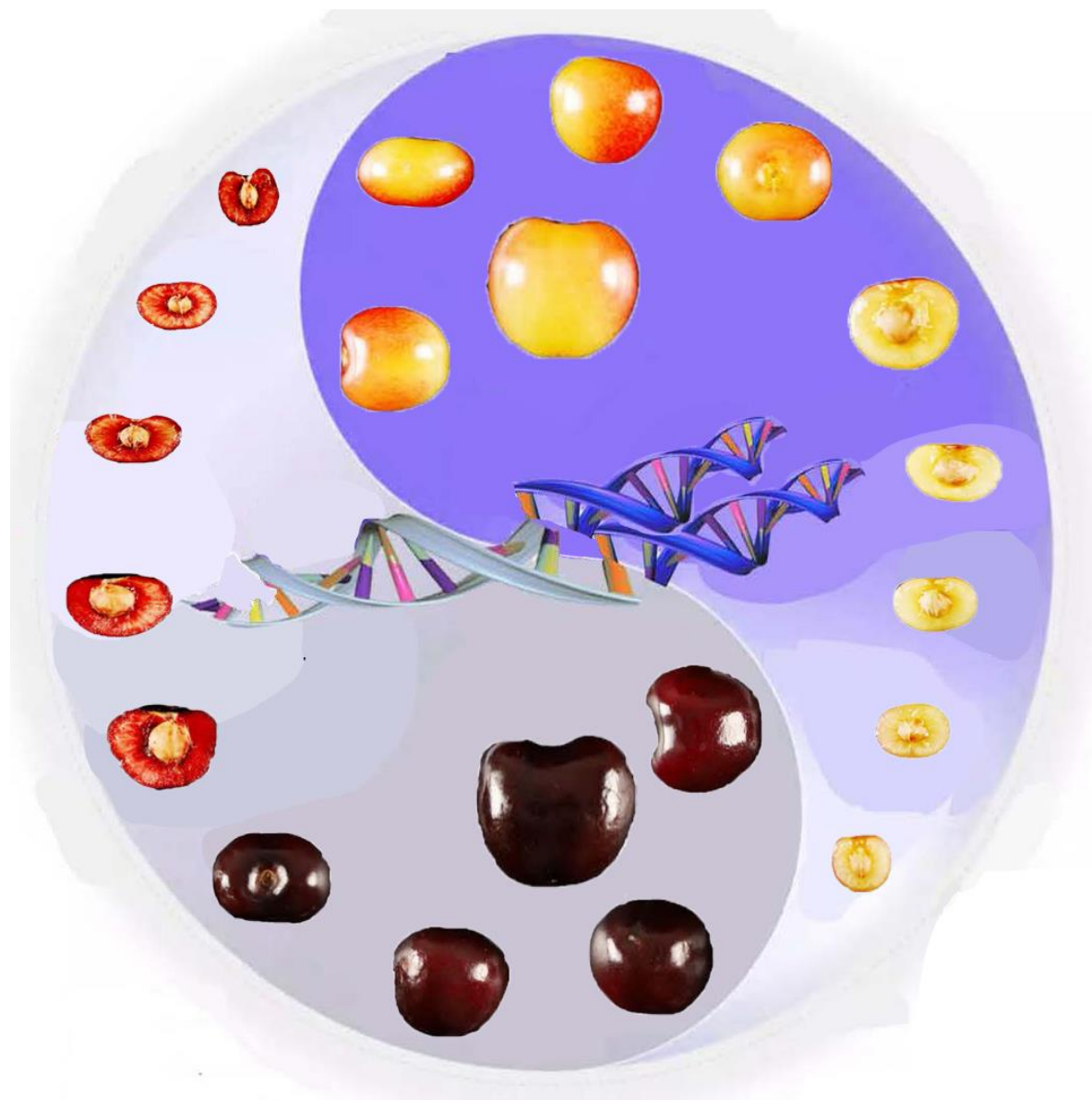
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Xin Zhang, Xuwei Duan, Jing Wang, Xiaoming Zhang, Guohua Yan, Chuanbao Wu, Yu Zhou, Kaichun Zhang. 2024. Insights into the evolution and fruit color change-related genes of chromosome doubled sweet cherry from an updated complete T2T genome assembly. *iMetaOmics* 1: e13. <https://doi.org/10.1002/imo2.13>



# 简介

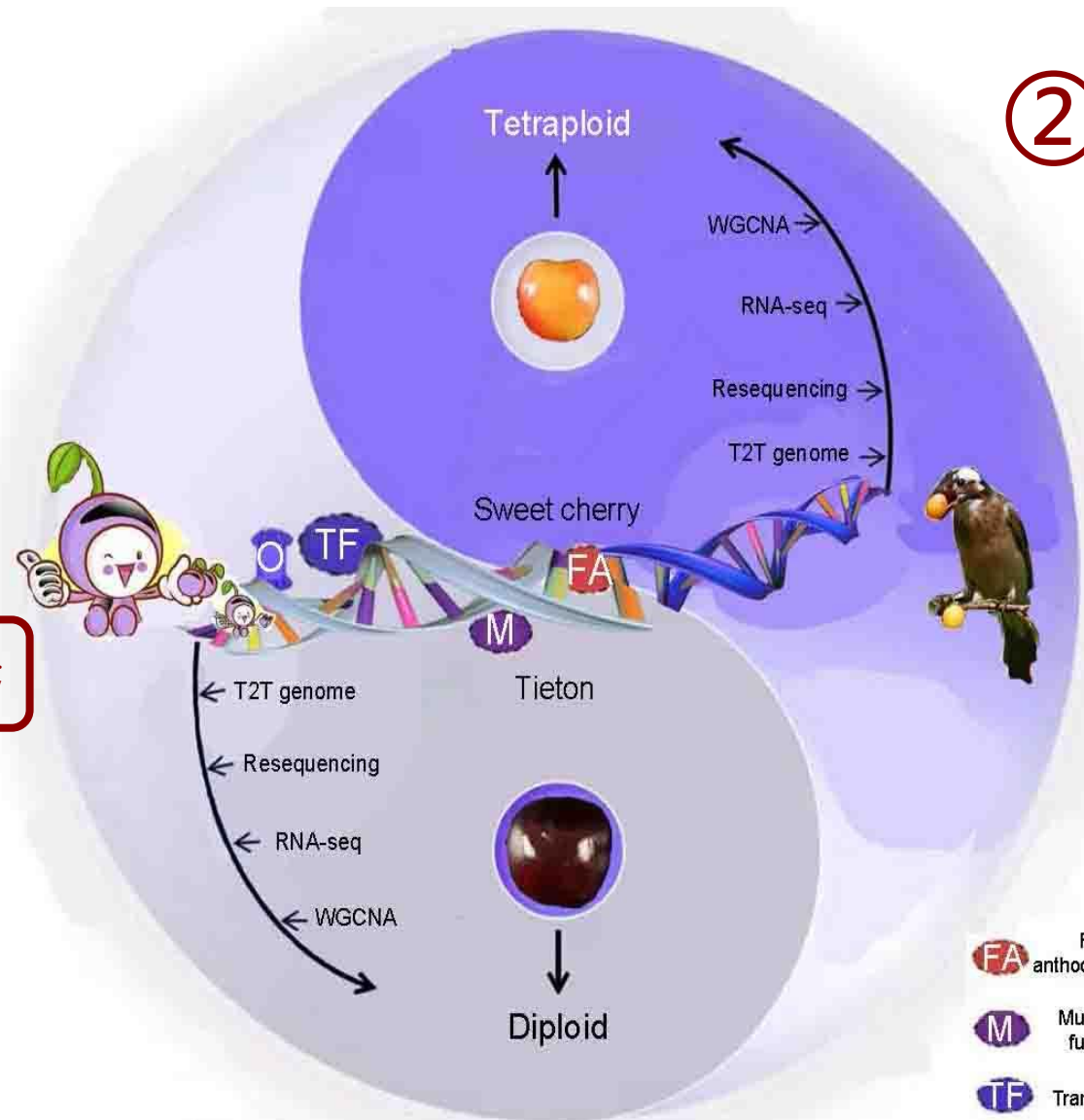




# 亮点

1

甜樱桃的完整T2T基因组组装;



2

甜樱桃的染色体加倍;

3

影响甜樱桃多倍体果色基因及突变的多组学挖掘。

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

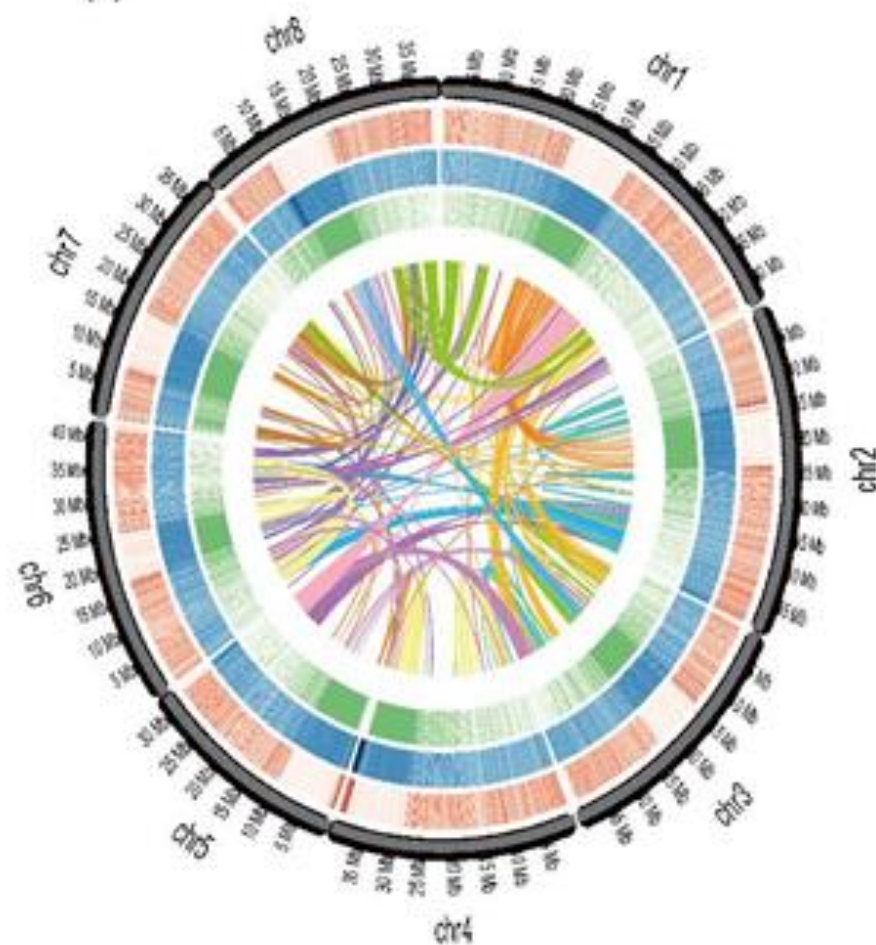
# 基因组组装和注释

本研究组装了美早完整的基因组。组装、注释及应用指标均有明显提高。

(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%
	LTR assembly index (LAI)	15.60	25.45
Annotation	Gene_number	39,984	58,204
	Total_CDS_length (bp)	41,779,462	88,964,838
	CDS_Number	173,294	366,035
	BUSCOs (%)	93.50%	98.4%
Application	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	

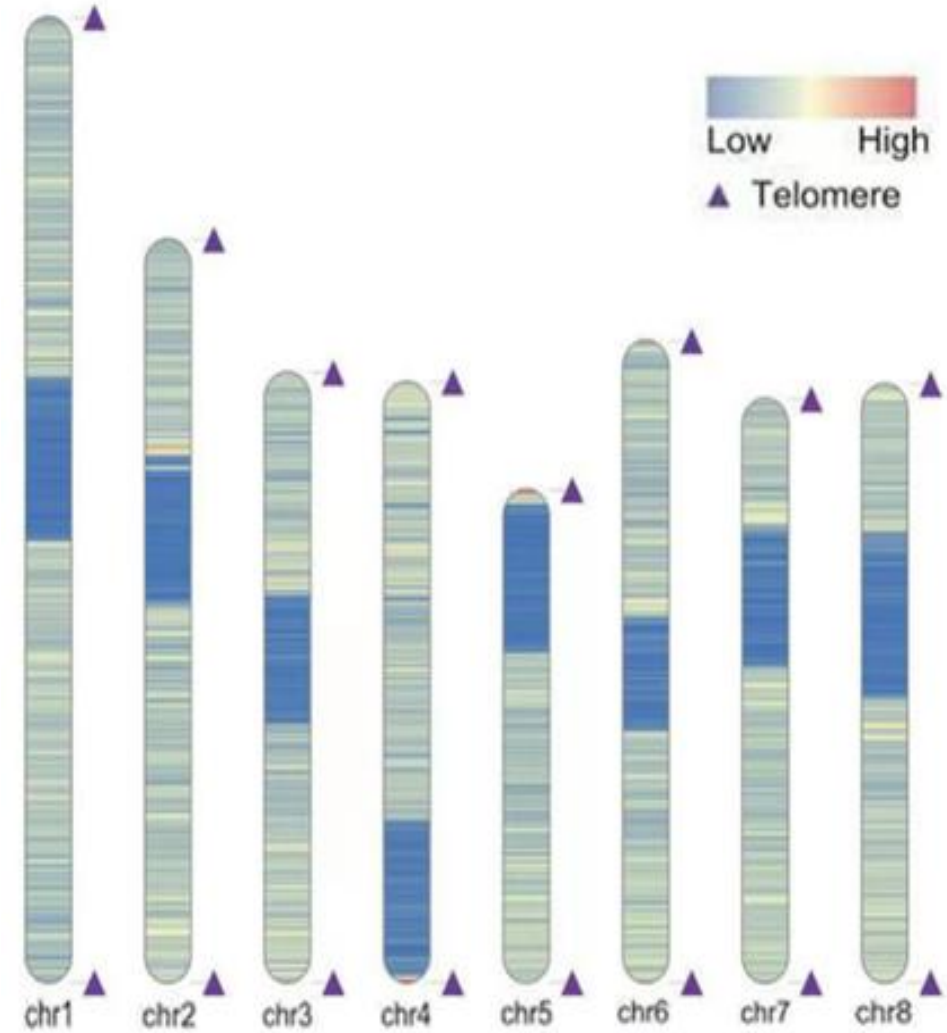
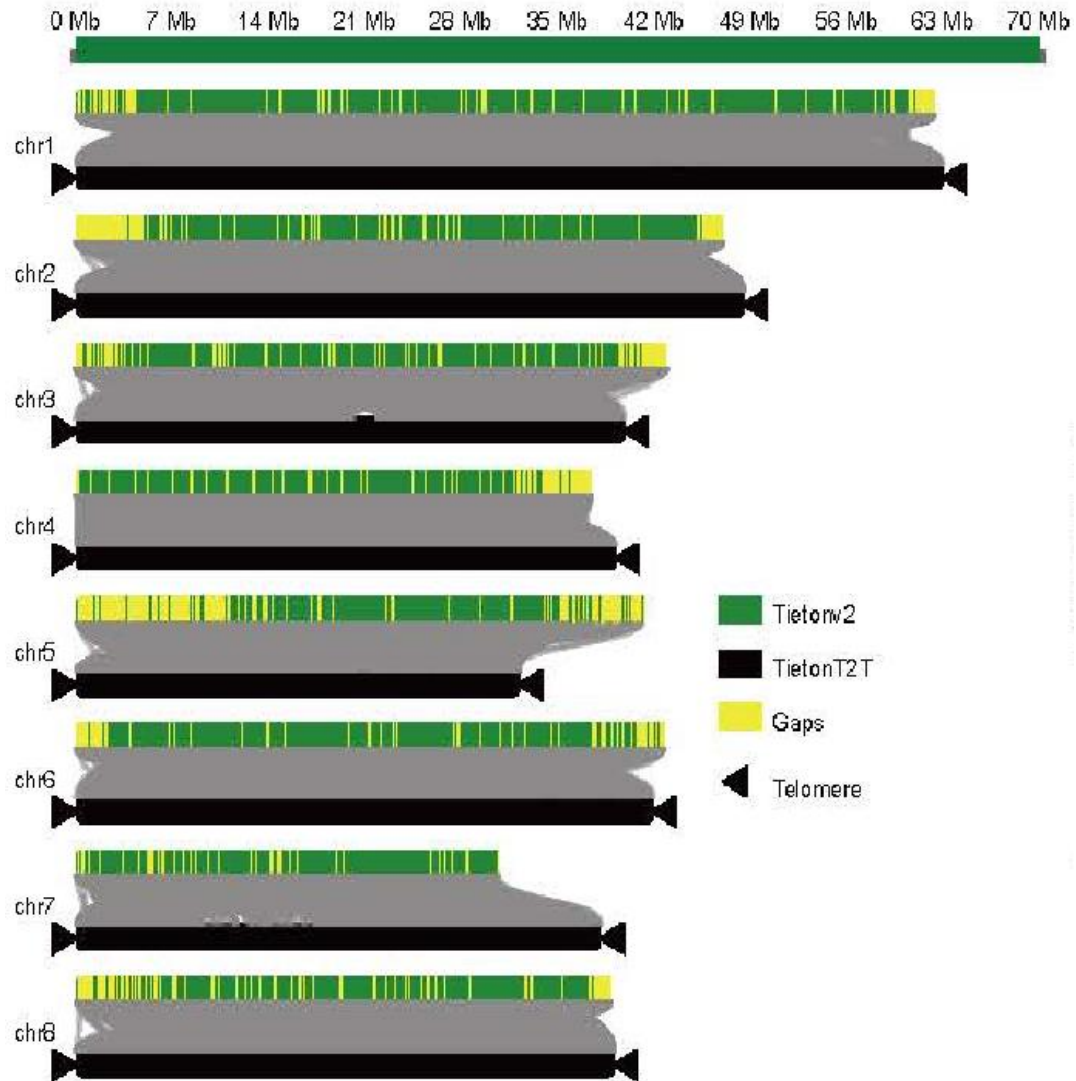
(B)





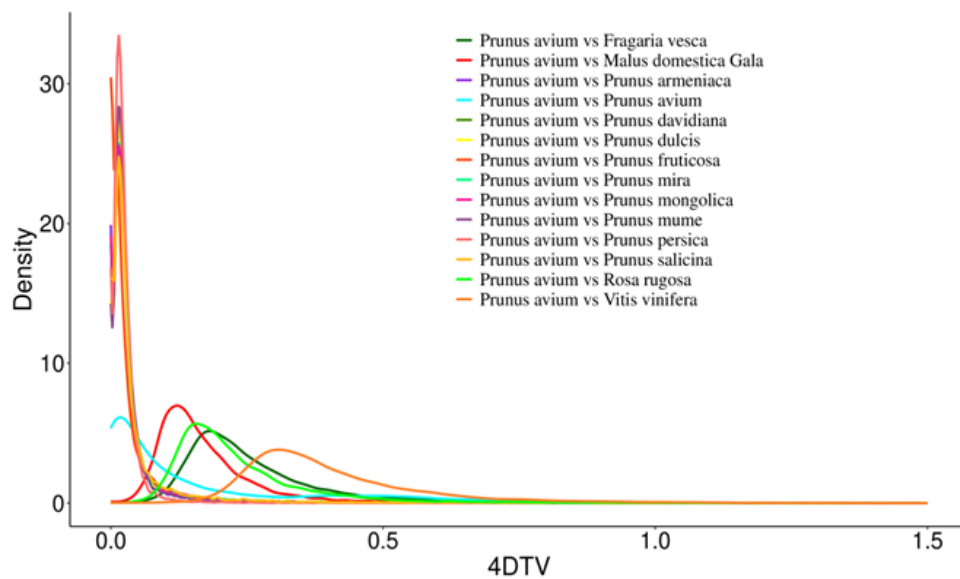
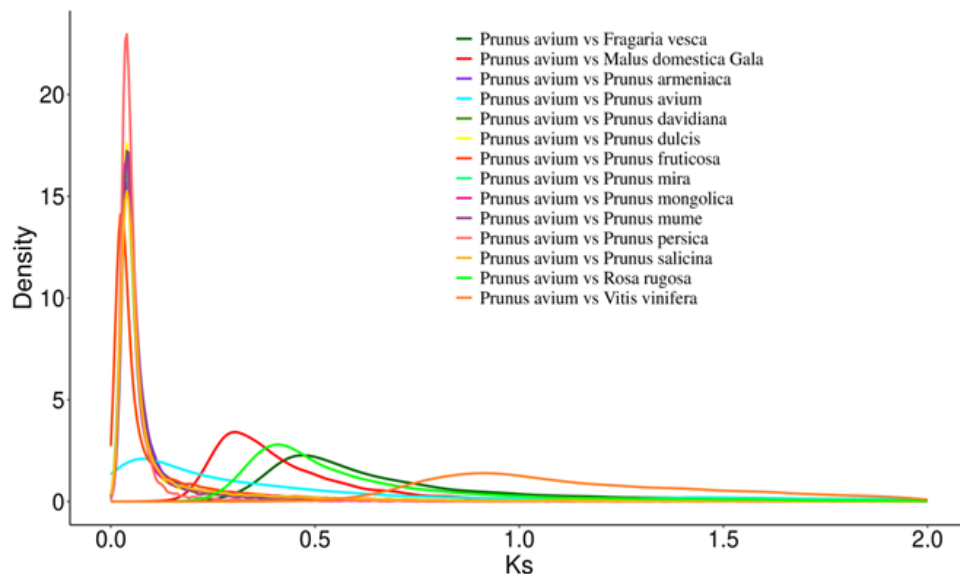
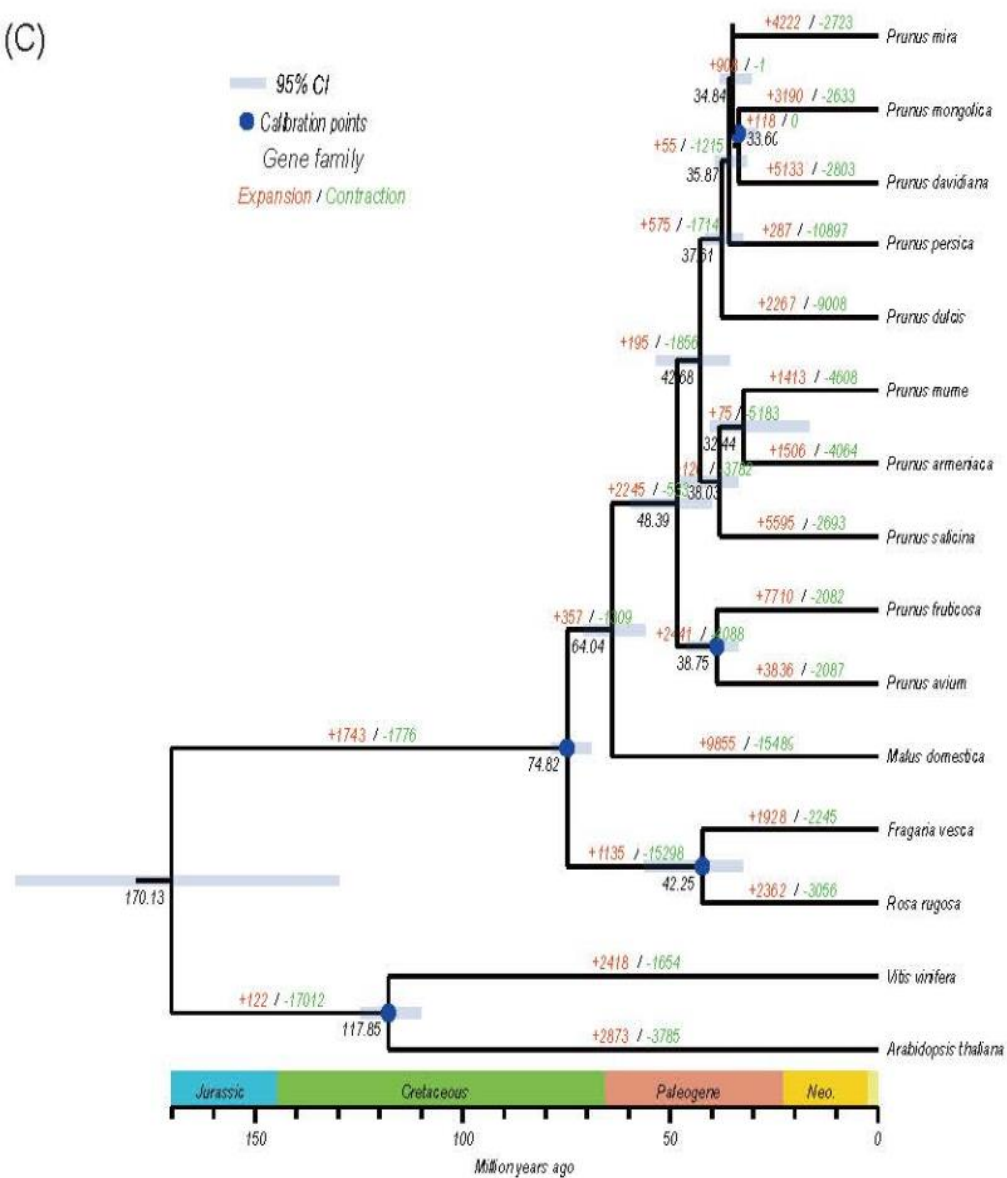
# 基因组组装和注释

美早完整的T2T基因组检测：缺口，着丝粒和端粒。



# 比较基因组分析

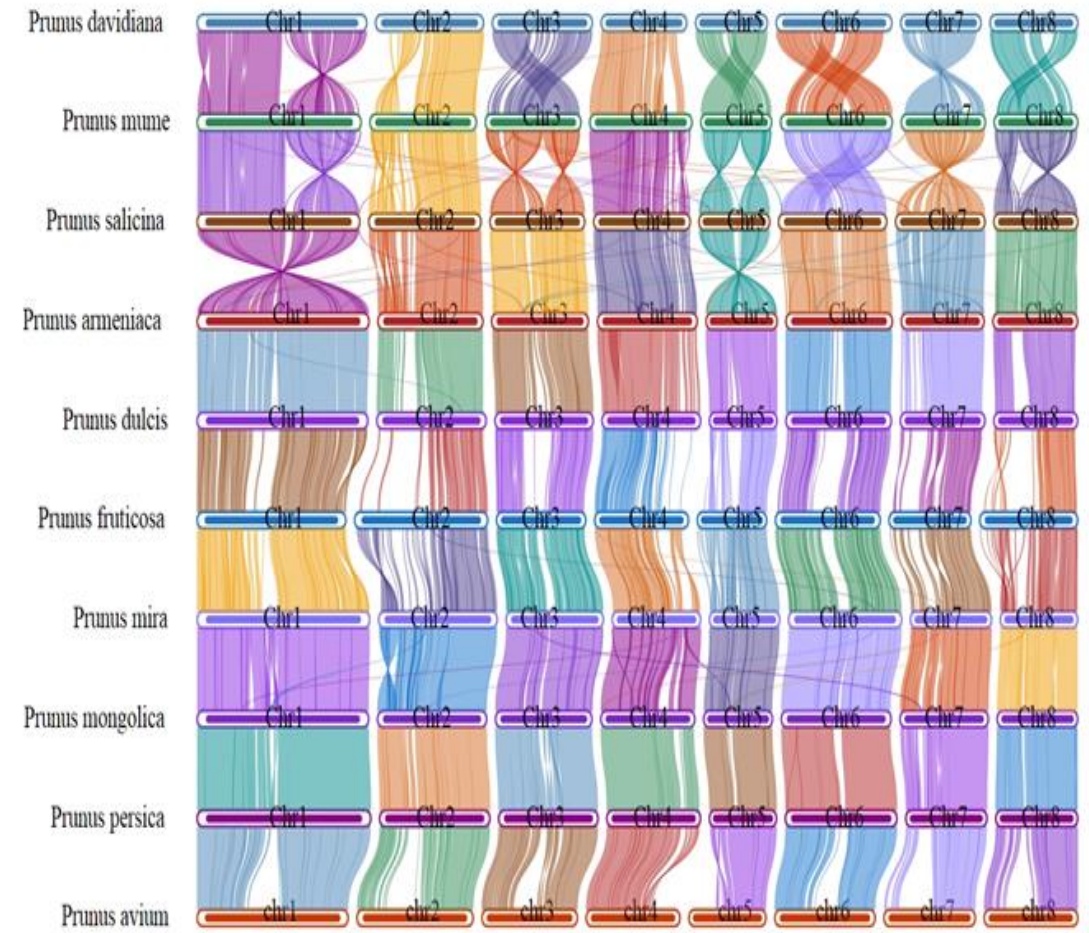
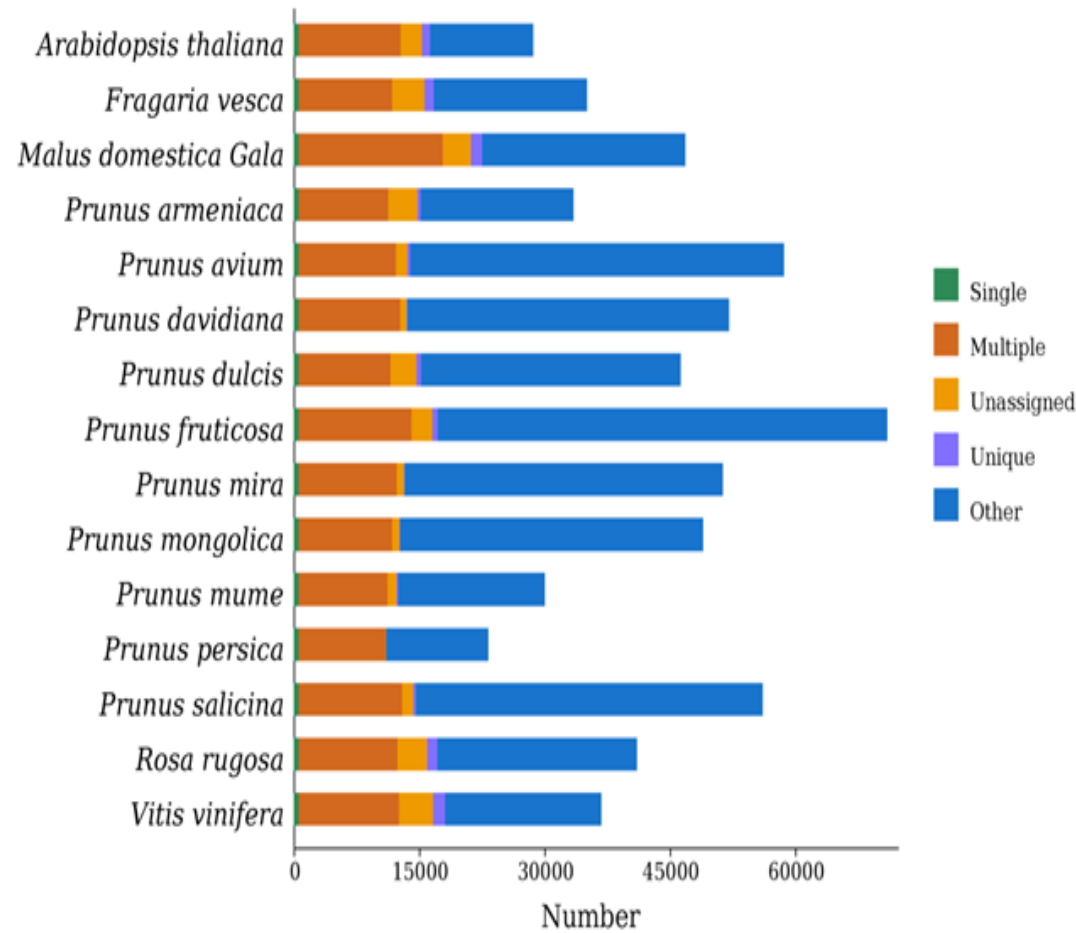
(C)



进化关系和全基因组加倍事件分析



# 比较基因组分析



基因家族分析及共线性分析



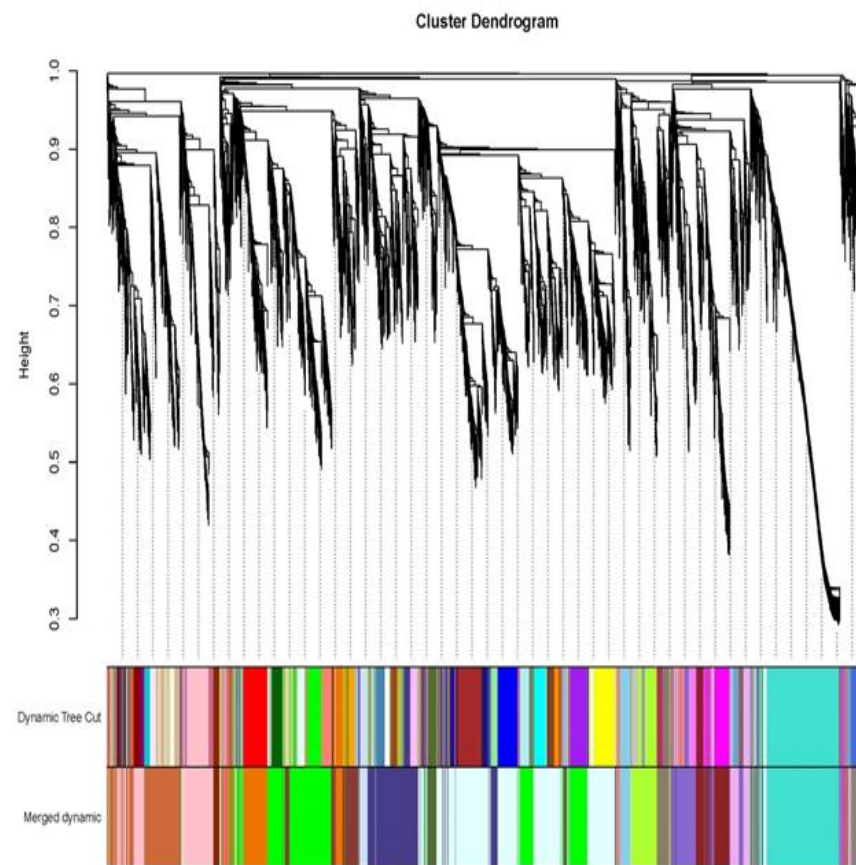
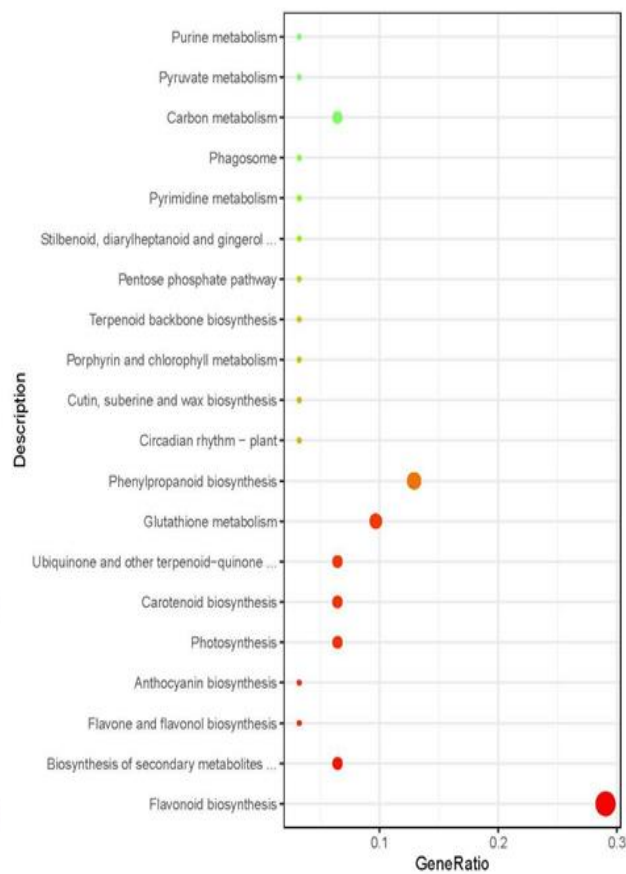
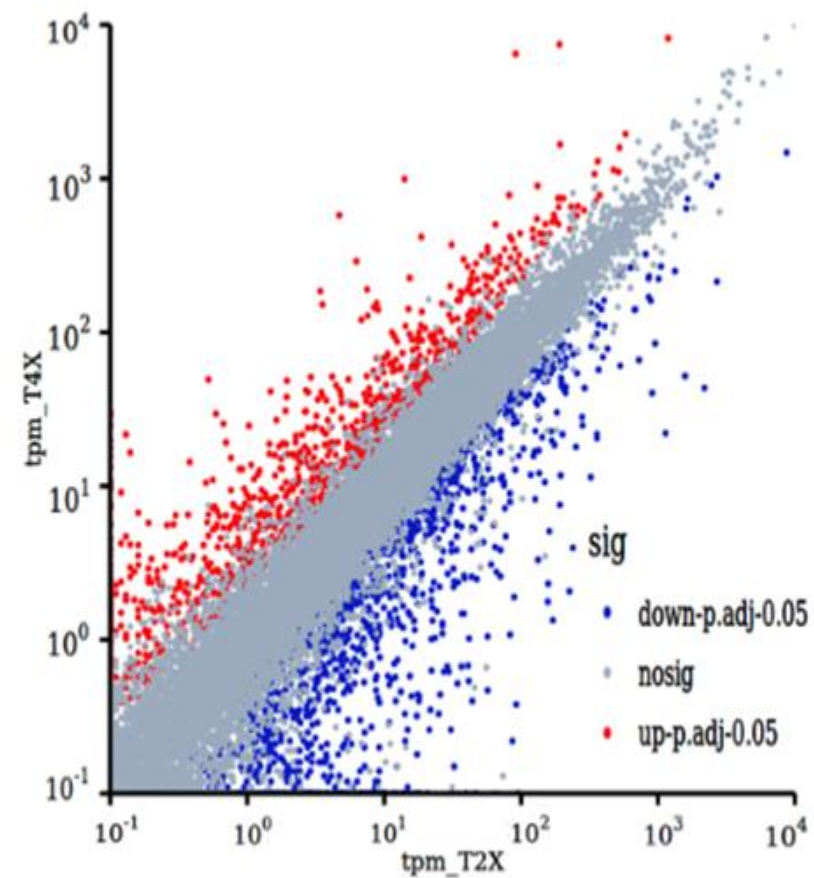
# 染色体加倍



甜樱桃美早加倍前后的果实



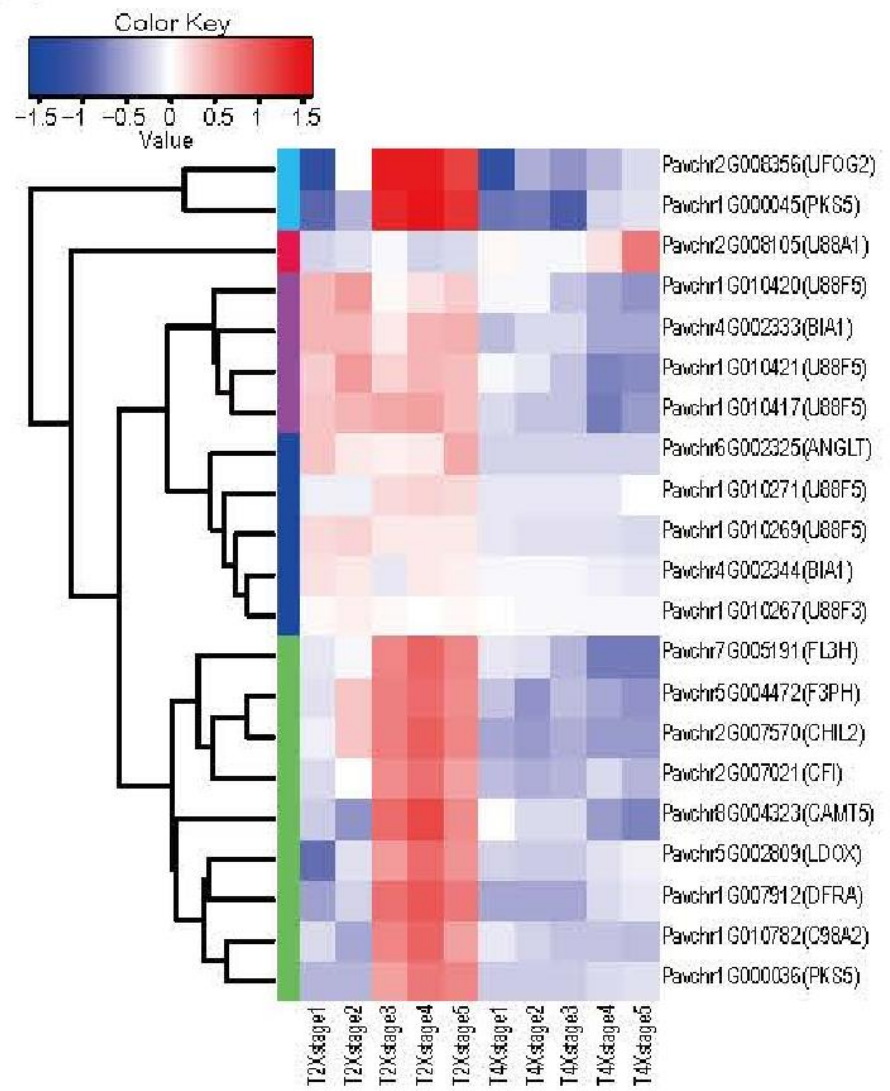
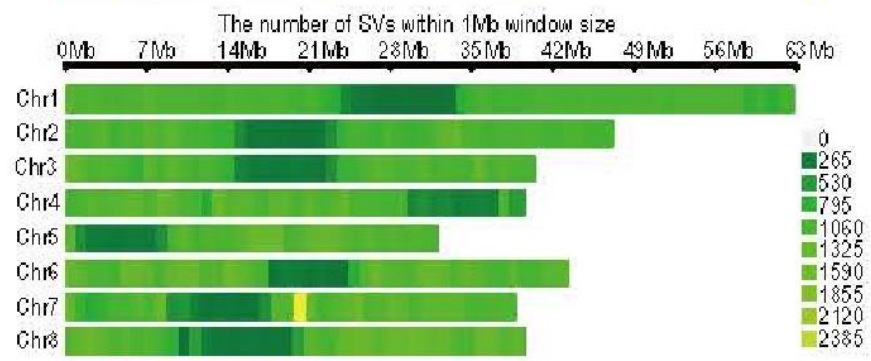
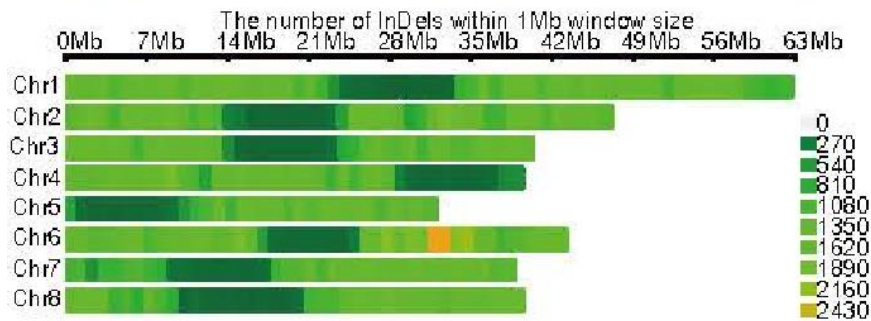
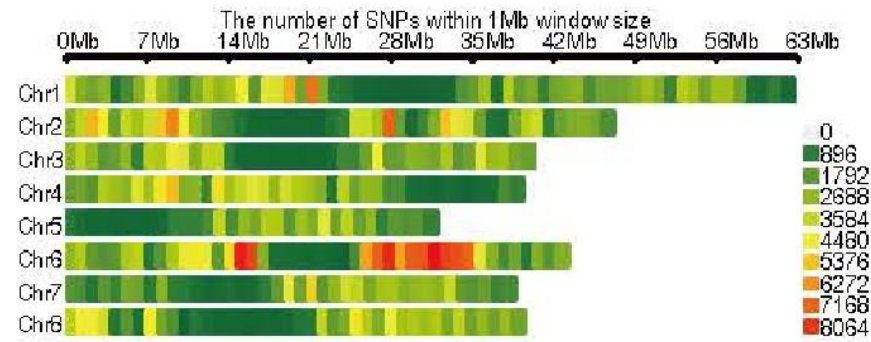
# 转录组和突变分析



转录组及WGCNA分析



# 转录组和突变分析





# 总结

- ❑ 在这项研究中，我们组装了一个甜樱桃主栽品种的完整基因组——T2T基因组；
- ❑ 在蔷薇科中对新组装的基因组代表的甜樱桃进行了比较基因组和进化研究；
- ❑ 以上述数据和研究为基础对染色体加倍后美早四倍体果色变化的候选基因和突变进行了多组学挖掘；
- ❑ 数据及方法获取：  
<https://db.cngb.org/search/project/CNP0004619/>  
<http://www.imeta.science/imetaomics/>

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# 课题组介绍

## Team Introduction



**Kaichun Zhang** Professor

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

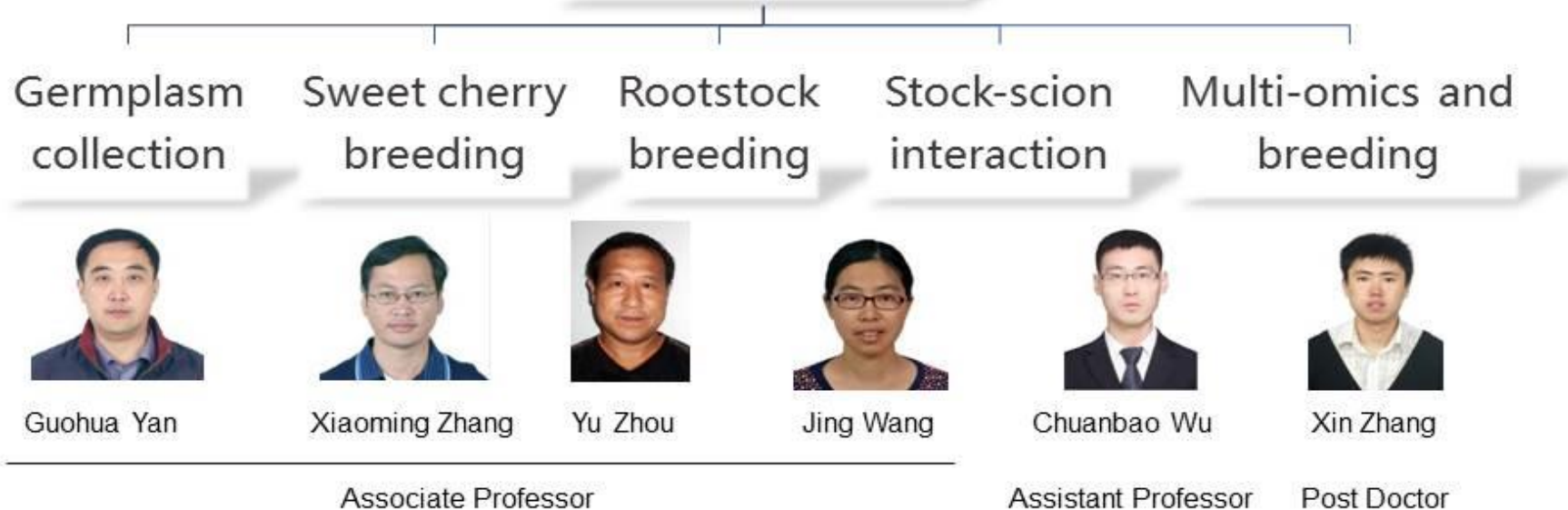


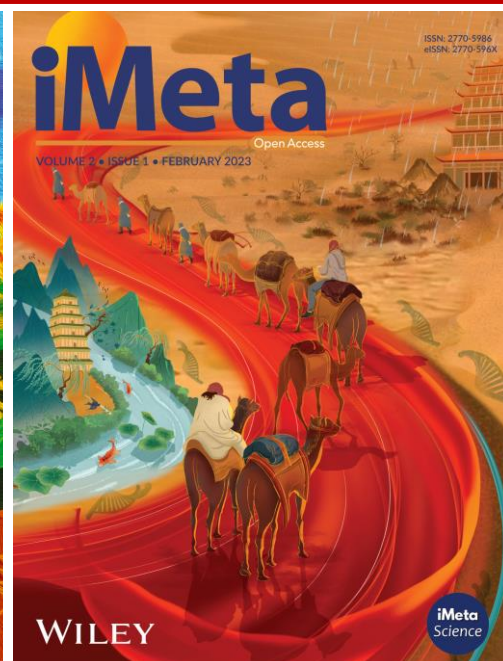
**Xuwei Duan**

Associate Professor

The leader of cherry group

## Research area





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