IAEA
International Atomic Energy Agency
Atoms for Peace and Development

Regional Training Course on Efficient Screening Methods for Improved Nutritional Quality in Mutant Populations

Cibinong, Indonesia,13 rd- 17th April, 2026

Multi-omics genetic resource research and improvement the quality and resistance breeding of peppers(*Capsicum* spp.)

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Cibinong, Indonesia,15th April, 2026

Institute of Vegetables and Flowers， CAAS

Beijing, China

Capsicum is one of the main vegetable crops in China

in China :

- **Aera:** 2.15 million ha/y, 9.28% of vegetables; 38.9% of the world's pepper.
- **Production:** 63.994 million tons, 7.76% of vegetable production.
- **Benefits:** 60 billion $/y; 11.36% of total vegetable value;1.14% to farmers' income.
- **Development:** The area has increased by 30% in ten years; The industrial chain with the processing.

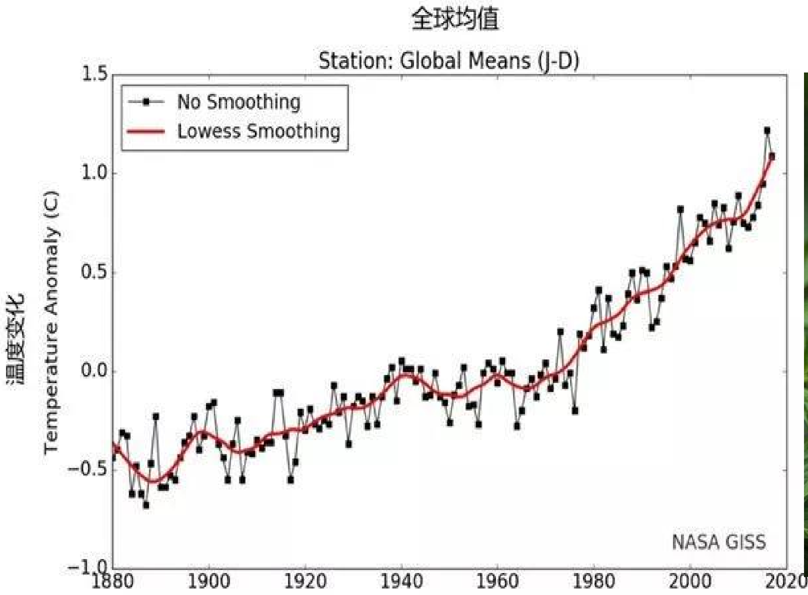
Northern Sunlight Greenhouse

High mountain pepper

Pepper in Base for transporting southern vegetables north

Global climate changing brings new challenges to production

- Global climate change has resulted in shifts in climatic zones, leading to serious diseases such as epidemics and anthracnose in high-temperature environments;
- From 1951 to 2017, the temperature increase rate in our country reached 0.24° C every 10 years. Viral diseases such as TMV and CMV are severe, with new epidemic diseases like PMMoV and TSWV emerging.
- Resistance genes can easily lose their function under high-temperature conditions, resulting in serious losses.



Germplasm : Phynotyping and Resequencing for Genotyping

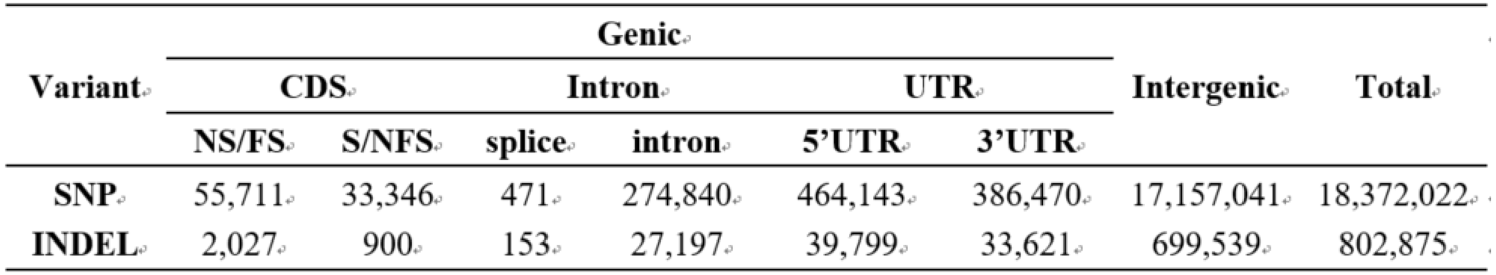
Accessions of *Capsicum of core collections*

Species	No. of A
Capsicum annuum	**309**
Capsicum annuum var. glabriusculum	2
Capsicum frutescens	10
Capsicum chinense Jacquin	10
Capsicum pubescens Ruiz & Pavon	2
Capsicum baccatum var. pendulum	5
Capsicum baccatum var. baccatum	1
Capsicum cardenasii	1
Capsicum chacoense	2
Capsicum eximium	1
Capsicum galapagoense	1
Capsicum rhomboideum	1
Capsicum flexosum	1
Capsicum minutiflorum	1
Total	347

(1) Sequenced on the Illumina Solexa platform.

(2) Clean reads were mapped to the Zunla-1 3.0 reference genome using BWA. Samtools and GATK were used to call the SNP/InDel variants.

Positions of the SNPs and InDels identified in the pepper population*.

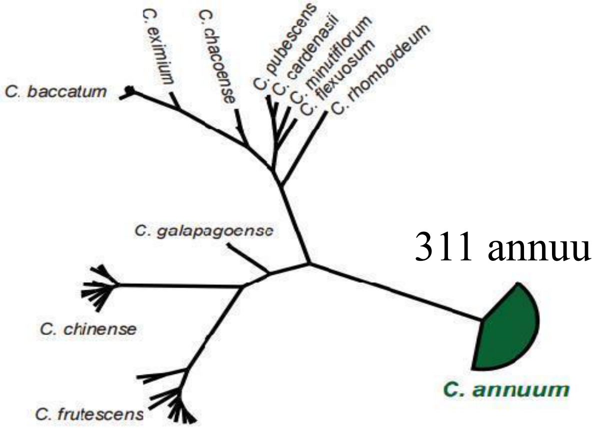


Variant	Genic						Intergenic	Total
	CDS		Intron		UTR			
	NS/FS	S/NFS	splice	intron	5'UTR	3'UTR		
SNP	55,711	33,346	471	274,840	464,143	386,470	17,157,041	18,372,022
INDEL	2,027	900	153	27,197	39,799	33,621	699,539	802,875

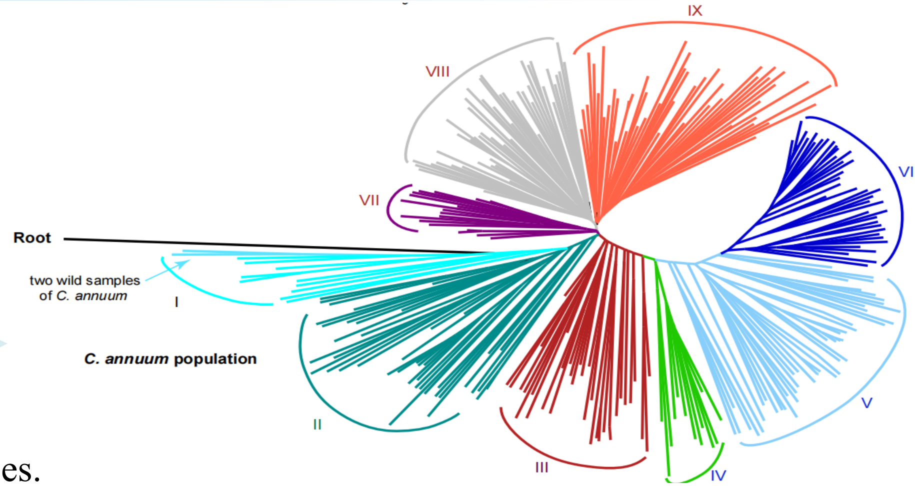
*: Abbreviations: CDS: coding sequences; UTR: untranslated region; NS: nonsynonymous and S: synonymous mutations of SNPs; FS: frameshift and NFS: non-frameshift mutations of InDel. (https://bigd.big.ac.cn/gsa)

Cao et al., 2022, Molecular Plant

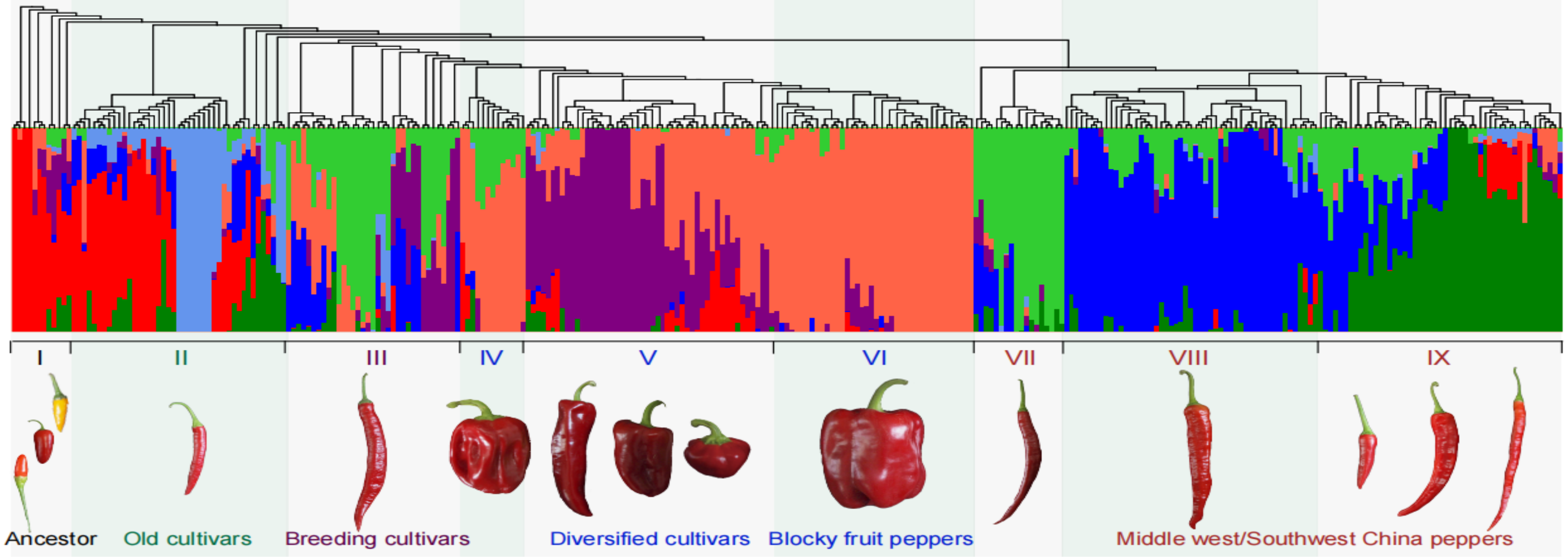
Main trajectories of *C. annuum* domestication



311 annuum pepper



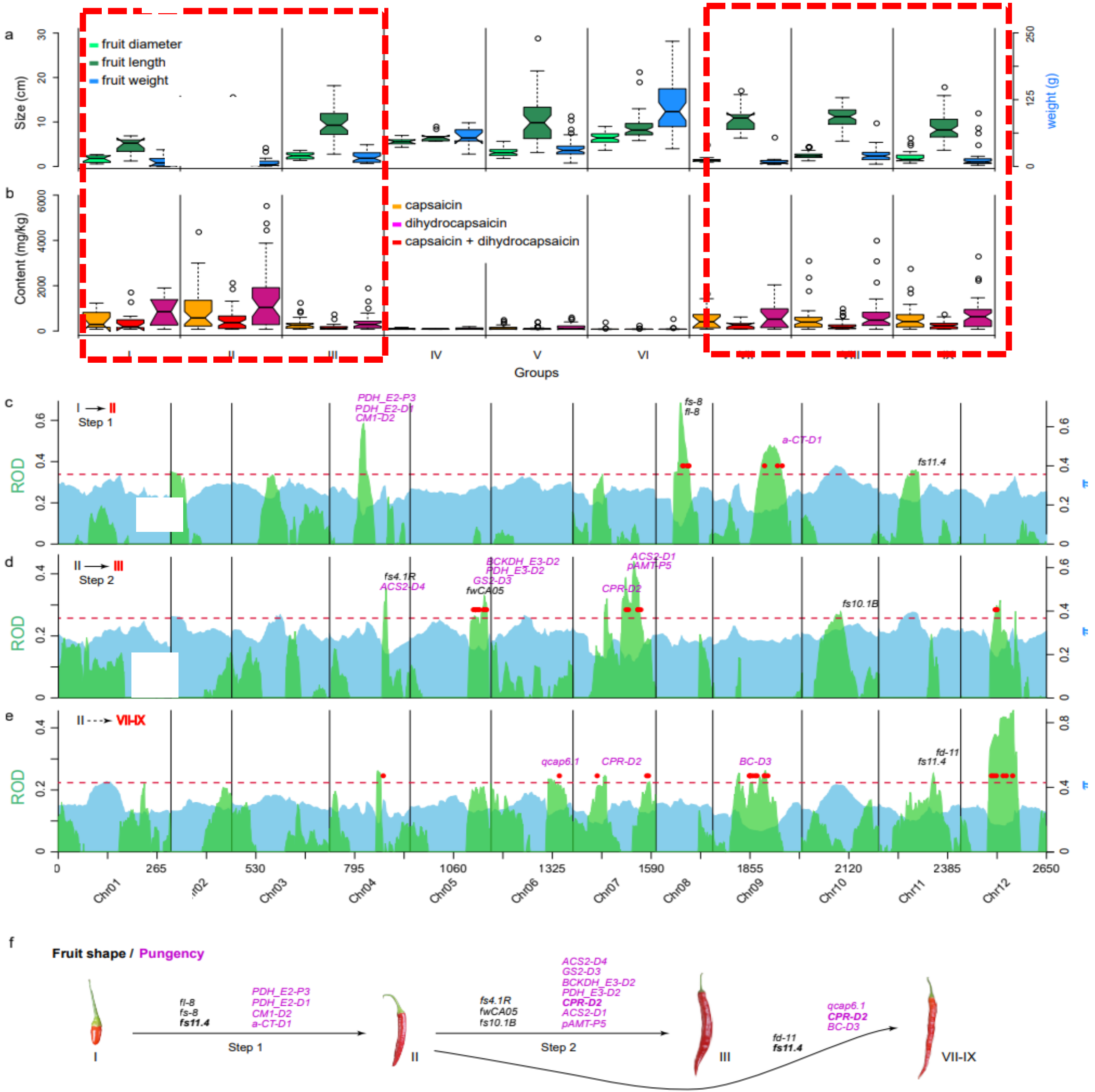
- Phylogenetic tree of 347 resequenced accessions from 12 *Capsicum* species.



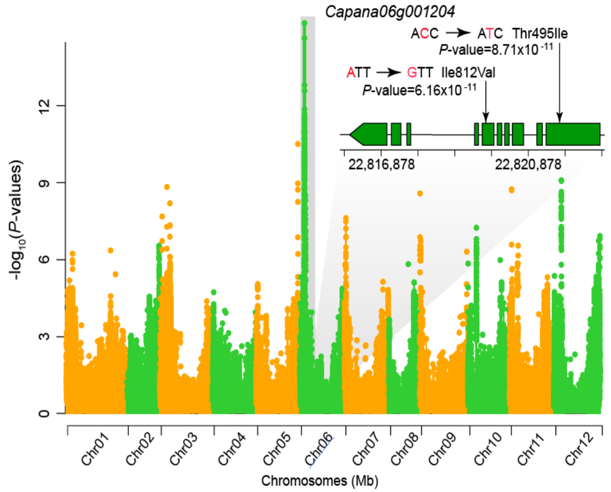
- Phylogenetic tree of the 311 *C. annuum* accessions. Different colored branches indicate the nine groups discussed in the text.

Cao et al., 2022, Molecular Plant

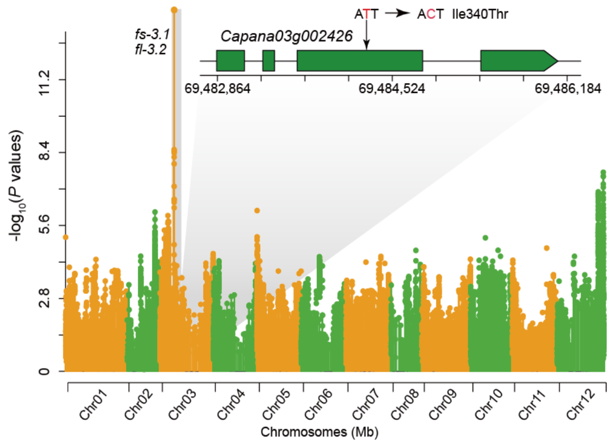
Domestication map of narrow fruit peppers, *Flip1 & TRM25* genes



***Flip1* gene** control important traits—Fruit capsaicinoids content

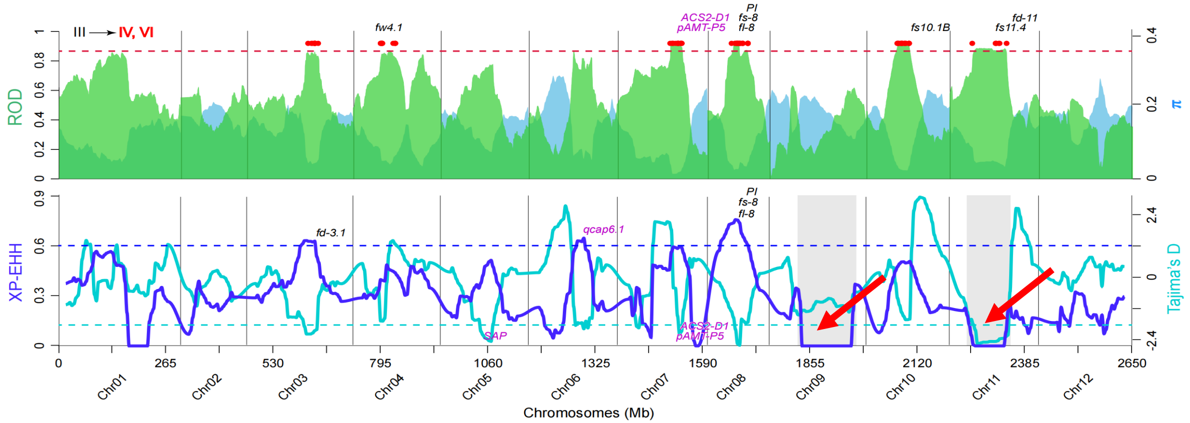


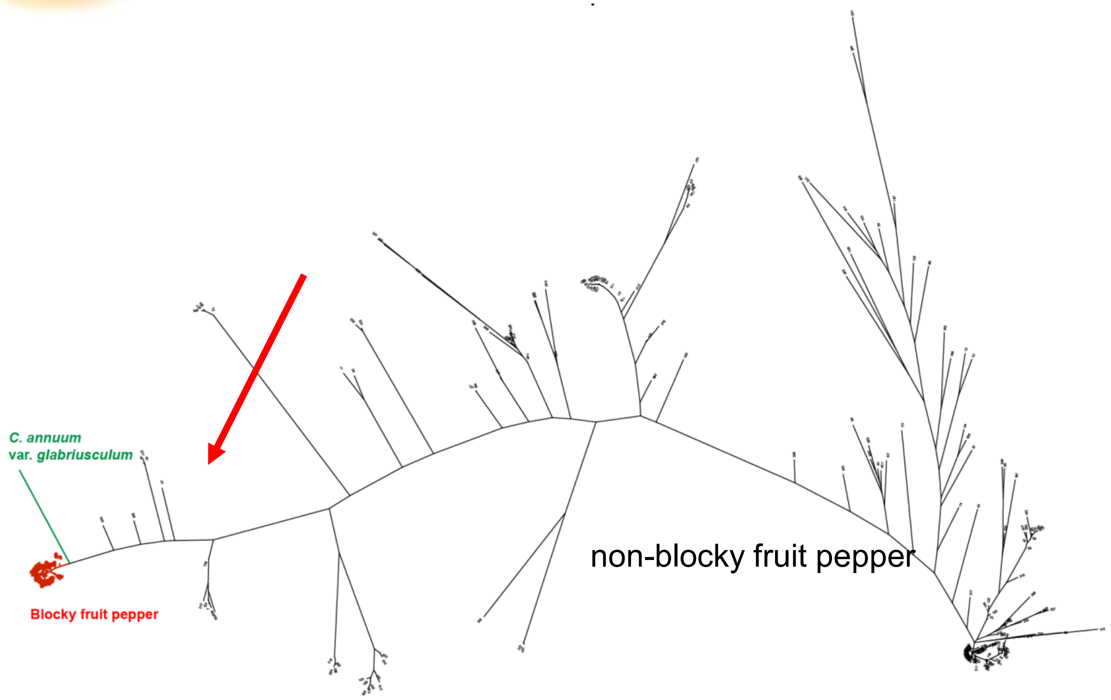
***TRM25* gene** control important traits—Fruit shape

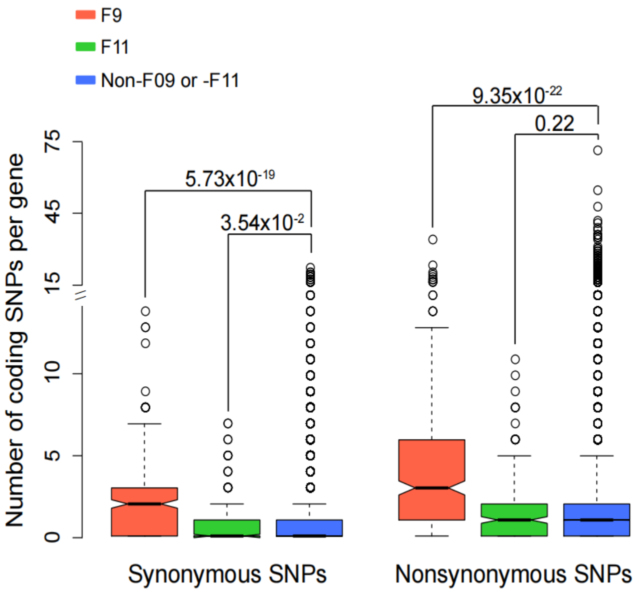


Cao et al., 2022, Molecular Plant

Evolution of the blocky fruit peppers, F09 and F11 introgressions

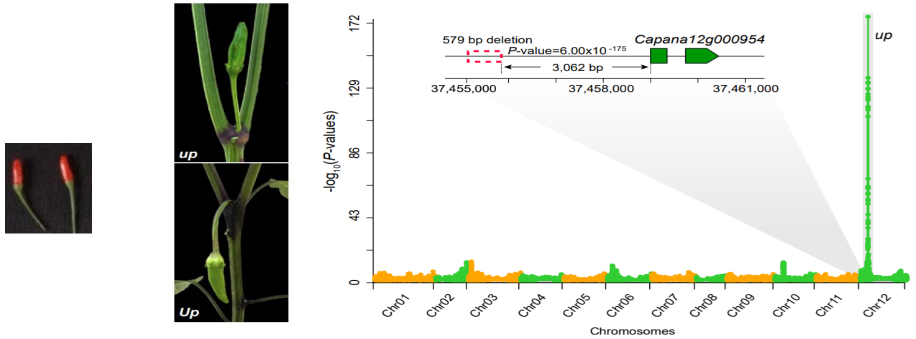




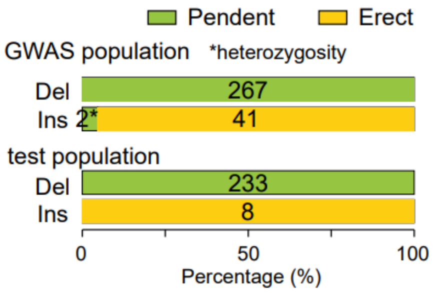


Cao et al., 2022, Molecular Plant

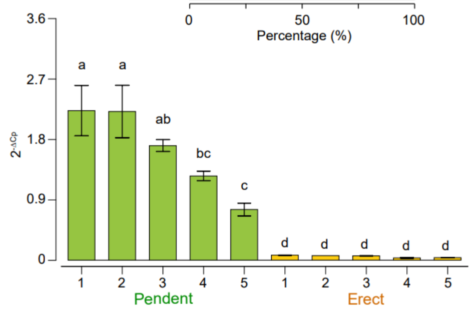
Identification of Fruit orientation control gene *up Capana12g000954*



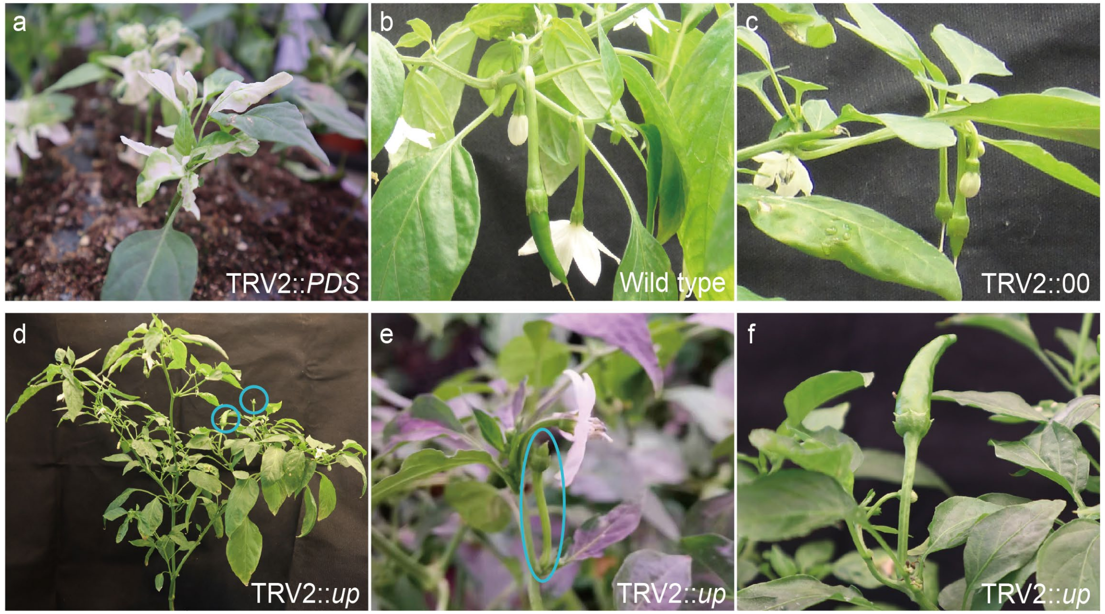
- GWAS association signal of the 579-bp deletion in the promoter region of *Capana12g000954* (*up*).

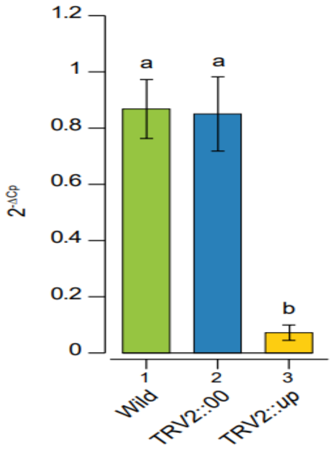


- Frequencies of the deletion in the GWAS and test populations



- qRT-PCR analysis of *up* expression in young fruit pedicels with different fruit orientations (pendent vs erect).

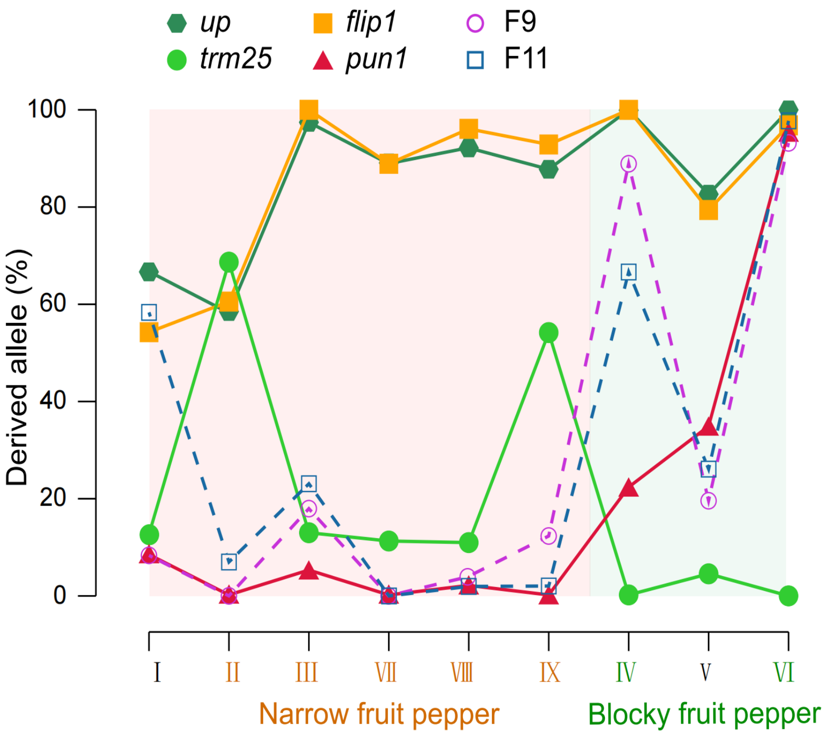


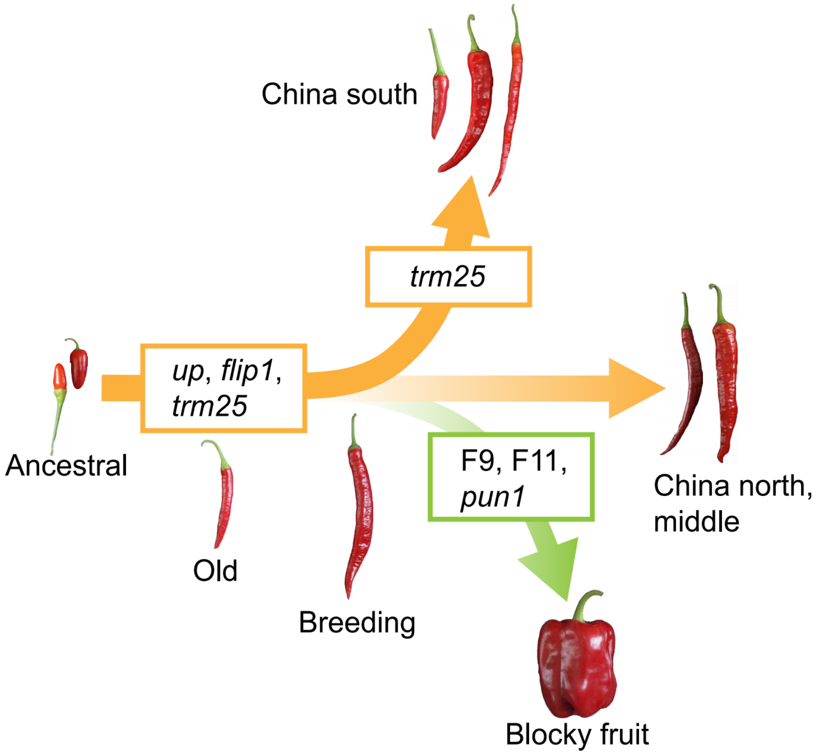


- The erect fruit of "Changyang chili" after the VIGS treatment with TRV2::*up*, which was pendent in its wild type.

Cao et al., 2022, Molecular Plant

Conclusion: Key events shaped pepper fruit domestication and diversification





Key events that shaped pepper fruit domestication and diversification.

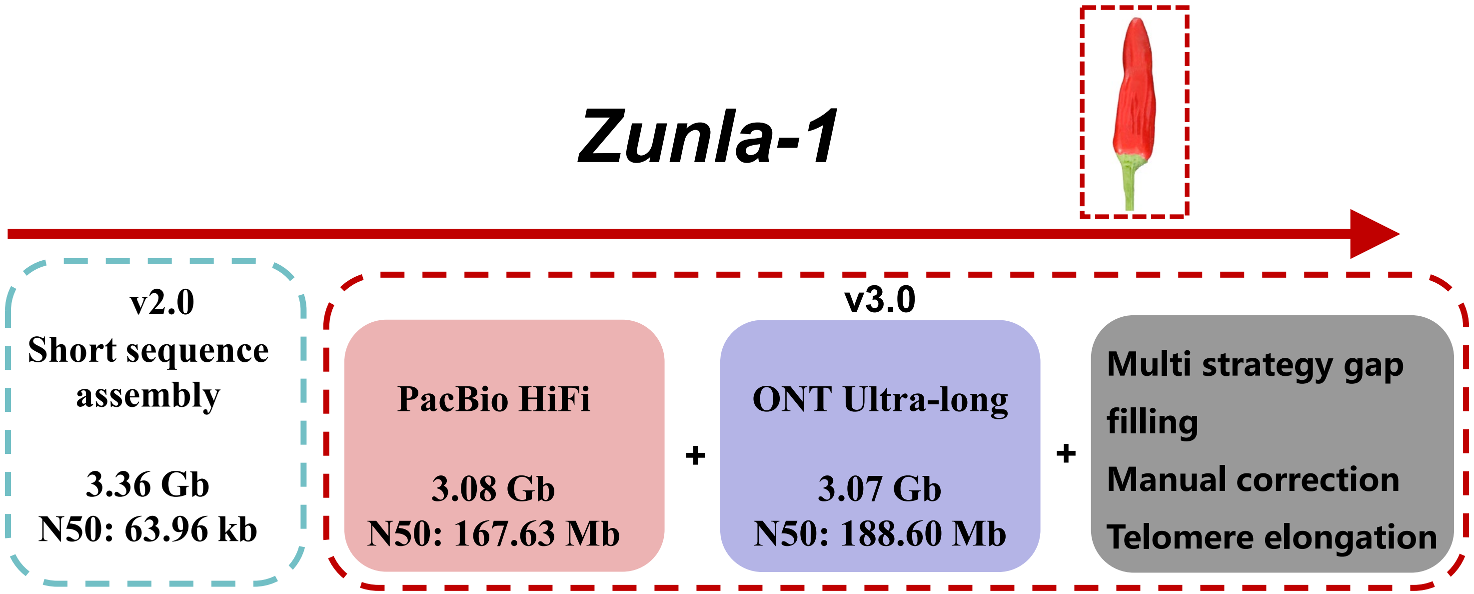
- Frequency distributions of the mutations in the *up* and *trm25* alleles, controlling respectively fruit orientation and shape; of the *flip1* and *pun1* alleles, controlling fruit pungency; and of the F9 and F11 introgressions, associated with blocky fruit pepper, in the nine *C. annuum* groups.
- Chronodiagram of the key genetic events controlling fruit characteristics during pepper domestication and differentiation.

Cao et al., 2022, Molecular Plant

Zunla-1 reference genome reassembly

No gaps Zunla-1 reference genome reassemble as a reference

- *Zunla-1* reference genome was first published in 2014
- Reassemble using HiFi+Ultra long sequencing method



Zunla-1

v2.0
Short sequence assembly

3.36 Gb
N50: 63.96 kb

v3.0

PacBio HiFi

3.08 Gb
N50: 167.63 Mb

\+

ONT Ultra-long

3.07 Gb
N50: 188.60 Mb

\+

Multi strategy gap filling
Manual correction
Telomere elongation

✓ Filled all the gaps

✓ Total chromosome length increased by 16%

✓ Fix a large number of assembly errors

（http://www.bioinformaticslab.cn/PepperBase/）

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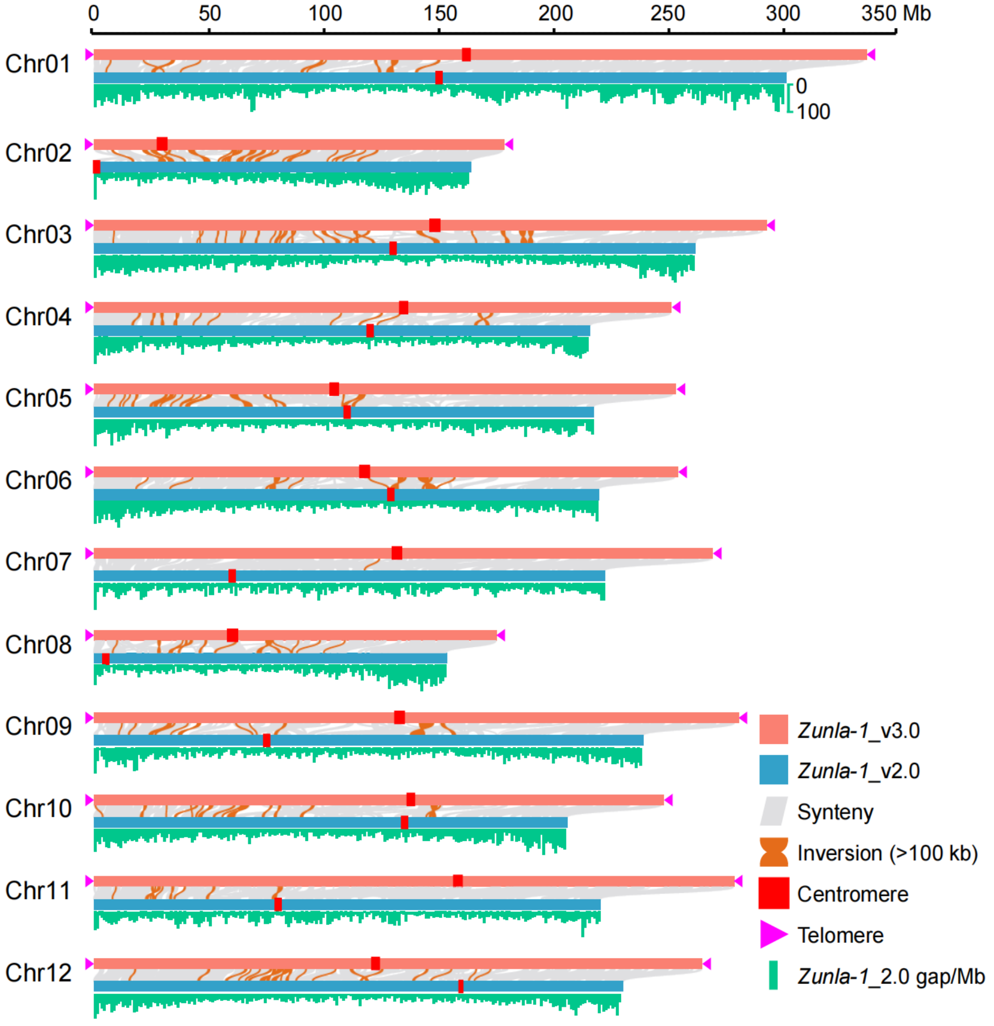
Assemble a complete and gapless T2T genome



Zhang et al., 2024, Plant Communications

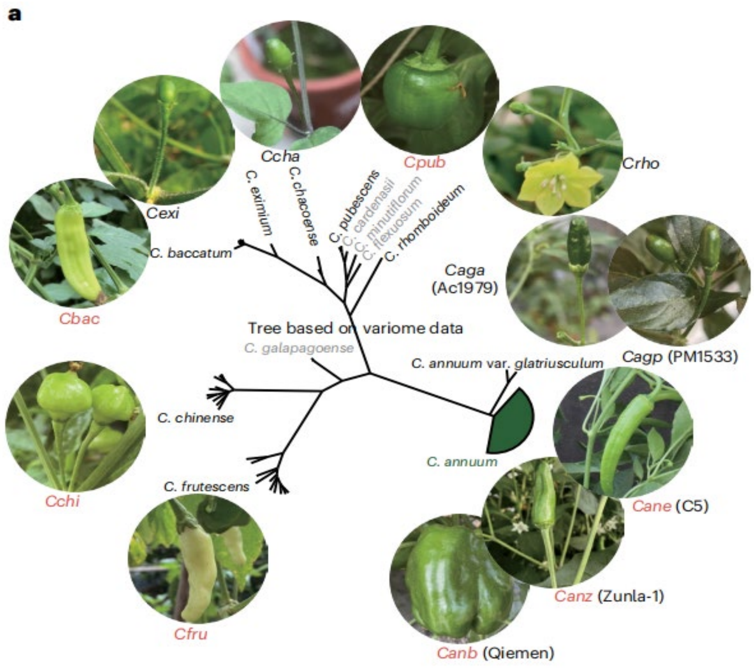
Genomic assembly of wild and cultivated Capsicum

Near-complete assemblies of wild and domesticated peppers

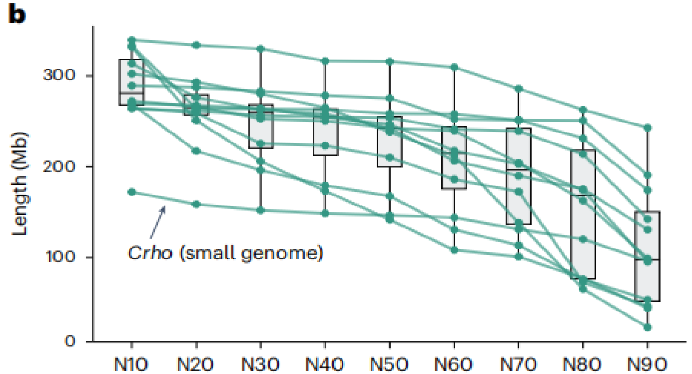
11 Genomes of *Capsicum*

- ✓ **5 cultivated species (6 accessions)**
- ✓ **4 wild species (5 accessions)**

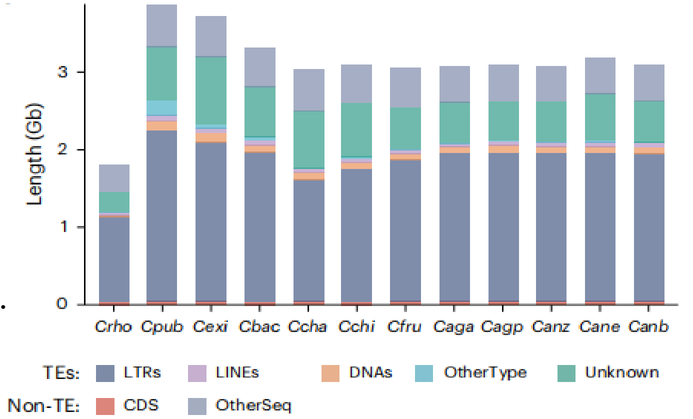
HiFi, ONT and Hi-C



The phylogeny and photos of selected Capsicum materials for genome assembling.



The NX values of assembled contigs for each accession



The sequence composition of the assembled genomes.

Table. Summary of assembly results for the pepper accessions.

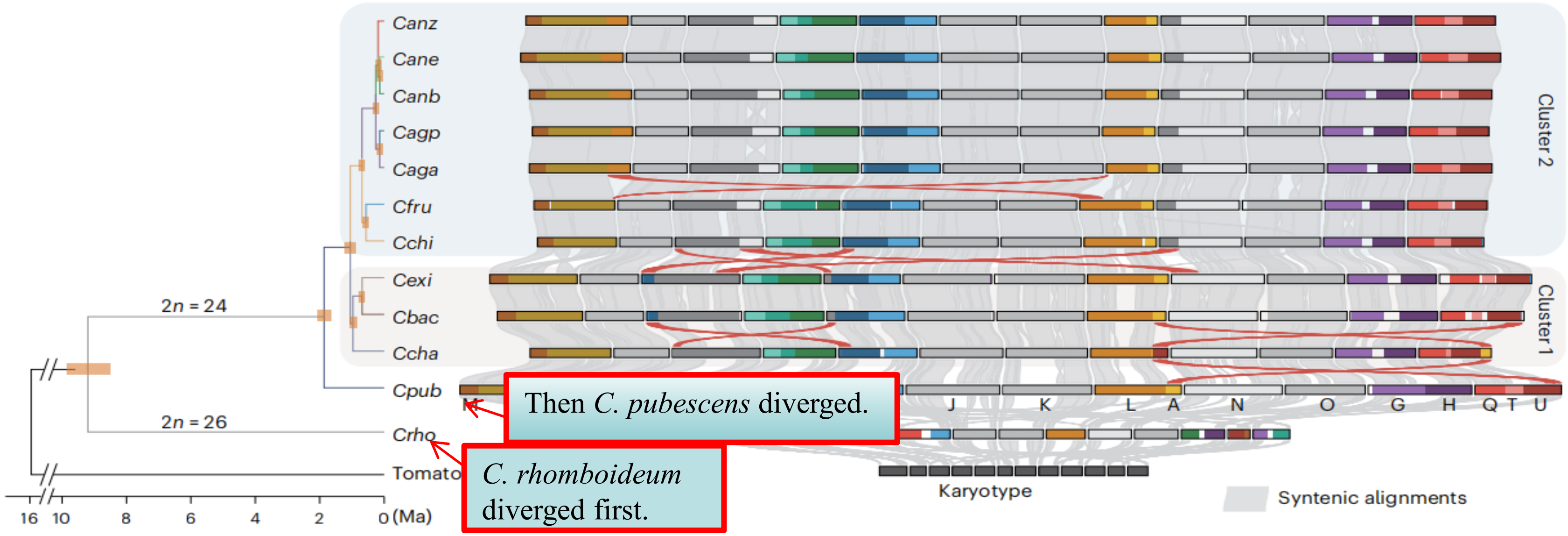
Name	Size (Gb)	Contig N50 (Mb)	Contig N90 (Mb)	Completeness	Quality value
Canb	3.10	242.45	130.77	99.77%	62.27
Cane	3.18	141.64	44.18	99.37%	66.32
Canz	3.08	167.63	53.50	99.65%	62.26
Cagp	3.09	258.43	174.11	99.79%	62.82
Caga	3.08	242.43	99.06	99.74%	63.82
Cchi	3.09	246.64	95.45	99.72%	66.47
Cfru	3.06	253.81	142.39	99.43%	66.73
Ccha	3.04	210.24	46.50	99.55%	63.03
Cexi	3.73	315.77	242.84	99.13%	65.22
Cbac	3.32	275.39	190.81	99.60%	64.64
Cpub	3.88	238.09	23.16	99.25%	62.75
Crho	1.80	146.59	96.17	99.42%	66.34

The quality value scores of all assemblies were above 62, meeting the standards for reference-grade genomes.

（https://ngdc.cncb.ac.cn/gwh/）

Zhang et al., 2025, Nature Plants

Karyotype-resolved evolutionary history of the Capsicum genus

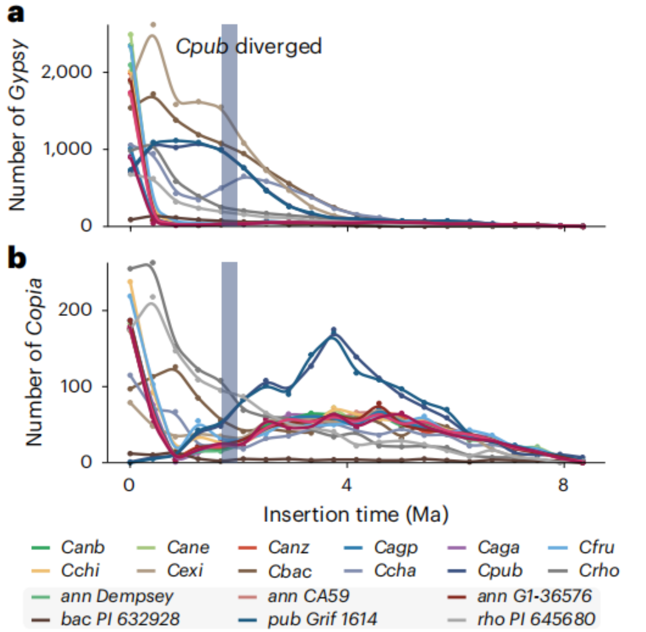


Then *C. pubescens* diverged.

C. rhomboideum diverged first.

The phylogenetic tree and the syntenic relationships among *Capsicum* genomes.

C. rhomboideum has the highest number of chromosomes, at 13, but the smallest genome size.

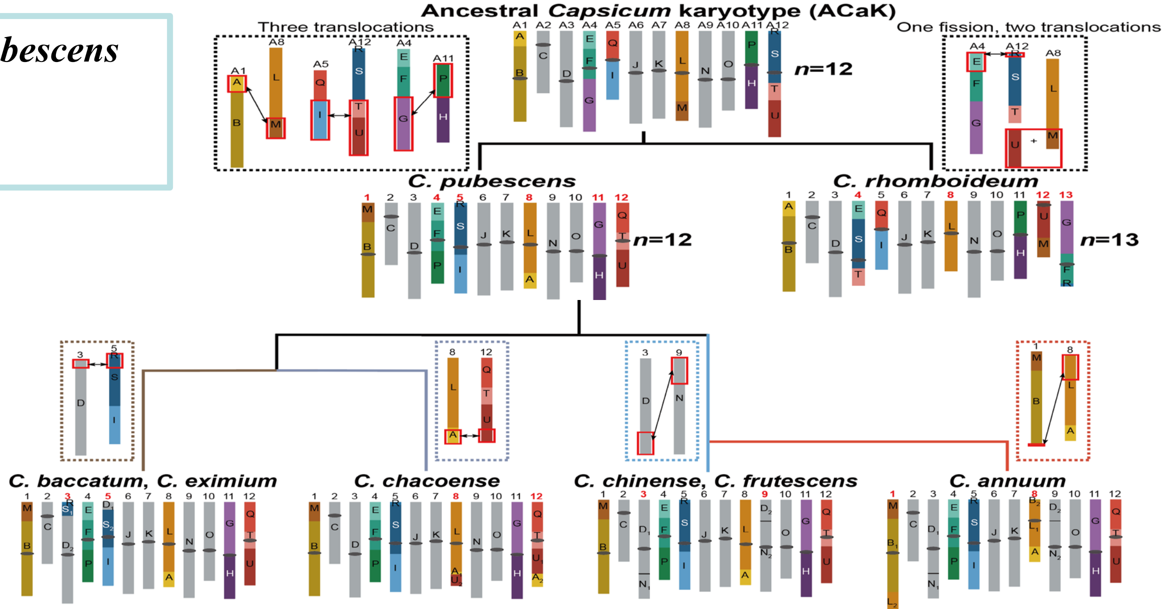


The distribution of insertion times for Gypsy (a) and Copia (b) full-length retrotransposons.

The differential accumulation of TEs from families such as Gypsy and Copia contributed to the diversity of genome expansion in peppers.

Both *C. rhomboideum* and *C. pubescens* experienced three chromosomal reshuffling events.

At least one chromosome translocation occurred in the differentiation of other species.

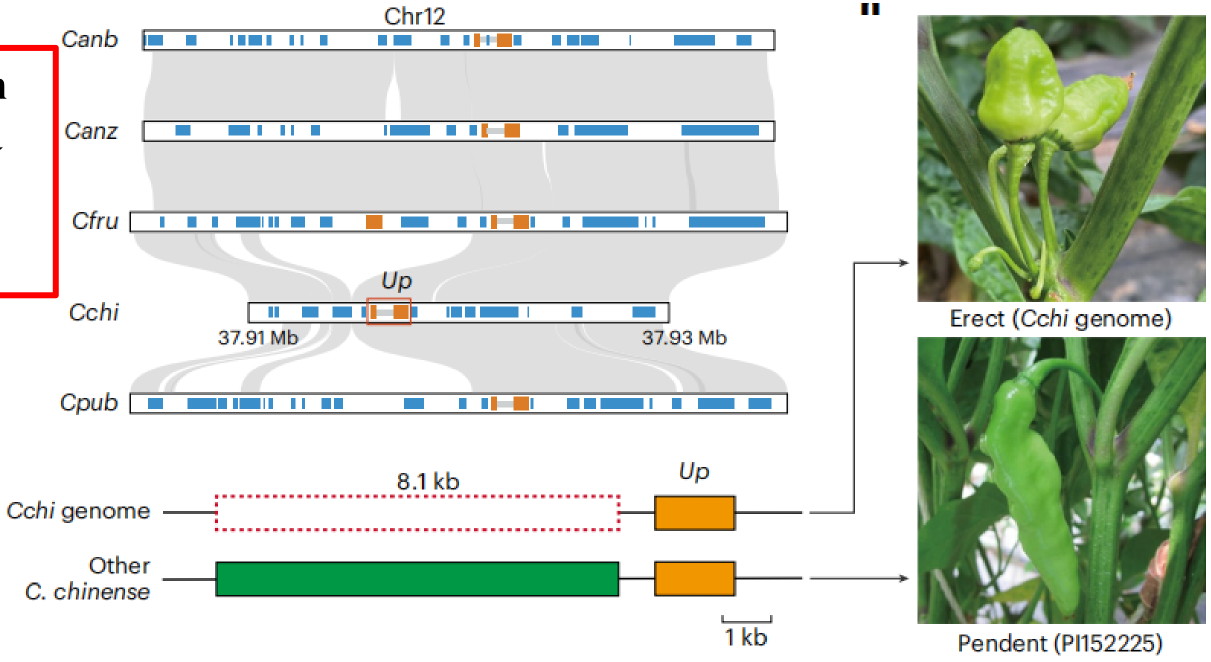


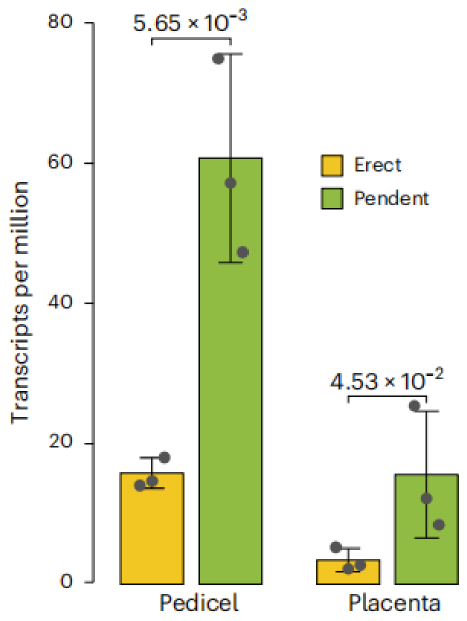
Karyotype and centromere evolution of *Capsicum*.

Zhang et al., 2025, Nature Plants

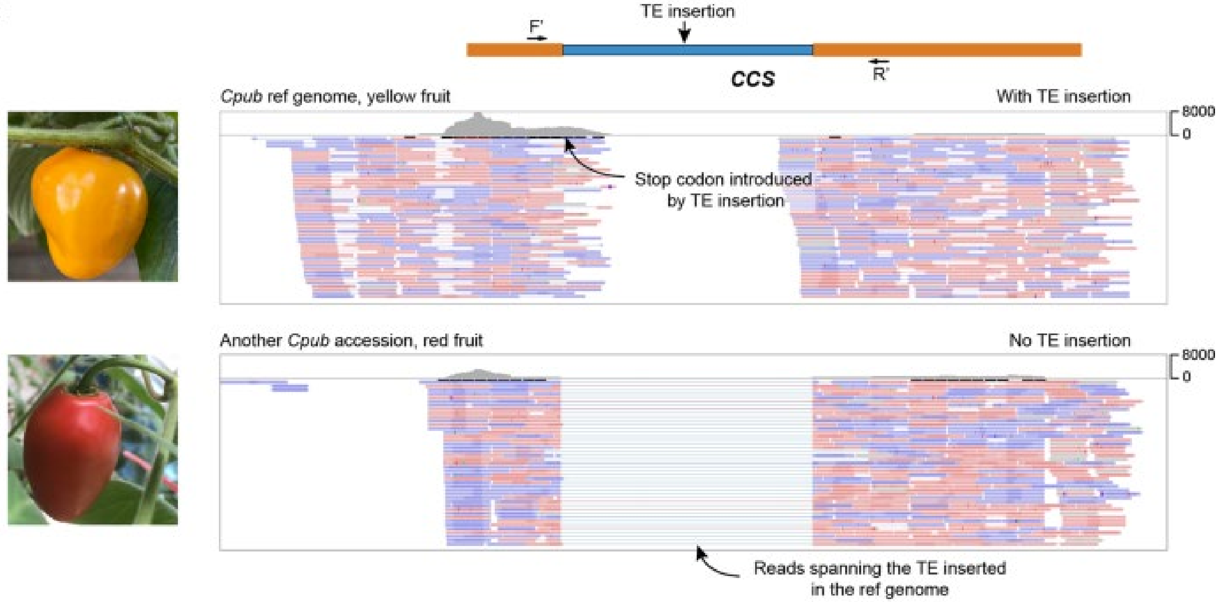
SV and TE lead to change in fruit orientation and color

The 8 kb deletion upstream of the *Up* gene resulted in a change in the fruit orientation of *C. chinense*.





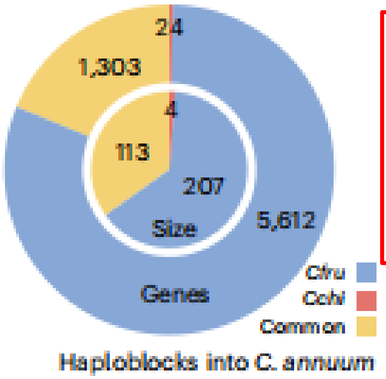
A transposon insertion in CCS gene in *C. pubescens* caused the fruit color from red to yellow.



Zhang et al., 2025, Nature Plants

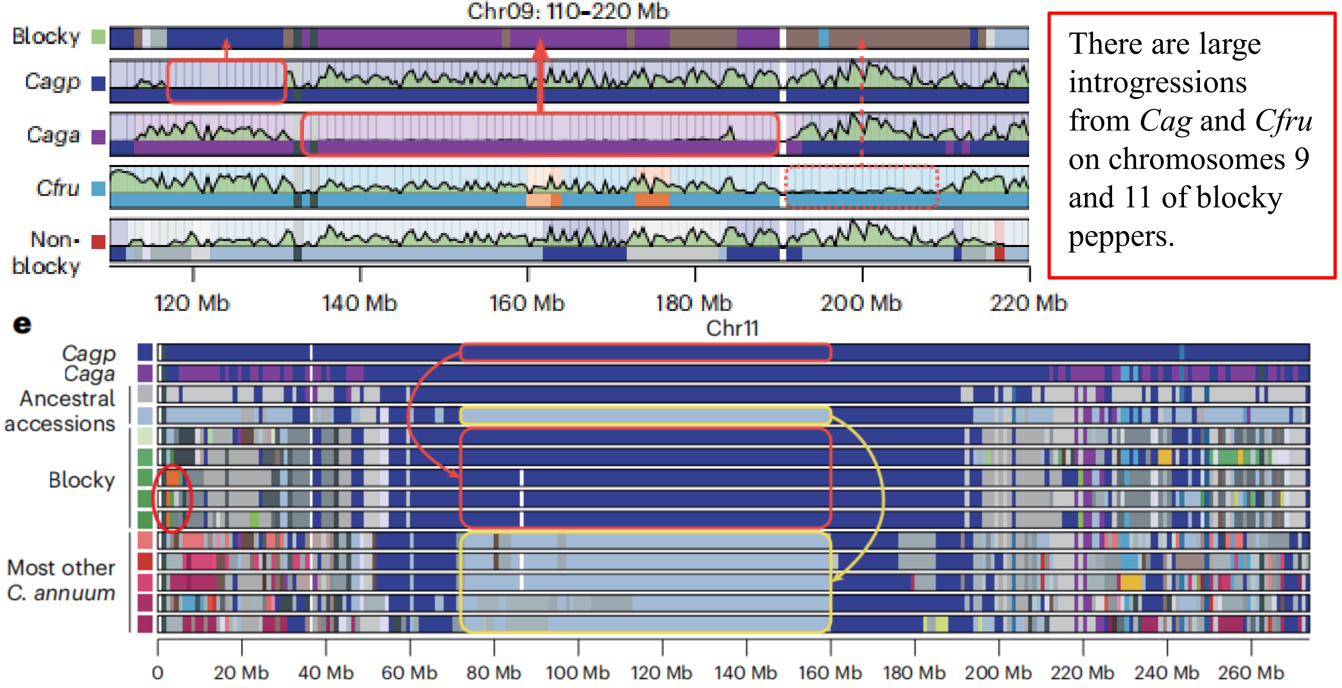
Introgressions increased the genetic diversity of *C. annuum*

We generated deep resequencing data
(>40× coverage) for a core collection of 124 pepper germplasms.

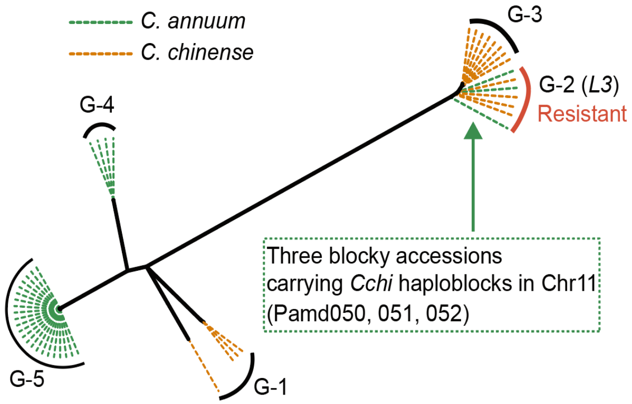


Contributions of *Cfru* and *Cchi*
haploblocks to *C. annuum*.

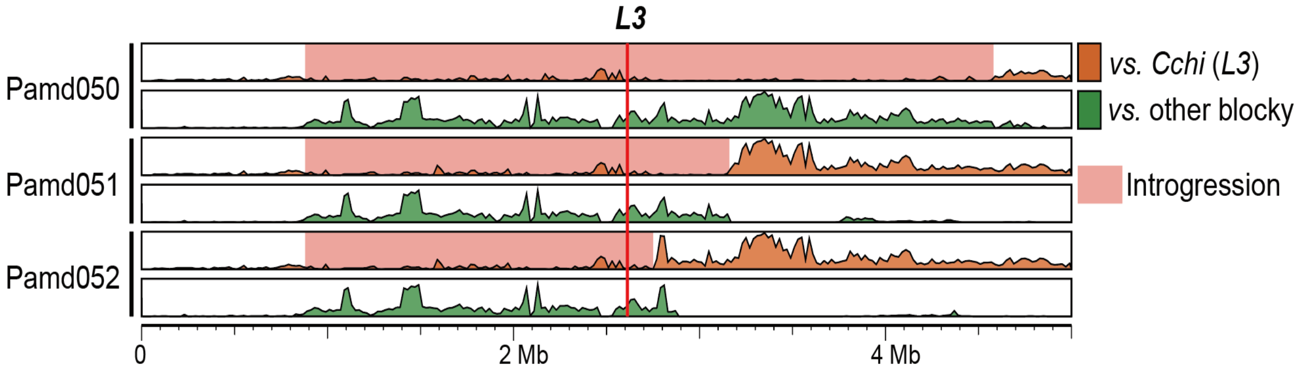
Most of these introgressed haploblocks in *C. annuum* were from *C. frutescens*, while the *C. chinense*-derived haploblocks were rare.



There are large introgressions from *Cag* and *Cfru* on chromosomes 9 and 11 of blocky peppers.



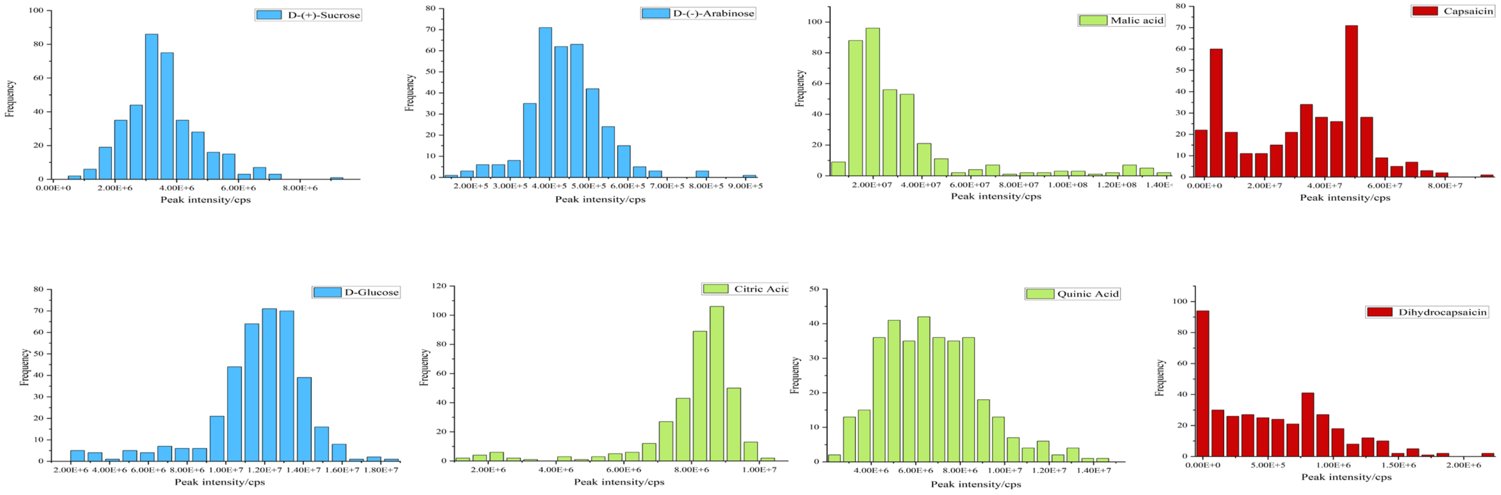
Three blocky accessions
carrying *Cchi* haploblocks in Chr11
(Pamd050, 051, 052)



Zhang et al., 2025, Nature Plants

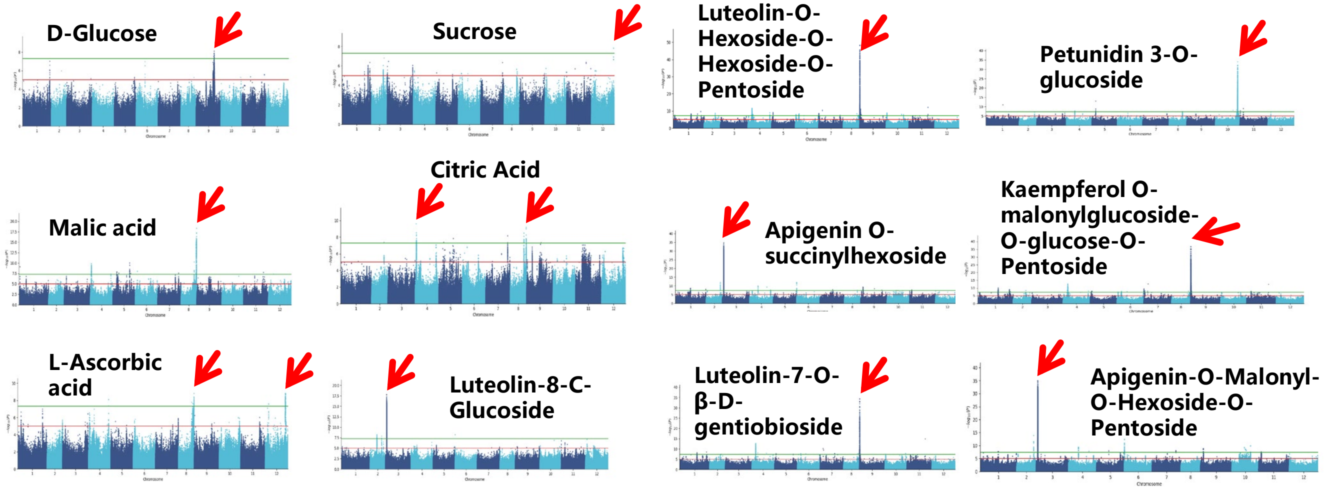
Identification of pepper metabolome and GWAS analysis

- **Extensive targeted metabolomics profiling and genome-wide genotyping were performed on 347 pepper core germplasm resources, identifying 622 known metabolites and locating 992,630 associated loci via GWAS.**
- **Precise identification and genetic mapping of pepper metabolites provide resources and molecular markers for breeding programs targeting taste and nutritional quality in pepper.**



Frequency distribution bar chart of Saccharides, Organic Acids, and Capsaicinoids

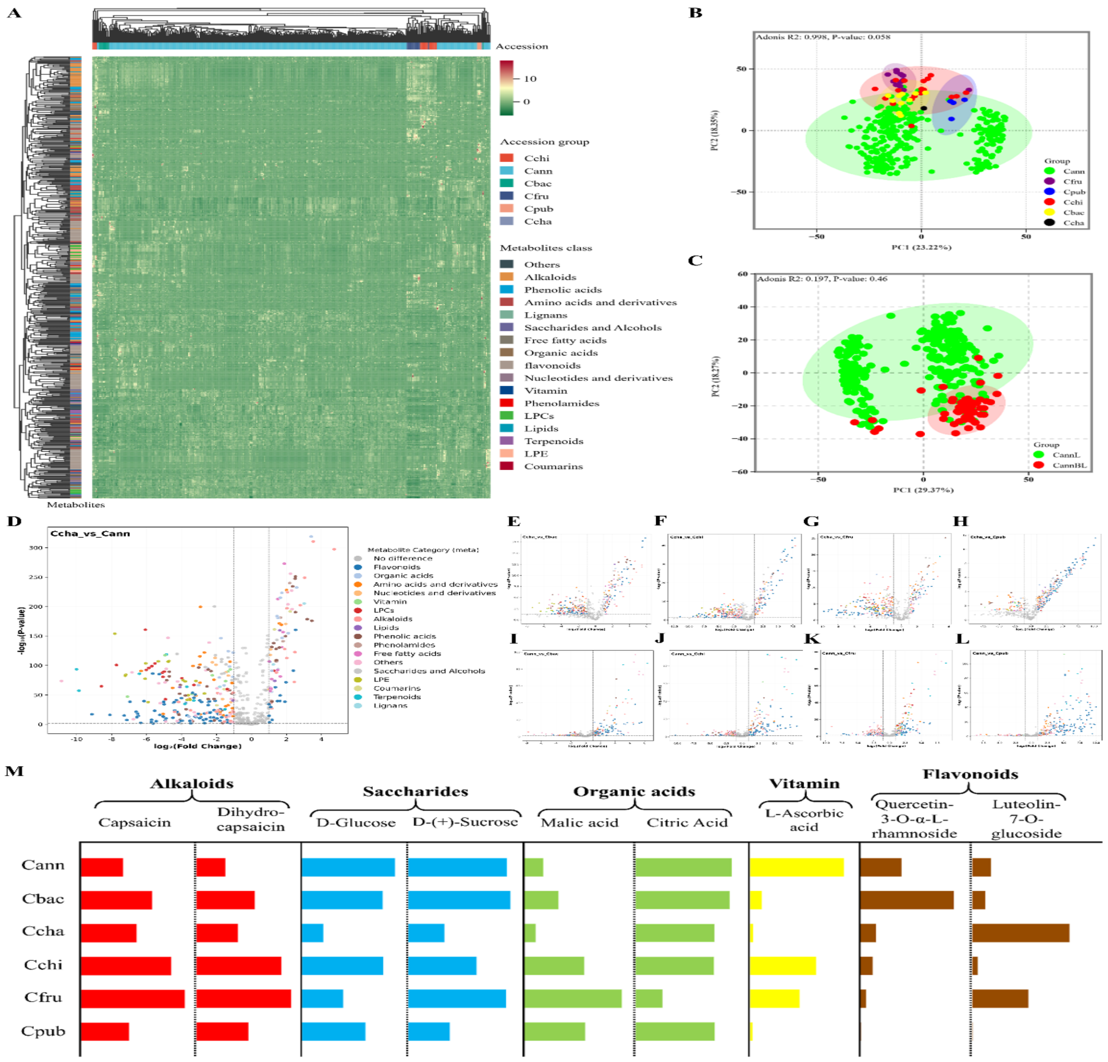
Pepper resources with high Vc content and excellent horticultural traits

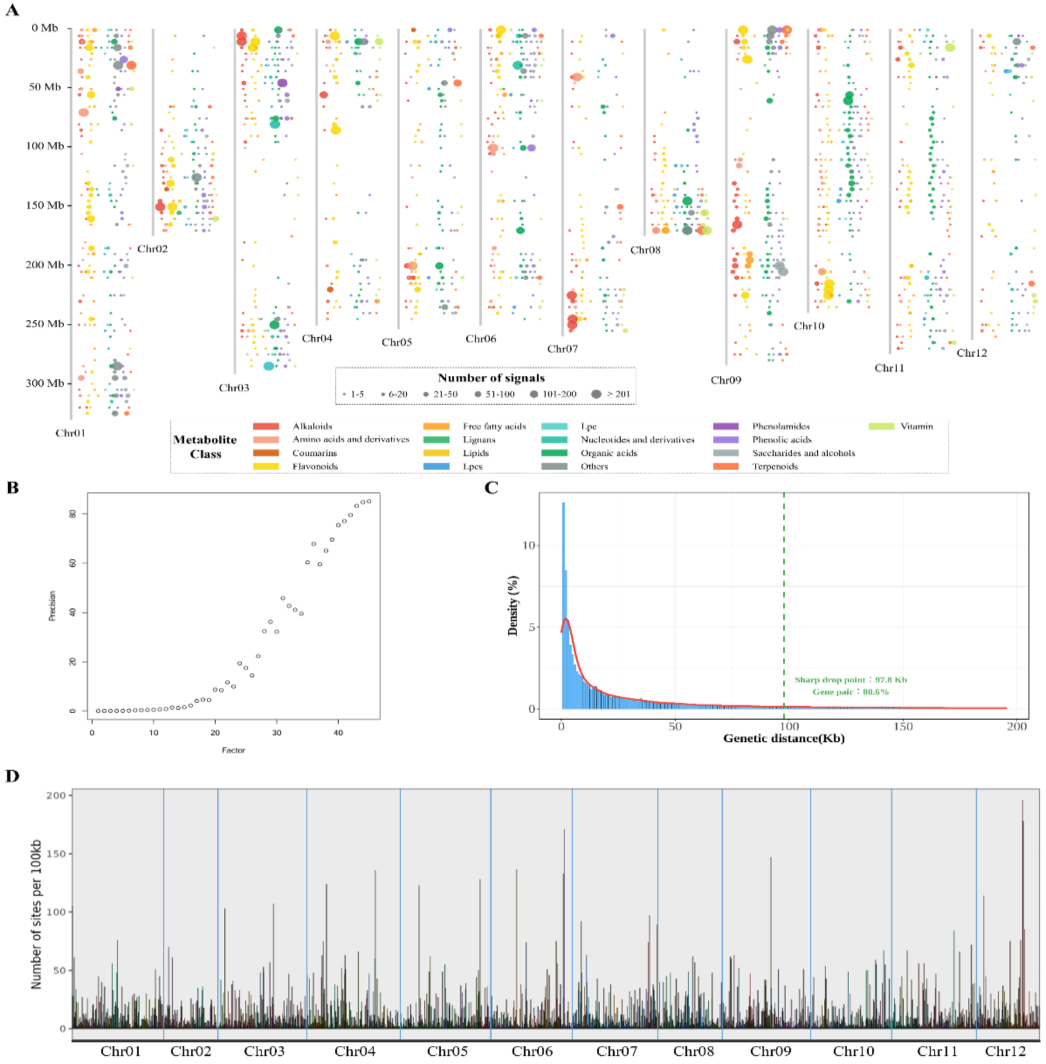


Metabolites GWAS manhattan plot

Article in writing

Capsaicin and dihydrocapsaicin ,D-glucose and D-(+)-sucrose spices difference and Distribution of mGWAS signals for different metabolic classes





Significant interval of ascorbic acid content was located at the end of chromosome 8 about 170~174Mb, where we found a GAUT3 (galacturonosyltransferase 3) involved in the galactose synthesis pathway

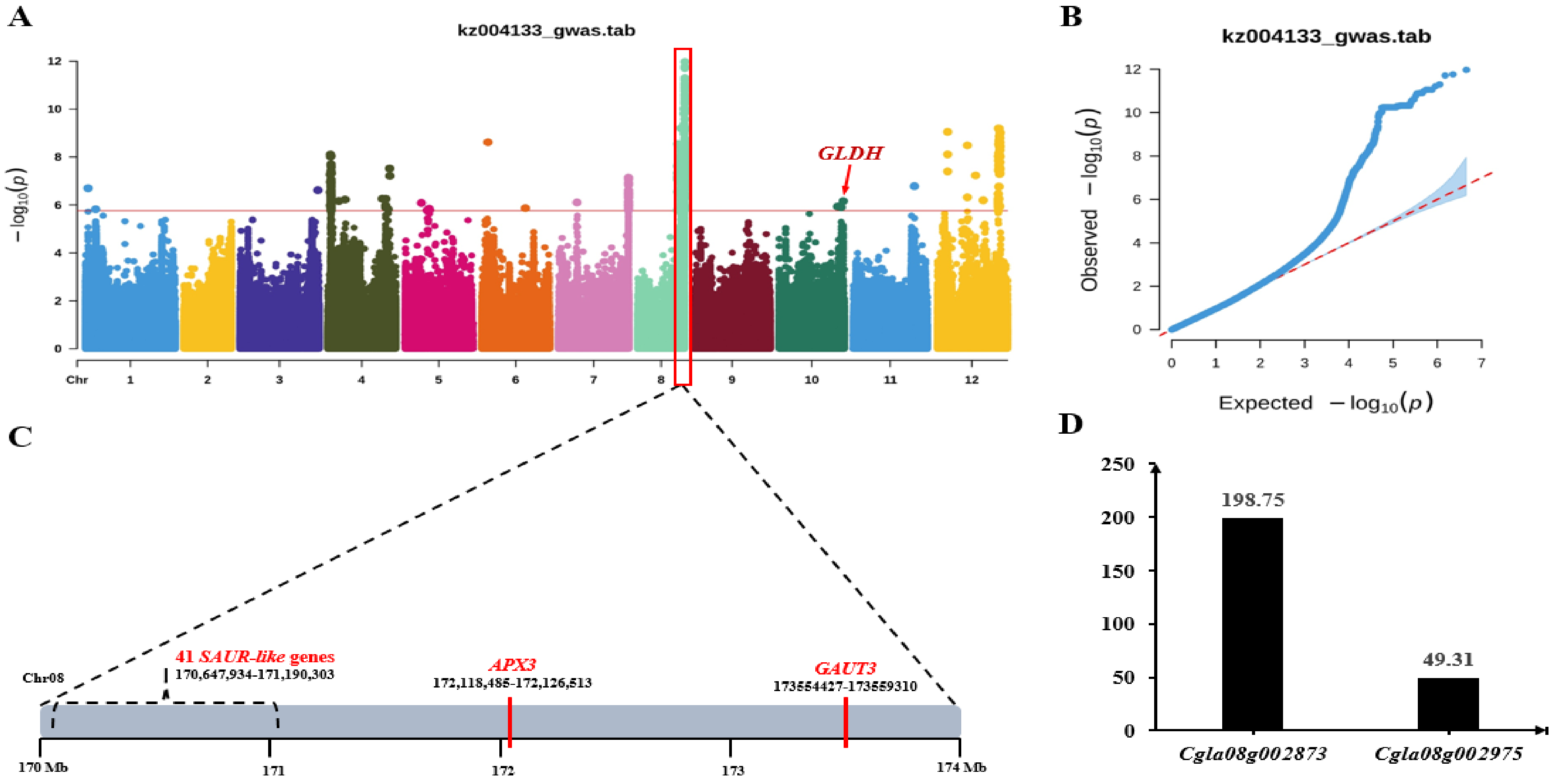


Fig. GWAS and candidate gene analyses of Vc.

Genetic mapping of anthracnose resistance in *Capsicum chinense*

Resistant material
PBC932（*C. chinense*）

Susceptible material
PI152225（*C. chinense*）

An F_2 population of 200 individual plants was subjected to 5× whole-genome resequencing.

Reference genome: PBC932（Zhang et al., 2025）

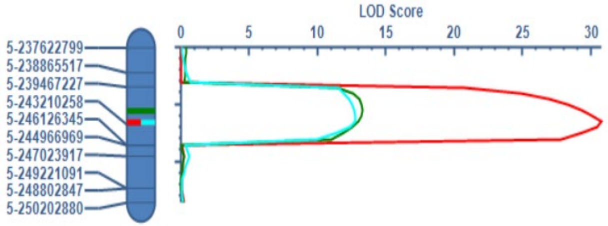
Statistics of genetic linkage group information

linkage	marker_number	length(cM)	average_length(cM)
lg1	175	173.35	0.99
lg2	90	100.39	1.12
lg3	84	120.52	1.43
lg4	64	51.35	0.8
lg5	107	126.27	1.18
lg6	111	110.81	1.0
lg7	109	147.03	1.35
lg8	160	217.92	1.36
lg9	161	210.39	1.31
lg10	112	186.65	1.67
lg11	123	145.54	1.18
lg12	138	159.3	1.15
total	**1434**	**1749.52**	**1.22**

Green ripening stage

QTL

The candidate interval is located on chromosome 5 from 239,467,227 to 244,966,969 Mb. A total of 159 genes were identified.

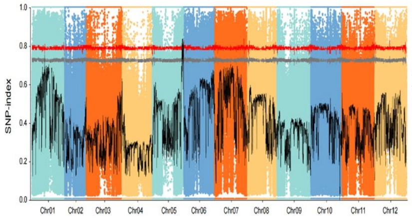


QTL analysis of anthracnose resistance

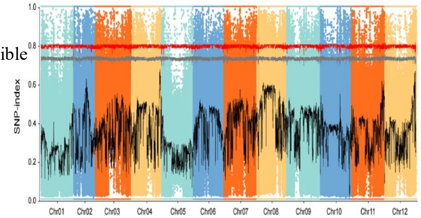
TraitName	Position	LeftMarker	RightMarker	LOD	PVE(%)	Add
First	12	5-249221091	5-243210258	31.3	57.8	4.2
Second	16	5-243210258	5-239467227	13.3	48.9	3.6
Third	14	5-243210258	5-239467227	12.8	55.6	4.3

BSA

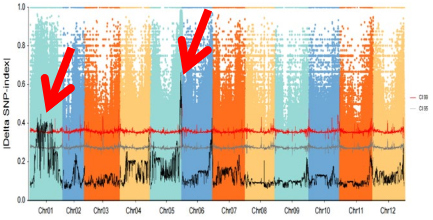
The candidate interval spans 173,000,000–251,900,000 Mb on chromosome 5 and contains 1,062 genes.



Susceptible pool

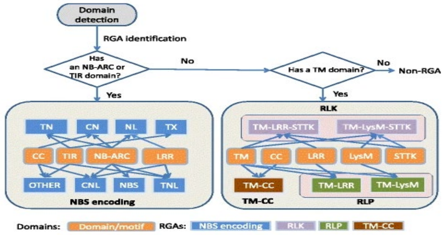


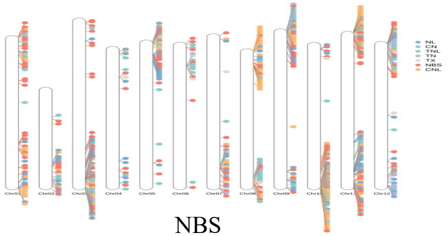
Resistant pool



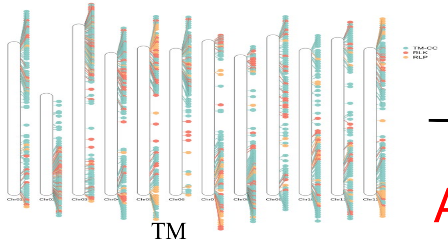
RGAs

A total of 1,664 resistance RGAs were identified.





NBS



TM

Combined with haplotype analysis

A total of 15 disease resistance genes were identified, among which genes ***Cchi05g001868*** and ***Cchi05g001967*** are the most likely candidates controlling anthracnose resistance in the green ripening stage of pepper fruit.

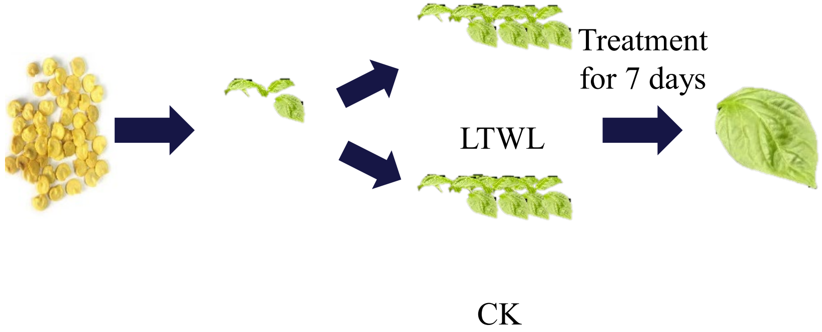
Article in writing

Research progress -Identification of Evaluation Indicators and Mining of Key Genomic Loci for Low-Temperature and Weak-Light Tolerance in Pepper (*Capsicum annuum* L.)

Article in writing

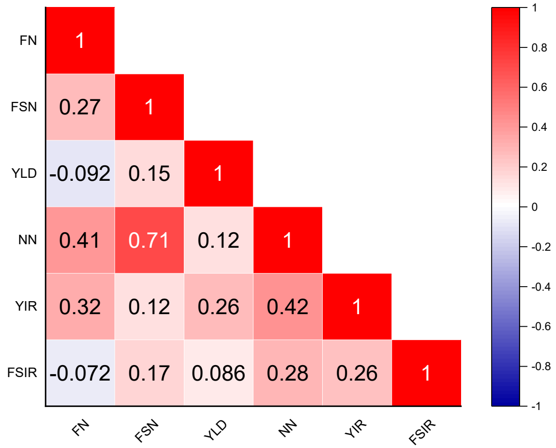
Phenotypic identification

Investigation on fruit setting, node number, flower setting and yield under LTWL at ripening stage



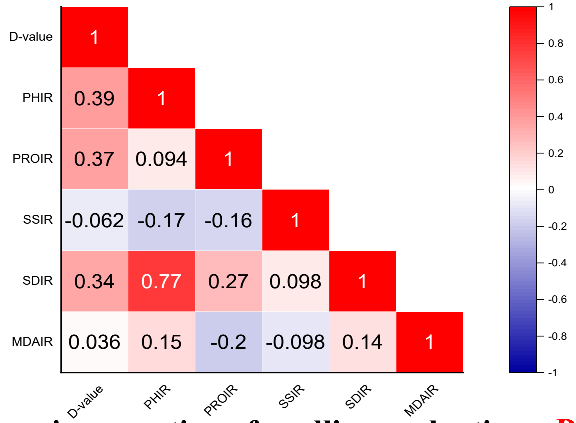
Investigation on physiological indexes under LTWL at seedling stage

Establish appraisal system



	FN	FSN	YLD	NN	YIR	FSIR
FN	1					
FSN	0.27	1				
YLD	-0.092	0.15	1			
NN	0.41	0.71	0.12	1		
YIR	0.32	0.12	0.26	0.42	1	
FSIR	-0.072	0.17	0.086	0.28	0.26	1

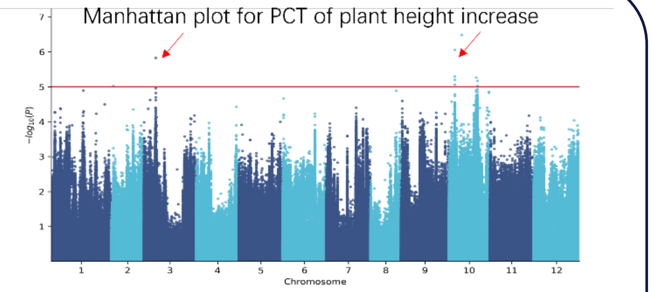
Regression equation of ripening evaluation : $D = -2.46 + 0.086 \times NN + 2.95 \times YLD + 2.67 \times FSIR + 0.99 \times YIR$, ($R^2 = 0.976$, $P < 0.001$).

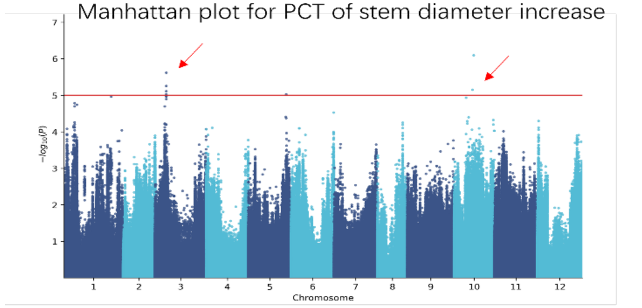


	D-value	PHIR	PROIR	SSIR	SDIR	MDAIR
D-value	1					
PHIR	0.39	1				
PROIR	0.37	0.094	1			
SSIR	-0.062	-0.17	-0.16	1		
SDIR	0.34	0.77	0.27	0.098	1	
MDAIR	0.036	0.15	-0.2	-0.098	0.14	1

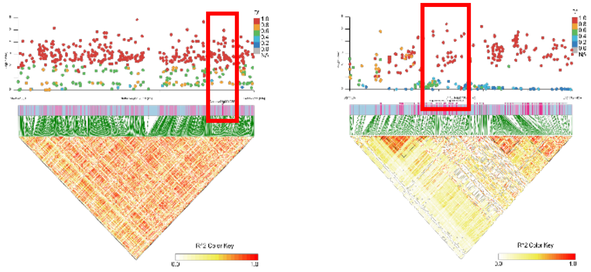
Regression equation of seedling evaluation : $D = -0.16 + 3.85 * PHIR + 0.35 * PROIR - 0.08 * SSIR + 0.40 * SDIR - 0.10 * MDAIR$.

Candidate genes





GWAS analysis

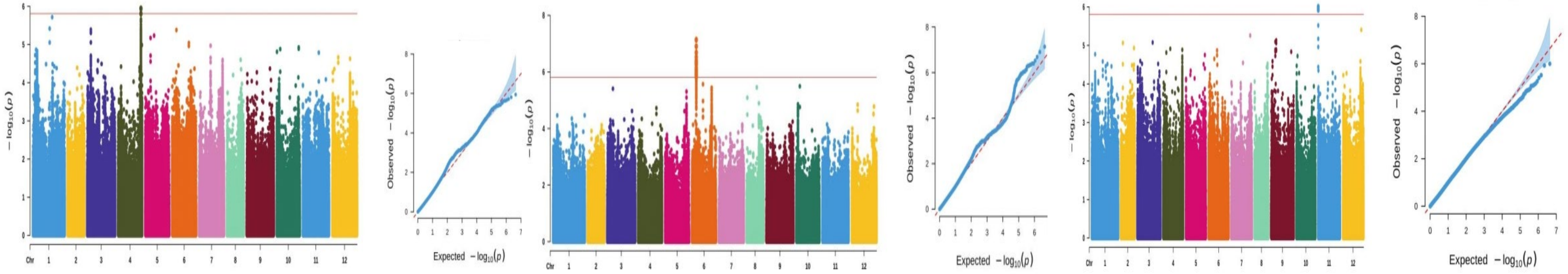


***capana04g001281*, *capana05g000007*, and *capana05g000008* at the missense mutation sites were presumed to be the most likely candidate genes.**

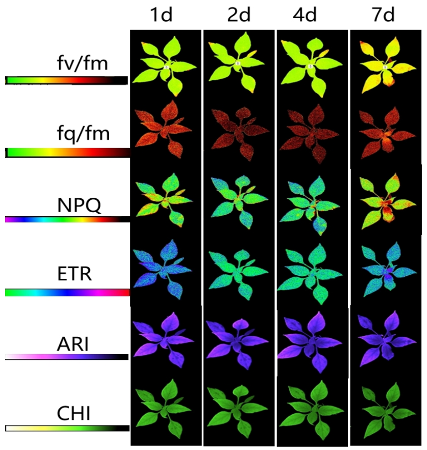
Phenotyping provids insights into the genetic basis of salt tolerance

● Germination -Stage Screening

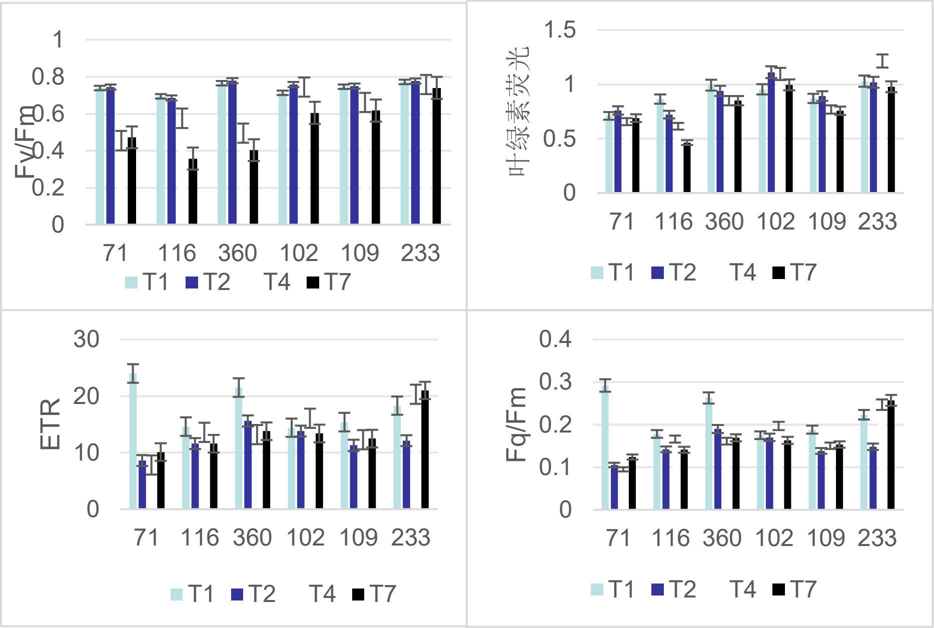
- ➢ 203 pepper core germplasm accessions
- ➢ At the germination stage
- ➢ 44 SNP loci significantly related to salt tolerance on chromosomes 4, 6, and 11. Integrated analysis of functional annotation and transcriptome data highlighted 12 candidate genes,



● seedling-stage phenotypic dataset



PSII maximum quantum yield (Fv/Fm), PSII effective quantum yield (Fq/Fm), electron transport rate (ETR), non-photochemical quenching (NPQ), anthocyanin index (ARI), and chlorophyll index (CHI) imaged at 1, 2, 4, and 7 days after salt stress.



Fv/Fm, chlorophyll fluorescence, Fq/Fm, and ETR in relatively sensitive (71, 116, 360) and relatively tolerant (102, 109, 233) accessions at 1 (T1), 2 (T2), 4 (T4), and 7 (T7) days after salt stress.

● Adult stage under saline-alkaline conditions

Pepper growth in saline-alkaline soil

Pepper growth in normal soil

螺丝椒M-2

中椒黄钻3号

中椒L13

Numex R-Naky

耐寒甜椒

保山椒

Mean Yield Comparison: Experimental vs. Control

Trait	Treatment Group Mean	Control Group Mean	Reduction (%)	Significance ($p < 0.05$)
Single Fruit Weight (g)	10.1 ± 8.2	27.9 ± 12.5	63.8 %	Significant

Trait Mean Comparison: Experimental vs. Control

Trait	Treatment Group Mean	Control Group Mean	Reduction (%)	Significance ($p < 0.05$)
Plant height (cm)	27.2 ± 6.48	57.7 ± 14.73	52.9%	Significant
Plant width (cm)	21.8 ± 6.49	51.7 ± 9.89	57.8%	Significant

Creating *Capsicum* Research and Breeding Materials Through Electron Accelerator Radiation-Induced Mutagenesis

Article in writing

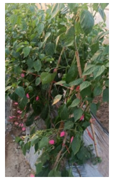
Radiation treatment using a linear electron accelerator (electron beam energy 2 mev, average power 1 kw, minimum resolution dose 5 Gy)

Different seed states

Different irradiation doses

Different irradiation durations

M1, chimera



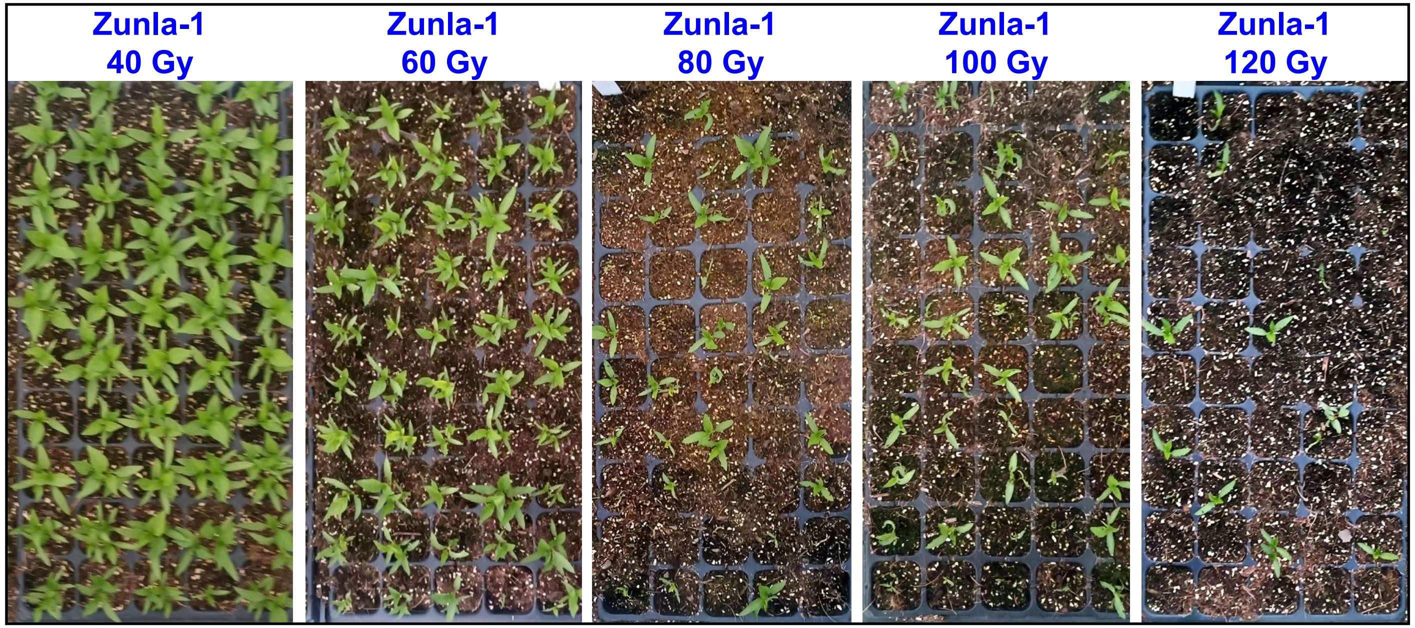
M2, phenotypic screening

M3

Verifying the authenticity and stability of mutant traits

Treatment with different irradiation doses (40 Gy, 60 Gy, 80 Gy, 100 Gy, and 120 Gy) during the germination stage of *capsicum* seeds (Zunla-1, CM334, and Qiemen)

M1



M2

The upcoming work:
Phenotypic Mutation Screening and Statistics

Development of 5K and 20K Liquid Phase Chips for pepper

Article in writing

- ➢ **A medium-density 5K liquid-phase chip and a high-density 20K liquid-phase chip for pepper have been developed. These chips encompass key loci associated with disease resistance, agronomic traits, and fruit taste and nutritional quality (including capsaicin, sugars, organic acids, vitamins, anthocyanins, and flavonoids), providing robust technical support for molecular design breeding in pepper.**

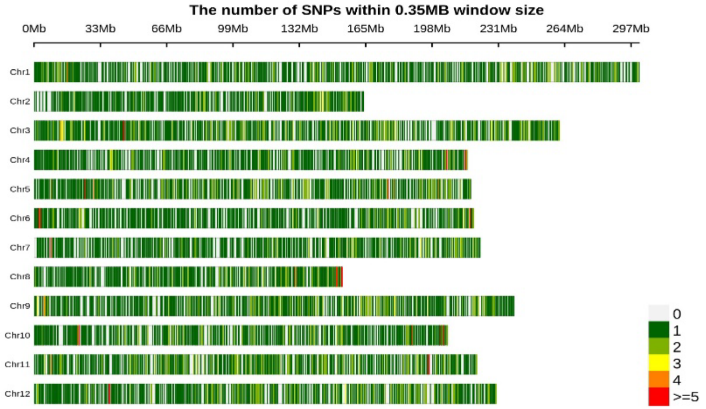
The pepper liquid-phase chip comprises a total of 312 functional sites associated with traits, including 53 disease resistance loci, 48 agronomic trait loci, and 211 fruit quality loci.

Pepper 5K Liquid Phase Chip

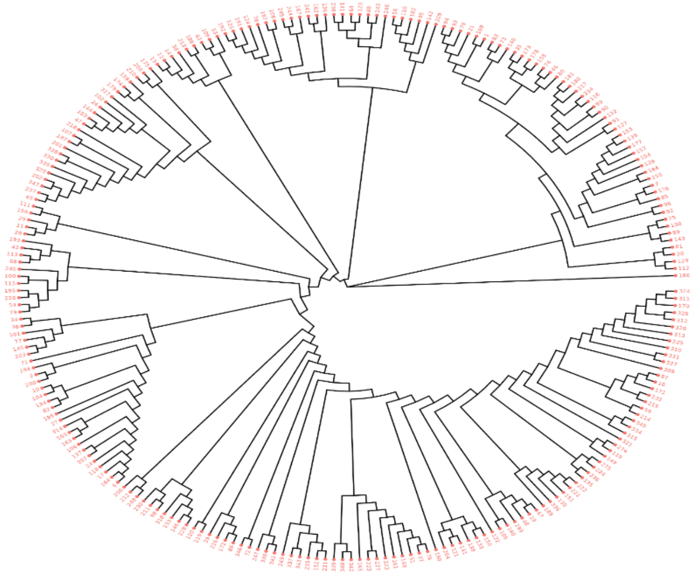
- √ **The 5,297 loci of the pepper genome are evenly distributed across the genome.**
- √ **High site polymorphism with an average MAF of 0.44**
- √ **Within the chip, 276 loci are located on genes, while 4,280 loci are situated in intergenic regions.**
- √ **Developed based on deep sequencing sites, with an average site detection rate exceeding 99%.**

Pepper 20K Liquid Phase Chip

- √ **Detection of 20,292 genetic markers across the pepper genome, uniformly distributed throughout the genome with an average spacing of 160.73 kb.**
- √ **High site polymorphism with an average MAF of 0.38**



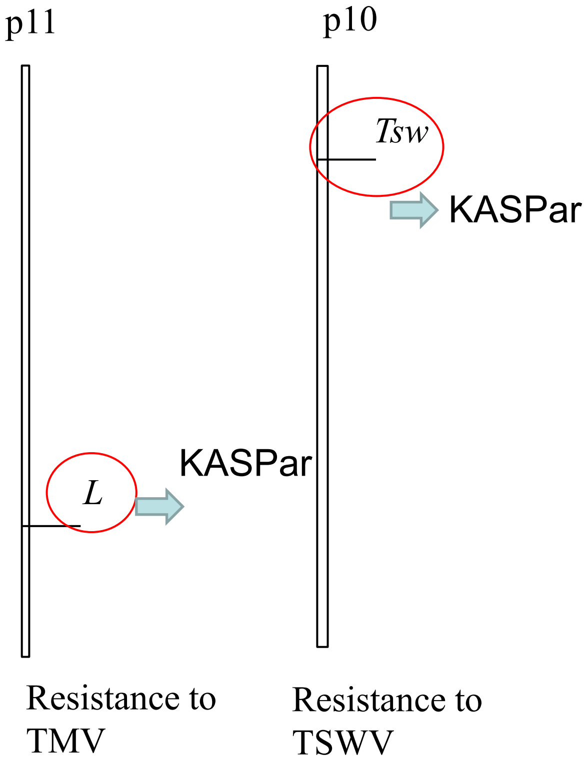
Distribution of 5K Chip Sites Across the Genome

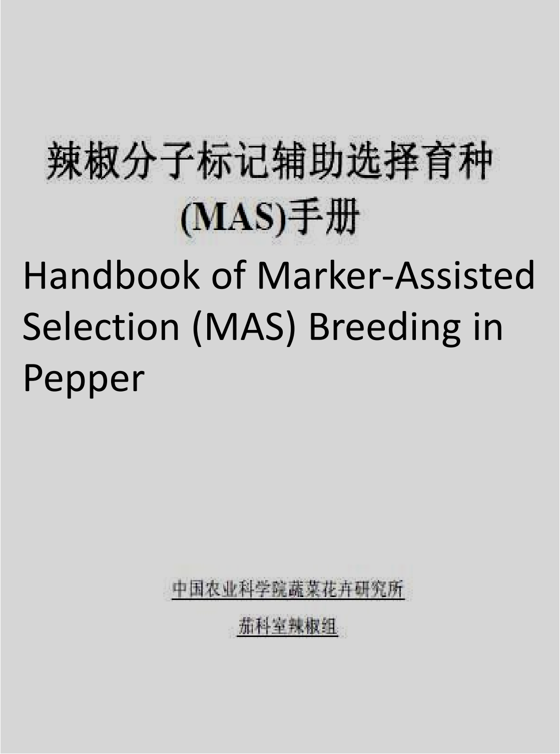


Phylogenetic Tree of 5K Chip SNPs

Establishment of a Molecular Marker Application System

- Determined that resistance to PMMoV and TSWV, controlled by the L^3 and Tsw genes respectively, both follow monogenic dominant inheritance. Developed KASP markers.




辣椒分子标记辅助选择育种(MAS)手册

Handbook of Marker-Assisted Selection (MAS) Breeding in Pepper

中国农业科学院蔬菜花卉研究所
茄科室辣椒组

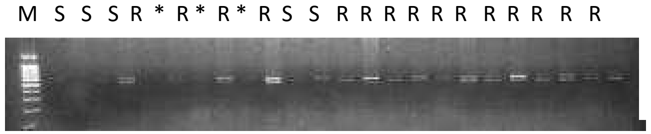
7 Patents

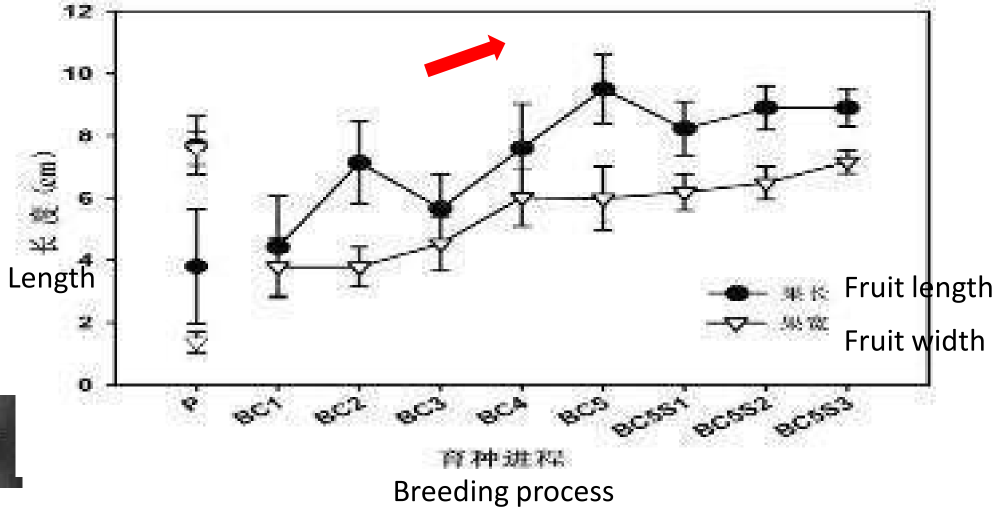
- *Selection accuracy using molecular markers for 9 traits and 11 genes exceeded 90%.Selection accuracy for markers reached 98% and 94% respectively.*

Pepper traits	Gene	Mark	Accuracy	References
Resistance to TMV（PMMoV）	*L^3，L^4*	*SCAR*	*98.2%*	*Kim,2005;Yu et al，Internal materials*
Resistance to TSWV	*Tsw*	SCAR	94%	Moury, 2000；Wang et al, *Patent application*
Resistance to PVY	*Pvr4*	*CAPS*	*97%*	*Wang et al，2008*
Resistance to Scab	*Bs2，Bs3*	SCAR/CAPS	98%	Tai，1999
Resistance to Anthracnose	*Major Gene P5*	Indel	92.9%	*Sun et al,2015;Wang et al，Patent*
Resistance to Root-Knot Nematode	*Me1，N*	SCAR	99.9% /97%	*Wang et al,2009;* *Zhao et al, 2019；Zhang et al，2 patents*
Resistance to CMV	*UN54228*	KASP	99%	*Zhao et al，2009；Zhang et al，Patent*
Resistance to Powdery Mildew	*QTL5*	SSRH6-96	97%	*Wang et al，2009*
Resistance to Phytophthora Blight	*P5.1*	KASP	90%	*Wang et al，Patent*
Capsanthin	*QTL-12-1*	ES236	90%	*Zhang et al，2010*

Example: Molecular Marker-Assisted Breeding – Development of TSWV-resistant Pepper Materials

Introduction No.:200374	**April 2003**
PI152225: 200374	**2007Spring Sunlight Greenhouse 39**
F1(0516×PI152225)	**2007Spring Sunlight Greenhouse 20×39**
BC1（**0516×**PI152225）	2007Autumn Sunlight Greenhouse 10×3
MAS	
BC2(0516×PI152225)	2008Autumn Sunlight Greenhouse 50×6
MAS	
BC3(0516×PI152225)	2009Spring Sunlight Greenhouse 37-2×1
MAS	
BC4(0516 ×PI152225)	2009Autumn Sunlight Greenhouse 49×8
MAS	
BC5 (0516× PI152225)	**2010Spring Greenhouse 5×32**
Disease resistance identification MAS	
BC5 (0516×PI152225) I1	**2010**Autumn Sunlight Greenhouse 47-1 Selfing
MAS	
BC5 (0516×PI152225) I2	2011Spring Greenhouse 15-1 Selfing
Homozygous inbred line: BC5 (0516×PI152225) I3	**2012Spring Greenhouse 80 Selfing**
Disease resistance identification	**Cross combinations made**





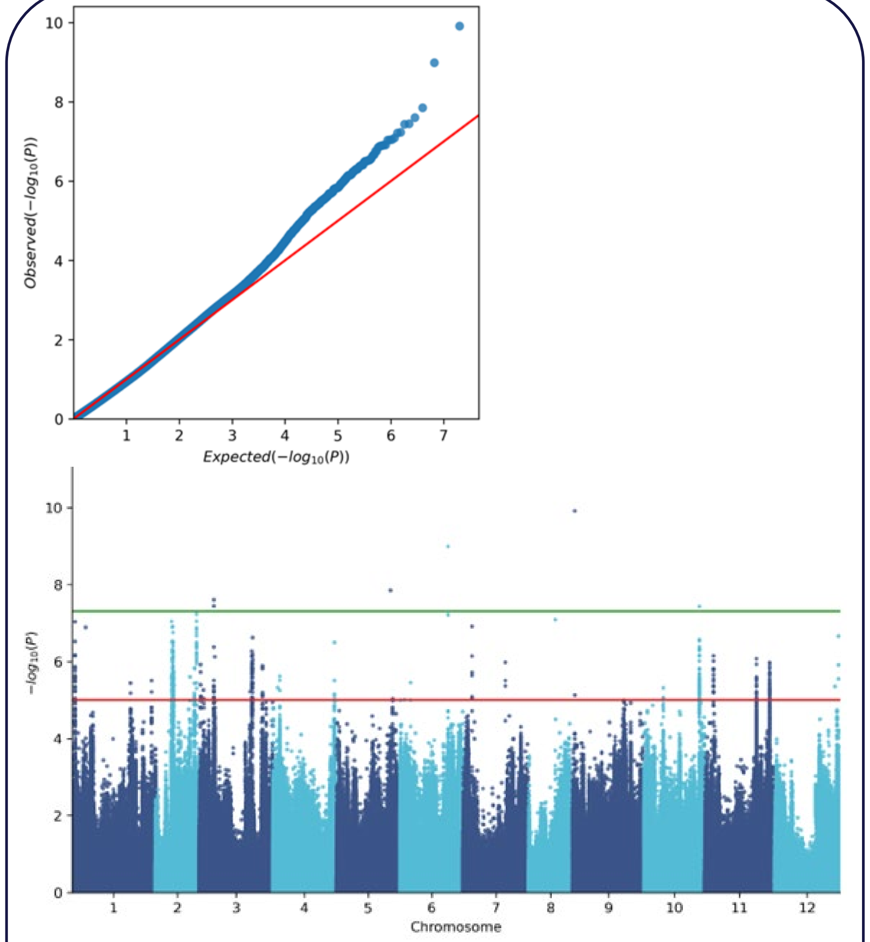
0516（Tsw） 0516 CK

China Vegetables, 2016; China Vegetables, 2019

Research progress -Molecular Design Breeding for New High-Capsanthin Pepper (*Capsicum annuum* L.) Germplasm Resources

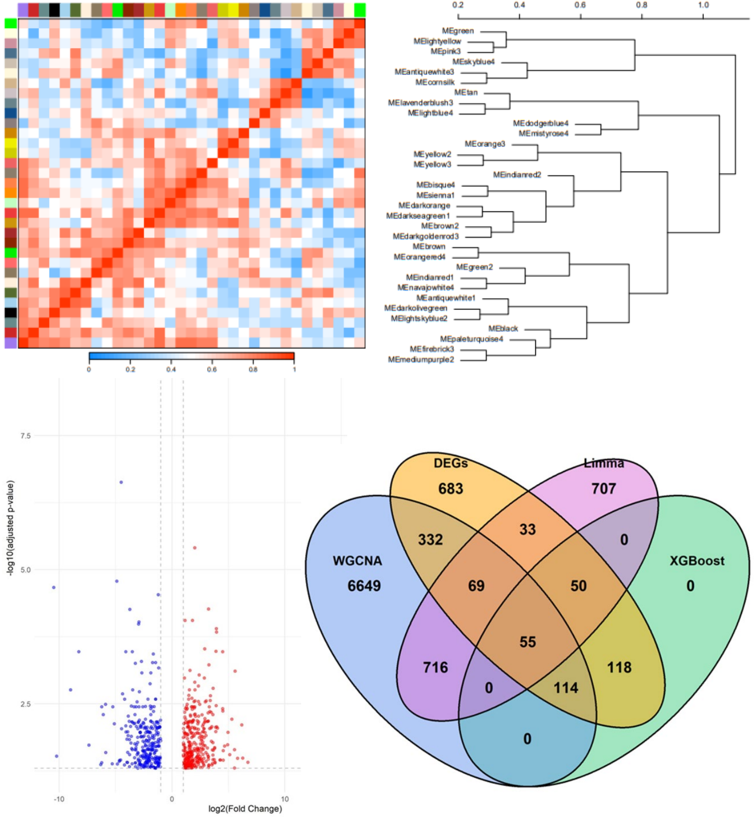
Article in writing

GWAS Analysis



Using phenotypic data from 274 samples and 10,005,012 high-quality SNPs, identifying 41 significant SNPs .

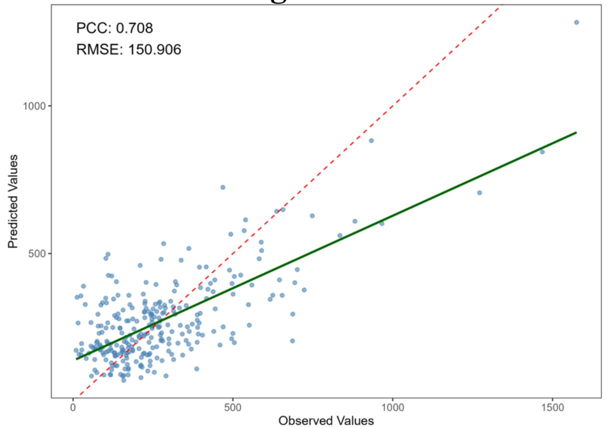
Transcriptome Analysis



Using transcriptome data from the peel during the color-changing period of 10 extreme phenotypic materials, differential expression analysis, XGBoost analysis, linear regression in Limma, and WGCNA were performed to identify pivotal genes with overlapping significance.

Design Breeding

Based on previous research findings, 57 hybrid combinations were selected and bred in Sanya in 2024. The resulting F1 generation was transplanted to Beijing, and phenotypic data were detected using HPLC.



The optimal GS model will be explored by combining the phenotypic data of the F_1 generation and their parents.

Zhongjiao No.1615

✓Large fruits， square lantern shape
✓150-200 grams in weight
✓Green to red
✓Resistant to TMV (P0,1,2)L3，
✓Tolerant to CMV and Phytophthora blight.
✓Suitable for protected production
✓Protected production

Farmer： Wang Jianyong from Sishang Village,
Luannan County Tangshan City

Zhongjiao No.220

Sweet pepper
Mid maturity (40days from planting to harvesting)
Large fruits with long blocky shape, firm and attractive
The flesh thickness is about 0.6cm, the transverse diameter is about 11.0cm and the longitudinal diameter is about 14.0cm.
200-250 grams in weight, high yield
Green to red
The plants grow vigorous
Resistant to TMV(0,1,2) and CMV
Suitable for protected production

Zhongjiao Longblock(1902)

Zhongjiao No.5657

low Temperature and weak Light
Suitable for protected production

Zhongjiao Eearly

Sweet pepper

Early maturity (28 days from planting to harvesting)

Large fruits with bell shape, thin skin, high Vc content and good taste

The flesh thickness is about 0.4cm, the transverse diameter is about 7.0cm and the longitudinal diameter is about 9.6cm.

120-150 grams in weight, high yield

Green to red

Resistant to TMV

Suitable for outdoor and protected production

Zhongjiao Mear2

Sweet pepper

Mid-early maturity(36days from planting to harvesting)

Large fruits with blocky shape, firm, uniform, attractive

Good tolerance to storage and shipment.

The flesh thickness is about 0.45cm, the transverse diameter is about 7.0cm and the longitudinal diameter is about 10.0cm.

100-120 grams in weight, high yield

Green to red

Resistant to TMV (0,1,2)

Suitable for outdoor and protected production

Zhongjiao Mear2-Plus

Resistance to TMV (0,1,2) and TSWV(0)

Zhongjiao No.8281

Sweet pepper
Mid-late maturity
Large fruits with blocky shape
Firm, tolerance to storage and shipment
Flesh thickness is about 0.6cm,
8.0cm ×9.0cm
150-200 grams in weight
Green to red
Plants grow vigorous
Resistant to TMV(0,1,2)
Suitable for outdoor and protected production

Varieties before in South Asian

Zhongjiao No.8281 in South Asian

Zhongjiao Hongzuan No.1

Color pepper varieties
Mid-late maturity (90days from planting to harvesting of red fruits)
Sweet, square lantern
Green to red
The flesh thickness is about 0. 7cm, the transverse diameter is about 8.8 cm and the longitudinal diameter is about 9.6 cm.
200 grams in weight, high yield.
Long shelf life
Resistant to TMV (0,1,2)
Suitable for protected production

Zhongjiao Huangzuan No.2

Color pepper varieties
Mid-late maturity (90days from planting to harvesting of yellow fruits)
Sweet, square lantern
Green to yellow
The flesh thickness is about 0.8 cm, the transverse diameter is about 9.0 cm and the longitudinal diameter is about 9.6 cm.
220 grams in weight, high yield.
Long shelf life
Resistant to TMV (0,1,2)
Suitable for protected production

Zhongjiao Huangzuan No.3

北方保护地专用彩色甜椒品种

Zhongjiao Hongzuan No.2

Color pepper varieties
Mid-late maturity (90days from planting to harvesting of red fruits)
Sweet, square lantern
Green to red
Diameter is about 8.8 cm and the longitudinal diameter is about 9.6 cm.
200 grams in weight, high yield.
Long shelf life
Resistant to TMV (0,1,2)
Suitable for protected production

北方保护地专用彩色甜椒品种 Zhongjiao Hongzuan No.2

Zhongjiao YiPaprika

Cattle horn shape
Mid-early maturity (35days from planting to harvesting of green fruits)
Slightly spicy, good taste, excellent commercial quality and good storage tolerance
45-62 grams in weight, about 12.0*4.0cm
Green to red
Good tolerance to viruses, heat and cold
Suitable for outdoor and protected production

Zhongjiao Sparkle

55-80 grams in weight, about 15.0*5.0 cm, high yield

protected production

Zhongjiao No.H2 For processing

Sheep horn shape
Mid-early maturity
30 grams in weight, about 15.0*3.0cm
Slightly spicy .
Suitable for processing
High redpiment
Suitable for outdoor production

中椒L5

中椒L13

中椒H195号

Color (18)，SHU: 200,000，fruity

Characters：

- 20g/fruit，7cmX3.5cm。
  Resistant to CMV

Zhongjiao D1、D2、D3、D4

Zhongjiao D2:
Single upward-growing fruits;
10 cm long; 1 cm wide,
4 g single-fruit weight;
Green to bright red
Resistance to CMV
Fresh pepper yield of about 22,500 kg/ha.
5,000 SHU

Zhongjiao D3:
Single upward-growing fruits;
12 cm long, 1.2 cm wide,
6 g single-fruit weight;
green to red
Resistance to CMV
Fresh pepper yield of about 33750 kg/ha.
9,000 SHU

Zhongjiao D4:
Single upward-growing fruits;
12cm long
1.1cm wide
7g single-fruit weight;
Green to redd
Resistance to CMV
27,000 SHU

Zhongjiao No.105 and Zhongjiao No.107 were designated as leading varieties by the Ministry of Agriculture and Rural

- All Varieties have addressed issues such as the northward transportation of southern vegetables, highland vegetable cultivation, and newly emerging epidemic diseases in northern protected cultivation, becoming major cultivars.
- All :1.5 M ha extended, 300 Billion $ beneficial to society.

Zhongjiao 105 Grown in Maoming, Guangdong Province

Zhongjiao 106 Planted in Changyang, Hubei Province

Zhongjiao 107 Cultivated in Liaoning Region

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Lihao Wang	Doctoral Supervisor, Research Fellow, Project Leader
Zhengjhai Zhang	Doctor, Associate Research Fellow
Yacong Cao	Doctor, Associate Research Fellow
Huamao Wu	Doctor, Associate Research Fellow
Qiang Su	Doctor, Assistant Research Fellow
Research Assistant:	Jialiang Chen; Yuhuan Li; Shuangshuang Ren; Aiqiong Zhou; Weihua Zhang; Lingling Ma
Doctoral candidate:	Daiyuan Zhou; Xiaolin Xing; Hongbo Ding; Khin Thandar; Zihan Cheng
Master degree candidate:	Jiachi Yan; Na He; Junyue Sun; Huan Xu; Zhuo Liu; Fangqi Zhao; Jiawei Kang; Dan Zhong; Xueyan Dai; Rui Wang; Rongxuan Li; Yiting Chen; Yutong Zhu; Jingyi Chen; Nibigira Vanessa; Na Zhang; Peineng Qi; Qinhao Zhang

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- **Funded by the Science and Technology Innovation Program of the Chinese Academy of Agricultural Sciences**
- **Project of Hainan Yazhou Bay Seed Laboratory**

Dept. of Solunaceous

Tomato (fresh/processing)

Pepper

Eggplant

The department consist 4 research groups of genetic breeding of fresh tomato, processing tomato(*S. lycopersicum*), sweet (hot) pepper (*Capsicum spp*.), and eggplant (*Solanummelongena*) respectively. Facing to the major problems in production of Solanaceous crops, they engage in the discovery of genetics knowledge on main agronomic charzcters, genetics and mechanism of quality, disease resistance and stress to tolerance to improve crop yield, quality and resistance to abiotic and biotic stresses in solanums. Exploration and application of novel breeding strategies including male sterility, cell engineering technique, molecular marker-assisted breeding, whole genomic selection, genetic engineering etc. They also dedicate to germplasm enhancement and development of new varieties.

THANKS!