

WHITE PAPER

Advancing Pepper Genomics: The GenoBaits Pepper Panel Series

Summary

This white paper outlines the SNP selection, design, and application of MolBreeding's Pepper GBTS Panel Series, a comprehensive genomic resource aimed at advancing pepper breeding programs. We summarize the key traits currently prioritized in the global public research domain.

SNP markers have been assembled into a single array, with annotations detailing their associations with specific traits. This will provide breeders and researchers with enhanced insights into the genetic architecture of their materials and the underlying genes. By leveraging this resource, breeding programs can accelerate the selection and integration of superior genes into pepper varieties, effectively addressing market demands and overcoming environmental challenges.

Introduction

Capsicum (*Capsicum* spp.), commonly known as pepper, is an important vegetable and spice crop that originated in the American tropics. Its adaptability and versatility allow for cultivation worldwide, yielding fresh vegetables, dried spices, and valuable nutrients, pigments, and flavor compounds. However, the large and highly repetitive 3 Gb genome of pepper makes whole-genome sequencing costly.

Genotyping by Targeted Sequencing (GBTS) offers a cost-effective, scalable, and efficient alternative. Unlike traditional GBS, which relies on random reduced-representation sequencing and may introduce bias due to factors such as restriction enzyme site distribution, chromatin accessibility, and genotype-specific variation (He et al., 2014), GBTS panels provide a more robust and comprehensive dataset. Compared to whole-genome sequencing (WGS) and endpoint assays like KASP and TaqMan, GBTS panels deliver high-quality genome-wide variation profiling with excellent reproducibility and computational efficiency, making them suitable for large-scale pepper breeding programs (Li et al., 2024).

In collaboration with China Agricultural University, MolBreeding developed **three ready-to-use Pepper GBTS Panels** using publicly available genomic resources. These panels provide comprehensive genome coverage to support genetic diversity analysis, trait-associated loci mapping, hybrid purity testing, and marker-assisted selection.

SNP Selection, Probe Design & Validation

The sequencing data from **2,361** pepper germplasms from five domesticated species (*C. annuum*, *C. chinense*, *C. frutescens*, *C. baccatum*, and *C. pubescens*) are



downloaded from public domain and aligned to the CA_59 reference genome. (Li et al., 2024; Liao et al., 2022). Over a million SNPs are identified from these re-sequencing data.

Collectively, these germplasm resources harbor substantial genetic variation across the pepper genome ($2n = 2x = 24$), these genome-wide polymorphic sites are acquired and further filtered based on following criteria:

- Minimum sequencing depth $\geq 10\times$
- Minor allele frequency (MAF) > 0.05
- Missing rate $< 20\%$
- Heterozygosity $< 5\%$
- Linkage disequilibrium (LD) < 0.4 , to reduce redundancy and ensure informative coverage

A total of **45,389** polymorphisms are selected to be designed in 110bp probes in optimal regions to capture the target variants. The probe regions are further filtered to exclude sequences that could impair capture efficiency or genotyping accuracy, including highly repetitive regions, low-complexity or ambiguous bases, and multi-copy or paralogous loci identified through whole-genome BLAST analysis.

The pepper probe panel are further validated using **420** diverse variety accessions (Li et al., 2024):

1. Panel performance across all accessions has high efficiency. Within the 420 samples, 95% samples have over 97.72% call rate among the target rate.
2. 45K pepper gene chip effectively resolves population structure, consistently clustering accessions with shared genetic backgrounds and breeding histories. In addition, it also reliably distinguishes accessions with similar key phenotypic traits—particularly fruit type and pungency (Figure 1 & 2, Li et al., 2024).



Figure 1 Population structure analysis of 410 pepper germplasms. (A) The 410 pepper germplasms can be classified into six distinct populations. (B) Cross-validation (CV) error assessment for the K value. Population I consisted mainly of 21 accessions with goat horn-shaped, helical fruits; *C. chinense* accessions clustered in Population II; Populations III and IV are dominated by skyward-pointing cultivars; and Populations V and VI are characterized largely by lantern-shaped and sweet pepper types, respectively.

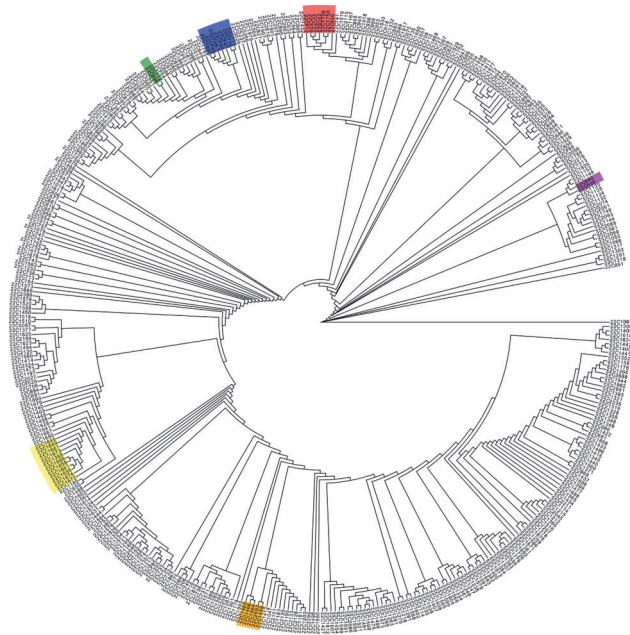


Figure 2 IQtree analysis of the 410 pepper germplasms. In the IQ-TREE analysis, sister lines and closely related materials consistently cluster together. The orange box represents a cluster of sister lines, the yellow box corresponds to a *C. chinense*-dominated group with further subdivision among closely related lines, the red box contains self-pollinated backcross lines carrying the L4 gene, and the blue box comprises backcross progenies carrying the *msc-1* gene with long horn-shaped, mildly pungent fruits. The green box highlights a self-pollinated line clustering tightly with its parental line, further confirming the chip's ability to resolve fine-scale genetic relationships.

To further enhance the panel's value for breeding applications, a comprehensive review of current research is conducted on genes and QTLs underlying major agronomic, quality, and biotic/abiotic stress-related traits in pepper. Based on associations between genomic polymorphisms and these traits, relevant loci are annotated as trait-associated SNPs. The following section summarizes these key traits and highlights some classic genetic components that have been characterized across different *Capsicum* species.

Genetics of Agronomic, Quality, and Reproductive Traits in *Capsicum*

Agronomic traits (Table 1) such as plant architecture, and yield components are foundational to pepper production. Variation in traits like plant type, branching habit, and flowering can substantially influence plant productivity and adaptability. Genomic association studies have revealed extensive genetic variation underlying these traits across diverse pepper germplasm, with hundreds of trait associated single nucleotide polymorphisms (SNPs) identified for agronomic characteristics such as fruit size, plant habit, and yield components. (Fu et al., 2024; Han et al., 2023; Lee et al., 2020; Wu et al., 2019).

Agronomic Traits	Genes	# Associated Markers	Chrom.
Branching habit	<i>Capana09g001660</i> ; <i>PRA1A3</i> , <i>PK1</i> , <i>ATG1</i> ; <i>HDG2</i> ; <i>PURA1</i> ; <i>sck1</i> , <i>RH1</i> , <i>RFK1</i> , <i>NAK</i> ; <i>SNL1</i> ; <i>MGD</i> ; <i>Capana01g004004</i> , <i>Capana01g004005</i> ; <i>XYLT1</i> , <i>SERINC3</i> , <i>PI206</i> , <i>ING1</i> , <i>GATA1</i> , <i>CPN60-2</i> ; <i>YOR131C</i> , <i>SUVH2</i> , <i>RH13</i> , <i>POLR3F</i> , <i>PCMP-H32</i> , <i>MYB59</i> , <i>AMT1-1</i>	15	chr9; chr7; chr1; chr3
Plant type	<i>Capana09g001488</i> , <i>Capana09g001489</i> , <i>Capana09g001491</i> ; <i>DDB2</i> ; <i>LUG</i> ; <i>Capana09g001502</i> ; <i>VAMP725</i> , <i>PANC</i> ; <i>ATJ2</i> ; <i>PUB13</i> , <i>CYCD3-2</i> ; <i>Y-3</i> , <i>GTE7</i> ; <i>SMO2-2</i> , <i>RAB2BV</i> , <i>NPP2</i> , <i>MTPB</i> , <i>HRGPNT3</i> ; <i>TOC75-3</i> , <i>toa1</i> , <i>SMO2-2</i> , <i>RAB2BV</i> , <i>NPP2</i> , <i>MTPB</i> , <i>HRGPNT3</i> , <i>APUM2</i> , <i>APUM1</i> ; <i>TOM22-2</i> , <i>PUP9</i> , <i>PUP10</i> , <i>PER40</i> , <i>IIL1</i> , <i>CRRSP3</i> , <i>CAB3C</i> , <i>Ankrd27</i> , <i>Alg14</i>	14	chr9; chr11; chr6; chr4

Table 1 Key agronomic traits in pepper breeding.

Agronomic Traits	Genes	# Associated Markers	Chrom.
Branching habit	<i>Capana09g001660; PRA1A3, PK1, ATG1; HDG2; PURA1; sck1, RH1, RFK1, NAK; SNL1; MGD; Capana01g004004, Capana01g004005; XYL1, SERINC3, PI206, ING1, GATA1, CPN60-2; YOR131C, SUVH2, RH13, POLR3F, PCMP-H32, MYB59, AMT1-1</i>	15	chr9; chr7; chr1; chr3
Plant type	<i>Capana09g001488, Capana09g001489, Capana09g001489, Capana09g001491; DDB2; LUG; Capana09g001502; VAMP725, PANC; ATJ2; PUB13, CYCD3-2; Y-3, GTE7; SMO2-2, RAB2BV, NPP2, MTPB, HRGPNT3; TOC75-3, toa1, SMO2-2, RAB2BV, NPP2, MTPB, HRGPNT3, APUM2, APUM1; TOM22-2, PUP9, PUP10, PER40, IL1, CRRSP3, CAB3C, Ankrd27, Alg14</i>	14	chr9; chr11; chr6; chr4
Main stem color	<i>ZFP3, ycf2-B, RPL7C, ERF003</i>	2	chr6
Main stem pubescence	<i>RBOHH; WOXX3</i>	11	chr11
Corolla color	<i>Capana08g001752, Capana08g001753; N, GLP2A; TIF3C1, Stard10, NUP160, KOR, FRO7, DFR; 3_Apr, 2_Apr; R1B-12, nep1, med25, ECA3; SPG20; UGT85A5, HSP17.6-L</i>	12	chr8; chr4; chr11; chr2; chr9
Style color	<i>Capana11g000688; TKRP125, Nfrkb; AMY1.1; Capana11g000686; Capana11g000688; Capana11g000699; Capana10g001431;</i>	15	chr10,11
Dry matter content	<i>Capana02g000627, Capana02g000628, Capana02g000629</i>	1	chr2
Flower pedicel growing state	<i>ATG12, ABP19A; EFL3, C1</i>	2	chr12
Leaf margin	<i>AERO1; Capana04g001485, Capana04g001486; Capana04g001487; PVS1, MEE40, LKAP, Gpatch8; RLP12, BZR1</i>	10	chr1; chr4; chr8; chr12
Leaf pubescence	<i>DDB_G0290631; Capana10g001519, Capana10g001520</i>	6	chr12; chr10
Number of flowers per axil	<i>atad1a; Notum; RKL1, pkgA, NUDT17, DDB_G0272282; TIR1; R1B-13, R1A-6, R1A; VPS62, LTP8, HEX1; Capana09g001185; ENO1; LUG; SPCC550.15c; UBP12, R1A-6</i>	23	chr6; chr1; chr9;
Trichome formation	<i>C2H2 ZFP</i>	2	chr2

Table 1 Key agronomic traits in pepper breeding.

Fruit morphology traits (Table 2)—**Fruit size and weight** have been major targets of domestication, ranging from blocky bell peppers to elongated chilies. Interestingly, *C. annuum* and *C. baccatum* achieved similar domestication goals through selection on different genomic regions. In *C. annuum*, strong domestication signals for fruit weight and shape are primarily located on chromosomes 3 and 5, overlapping QTLs such as *fs3.1* and *Han3.1*, whereas in *C. baccatum*, selection targeted

chromosomes 2, 9, and 12, including QTLs like *FT2.1*, *FT9.1*, reflecting independent evolutionary paths to alter fruit morphology (F. Liu et al., 2023). For example, the *fs3.1* locus was one of the first major quantitative trait loci (QTLs) identified for **fruit shape**. Key hub genes, such as *CalQD1*, regulate the fruit length–width ratio by integrating cell cycle control, auxin signaling, and microtubule dynamics through interactions with *CaOPF20*, and cytoskeletal proteins (T. Liu et al., 2024; Mao et al., 2025). Additional loci influencing specialized traits—such as wrinkled surfaces (*wr11*, *wr12*), helical fruit shape (*heli1.1*), and fruit glossiness (*FCD1*)—offer breeders valuable targets for developing fruit types tailored to diverse market and cultural preferences (Ahmed et al., 2024; Li et al., 2024; J. Wang et al., 2023).



Hot and sweet peppers. Photo credit Tripodi, Pasquale & Kumar, Sanjeet. (2019). The *Capsicum* Crop: An Introduction. 10.1007/978-3-319-97217-6_1.

Fruit Morphology Traits	Genes	# Associated Markers	Chrom.
Fruit cracking	<i>EXP4</i>	1	chr2
Fruit glossy	<i>Capana07g000135</i>	1	chr7
Fruit length	<i>Fs3.1/F13.2; TRM25</i>	1	chr3
Fruit ripening	<i>PBG1</i>	2	chr9
Fruit shoulder shape	<i>Capana11g000816</i>	2	chr11
	<i>Capana09g001222</i>	1	chr9
	<i>MUDENG; GATL4; CYCB2-1</i>	1	chr1
Fruit width	<i>SPAC24H6.01c, prfB, Dimt1, CK11, CAL1, AVP1</i>	4	chr8
	<i>Zmat2, SPAC24H6.01c, SAR1A, PCMP-E70, lpdA, CK11, CAL1, AVP1</i>	1	chr8
Helix fruit shape	<i>heli1.1</i>	6	chr11
	<i>heli1.2</i>	1	chr11
	<i>heli2.1</i>	2	chr2

Table 2 Key fruit morphology traits in pepper breeding.

Fruit quality (Table 3) in pepper encompasses traits such as color, nutritional composition, texture, and pungency. Pepper fruits show remarkable variation in carotenoid and anthocyanin content, which determine the colors of both immature and mature fruits and influence their culinary and market value. Genetic variation in the biosynthetic pathways for these pigments, shaped by both natural allelic diversity and human selection, underlies this diversity (F. Liu et al., 2023; L. Wang et al., 2023). For example, *AN2*, an *R2R3-MYB* transcription factor, is a central regulator of anthocyanin accumulation, while other genes involved in carotenoid and anthocyanin biosynthesis, transport, and regulation—including *CHS*, *F3H*, *F3'H*, *PP2C35*, *PSY*, and *CCS*—participate in the complex pathways summarized in Table 3.

Fruit Quality Traits	Genes	# Associated Markers	Chrom.
Sugar content	<i>SWEET9</i>	1	chr2
Immature fruit color (chlorophyll synthesis)	<i>CHLG</i>	3	chr7,9,11
	<i>CPOX</i> ; <i>UROD</i>	5	chr10
	<i>DVR</i> ; <i>GluTR</i> ; <i>PBGS</i>	3	chr1
	<i>GSA-AM</i>	4	chr5,7,10
	<i>MgCh</i>	2	chr2
	<i>MgPMT</i>	1	chr11
	<i>PBGD</i>	1	chr7
	<i>POR</i> ; <i>PPOX</i>	4	chr3,10
Fruit color (carotenoid)	<i>PSY2</i>	1	chr
Fruit color (stay-green phenotype)	<i>SGR1(c)</i>	1	chr1
Fruit color(green stripes on fruit surface)	<i>CaPP2C35</i>	3	chr10
Mature fruit color	<i>E(bx)</i> , <i>CSLA2</i> , <i>ADT6</i> ; <i>RPL12</i> , <i>petA</i> ; <i>saal1</i> , <i>PDAT2</i> , <i>mki67ipl</i> , <i>E(bx)</i> , <i>dsK1</i> , <i>CSLA2</i> , <i>arnA</i> , <i>ALPHAC-AD</i> , <i>ACT-2</i>	3	chr6
Mature fruit color (anthocyanin biosynthesis)	<i>CHS</i>	1	chr5
	<i>F3H</i>	2	chr2,12
	<i>F3'H</i>	2	chr3
	<i>GST</i> ; <i>PAL1</i>	3	chr9
	<i>PMT2</i>	4	chr1,3,11,12
	<i>UFGT</i> ; <i>OXR1</i> ; <i>Capana10g001414</i> ; <i>ACS10</i> ; <i>An2</i> ; <i>Capana10g001381</i> , <i>Capana10g001382</i> , <i>Capana10g001417</i> , <i>Capana10g001418</i> , <i>Capana10g001419</i>	20	chr10
	<i>yipf1</i> , <i>SLC25A17</i> , <i>CPT1</i> , <i>CCX4</i> , <i>CAISE5</i> , <i>BG</i>	1	chr8

Table 3 Key fruit quality traits in pepper breeding.

Pungency, caused by capsaicinoid accumulation, is a hallmark quality trait in *Capsicum*. Wild peppers are typically pungent, and human selection has generated varieties ranging from mild sweet peppers to extremely hot chilies. Genes influencing pungency include *Pun1* (*AT3/CS*), encoding an acyltransferase whose loss-of-function alleles produce non-pungent fruits (Stewart Jr et al., 2005), and the *Cap1/Pun3* locus (*MYB31*), which activates capsaicinoid biosynthetic genes in the fruit placenta. Natural promoter variations in *MYB31* can further enhance pungency, offering breeders a target to develop hotter or milder varieties (Z. Zhu et al., 2019).

Reproductive traits, including flowering time, fertility, and pollination biology, also shape pepper productivity. Two major QTLs, *Ffn2.1* and *Ffn2.2*, on chromosome 2 are strongly associated with first flower node (FFN), a key indicator of fruit earliness (X. Zhang et al., 2019). For pollination, most cultivated peppers are selfpollinating, but male sterility systems—both nuclear and cytoplasmic (CMS)—have been exploited to produce hybrids efficiently. Key male-sterility loci, such as *ms8* and *msc-2*, enable hybrid seed production without labor-intensive emasculation (Bartoszewski et al., 2012; Cheng et al., 2020). Additionally, *restorer-of-fertility* (*Rf*) loci, including candidate genes *Capana06g002967* and *Capana06g002969*, can be used to reverse male sterility (Wu et al., 2019).

Overall, the genetic diversity underlying agronomic, quality, and reproductive traits in pepper provides a rich resource for breeders. By combining natural variation with molecular tools, breeders can tailor cultivars for yield, quality, and market-specific characteristics.

Pungency and Reproductive traits	Genes	# Associated Markers	Chrom.
Pungency/Placental development	<i>Comt</i>	2	chr2,3
	<i>Kas</i>	1	chr1
Pungency	<i>CaERF102</i>	1	chr6
	<i>CaERF111</i>	1	chr4
	<i>SCM002821.1_6775936</i> 2	1	chr10
	<i>Spicy1-15</i> (SNP)	20	chr1,4,6,9,10,12
	<i>viaf</i> , <i>SPL9</i> , <i>nse4</i> , <i>GMPM1</i> , <i>APL</i>	2	chr10
Anther development	<i>DTX35</i>	1	chr3
Male sterility	<i>Rf</i>	4	chr6
	<i>msc-1</i>	1	chr2
	<i>msc-2</i>	1	chr5

Table 4 Key pungency and reproductive traits in pepper breeding.

Genetics of Tolerance/Resistance to Abiotic and Biotic Stress in *Capsicum*

Modern pepper breeding emphasizes not only yield and fruit quality but also tolerance to abiotic stresses (e.g., drought, salinity, and temperature extremes) and resistance to biotic stresses (e.g., viruses, bacteria, fungi, and insect pests). While management practices can mitigate some impacts on yield, breeding and selecting resistant cultivars remain the most cost-effective and sustainable solutions (Pohan et al., 2021).

Abiotic Stress Tolerance

Abiotic stress tolerance (Table 5) in pepper is governed by complex genetic and regulatory networks (J.-K. Zhu, 2016). As extreme weather events become more frequent, breeding cultivars tolerant to heat, cold, drought, and floods is increasingly vital. Advances in molecular genetics have revealed numerous stress-responsive regulators that encode transcription factors, kinases, transporters, and detoxification enzymes (X. Zhang et al., 2024).

1. Mechanisms of Tolerance

1.1 Thermal Stress

Key regulatory gene families, including *HSF*, *NAC*, and *CIPK*, are central to thermal stress responses in pepper:

- **Heat Stress:** This activates the *CaHsp70* family, particularly *CaHsp70-2*, which enhances thermotolerance by inducing downstream heat-responsive genes (Guo et al., 2016). Additionally, small heat shock proteins such as *CaHSP16.4* and *CaHSP25.9* improve heat and drought tolerance by reducing reactive oxygen species (ROS) accumulation (Feng et al., 2019). The transcription factor *CaHsfA1d* further contributes to heat tolerance by promoting glutathione-related antioxidant pathways (Gai et al., 2020).

- **Cold Stress:** The *CBL–CIPK* signaling pathway is crucial; *CaCIPK13* positively regulates cold tolerance, and its loss leads to increased oxidative damage and reduced expression of cold-responsive and antioxidant-related genes (Ma et al., 2022). The conserved *ICE1–CBF–COR* transcriptional cascade governs cold adaptation, linking stress perception with protective downstream gene activation (J.-K. Zhu, 2016).

1.2 Salt Stress

Salt tolerance is modulated by various genes involved in ion homeostasis, antioxidant defense, and stress signaling. Key positive regulators include:

- **NHX antiporters** (e.g., *CaNHX1*, *CaNHX3*), which maintain Na^+/K^+ balance (Luo et al., 2021; H.-X. Zhang et al., 2020).

- *CabHLH035*, which activates *CaSOS1* and *CaP5CS* to promote proline accumulation (Z. Zhang et al., 2022).

Conversely, antioxidant genes like *CaSBP12* and *CaCP15* serve as negative regulators of salt and osmotic stress responses (H.-X. Zhang et al., 2020; Zhou et al., 2023).

1.3 Heavy Metal Stress

CaPCS and *CaHMA1* mediate cadmium detoxification in pepper (Hu et al., 2021; Xu et al., 2023). Additionally, MYB transcription factors enhance lignin and flavonoid synthesis, which helps reduce oxidative damage (Xie et al., 2022).



Abiotic tolerance Traits	Genes	# Associated Markers	Chrom.
Cadmium tolerance	<i>CaHMA1</i>	2	chr2
Cold tolerance	<i>CaCIPK13</i>	1	chr5
	<i>CaNAC1</i>	1	chr5
	<i>CaPLDα4</i>	1	chr3
	<i>CaPOA1</i>	2	chr8
Drought tolerance	<i>CaAIMK1</i>	1	chr7
Heat tolerance	<i>CaHsfA1</i>	1	chr1
	<i>CaHSP60-6</i>	1	chr11
Salt tolerance	<i>CaARR4</i>	1	chr5
	<i>CaARR8</i>	1	chr9
	<i>CaARR9</i>	1	chr11
	<i>CabHLH035</i>	2	chr1
	<i>CabZIP25</i>	1	chr4
	<i>CaHAK7</i>	2	chr9,10
	<i>CaSBP12</i>	1	chr10
	<i>CaWRKY27</i>	1	chr9

Table 5 Key abiotic tolerance traits in pepper breeding.

Biotic Resistance in Capsicum

Biotic resistance (table 6) in pepper involves both vertical (qualitative) and horizontal (quantitative) mechanisms, forming a multi-layered immune system.

1. Mechanisms of Resistance

1.1 Vertical Resistance

Vertical resistance is often race-specific and mediated by major resistance (R) genes from classical families such as *NLRs* (nucleotide-binding leucine-rich repeats), *RLKs* (receptor-like kinases), and *RLPs* (receptor-like proteins). These genes recognize specific pathogen effectors and initiate defense responses, including the hypersensitive response (HR), which restricts pathogen spread.

1.2 Horizontal Resistance

In contrast, horizontal resistance is quantitative and non-race-specific, involving multiple genes that provide partial but durable protection against diverse pathogens. While it does not typically trigger a visible HR, horizontal resistance complements R-gene-mediated vertical resistance, forming a robust defense strategy for pepper.

2. Key Pathogens and Resistance Genes

2.1 Fungal Pathogens

Among fungal threats, *Phytophthora capsici* of Leonian race 2 significantly impacts pepper (Siddique et al., 2019). The gene *CaChiVI2* enhances tolerance to heat and drought by reducing ROS and modulating defense gene expression (Ali et al., 2020).

2.2 Bacterial Pathogens

Classical vertical resistance genes such as *Bs2* and *Bs3* confer race-specific protection against bacteria like *Xanthomonas* spp. (Herbers et al., 1992; Truong et al., 2011). Conversely, recessive genes *bs5* and *bs6* provide non-race-specific resistance, with *bs5* linked to a deletion in the *Ca_CYSTM1* gene (Sharma, 2023; Szabó et al., 2023).

2.3 Viral Pathogens

The *potyvirus* genus, including Pepper severe mosaic virus (*PepSMV*) and Pepper yellow mosaic virus (*PepYMV*), poses significant threats (Inoue-Nagata et al., 2022). Resistance is attributed to:

- Recessive alleles *pvr1* and *pvr2*, providing broad-spectrum resistance (Kang et al., 2005; Rubio et al., 2008).
- Dominant gene *Pvr4* (*Pvr7*), which confers additional broad resistance (Devran et al., 2015; Venkatesh et al., 2018)).
- Recessive genes *pvr6* and *pvr3*, targeting specific viruses like *ChiVMV* and *PepMoV* (Fang et al., 2021).

2.4 Begomoviruses

Resistance genes *Pep1-1* and *Pep1-2* confer resilience to *Pepper yellow leaf curl virus*, aiding in managing these infections (Koeda et al., 2021, 2022).



Insect Resistance Research

Research on insect resistance is less advanced due to its polygenic nature and environmental influences. However, advances in multi-omics technologies and AI-driven phenotyping are facilitating the discovery of new resistance genes. For instance, a QTL for thrips resistance has been identified on chromosome 6, explaining approximately 50% of the variation in thrips larval development (van Haperen et al., 2021). Additionally, QTLs on chromosomes 2 and 4 have been linked to resistance against thrips and aphids (Sun et al., 2020). Resistance to root-knot nematodes in pepper is dominantly controlled by several *Me*-genes and the *N*-gene, clustered on chromosome P9 (Barbary et al., 2015; Fazari et al., 2012).

Breeding Strategies

Modern breeding integrates both vertical and horizontal resistance by pyramiding specific R genes onto backgrounds of broad quantitative resistance. This strategy aims to develop durable cultivars that maintain yield stability while minimizing chemical inputs.

Biotic resistance Traits	Genes	# Associated Markers	Chrom.
Bacterial spot resistance	<i>Bs3</i>	2	chr2
	<i>bs5</i>	1	chr3
Begomovirus resistance	<i>pepy-1</i>	4	chr5
Phytophthora resistance	<i>BRL2</i>	1	chr5
	<i>CaChiVI2</i>	2	chr8
	<i>RPP13</i>	1	chr5
Potyvirus resistance	<i>pvr1/pvr1^{Δ1} /pvr1^{Δ2}; pvr2 and allelic variants</i>	6	chr4
	<i>OCT7</i>	4	chr1,3,6,9

Table 6 Key biotic resistance traits in pepper breeding.

Trait-Associated Markers

SNPs within functional genes, along with their ± 7 kb flanking regions, have been identified as trait-associated SNPs. The MolBreeding Pepper Panel acts as a genotyping tool to assess genetic diversity and support trait-informed marker selection. While the status of these SNPs may not directly indicate a trait or its resistance, they, or their combined haplotypes, are often associated with specific traits.

While these markers suggest associations, they do not guarantee causation. Further analysis linking phenotypic and genotypic data is essential for confirming these associations. Upon validation of key loci, new molecular functional markers can be developed for routine application in marker-assisted selection and breeding programs.

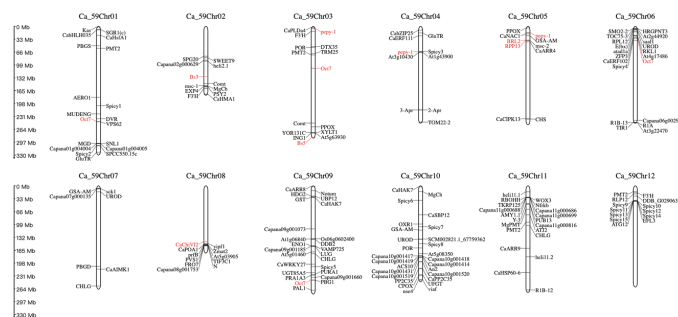


Figure 3 Genomic distribution of SNP markers associated with functional genes and QTL regions across the 12 pepper chromosomes in the GenoBaits 45K Pepper Panel.

GenoBaits Pepper 20K/10K Panel

The 20K panel has 20000 target SNPs and additional 10K mSNPs, with 160 trait-associated markers spanning 28 traits. Project application data are being accumulated, and performance results will be reported as they become available.

The 10K panel includes 10000 target SNPs and additional 5K mSNPs, with 120 target markers associated with 24 traits. Recent projects utilizing this panel have shown the following average performance:

- Alignment Rate: 90.02 %
- Coverage Uniformity 20%*: 91.81 %
- Mean Depth of reads: 33.88
- Target SNP Call Rate: 96.11 %

Product Name	SNP Count	Trait Count	Trait-associated SNP Count	Site Type
GenoBaits Pepper 45K Panel	44,646	30	278	SNP
GenoBaits Pepper 20K Panel	20,000	28	160	SNP
GenoBaits Pepper 10K Panel	10,000	24	120	SNP

Reference Genome: Genome assembly Ca_59_1.0 (GCA_021292125.1)

Table 7. Overview of Three GBTS Ready-to-Use Pepper Panels

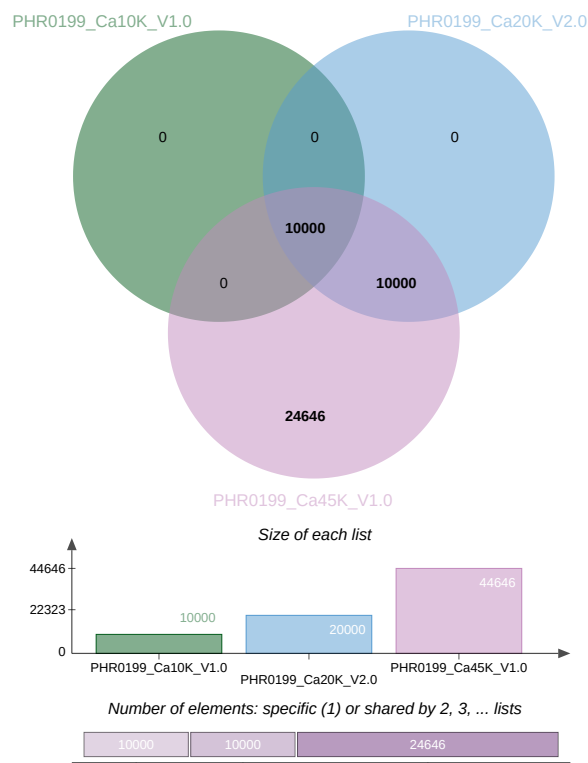


Figure 4. Venn diagram illustrating the overlap of SNP markers among three pepper panels.

Ready-to-Use Pepper GBTS Panels

Three high-quality pepper genotyping panels—10K, 20K, and 45K—have been developed based on trait-associated (foreground) and background SNPs. The 10K and 20K panels consist of evenly distributed subsets of the 45K panel (see Tables 7; Figures 4 & 5).

GenoBaits Pepper 45K Panel

The 45K panel offers high resolution, featuring 44,646 target SNPs along with an additional 27,000 mSNPs (flanking SNPs identified on fragments captured by probes). This panel includes 278 trait-associated markers that cover 30 traits across agronomic, quality, pungency, reproductive, abiotic, and biotic categories, facilitating informed breeding decisions. More details regarding the selection and validation of these 45K markers are available in the study by Li et al. (2024). The following metrics summarize the actual performance data from recent genotyping projects:

- Alignment Rate: 94.87%
- Coverage Uniformity (20%)*: 95.96%
- Mean Depth of Reads: 122.9
- Target SNP Call Rate: 98.50%

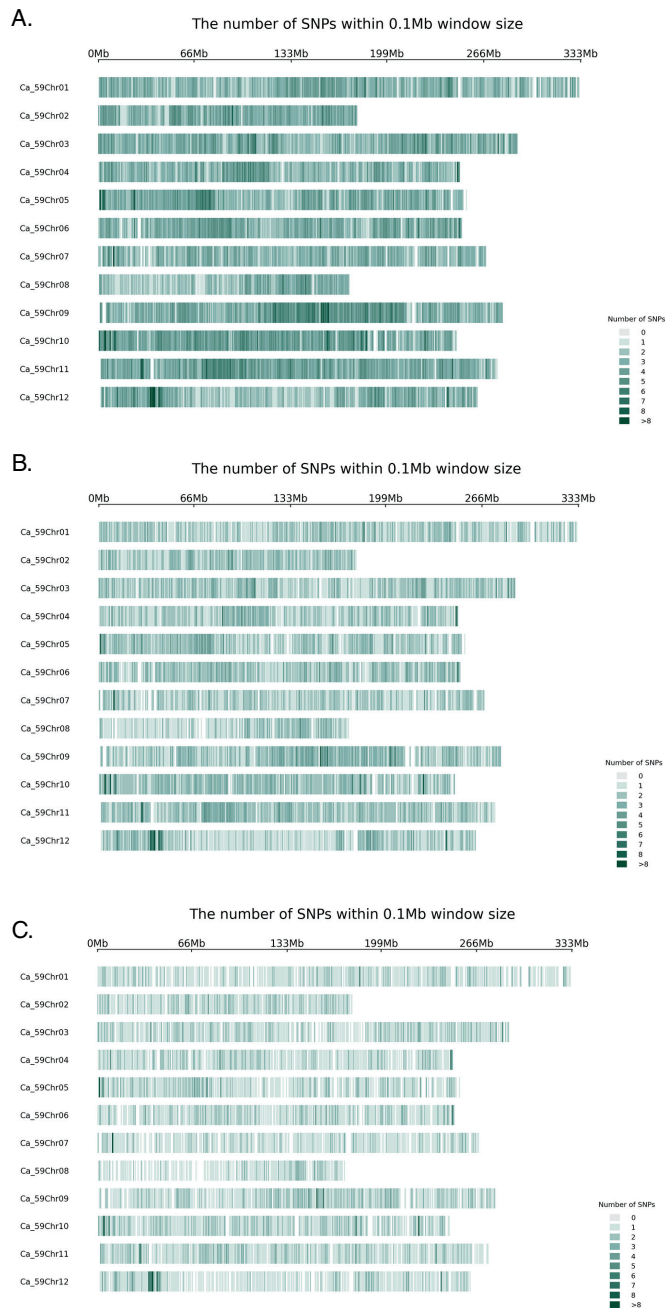


Figure 5. Distribution of Markers in Three Pepper Panels 45K, 20K, 10K. All SNPs are evenly distributed across 12 chromosomes.

Phylogenetic Tree & PCA Analysis Using Pepper 45K Loci

The reliability and accuracy of the 45K Pepper GenoBaits® Panel are confirmed through phylogenetic and diversity analyses, demonstrating that the selected SNPs effectively capture genetic relationships among cultivars and landraces. Sequencing data from 436 wild and cultivated accessions across nine *Capsicum* taxa are analyzed (PRJNA800056 and PRJNA801499) to extract the 45K SNP loci for relationship reconstruction (Table 8).

The genus *Capsicum* includes over 30 species, with five domesticated species—*C. annuum*, *C. frutescens*, *C. chinense*, *C. baccatum*, and *C. pubescens*—commonly cultivated for consumption. A comprehensive genomic analysis of 500 accessions spanning all major domesticated pepper species and their wild relatives utilized a high-quality “graph pan-genome” created from chromosome-level assemblies of representative accessions from the Annuum, Baccatum, and Pubescens clades (F. Liu et al., 2023). This analysis identified three deeply diverged lineages: the Pubescens clade (*C. pubescens*), the Baccatum clade (*C. baccatum*, *C. chacoense*), and the Annuum clade (*C. annuum*, *C. chinense*, *C. frutescens*).

Phylogenetic trees and PCA analyses from the 45K panel confirmed clustering into three deep clades and seven distinct lineages, mirroring the patterns of *Capsicum* evolution and domestication (Figure 6A-B). While minor discrepancies in branching order are noted compared to whole-genome phylogenies—where Pubescens is consistently identified as the earliest-diverging lineage, followed by Baccatum, and Annuum as the most recently diversified (F. Liu et al., 2023; Sebastin et al., 2024)—the overall clustering pattern remained robust. The panel-based tree placed Baccatum at the basal position and Pubescens as intermediate. This shift likely results from the incomplete recovery of about 40% of targeted loci from publicly sourced sequencing data for Pubescens and Baccatum, which can diminish phylogenetic resolution.

Overall, the congruence observed in the phylogenetic trees illustrates that all of MolBreeding’s Pepper panels effectively discriminate evolutionary relationships and domestication signals across diverse pepper germplasm, supporting their utility in germplasm evaluation and introgression-based improvement strategies.

Project ID	Species	Number of sample
PRJNA800056	<i>C. annuum</i> var. <i>annuum</i> .	66
	<i>C. annuum</i> var. <i>glabriusculum</i>	26
	<i>C. baccatum</i> var. <i>baccatum</i>	8
	<i>C. baccatum</i> var. <i>pendulum</i>	99
	<i>C. chacoense</i>	15
	<i>C. chinense</i>	92
	<i>C. frutescens</i>	87
	<i>C. pubescens</i>	37
	<i>C. baccatum</i> var. <i>pendulum</i>	3
	<i>C. annuum</i> var. <i>annuum</i>	66
PRJNA801499	<i>C. baccatum</i> var. <i>pendulum</i>	3
	<i>C. chacoense</i>	1
	<i>C. pubescens</i>	2

Table 8. Summary of *Capsicum* accessions included in Bioproject PRJNA800056 and PRJNA801499.

Conclusion

MolBreeding's Pepper Panels are tailored for modern molecular breeding programs, utilizing high-density probes that have been efficiently captured and thoroughly validated across diverse *Capsicum* species. This design ensures broad applicability and extensive polymorphic site coverage. The panels facilitate accurate germplasm evaluation, phylogenetic analysis, hybrid testing, and the discovery of trait-associated loci, empowering breeders to rapidly unlock genetic potential and promote pepper improvement worldwide.

Call to Action

We invite the pepper research and industry community to collaborate with us in utilizing Pepper GenoBaits Panels to accelerate breeding and genetic discovery. Through this collaboration, we aim to unlock more potential of pepper genetics in modern breeding programs, enabling the development of superior cultivars with enhanced yield, disease resistance, and flavor quality, and shaping a more innovative and sustainable future for pepper cultivation.

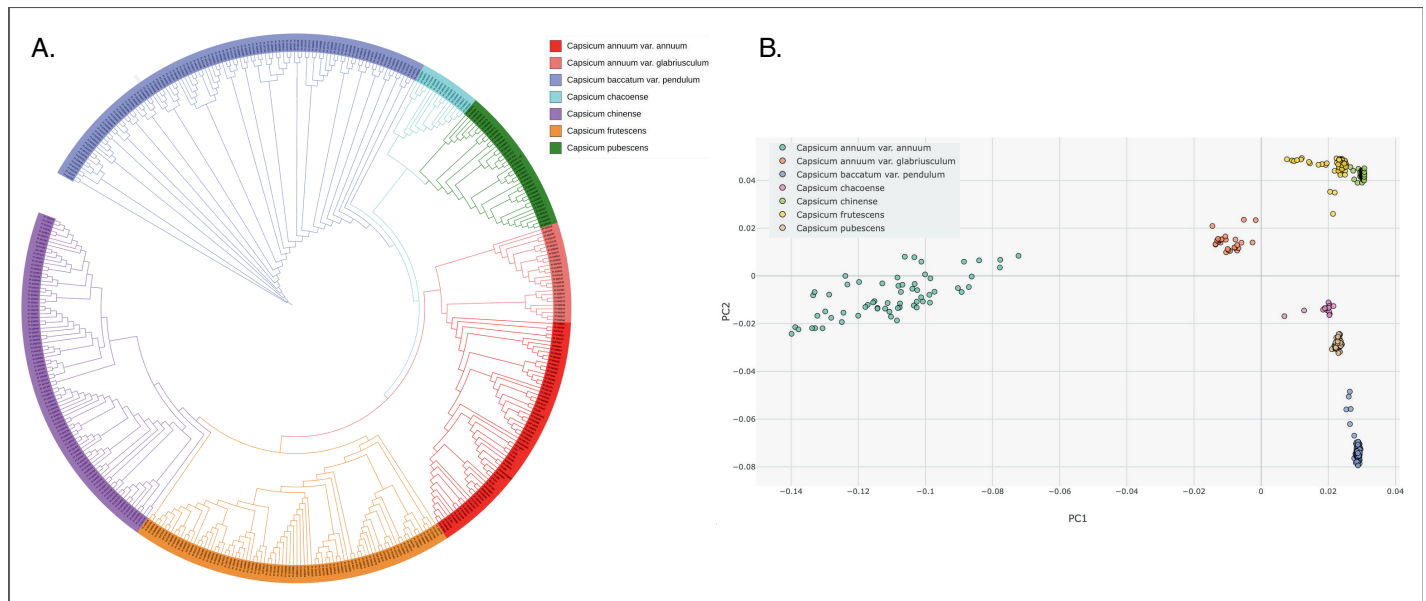


Figure 6. (A) Phylogenetic tree. (B) PCA plot based on the GenoBaits 45K Pepper panel markers, revealing seven distinct lineages, which is highly consistent with the phylogenetic tree.

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