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Heterosis-driven breeding in chilli (*Capsicum annuum* L.) across three diverse agro-climatic regions of Himachal Pradesh

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Abstract

Chilli has immense global importance because of its export value and medicinal properties. The present study focused on the development and evaluation of high-yielding and resilient cultivars of chilli (*Capsicum annuum* L.) across three distinct locations (E1-University of Horticulture and Forestry (UHF), Nauni; E2-Regional Horticultural Research and Training Station (RHR&TS), DhaulaKuan, Sirmour; E3-RHR&TS, Bajaura, Kullu), each specified by varying altitude and temperature conditions. A total of 21 hybrids and 7 parents were evaluated during 2021–22 and 2022–23 using a randomised complete block design (RCBD) in a half-diallel mating design. In this study, the assessed genotypes showed wide variability and significant variations. Crosses viz., Him Palam Mirch 2 × Punjab Guchhedar and Him Palam Mirch 2 × Him Palam Mirch 1 were found promising based on per se performance. The highest standard heterosis was exhibited by Him Palam Mirch 2 × Punjab Guchhedar and the highest heterobeltiosis was exhibited by Pusa Sadabahar × DKC-8 across all the environments and pooled analysis for fruit yield and other yield-associated characters. For quality characters such as oleoresin (%) and total soluble solids (TSS) (°B), hybrids viz., Pusa Jwala × Pusa Sadabahar and Pusa Jwala × DKC-8 outperformed other hybrids across all the environments. Therefore, these hybrids can be utilised effectively for their hybrid vigour to develop high-yielding chilli hybrids with superior quality traits and multi-location heterosis evaluation permits breeders to identify hybrids with consistent performance.

Keywords: chilli; genetic variability; half-diallel; heterobeltiosis; wide adaptability

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1. Introduction

Chilli, popularly referred to as hot pepper, is a member of the genus *Capsicum* belonging to the family Solanaceae, with its centre of origin in Central and South America (1). Cultivated species in this genus include *Capsicum annuum* L., *Capsicum chinense* Jacq., *Capsicum frutescens* L., *Capsicum baccatum* L. (Ruiz & Pavon) and *Capsicum pubescens* (Ruiz & Pavon) (2). *Capsicum annuum* is the most widely grown of all these species, including both pungent chilli and non-pungent bell pepper cultivars. *C. annuum* is the most important vegetable spice crop in India and the country continues to lead the world in chilli production, consumption and exports. The area and production of chilli were 1.28 million hectares and 2.04 million tonnes in 2021 (3). India produces 42 % of chilli and exports 17 % of its total production to countries like Indonesia, Bangladesh, Malaysia, the USA, the United Arab Emirates, Sri Lanka, the United Kingdom and Nepal. The export products made from chilli include dry chillies, pickles, chilli powder and oleoresin. Although India ranks first globally in terms of chilli acreage and production, productivity remains stagnant due to underutilised advanced production methodologies, because the yield has increased from 1.52 tonnes per hectare to 1.59 tonnes per hectare from 2012 to 2021 (3). This slight increase in yield clearly indicates that improvement in yield and productivity has been limited over time. Cultivation of high-yielding F_1 hybrids is a key aspect in achieving productivity increases (4).

Chilli is in high demand across global markets due to its nutritional and medicinal properties. Chilli provides a rich source of bioactive components, specifically ascorbic acid (vitamin C) and capsaicinoids containing the primary component capsaicin, which is highly valued for its anti-inflammatory, anti-cancer, analgesic and antioxidant properties (5). The export

demand for chilli in the commodity market worldwide depends upon taste, oleoresin content and pungency (6). More than 20 capsaicinoids have been identified across various *Capsicum* species (6–8). Apart from capsaicinoids, chilli is valued for its oleoresin and vitamin C content (9). Oleoresin compounds in chilli contain significant amounts of antioxidant and antimicrobial properties (10) and have a huge demand in the food processing sector as it serves as a natural source of colour and flavours in various products like ready-to-eat snacks, beverages and meat products (11, 12).

The genetic constitution of a genotype alone cannot determine trait development. Environmental factors, along with biotic and abiotic stresses, contribute equally. The yield potential and adaptability under various environments of a plant largely depend on plant type. Among different plant characteristics, plant spread or canopy development, has been positively correlated with fruit yield in chilli (13, 14). Vigorous plants produce a maximum number of primary, secondary and tertiary branches, ultimately increasing the number of prospective sites for flower bud initiation and fruit setting (15). Conversely, dwarf or short-statured plants possess distinct advantages, as they exhibit earlier fruiting stages. Yield per hectare can be increased by adopting varieties with compact plant canopies, as they allow closer inter-plant spacing and high-density planting, which results in more efficient usage of available land and inputs (13, 16). Broadly, canopy management and plant vigour have their own advantages and the agronomic practices primarily determine the relative value of either trait. Similarly, fruit features have an important role in determining production. Pericarp thickness, for example, has been shown to be positively connected with individual fruit weight (17) and overall fruit yield per plant (18). Genotypes with larger seeds tend to be nutritionally superior, as such seeds contain a higher concentration of nutrients. These fruit qualities and characteristics influence yield both directly and indirectly and also have a noticeable impact on the market value of chilli-derived products such as oleoresin, capsaicin extract and powdered chilli (15).

Temperature drastically affects plant development and yield in chilli. From 1901 to 2017, India's average yearly temperature rose by about 2.06 °C (19), which could have serious negative impacts on agricultural production. Both high and low temperatures affect plant growth by reducing leaf expansion, inhibiting branching and delaying overall development (20–22). Both low and high temperatures can cause non-viable pollen grains to develop and changes in temperatures may affect flower drop, fruit drop, size and quality (23). Many studies revealed that high temperatures reduced fruit set and development (22, 24, 25). Eventually, genotypes must undergo multi-environmental trials.

Capsicum annuum is predominantly a self-pollinated crop with complete (bisexual) and pentamerous flowers (26) with a flexible reproductive system, but it has been recognised as an often cross pollinated (often allogamous) species, with outcrossing rates as high as 90 % under certain conditions (27) and this genetic behaviour causes genetic diversity for both quantitative and qualitative parameters (28–30), which may be positively used in breeding programs. Diallel analysis is frequently used to increase chilli yield and quality.

However, parental genotypes should not only be considered based on previous performance, but this selection process does not always yield the desired breeding outcomes (31), which underlines the necessity for more rigorous selection procedures. Scientific studies have proved that heterosis can improve various qualities by introducing novel gene combinations (32) and yield increases are frequently associated with improved performance of yield-related attributes. Key characteristics can be improved in chilli through heterosis breeding. Previous research has found heterosis in fruit number (32), fruit yield (33) and quality indices such as soluble solids, oleoresin content (34) and ascorbic acid (35). Although these findings are encouraging, the consistent performance of genotypes across multiple environments remains a difficulty that requires more investigation, so the present investigation is focused on the development of hybrids and evaluation of parental and F_1 genotypes at different locations.

2. Materials and Methods

Parental material

The parental material consisted of seven open-pollinated varieties and 21 F_1 hybrids generated through crosses among the parental lines. The distinct agronomic features of the parental lines with origins are presented in Table 1.

Research sites

The experiment was conducted at three locations representing distinct agro-climatic conditions. The first location was Dr. Yashwant Singh Parmar University of Horticulture and Forestry (YSP UHF), Nauni, Solan, Himachal Pradesh, India, situated at 30°51′54″N, 77°10′08″E and 1300 m above sea level. The second location was the Experimental Research Farm, Dr. YSP UHF, Regional Horticulture Research and Training Station (RHR&TS), Dhaula Kuan, Sirmour, Himachal Pradesh, India, situated at 30°30′20″N, 77°20′30″E and 468 m above sea level. The third location was the Experimental Research Farm, Dr. YSP UHF, RHR&TS, Bajaura, Kullu, Himachal Pradesh, India, situated at 32.8°N, 74.7°E and 1090 m above sea level. The agro-climatic characteristics of the three experimental locations are presented in Fig. 1.

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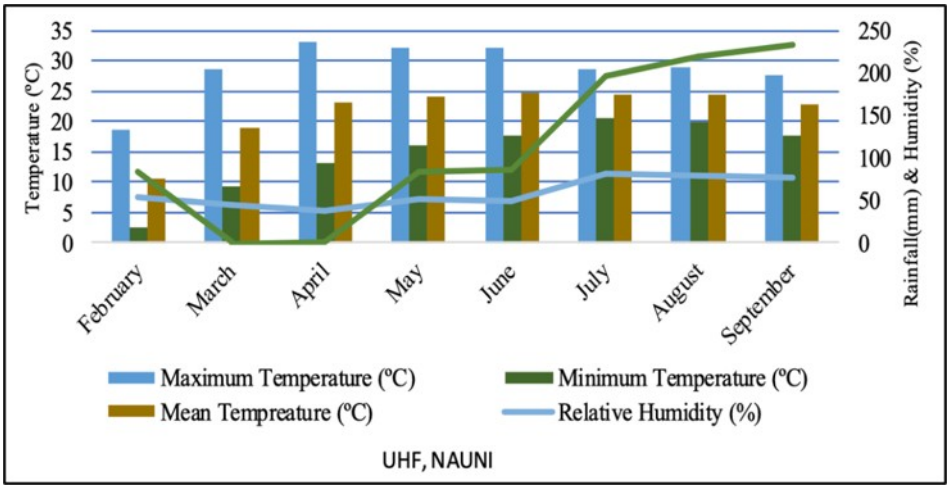
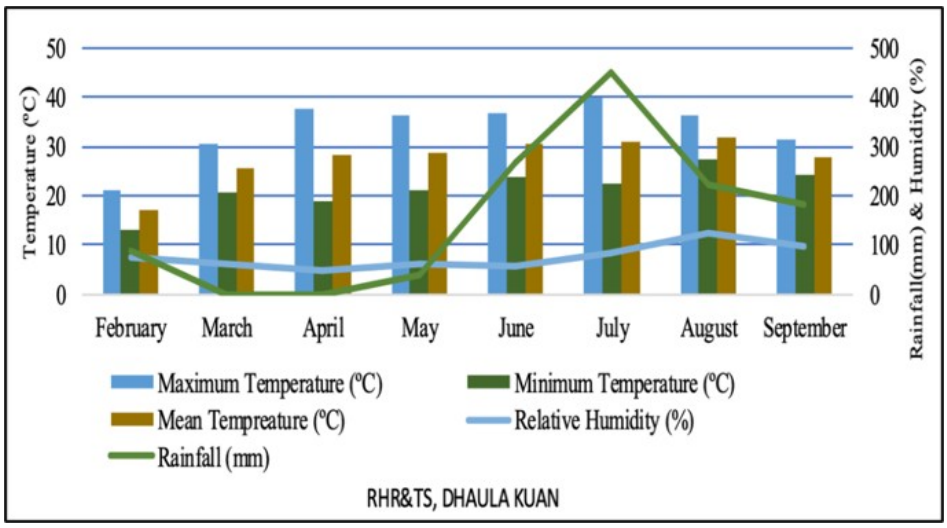
Table 1. List of all the genotypes used in the experiment along with sources and acronyms used

Sl. No.	Acronyms	Genotypes	Agronomic characteristics	Source
1	P1	Him Palam Mirch 2	Fruits are erect, solitary, red and medium long	CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur
2	P2	Him Palam Mirch 1	Fruits are erect, cluster bearing, red and medium sized	CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur
3	P3	Surajmukhi	It is medium tall with profuse branching and perennial. Fruits are dark green and turns deep red at maturity. It is tolerant to leaf curl virus. Suitable for distant markets	CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur
4	P4	Pusa Jwala	Plants are medium in height; fruits are long and thin. Tolerant to thrips, mosaic and leaf curl virus.	Indian Agricultural Research Institute, New Delhi
5	P5	Punjab Guchhedar	Plants stature is tall. Small sized fruits, erect with 5–16 fruits per cluster. Highly tolerant to leaf curl virus and fruit rot. Highly resistant to mosaic. Fruit yield is 60 q/acre	Punjab Agricultural University, Ludhiana
6	P6	Pusa Sadabahar	Plant stature is 60.0–85.0 cm. Upright growth habit. Dark green and broad leaves. Fruits bear in clusters of 6 to 14 that enable bunch harvesting	Indian Agricultural Research Institute, New Delhi
7	P7 (check)	DKC-8 (check)	Medium tall plant stature with profuse branching, perennial. Dark green fruits which turn deep red at maturity, highly pungent	Dr YSPUHF, Nauni

CSK: Chaudhary Sarwan Kumar; YSPUHF: Yashwant Singh Parmar University of Horticulture and Forestry.





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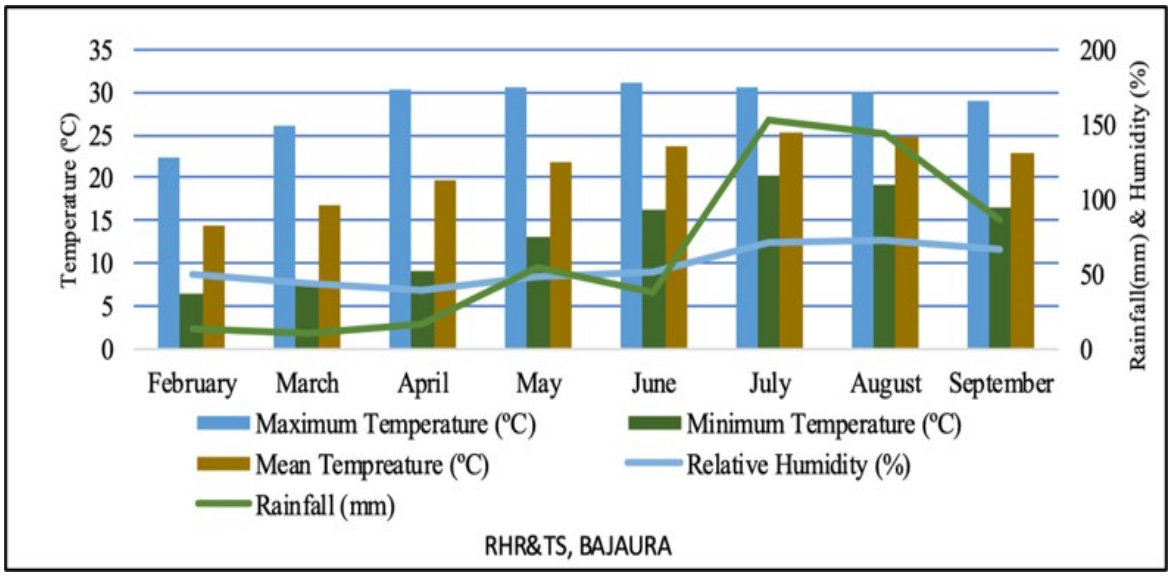

Fig. 1. Meteorological data on temperature, relative humidity and rainfall (February to September, 2022) at UHF,Nauni; RHR&TS, Dhaula Kuan; and RHR&TS, Bajaura.

Development of F_1 hybrids and evaluation of genotypes

Seven open-pollinated cultivars were used as parental genotypes and manually crossed using a half diallel mating design (13) during the first year of study. The crossing operations were carried out between 09:00 and 11:30 hr. To prevent contamination from external pollen sources, the parental plants were completely isolated during the crossing phase by putting them in 24-mesh net cages. During the second year, the genotypes (7 parental lines including the check and 21 F_1 hybrids) were evaluated at three different locations. The genotypes were sown in a randomised complete block design (RCBD) with 3 replications at each location and the data were recorded for 10 plants per plot of size 2.25 × 1.8 m with spacing of 45 cm between inter and intra row each, across all the locations respectively. The package of practices recommended for chilli crop by the Directorate of Extension Education, Dr. YSP University of Horticulture and Forestry, Nauni, Solan, were followed during transplanting (36). The traits selected under assessment were days to 50 % flowering, plant spread, number of primary branches per plant, fruit length, fruit width, red ripe fruit yield per plant, thousand seed weight, total soluble solids and oleoresin. Red ripe fruits per plant were obtained at each picking from ten selected healthy plants and were averaged during the last picking to estimate heterosis for the individual traits under investigation. The date of sowing and transplanting of seedlings across all the locations is given in Table 2.

Table 2. Experimental locations with date of sowing and transplanting of genotypes

Locations	Date of sowing	Date of transplanting
YSPUHF, Nauni	01/Mar/2022	07/May/2022
RHR&TS, Dhaula Kuan	27/Feb/2022	11/Apr/2022
RHR&TS, Bajaura	15/Mar/2022	5/May/2022

RHR&TS: Regional Horticultural Research and Training Station; YSPUHF: Yashwant Singh Parmar University of Horticulture and Forestry.

Analysis of variance (ANOVA) and estimation of heterosis

The analysis of raw data for quantitative and qualitative traits was performed using R and PBTools, while a heatmap was generated using the function 'pheatmap()' in R software, whereas figures were generated via Microsoft (MS) Excel and PAST version 4.15. The analysis of variance (ANOVA) table across pooled environments for all the studied traits is presented in Table 3. The genotype × environment interaction (GEI) is found significant for most of the traits, indicating that the performance and magnitude of heterosis are significantly influenced by the environments. Therefore, it creates the necessity to evaluate the genotypes for heterosis studies across environments. The extent of heterosis was calculated based on data from different quantitative and fruit quality traits. Heterosis values were expressed as the percentage increase or decrease in the mean performance of F_1 over the better parent (heterobeltiosis) and the standard variety (standard heterosis) (37).

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Table 3. Analysis of variance (mean squares) over environments for different characters in chilli

Sl. No.	Characters	Source of variation: Env. (E)	Rep/ Env.	Genotypes (G)	Parents (P)	Hybrids (F1)	P vs F1	G × E	P × E	F1 × E	(P vs F1) × E	Pooled Error
		2	6	27	6	20	1	54	12	40	2	162
1.	Days to 50 % flowering	331.45*	4.02	67.37*	81.77*	63.87 *	50.82*	2.50	2.38	2.66	0.03	2.76
2.	Number of branches per plant	18.17*	0.84	3.49*	2.39*	3.80*	3.86*	0.27	0.20	0.29	0.11	0.56
3.	Plant spread (cm)	688.90*	4.05	155.88*	22.55*	203.21*	9.22	12.20*	6.80*	12.34*	41.815*	2.86
4.	Fruit length (cm)	5.25*	0.22	21.52*	18.87*	22.95*	8.87*	0.10	0.04	0.11	0.30	0.14
5.	Fruit width (cm)	0.02*	0.001	0.09*	0.06*	0.10*	0.01*	0.002*	0.00	0.002 *	0.003*	0.001
6.	Red ripe fruit yield per plant (g)	92799.20*	116.86	108779.50*	46562.23*	121345.80*	230757.40*	4095.79*	1995.07*	4906.74*	481.26*	98.42
7.	1000 seed weight (g)	1.68*	0.01	0.58*	0.40*	0.65*	0.38*	0.065*	0.04*	0.08*	0.02	0.01
8.	Oleoresin (%)	19.22*	0.08	19.25*	18.88*	20.31*	0.17	2.63*	0.05	3.42*	2.33*	0.11
9.	TSS (°B)	14.49*	0.57	5.04*	9.78*	3.75*	2.49*	1.94*	0.20	2.46*	1.86*	0.32

*Significant at 5 % level of significance.

Heterobeltiosis

It is determined by the difference between F_1 and the better parent (38) and is calculated by using the following formula:

$$\text{Heterobeltiosis (\%)} = \frac{\overline{F1} - \overline{BP}}{\overline{BP}} \times 100 \quad \text{Eq. 1}$$

Where:

$\overline{F1}$ = Mean performance of F_1

$\overline{BP}$ = Mean value of better parent of respective cross combination

Standard heterosis

$$\text{Standard heterosis (\%)} = \frac{\overline{F1} - \overline{SC}}{\overline{SC}} \times 100 \quad \text{Eq. 2}$$

$\overline{F1}$ = Mean performance of F_1

$\overline{SC}$ = Mean performance of standard check

The standard error of difference for heterobeltiosis and standard heterosis was calculated as follows:

$$\text{S. E. (d)} = \sqrt{\frac{2Me}{r}} \quad \text{Eq. 3}$$

Where:

M_e = Error mean square (M_e)

r = Number of replications

The test of significance of heterobeltiosis and standard heterosis was done by '*t*' test as under:

t-test for heterobeltosis

$$t = \frac{\overline{F1} - \overline{BP}}{S.E._{(d)}} \quad \text{Eq. 4}$$

t-test for economic heterosis

$$t = \frac{\overline{F1} - \overline{SC}}{S.E._{(d)}} \quad \text{Eq. 5}$$

We compared the estimated "*t*" value to the table value of "*t*" at the 5 % and 1 % levels of significance for the error degrees of freedom. In both instances of heterosis, crucial differences (CD) were calculated using the following formula:

$$CD = SE(d) \times t_{0.05} \text{ at error d.f.} \quad \text{Eq. 6}$$

3. Results and Discussion

Days to 50 % flowering

Early flowering is always desirable in chilli (34, 39). The assessments of heterobeltiosis ranged from -1.11 to -14.44 in E1, -14.37 to 3.01 in E2 and -15.34 to 1.67 in E3 environments respectively. Ten hybrids in E1 and E2 and seven in E3 exhibited earlier flowering than their relevant parents, presenting heterosis in the required (negative) direction for days to 50 % flowering. The highest desirable heterobeltiosis was witnessed in the

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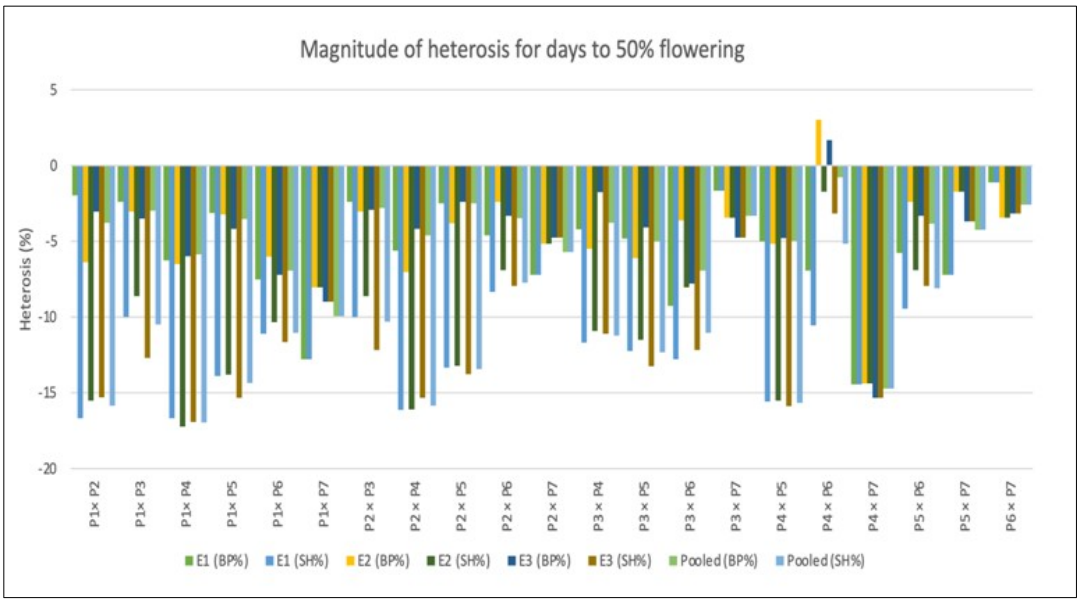
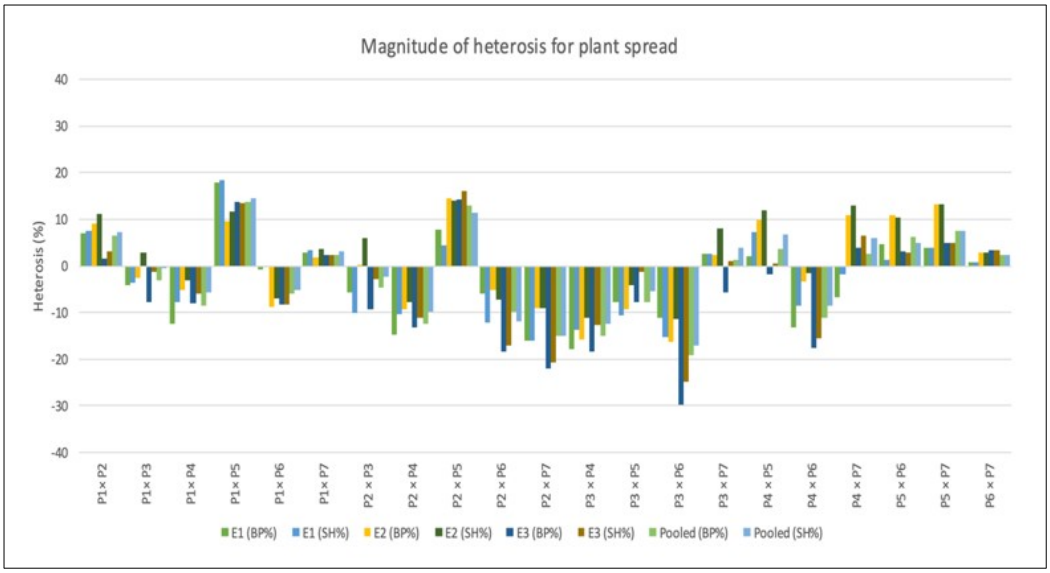
hybrid P4 × P7, having values of -14.44 % in E1, -14.37 % in E2 and -15.34 % in E3 respectively (Fig. 2). Pooled data analysis revealed that heterobeltiosis ranged from -0.77 % (P4 × P6) to -14.73 % (P4 × P7). The highest negative heterobeltiosis was observed in P4 × P7 (-14.73 %), followed by P1× P7 (-9.94 %).

Economic heterosis over the standard check variety (P7) was discovered to be significant in 19, 17 and 18 crosses in E1, E2 and E3 respectively, in the required (negative) direction. The values of standard heterosis varied from -1.11 to -16.67 % in E1, -1.72 to -17.24 % in E2 and -3.17 to -16.93 % in E3 environments over check P7. In E1, the crosses P1× P4 (-16.67 %) and P1× P2 (-16.67 %), in E2, the crosses P1× P4 (-17.24 %) and P2 × P4 (-16.09 %) performed well, while in E3, P1× P4 (-16.93 %) and P4 × P5 (-15.87 %) recorded desirable heterotic effects. Pooled analysis across locations further signified that P1× P4 (-16.94 %) exhibited the highest significant negative heterosis over the standard check (P7), followed by P2 × P4 (-15.84 %) (Table 4). The direction and magnitude of heterosis varied among crosses and locations, as genes responsible for flowering are highly responsive to climatic conditions, causing the same hybrids to flower at different times under varied environmental conditions (40, 41). The consistent performance of P4 × P7 across all the environments indicates the complementary genetic background of its parents and the favourable interaction among the parental alleles responsible for controlling flowering (42). The superiority of early flowering in chilli hybrids has also been reported earlier by previous researchers (33, 34, 39, 40, 42–44).





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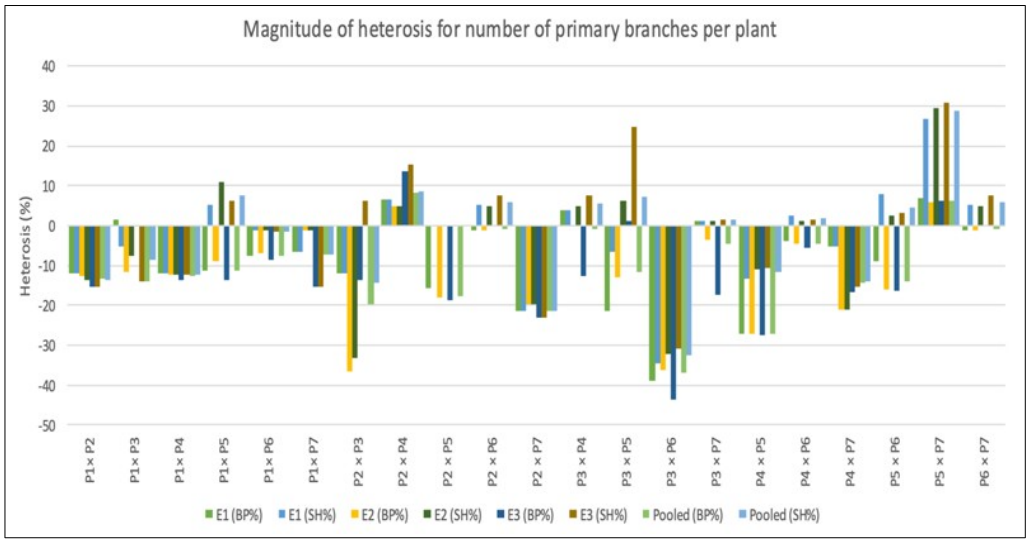

Fig. 2. Magnitude of heterosis for days to 50 % flowering, plant spread and primary branches per plant.

Table 4. Estimation of heterobeltiosis (BP) and standard heterosis (SH) for days to 50 % flowering

Sl. No.	[a]Genotype	Better Parent (BP %)				Standard Heterosis (SH %)			
		E1	E2	E3	Pooled	E1	E2	E3	Pooled
1	P1 × P2	-1.96	-6.37	-3.03	-3.79	-16.67*	-15.5*	-15.3*	-15.84 *
2	P1 × P3	-2.41	-3.05	-3.51	-2.99	-10.00*	-8.62 *	-12.70 *	-10.50 *
3	P1 × P4	-6.25*	-6.49*	-5.99*	-5.85*	-16.67*	-17.24 *	-16.93 *	-16.94 *
4	P1 × P5	-3.12	-3.23	-4.19	-3.53	-13.89 *	-13.79 *	-15.34 *	-14.36 *
5	P1 × P6	-7.51 *	-6.02 *	-7.22 *	-6.94 *	-11.11 *	-10.34 *	-11.64 *	-11.05 *
6	P1 × P7	-12.78 *	-8.05 *	-8.99 *	-9.94 *	-12.78 *	-8.05 *	-8.99 *	-9.94 *
7	P2 × P3	-2.41	-3.05	-2.92	-2.79	-10.00 *	-8.62 *	-12.17 *	-10.31 *
8	P2 × P4	-5.63 *	-7.01 *	-4.19	-4.59	-16.11 *	-16.09 *	-15.34 *	-15.84 *
9	P2 × P5	-2.50	-3.82	-2.40	-2.49	-13.33 *	-13.22 *	-13.76 *	-13.44 *
10	P2 × P6	-4.62	-2.41	-3.33	-3.47	-8.33 *	-6.90 *	-7.94 *	-7.73 *
11	P2 × P7	-7.22 *	-5.17 *	-4.76 *	-5.71 *	-7.22 *	-5.17 *	-4.76 *	-5.71 *
12	P3 × P4	-4.22	-5.49 *	-1.75	-3.79	-11.67 *	-10.92 *	-11.11 *	-11.23 *
13	P3 × P5	-4.82	-6.10 *	-4.09	-4.99 *	-12.22 *	-11.49 *	-13.23 *	-12.34 *
14	P3 × P6	-9.25 *	-3.61	-7.78 *	-6.94 *	-12.78 *	-8.05 *	-12.17 *	-11.05 *
15	P3 × P7	-1.67	-3.45	-4.76 *	-3.31	-1.67	-3.45	-4.76 *	-3.31
16	P4 × P5	-5.00	-5.16 *	-4.79	-4.98	-15.56 *	-15.52 *	-15.87 *	-15.65 *
17	P4 × P6	-6.94 *	3.01	1.67	-0.77	-10.56 *	-1.72	-3.17	-5.16 *
18	P4 × P7	-14.44 *	-14.37 *	-15.34 *	-14.73 *	-14.44 *	-14.37 *	-15.34 *	-14.73 *
19	P5 × P6	-5.78 *	-2.41	-3.33	-3.85	-9.44 *	-6.90 *	-7.94 *	-8.10 *
20	P5 × P7	-7.22 *	-1.72	-3.70	-4.24	-7.22 *	-1.72	-3.7	-4.24
21	P6 × P7	-1.11	-3.45	-3.17	-2.58	-1.11	-3.45	-3.17	-2.58
	Number of significant crosses in desirable direction	10	10	07	07	19	17	18	18
	SE ±	2.6	2.43	1	0.55	2.6	2.43	1	0.55

* Significant at 5 % level of significance where, E1 = UHF, Nauni, E2 = RHR&TS, DhaulaKuan and E3 = RHR&TS, Bajaura. aGenotype acronyms given in Table 1.

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Plant spread

Heterobeltiosis for plant spread showed vast variations across the locations, varying from -17.86 % (P3 × P4) to 17.81 % (P1× P5) in E1, -16.24 % (P3 × P6) to 14.52 % (P2 × P5) in E2 and -29.86 % (P3 × P6) to 14.36 % (P2 × P5) in E3. Significant and positive heterobeltiosis was observed in 3 hybrids in E1, 7 in E2 and 3 in E3, indicating the presence of exploitable genetic variability for this trait. Environments viz. E1, the crosses P1× P5 (17.81 %), P2 × P5 (7.88 %), P1× P2 (7.10 %) documented the highest positive heterobeltiotic effects and in E2, P2 × P5 (14.52 %), P5 × P7 (13.33 %), P4 × P7 (10.91 %) were acknowledged as superior combinations. Equally, in E3, P2 × P5 (14.36 %), P1× P5 (13.68 %), P5 × P7 (5.04 %) presented desirable heterotic responses.

Pooled analysis (Fig. 2) further confirmed that better parent heterosis ranged from -19.14 % (P3 × P6) to 13.64 % (P1 × P5). The cross P1 × P5 (13.64 %) conveyed the highest positive heterobeltiosis, followed by P2 × P5 (12.95 %), indicating their steady superiority across all the environments. Economic heterosis over the check variety (P7) also confirmed vast variations and varied from -16.15 % (P2 × P7) to 18.40 % (P1× P5) in E1, -11.48 % (P3 × P6) to 13.95 % (P2 × P5) in E2 and -24.93 % (P3 × P6) to 16.18 % (P2 × P5) in E3 locations. 3, 9 and 4 hybrids in E1, E2 and E3 respectively, unveiled significant positive standard heterosis for plant spread, suggesting that these crosses are worthy under different environmental conditions. Among the F_1 hybrids, P1 × P5 (18.40 %), P4 × P5 (7.38 %) and P1× P2 (7.63 %) performed best in E1. In E2 location, the crosses P2 × P5 (13.95 %), P5 × P7 (13.33 %) and P4 × P7 (12.96 %) showed excellent performance, whereas in E3 environment, P2 × P5 (16.18 %), P1 × P5 (13.53 %) and P4 × P7 (6.50 %) were identified as assuring combinations (Fig. 2). The pooled estimates over environments further revealed that P1 × P5 (14.56 %) recorded the highest significant positive heterosis over the standard check, followed by P2 × P5 (11.47 %) (Table 5), indicating their potential for successful plant spread in chilli. Significant and positive heterosis of hybrids over parents reveals superior vegetative vigour resulting from favourable complementary distribution of parental genomes, leading to improved canopy growth in the F_1 hybrids (45). The variations among crosses across locations for plant spread are because of varied temperature, radiation, and soil nutrients, as these factors strongly influence canopy growth and plant stature, causing single hybrids to express different levels of plant spread under contrasting environments (15). These results are in conformity for existence of significant heterotic effects for plant spread in chilli hybrids (15, 39, 46).

Table 5. Estimation of heterobeltiosis (BP) and standard heterosis (SH) for plant spread (cm)

Sl. No.	[a]Genotype	Better Parent (BP %)				Standard Heterosis (SH %)			
		E1	E2	E3	Pooled	E1	E2	E3	Pooled
1	P1 × P2	7.10 *	8.96 *	1.44	6.51 *	7.63 *	11.11 *	3.05	7.36 *
2	P1 × P3	-4.23	-2.57	-7.68 *	-3.14	-3.75	2.96	-1.19	-0.63
3	P1 × P4	-12.38 *	-5.08	-8.03 *	-8.49 *	-7.88 *	-3.21	-5.84 *	-5.63 *
4	P1 × P5	17.81 *	9.56 *	13.68 *	13.64 *	18.40 *	11.73 *	13.53 *	14.56 *
5	P1 × P6	-0.87	-8.72 *	-8.23 *	-5.92 *	-0.38	-6.91 *	-8.36 *	-5.16
6	P1 × P7	2.86	1.69	2.39	2.35	3.38	3.7	2.39	3.17
7	P2 × P3	-5.65 *	0.35	-9.29 *	-4.74	-10.14 *	6.05 *	-2.92	-2.29
8	P2 × P4	-14.76 *	-9.45 *	-13.21 *	-12.47 *	-10.39 *	-7.78 *	-11.14 *	-9.73 *
9	P2 × P5	7.88 *	14.52 *	14.36 *	12.95 *	4.51	13.95 *	16.18 *	11.47 *
10	P2 × P6	-5.90 *	-5.29	-18.41 *	-9.84 *	-12.14 *	-7.16 *	-17.11 *	-12.02 *
11	P2 × P7	-16.15 *	-9.01 *	-21.93 *	-15.15 *	-16.15 *	-9.01 *	-20.69 *	-15.15 *
12	P3 × P4	-17.86 *	-15.89 *	-18.46 *	-15.14 *	-13.64 *	-11.11 *	-12.73 *	-12.48 *
13	P3 × P5	-7.75 *	-9.35 *	-7.68 *	-7.80 *	-10.64 *	-4.2	-1.19	-5.42 *
14	P3 × P6	-11.04 *	-16.24 *	-29.86 *	-19.14 *	-15.27 *	-11.48 *	-24.93 *	-17.05 *
15	P3 × P7	2.63	2.34	-5.58 *	1.4	2.63	8.15 *	1.06	4.02
16	P4 × P5	2.14	9.94 *	-1.81	3.53	7.38 *	11.98 *	0.53	6.77 *
17	P4 × P6	-13.10 *	-3.39	-17.49 *	-11.20 *	-8.64 *	-1.6	-15.52 *	-8.42 *
18	P4 × P7	-6.67 *	10.91 *	4.02	2.67	-1.88	12.96 *	6.50 *	5.88 *
19	P5 × P6	4.65	10.79 *	3.19	6.30 *	1.38	10.25 *	2.92	4.91
20	P5 × P7	3.88	13.33 *	5.04 *	7.49 *	3.88	13.33 *	5.04 *	7.49 *
21	P6 × P7	0.88	2.84	3.45	2.37	0.88	2.84	3.45	2.37
	Number of significant crosses in desirable direction	03	07	03	05	03	09	04	06
	SE ±	2.09	2.58	0.85	0.76	2.09	2.58	0.85	0.76

* Significant at 5 % level of significance where, E1 = UHF, Nauni, E2 = RHR&TS, DhaulaKuan and E3 = RHR&TS Bajaura. aGenotype acronyms given in Table 1.

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Number of primary branches per plant

The heterobeltiosis for number of primary branches per plant indicated considerable variation across all three tested locations. Better parent heterosis varied from -38.75 % to 6.74 % in E1, -36.47 % to 6.06 % in E2 and -43.75 % to 13.64 % in E3 environments. Among the crosses evaluated in E1, P5 × P7 (6.74 %), P2 × P4 (6.67 %) and P3 × P4 (4 %) exhibited the highest positive heterobeltiosis. In E2, P5 × P7 (6.06 %) and P2 × P4 (4.94 %) were identified as the best combinations. Likewise, in E3, P2 × P4 (13.64 %), P5 × P7(6.25 %) and P3 × P5 (1.25 %) showed desirable heterotic responses. Pooled analysis of data (Table 6) across locations specified that heterobeltiosis ranged from -36.86 % (P3 × P6) to 8.11 % (P2 × P4). However, the highest rank for heterobeltiosis in the desirable direction was observed in P5 × P7 (6.34 %), signifying its relative stability across three environments (Fig. 2).

The values of standard heterosis for the number of primary branches per plant also varied largely. It ranged from -34.67 % (P3 × P6) to 26.67 % (P5 × P7) in E1, -33.33 % (P2 × P3) to 29.63 % (P5 × P7) in E2 and -30.77 % (P3 × P6) to 30.77 % (P5 × P7) in E3. Only one hybrid in each environment exhibited significant positive standard heterosis over the check, indicating limited but distinct superiority for this trait. In E1, the crosses P5 × P7 (26.67 %), P5 × P6 (8 %) and P2 × P4 (6.67 %) showed better performance. In E2, P5 × P7 (29.63 %), P1 × P5 (11.11 %) and P3 × P5 (6.17 %) were superior. In E3, P5 × P7 (30.77 %), P3 × P5 (24.62 %) and P2 × P4 (15.38 %) recorded the highest standard heterosis (Table 6). Additionally, pooled analysis over environments further revealed that P5 × P7 (28.96 %) unveiled the highest significant positive heterosis over the standard check variety (P7) (Table 6) for the number of primary branches per plant. Both additive and non-additive genetic effects governed the number of primary branches in chilli; however, significant heterosis reported in this trait indicates the major role of dominance and non-additive interactions for the inheritance of this trait under different environments (15, 47). The complementary genetic constitution of parents Pusa Jwala, Punjab Guchhedar and DKC-8 played a major role in the superior and consistent performance of P5 × P7 and P2 × P4 across all the environments through the promotion of favourable allelic interactions, which are responsible for governing axillary bud initiation in chilli (42). The results obtained are in agreement with some earlier studies (32, 34, 39, 42, 44, 46, 47) where both negative and positive heterobeltiosis and standard heterosis were recorded for this trait.

Table 6. Estimation of heterobeltiosis (BP) and standard heterosis (SH) for number of branches per plant

Sl. No.	[a]Genotype	Better Parent (BP %)				Standard Heterosis (SH %)			
		E1	E2	E3	Pooled	E1	E2	E3	Pooled
1	P1 × P2	-12.00	-12.50	-15.38	-13.18	-12.00	-13.58	-15.38	-13.57
2	P1 × P3	1.43	-11.76	-30.00 *	-14.04	-5.33	-7.41	-13.85	-8.60
3	P1 × P4	-12.00	-12.35	-13.64	-12.61	-12.00	-12.35	-12.31	-12.22
4	P1 × P5	-11.24	-9.09	-13.75	-11.19	5.33	11.11	6.15	7.69
5	P1 × P6	-7.50	-6.98	-8.57	-7.63	-1.33	-1.23	-1.54	-1.36
6	P1 × P7	-6.67	-1.23	-15.38	-7.24	-6.67	-1.23	-15.38	-7.24
7	P2 × P3	-12.00	-36.47 *	-13.75	-19.57	-12.00	-33.33 *	6.15	-14.48
8	P2 × P4	6.67	4.94	13.64	8.11	6.67	4.94	15.38	8.60
9	P2 × P5	-15.73	-18.18	-18.75	-17.54	0.00	0.00	0.00	0.00
10	P2 × P6	-1.25	-1.16	0.00	-0.85	5.33	4.94	7.69	5.88
11	P2 × P7	-21.33	-19.75	-23.08	-21.27	-21.33	-19.75	-23.08	-21.27
12	P3 × P4	4.00	0.00	-12.50	-0.85	4.00	4.94	7.69	5.43
13	P3 × P5	-21.35	-13.13	1.25	-11.57	-6.67	6.17	24.62	7.24
14	P3 × P6	-38.75 *	-36.05 *	-43.75 *	-36.86 *	-34.67 *	-32.10 *	-30.77 *	-32.58 *
15	P3 × P7	1.33	-3.53	-17.50	-4.68	1.33	1.23	1.54	1.36
16	P4 × P5	-26.97 *	-27.27 *	-27.50 *	-27.24 *	-13.33	-11.11	-10.77	-11.76
17	P4 × P6	-3.75	-4.65	-5.71	-4.66	2.67	1.23	1.54	1.81
18	P4 × P7	-5.33	-20.99	-16.67	-14.41	-5.33	-20.99	-15.38	-14.03
19	P5 × P6	-8.99	-16.16	-16.25	-13.81	8.00	2.47	3.08	4.52
20	P5 × P7	6.74	6.06	6.25	6.34*	26.67 *	29.63 *	30.77 *	28.96 *
21	P6 × P7	-1.25	-1.16	0.00	-0.85	5.33	4.94	7.69	5.88
	Number of significant crosses in desirable direction	0	0	0	01	1	1	1	01
	SE ±	0.17	0.25	0.44	0.23	0.17	0.25	0.44	0.23

* Significant at 5 % level of significance where, E1 = UHF, Nauni, E2 = RHR&TS, DhaulaKuan and E3 = RHR&TS Bajaura.
[a]Genotype acronyms given in Table 1.

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Fruit length (cm)

Heterobeltiosis for fruit length exhibited considerable variation across environments, ranging from -38.58 % (P2 × P4) to 50.48 % (P5 × P7) in E1, from -36.40 % (P2 × P4) to 54.89 % (P5 × P7) in E2 and from -39.77 % (P2 × P4) to 47.49 % (P5 × P7) in E3. A total of four hybrids in each environment (E1, E2 and E3) exhibited significant positive heterobeltiosis over their respective parents for this trait. The most superior crosses were consistent across all three environments. In E1, P5 × P7 (50.48 %), P1 × P6 (36.02 %) and P1 × P5 (26.97 %) recorded the highest better parent heterosis. While in E2, P5 × P7 (54.89 %), P1 × P6 (34.27 %) and P1× P2 (31.55 %) outperformed other crosses. Likewise, in E3, P5 × P7 (47.49 %), P1 × P6 (33.24 %) and P1 × P2 (26.07 %) were the best combinations for heterotic responses. Pooled analysis (Table 7) further indicated that heterobeltiosis went from -38.21 % (P2 × P4) to 51.00 % (P5 × P7). The highest significant heterobeltiosis in the desirable direction was observed in P5 × P7 (51.00 %) and P1 × P6 (34.53 %), which indicated that these crosses have stable performance across environments (Fig. 3).

Standard heterosis for fruit length also varied widely. It ranged from -18.87 % (P2 × P5) to 60.23 % (P1 × P6) in E1, -17.26 % (P2 × P3) to 54.89 % (P5 × P7) in E2 and -20.27 % (P2 × P3) to 52.46 % (P1 × P6) under E3 conditions. A total of 9 hybrids in E1, 9 in E2 and 7 in E3 demonstrated significant positive economic heterosis over the check (P7), reflecting substantial hybrid advantage for this trait. Among these, P1 × P6 (60.23 %), P5 × P7 (50.48 %) and P1 × P5 (49.57 %) were superior under E1 conditions. In E2, P5 × P7 (54.89 %), P1 × P6 (53.42 %) and P1 × P2 (50.32 %) recorded the highest values. Likewise, under E3 conditions, P1 × P6 (52.46 %), P5 × P7 (47.49 %) and P1 × P2 (44.26 %) emerged as the best-performing crosses (Table 7). Pooled estimates across environments further revealed that P1 × P6 (55.39 %) exhibited the highest significant positive heterosis over the standard check, followed by P5 × P7 (51.00 %) (Table 7) for fruit length. The magnitude of heterosis for fruit length varied among locations because fruit growth is highly influenced by genotype-by-environment interactions (GEI) (41) and environmental factors modify the level of cell division and expansion during fruit development, which results in variable fruit length across locations (48). Hybrids with consistency of positive heterosis for fruit length across tested environments (P5 × P7 and P1 × P6) offer greater breeding value for the development of commercially desirable long-fruited genotypes adapted to different agro-climates (15). These findings are consistent with the recommendation of multi-location testing of hybrids before selection for commercial cultivation. The superiority of this trait in chilli hybrids has also been reported earlier by previous researchers (15, 34, 35, 39, 41, 49), which is in agreement with the present findings.

Fruit width

Fruit width exhibited considerable variation in heterobeltiosis across environments. Under E1, values extended from -24.50 % (P4 × P5) to 5.48 % (P1 × P6), while in E2 and E3 the corresponding ranges were - 22.73 % to 7.14 % and -25.00 % to 16.67 % respectively, with P5 × P7 showing the highest expression in both environments. The hybrid combinations that expressed significant positive heterobeltiosis are one in E1, three in E2 and five in E3, suggesting a stronger heterotic response under the following environments. In E1, P1× P6 (5.48 %), P1 × P2 (4.52 %) and P5 × P7 (4.30 %) emerged as better-performing combinations. A similar trend was observed in E2, where P5 × P7 (7.14 %), P1 × P2 (6.86 %) and P1× P5 (6.82 %) recorded higher values. In E3, the magnitude of heterosis further elevated in crosses P5 × P7 (16.67 %), P1 × P5 (10.31 %) and P2 × P6 (9.73 %) signifying the hybrids most responsive to these specific environments (Fig. 3). Across environments, pooled estimates (Table 8) showed that heterobeltiosis ranged from -24.05 % (P4 × P5) to 9.24 % (P5 × P7). The latter cross expressed the highest significant heterobeltiosis in the desirable direction, followed by P1 × P2 (5.84 %), suggesting relatively stable performance.

Standard heterosis followed a comparable pattern but with relatively higher magnitudes. Under E1 conditions, it ranged from -21.65 % (P4 × P5) to 12.37 % (P1 × P6); in E2, from -20.00 % (P4 × P6) to 11.86 % (P5 × P7); and in E3, from -23.16 % (P4 × P6) to 17.89 % (P5 × P7). The number of crosses was 7 in E1, 6 in E2 and 5 under E3 conditions, which revealed significant heterosis over the check variety. Under E1 conditions, P1 × P6 (12.37 %), P1 × P2 (10.85 %) and P5 × P7 (8.25 %), under E2 conditions, P5 × P7 (11.86 %), P1 × P5 (11.53 %) and P1 × P2 (11.34 %) were found superior. Likewise, under E3, P5 × P7 (17.89 %), P1 × P5 (12.63 %) and P3 × P5 (9.12 %) recorded the highest values for economic heterosis (Table 8). The pooled performance over the standard check further confirmed the superiority of P5 × P7 (12.63 %), followed by P1 × P2 (10.22 %), for fruit width (Table 8). Fruit width is also an economically important trait as it contributes directly to fruit weight and yield. Under multi-environment studies of chilli, the pattern of genotype × environment interaction effects on fruit width was already observed by previous researchers (50), as genes governing fruit width are highly influenced among locations. A major role of non-additive genes has been observed for fruit width with respect to significant and positive heterosis, although the contribution of additive effects may also be present depending on parental combinations (47). Hybrids viz., P5 × P7 and P1 × P2 performed consistently for positive heterosis across all the tested locations, suggesting strong breeding value of these hybrids to enhance fruit weight and yield. The superiority of hybrids for fruit width has also been reported by previous researchers (34, 35, 39, 47, 50), which supports the key findings of this study.

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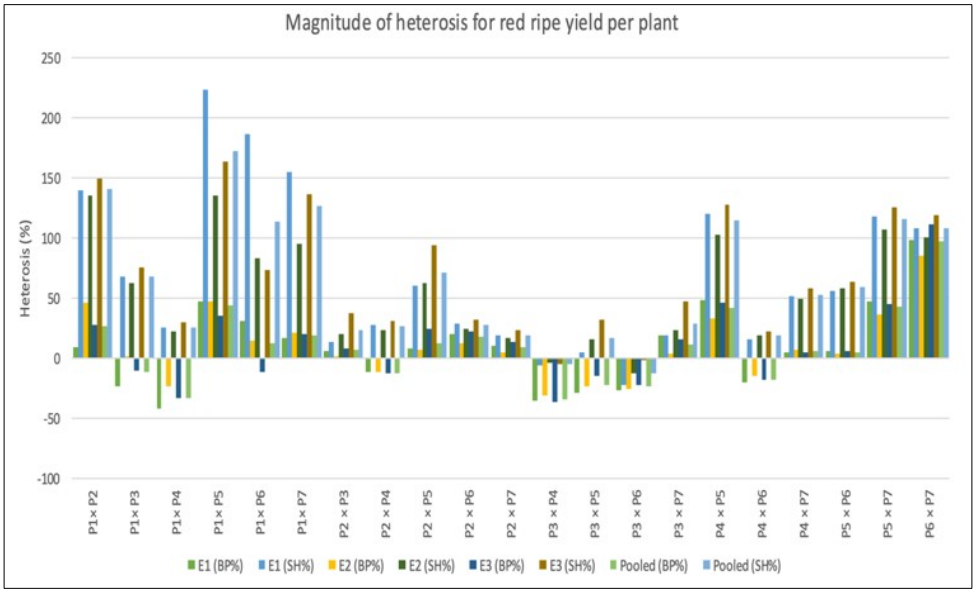
Table 7. Estimation of heterobeltiosis (BP) and standard heterosis (SH) for fruit length (cm)

Sl. No.	[a]Genotype	Better Parent (BP %)				Standard Heterosis (SH %)			
		E1	E2	E3	Pooled	E1	E2	E3	Pooled
1	P1× P2	25.43 *	31.55 *	26.07 *	27.69 *	47.76 *	50.32 *	44.26 *	47.48 *
2	P1× P3	-7.47 *	-2.35	-8.31	-6.02	9.01 *	11.58 *	4.92	8.54
3	P1× P4	-2.3	-0.71	-1.52	-1.5	44.99 *	47.89 *	42.08 *	45.02 *
4	P1× P5	26.97 *	24.14 *	22.97 *	24.73 *	49.57 *	41.84 *	40.71 *	44.06 *
5	P1× P6	36.02 *	34.27 *	33.24 *	34.53 *	60.23 *	53.42 *	52.46 *	55.39 *
6	P1× P7	-10.41 *	-12.39 *	-15.19 *	-12.62 *	5.54	0.11	-2.95	0.93
7	P2 × P3	-14.42 *	-19.80 *	-21.26 *	-18.46 *	-12.05 *	-17.26 *	-20.27 *	-16.50 *
8	P2 × P4	-38.58 *	-36.40 *	-39.77 *	-38.21 *	-8.85 *	-5.26	-13.11 *	-9.03
9	P2 × P5	-21.06 *	-12.24 *	-11.55 *	-14.98 *	-18.87 *	-9.47	-10.44	-12.93 *
10	P2 × P6	-5.08	-2.04	-7.56	-4.84	-2.45	1.05	-6.39	-2.55
11	P2 × P7	-15.20 *	-12.24 *	-17.70 *	-15.00 *	-12.85 *	-9.47	-16.67 *	-12.95 *
12	P3 × P4	-37.61 *	-35.34 *	-38.22 *	-37.02 *	-7.41	-3.68	-10.87	-7.28
13	P3 × P5	2.91	8.55	0	4.53	-17.06 *	-13.16 *	-18.03 *	-16.05 *
14	P3 × P6	-13.86 *	-9.8	-12.13	-11.92 *	-18.82 *	-15.26 *	-18.85 *	-17.62 *
15	P3 × P7	-2.35	6.84	5.85	3.44	-2.35	6.84	5.85	3.44
16	P4 × P5	-15.95 *	-20.71 *	-19.32 *	-18.66 *	24.73 *	18.11 *	16.39 *	19.76 *
17	P4 × P6	-23.81 *	-21.55 *	-23.07 *	-22.80 *	13.06 *	16.84 *	10.98	13.66 *
18	P4 × P7	-11.64 *	-8.83 *	-11.36 *	-10.59 *	31.13 *	35.79 *	27.87 *	31.64 *
19	P5 × P6	-4.3	-0.84	-5.21	-3.41	-9.81 *	-6.84	-12.46 *	-9.67 *
20	P5 × P7	50.48 *	54.89 *	47.49 *	51.00 *	50.48 *	54.89 *	47.49 *	51.00 *
21	P6 × P7	-12.69 *	-8.95	-16.07 *	-12.52 *	-12.69 *	-8.95	-16.07 *	-12.52 *
	Number of significant crosses in desirable direction	04	04	04	04	09	09	07	08
	SE ±	0.18	0.24	0.24	0.12	0.18	0.24	0.24	0.12

* Significant at 5 % level of significance where, E1 = UHF, Nauni, E2 = RHR&TS, DhaulaKuan and E3 = RHR&TS, Bajaura. [a]Genotype acronyms given in Table 1.



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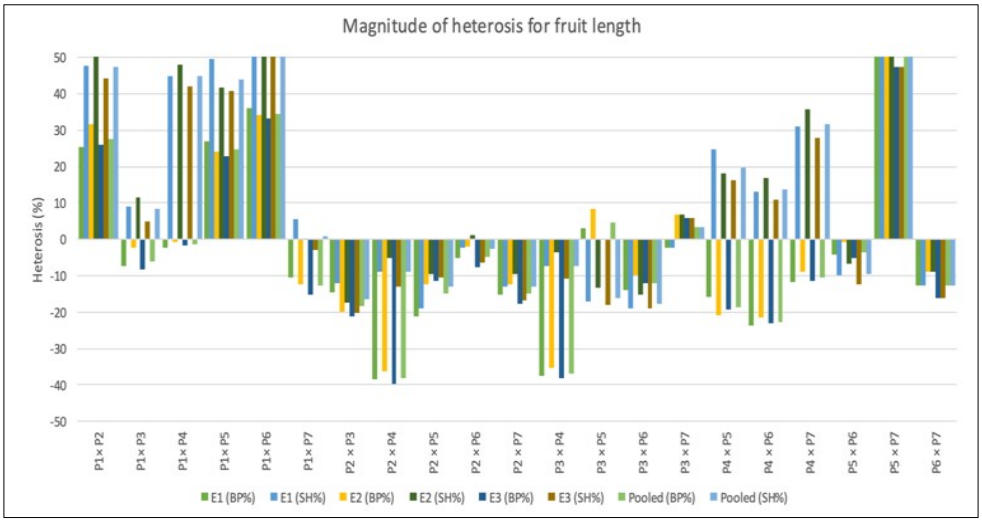

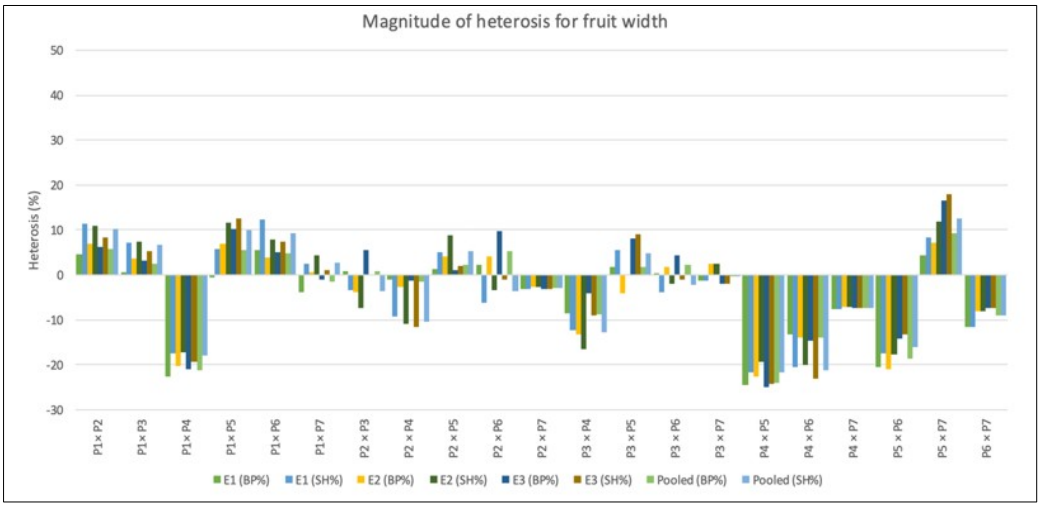

Fig. 3. Magnitude of heterosis for red ripe fruit yield per plant, fruit length and fruit width.

Table 8. Estimation of heterobeltiosis (BP) and standard heterosis (SH) for fruit width (cm)

Sl. No.	[a]Genotype	Better Parent (BP %)				Standard Heterosis (SH %)			
		E1	E2	E3	Pooled	E1	E2	E3	Pooled
1	P1 × P2	4.52	6.86 *	6.19 *	5.84 *	11.34 *	10.85 *	8.42 *	10.22 *
2	P1 × P3	0.65	3.59	3.09	2.43	7.22 *	7.46 *	5.26	6.66 *
3	P1 × P4	-22.58 *	-20.26 *	-20.96 *	-21.28 *	-17.53 *	-17.29 *	-19.30 *	-18.03 *
4	P1 × P5	-0.65	6.82 *	10.31 *	5.62 *	5.84 *	11.53 *	12.63 *	9.99 *
5	P1 × P6	5.48 *	3.92	5.15	4.85 *	12.37 *	7.80 *	7.37 *	9.18 *
6	P1 × P7	-3.87	0.65	-1.03	-1.43	2.41	4.41	1.05	2.64
7	P2 × P3	0.72	-3.87	5.56	0.72	-3.44	-7.46 *	0	-3.67
8	P2 × P4	-1.12	-2.59	-1.18	-1.64	-9.28 *	-10.85 *	-11.58 *	-10.56 *
9	P2 × P5	1.32	4.22	1.04	2.23	5.15 *	8.81 *	2.11	5.40 *
10	P2 × P6	2.25	4.01	9.73 *	5.40	-6.19 *	-3.39	-1.05	-3.56
11	P2 × P7	-3.09	-2.71	-3.16	-2.99	-3.09	-2.71	-3.16	-2.99
12	P3 × P4	-8.60 *	-13.38 *	-4.07	-8.76 *	-12.37 *	-16.61 *	-9.12 *	-12.74 *
13	P3 × P5	1.66	-4.22	7.99 *	1.67	5.50 *	0	9.12 *	4.82

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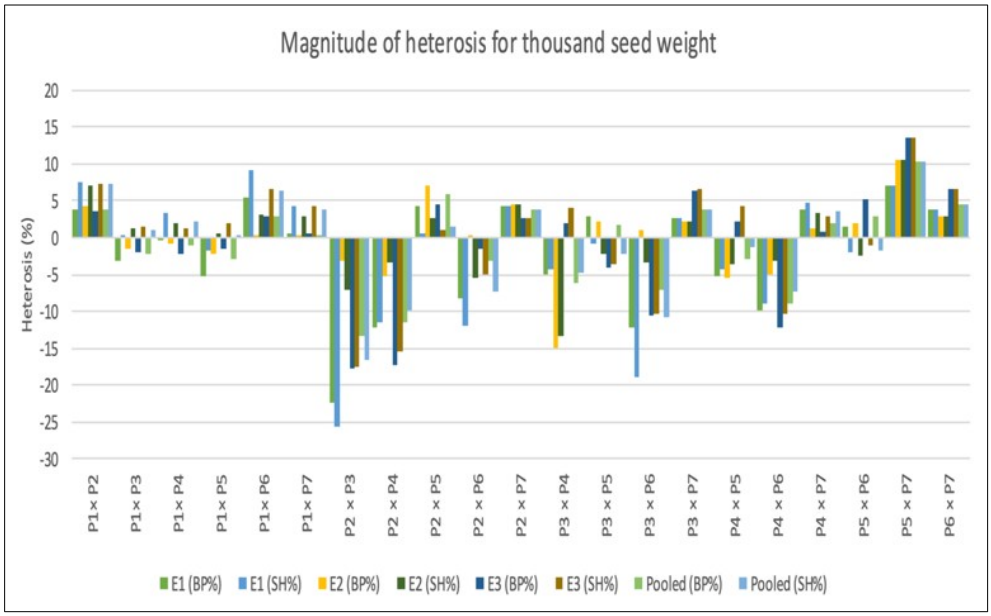
14	P3 × P6	0.36	1.76	4.44	2.16	-3.78	-2.03	-1.05	-2.3
15	P3 × P7	-1.37	2.37	-2.11	-0.34	-1.37	2.37	-2.11	-0.34
16	P4 × P5	-24.50 *	-22.73 *	-25.00 *	-24.05 *	-21.65 *	-19.32 *	-24.21 *	-21.70 *
17	P4 × P6	-13.16 *	-13.87 *	-14.79 *	-13.93 *	-20.62 *	-20.00 *	-23.16 *	-21.24 *
18	P4 × P7	-7.56 *	-7.12 *	-7.37 *	-7.35 *	-7.56 *	-7.12 *	-7.37 *	-7.35 *
19	P5 × P6	-20.53 *	-21.10 *	-14.24 *	-18.71 *	-17.53 *	-17.63 *	-13.33 *	-16.19 *
20	P5 × P7	4.30	7.14 *	16.67 *	9.24 *	8.25 *	11.86 *	17.89 *	12.63 *
21	P6 × P7	-11.68 *	-8.14 *	-7.37 *	-9.07 *	-11.68 *	-8.14 *	-7.37 *	-9.07 *
	Number of significant crosses in desirable direction	01	03	05	04	07	06	05	06
	SE ±	0.03	0.05	0.02	0.01	0.03	0.05	0.02	0.01

* Significant at 5 % level of significance where, E1 = UHF, Nauni, E2 = RHR&TS, DhaulaKuan and E3 = RHR&TS, Bajaura. [a]Genotype acronyms given in Table 1.

Red ripe fruit yield per plant

Fruit yield is an important economic trait in chilli and improvement in this character remains a major objective in breeding programmes. Significant variation in heterosis for fruit yield per plant was observed across environments. The heterobeltiosis ranged from -42.49 % (P1 × P4) to 98.18 % (P6 × P7) in E1, from -31.54 % (P3 × P4) to 85.49 % (P6 × P7) in E2 and from -36.65 % (P3 × P4) to 112.08 % (P6 × P7) in E3. Twelve hybrids in E1, ten in E2 and thirteen in E3 showed significant positive heterobeltiosis over their parents. The best performing crosses were P6 × P7 (98.18 %), P4 × P5 (48.15 %) and P1 × P5 (47.76 %) in E1; P6 × P7 (85.49 %), P1 × P5 (47.07 %) and P1 × P2 (46.58 %) in E2; and P6 × P7 (112.08 %), P4 × P5 (46.15 %) and P5 × P7 (45.39 %) in E3. Pooled analysis (Table 9) indicated that heterobeltiosis varied from 34.26- % (P3 × P4) to 97.14 % (P6 × P7). The highest heterobeltiosis in the desirable direction was recorded by P6 × P7 (97.14 %), followed by P1 × P5 (43.66 %) (Fig. 3). The consistent superiority of these crosses across environments suggests their potential for improving fruit yield. Standard heterosis also showed a wide range for this trait. It varied from -22.55 % (P3 × P6) to 223.53 % (P1 × P5) in E1, from -12.19 % (P3 × P6) to 135.81 % (P1 × P5) in E2 and from -4.65 % (P3 × P4) to 164.08 % (P1 × P5) in E3.



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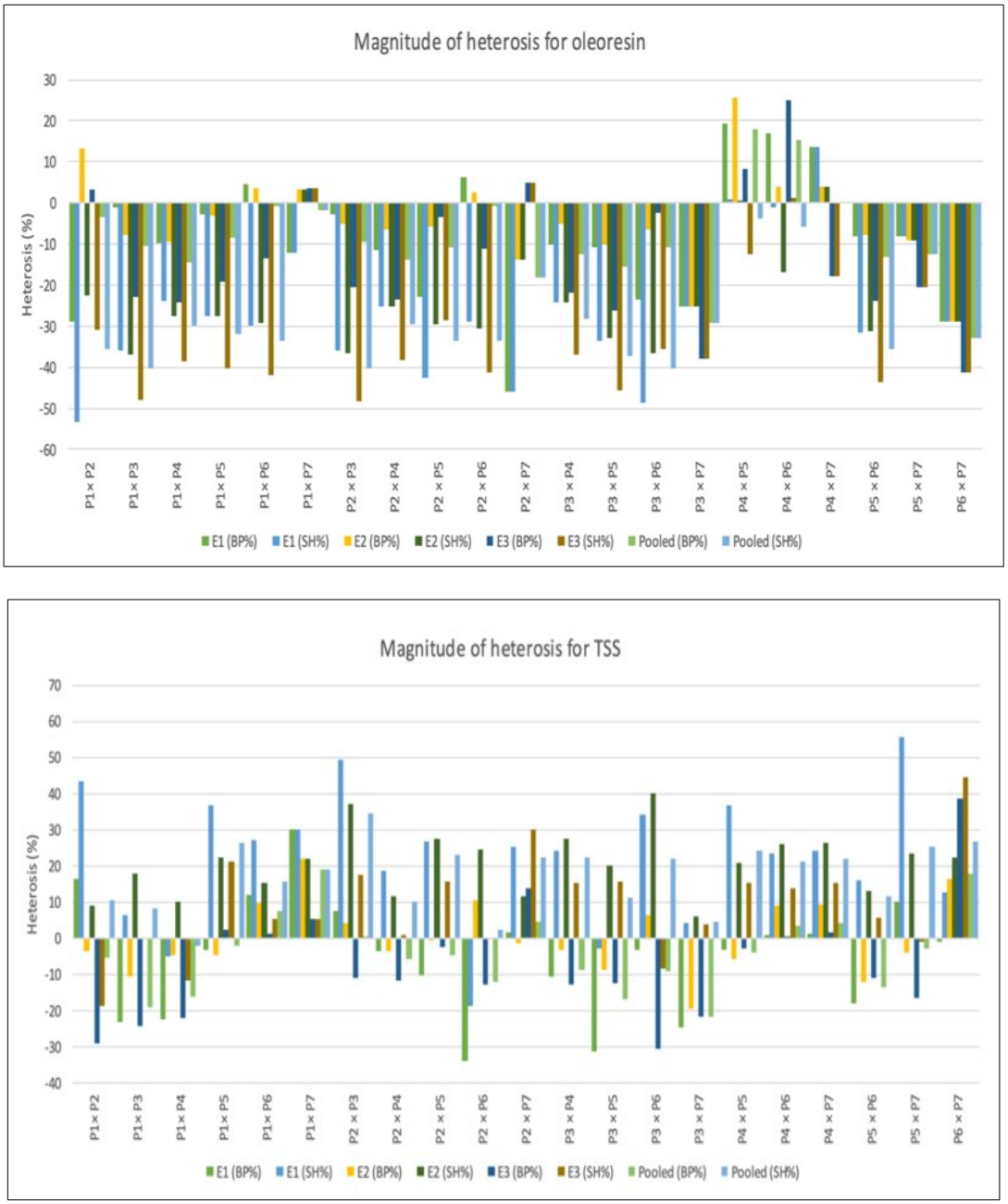

Fig. 4. Magnitude of heterosis for thousand seed weight, oleoresin and total soluble solids.

Eighteen hybrids in E1, nineteen in E2 and nineteen in E3 showed significant positive standard heterosis over the check (P7). The most promising crosses were P1 × P5 (223.53 %), P1 × P6 (186.56 %) and P1 × P7 (154.70 %) in E1; P1 × P5 (135.81 %), P1 × P2 (135.01 %) and P5 × P7 (107.12 %) in E2; and P1 × P5 (164.08 %), P1 × P2 (149.56 %) and P1× P7 (136.17 %) in E3 (Table 9). On a pooled basis, P1× P5 (172.73 %) followed by P1 × P2 (140.73 %) recorded the highest significant positive heterosis over the standard check for red ripe fruit yield per plant (Table 9). Fruit yield is a complex polygenic trait resulting from the combined effects of photosynthetic efficiency, assimilate production and partitioning and sink strength (51). Recent advances in genomic studies indicate that hybrid superiority is governed by coordinated regulation of numerous genes rather than the effect of single loci, with dominance, overdominance and epistatic interactions (52). Additionally, environmental factors such as temperature, rainfall and soil fertility modify photosynthetic activity, flowering regulation, fruit set and assimilate partitioning, thereby altering the expression of hybrid vigour (41). Therefore, the higher heterotic response for yield may be due to favourable gene combinations and better expression of yield-contributing traits under different environments. Similar results for significant heterosis in fruit yield have also been reported by previous researchers (14, 34, 41, 49, 53, 54).

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Seed weight (g/1000 seed)

Heterosis for seed weight showed noticeable variation across environments, with both positive and negative estimates observed among the hybrids. The magnitude of heterobeltiosis ranged from -22.37 % (P2 × P3) to 7.06 % (P5 × P7) in E1, from -15.04 % (P3 × P4) to 10.63 % (P5 × P7) in E2 and from -17.73 % (P2 × P3) to 13.63 % (P5 × P7) in E3. The number of hybrids showing significant positive heterobeltiosis was relatively low, with two in E1, four in E2 and five in E3. Some of the earlier studies also found non-significant G × E interactions for this trait under different temperature conditions, suggesting that 1000 seed weight is sometimes more genetically stable than other yield-contributing traits (15). In E1, P5 × P7 (7.06 %) recorded the highest positive heterobeltiosis, followed by P1× P6 (5.35 %) and P2 × P7 (4.21 %). In E2, the leading crosses were P5 × P7 (10.63 %), P2 × P5 (7.12 %) and P2 × P7 (4.46 %). Under E3 conditions, P5 × P7 (13.63 %) again showed maximum heterosis, followed by P6 × P7 (6.68 %) and P3 × P7 (6.31 %). Pooled estimates (Table 10) indicated that heterobeltiosis varied from -13.27 % (P2 × P3) to 10.41 % (P5 × P7). The highest significant heterobeltiosis in the desirable direction was expressed by P5 × P7 (10.41 %), followed by P2 × P5 (6.03 %). The repeated superiority of P5 × P7 across environments suggests its stability for improving seed weight. Standard heterosis for seed weight also followed a similar trend of variation. It ranged from -25.57 % (P2 × P3) to 9.25 % (P1 × P6) in E1, from -13.31 % (P3 × P4) to 10.63 % (P5 × P7) in E2 and from -17.45 % (P2 × P3) to 13.63 % (P5 × P7) in E3.

Table 9. Estimation of heterobeltiosis (BP) and standard heterosis (SH) for red ripe fruit yield per plant (g)

Sl. No.	[a]Genotype	Better Parent (BP %)				Standard Heterosis (SH %)			
		E1	E2	E3	Pooled	E1	E2	E3	Pooled
1	P1× P2	9.42 *	46.58 *	27.38 *	26.80 *	139.58 *	135.01 *	149.56 *	140.73 *
2	P1× P3	-23.46 *	1.27	-10.34 *	-11.55 *	67.59 *	62.37 *	75.65 *	67.93 *
3	P1× P4	-42.49 *	-23.82 *	-33.77 *	-33.85 *	25.92 *	22.14 *	29.76 *	25.59 *
4	P1× P5	47.76 *	47.07 *	34.80 *	43.66 *	223.53 *	135.81 *	164.08 *	172.73 *
5	P1× P6	30.87 *	14.12 *	-11.54 *	12.77 *	186.56 *	82.98 *	73.31 *	114.09 *
6	P1× P7	16.32 *	21.47 *	20.55 *	19.25 *	154.70 *	94.77 *	136.17 *	126.40 *
7	P2 × P3	5.63	1.61	7.58 *	6.74 *	13.33 *	20.41 *	37.02 *	22.91 *
8	P2 × P4	-11.72 *	-11.86 *	-12.76 *	-12.09 *	27.33 *	23.41 *	31.32 *	26.99 *
9	P2 × P5	8.00 *	7.12 *	24.77 *	12.65 *	60.30 *	62.27 *	94.10 *	70.86 *
10	P2 × P6	19.52 *	12.29 *	21.99 *	17.41 *	28.23 *	24.66 *	32.13 *	27.99 *
11	P2 × P7	10.43 *	4.98	13.98 *	9.33 *	18.48 *	16.55 *	23.45 *	19.18 *
12	P3 × P4	-35.11 *	-31.54 *	-36.65 *	-34.26 *	-6.41	-4.15	-4.65	-5.04
13	P3 × P5	-29.21 *	-23.57 *	-15.27 *	-22.91 *	5.08	15.78 *	31.81 *	16.92 *
14	P3 × P6	-26.29 *	-25.90 *	-22.73 *	-24.02 *	-22.55 *	-12.19 *	-1.59	-12.51 *
15	P3 × P7	18.50 *	3.68	15.39 *	11.67 *	18.98 *	22.86 *	46.96 *	28.58 *
16	P4 × P5	48.15 *	33.55 *	46.15 *	41.98 *	119.90 *	102.33 *	127.36 *	115.34 *
17	P4 × P6	-19.78 *	-14.95 *	-18.49 *	-17.60 *	15.70 *	19.09 *	22.68 *	19.02 *
18	P4 × P7	4.93	6.59 *	5.20 *	5.63 *	51.35 *	49.24 *	58.35 *	52.58 *
19	P5 × P6	5.36 *	4.08	5.43 *	4.89 *	56.38 *	57.67 *	64.01 *	59.09 *
20	P5 × P7	46.94 *	36.72 *	45.39 *	42.57 *	118.11 *	107.12 *	126.18 *	116.24 *
21	P6 × P7	98.18 *	85.49 *	112.08 *	97.14 *	108.24 *	100.96 *	119.24 *	108.65 *
	Number of significant crosses in desirable direction	12	10	13	14	18	19	19	19
	SE ±	17.93	16.19	4.7	11.04	17.93	16.19	4.7	11.04

* Significant at 5 % level of significance where, E1 = UHF, Nauni, E2 = RHR&TS, DhaulaKuan and E3 = RHR&TS, Bajaura. [a]Genotype acronyms given in Table 1.

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Table 10. Estimation of heterobeltiosis (BP) and standard heterosis (SH) for thousand seed weight (g/1000 seed)

Sl. No.	[a]Genotype	Better Parent (BP %)				Standard Heterosis (SH %)			
		E1	E2	E3	Pooled	E1	E2	E3	Pooled
1	P1× P2	3.81	4.19 *	3.6	3.87 *	7.65 *	7.06 *	7.38 *	7.36 *
2	P1× P3	-3.16	-1.5	-2.01	-2.22	0.42	1.22	1.56	1.06
3	P1× P4	-0.24	-0.79	-2.26	-1.08	3.45	1.95	1.3	2.24
4	P1× P5	-5.19 *	-2.21	-1.51	-2.98	-1.68	0.49	2.08	0.28
5	P1× P6	5.35 *	0.39	2.93	2.87	9.25 *	3.17	6.68 *	6.33 *
6	P1× P7	0.65	0.16	0.59	0.46	4.37 *	2.92	4.25 *	3.83 *
7	P2 × P3	-22.37 *	-3.13	-17.73 *	-13.27 *	-25.57 *	-7.14 *	-17.45 *	-16.60 *
8	P2 × P4	-12.25 *	-5.25 *	-17.18 *	-11.42 *	-11.44 *	-3.33	-15.45 *	-9.94 *
9	P2 × P5	4.18	7.12 *	4.58 *	6.03 *	0.5	2.6	1.04	1.4
10	P2 × P6	-8.16 *	0.17	-1.62	-3.19	-11.94 *	-5.36 *	-4.95 *	-7.42 *
11	P2 × P7	4.21	4.46 *	2.6	3.78 *	4.21	4.46 *	2.6	3.78 *
12	P3 × P4	-5.08 *	-15.04 *	1.96	-6.25 *	-4.21	-13.31 *	4.08 *	-4.67 *
13	P3 × P5	2.79	2.12	-3.98	1.72	-0.84	-2.11	-3.65	-2.18
14	P3 × P6	-12.28 *	0.93	-10.64 *	-7.19 *	-18.92 *	-3.25	-10.33 *	-10.75 *
15	P3 × P7	2.69	2.11	6.31 *	3.78 *	2.69	2.11	6.68 *	3.78 *
16	P4 × P5	-5.25 *	-5.49 *	2.13	-2.95	-4.37 *	-3.57 *	4.25 *	-1.32
17	P4 × P6	-9.75 *	-5.01 *	-12.24 *	-8.92 *	-8.92 *	-3.08	-10.42 *	-7.39 *
18	P4 × P7	3.83	1.35	0.77	1.98	4.79 *	3.41	2.86	3.69
19	P5 × P6	1.57	1.95	5.26 *	2.87	-2.02	-2.35	-1.04	-1.82
20	P5 × P7	7.06 *	10.63 *	13.63 *	10.41 *	7.06 *	10.63 *	13.63 *	10.41 *
21	P6 × P7	3.87	3	6.68 *	4.48 *	3.87	3	6.68 *	4.48 *
	Number of significant crosses in desirable direction	02	04	05	06	05	03	08	07
	SE ±	0.16	0.17	0.05	0.05	0.16	0.17	0.05	0.05

* Significant at 5 % level of significance where, E1 = UHF, Nauni, E2 = RHR&TS, DhaulaKuan and E3 = RHR&TS, Bajaura. [a]Genotype acronyms given in Table 1.

Significant positive standard heterosis was recorded in five hybrids in E1, three in E2 and eight in E3. Among the crosses, P1× P6 (9.25 %), P1× P2 (7.65 %) and P5 × P7 (7.06 %) performed better in E1; P5 × P7 (10.63 %), P1 × P2 (7.06 %) and P2 × P7 (4.46 %) in E2; and P5 × P7 (13.63 %), P1× P2 (7.38 %) and P1 × P6 (6.68 %) in E3 showed higher standard heterosis (Table 10). On a pooled basis, P5 × P7 (10.41 %) followed by P1 × P2 (7.36 %) exhibited the highest significant positive heterosis over the standard check for thousand-seed weight (Fig. 4). The moderate level of heterosis observed for this trait indicates that seed weight may be governed by additive as well as non additive gene effects. However, the stable performance of P1 × P2 and P5 × P7 indicates low GEI effects on these hybrids and the favourable complementary distribution between parental alleles, which controls seed development and assimilate distribution to developing seeds. Recent research in chilli has shown significant parental and line-tester effects for thousand-seed weight, proving that the genetic background of parents and cross-specific interactions contribute to this character (55). The present findings are in agreement with earlier reports by previous researchers (15, 46, 55, 56) who also observed improvement in seed weight through heterosis in chilli.

Oleoresin (%)

Oleoresin content unveiled a good range of better parent heterosis, indicating significant variability in hybrid performance but remained limited or very low for economic heterosis across the three environments. Under E1 conditions, the values ranged from -45.81 % (P2 × P7) to 19.43 % (P4 × P5). Likewise, under E2 conditions, heterobeltiosis ranged from -29.05 % to 25.66 % and in E3 from 41.20 % to 24.-95 %. Despite this range of heterobeltiosis, only a small number of hybrids showed significant positive heterobeltiosis, with 4 in E1, 2 in E2 and 1 cross under E3 conditions. Noticeably, crosses involving the P4 parent consistently performed better under all three environments, revealing that this parent possesses favourable parental alleles that regulate the secondary metabolism and result in greater metabolic flux regarding oleoresin biosynthesis (45). In E1, P4 × P5 (19.43 %), P4 × P6 (17.05 %) and P4 × P7 (13.52 %) recorded the maximum values for

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better parent heterosis. In E2, P4 × P5 (25.66 %) repeatedly showed maximum improvement, followed by P1× P2 (13.30 %). In the E3 environment, the highest heterobeltiosis was observed in P4 × P6 (24.95 %), suggesting a stable contribution of this parent in enhancing oleoresin content. These results were supported by the results of pooled analysis, with heterobeltiosis ranging from -32.99 % to 17.83 %. The crosses P4 × P5 (17.83 %) and P4 × P6 (15.23 %) recorded the highest positive effect (Fig. 4). This pattern gives conformity that P4 emerged as a good parent for improving oleoresin levels, although broad improvement remains moderate.

Comparatively, standard heterosis for oleoresin content was found low and inconsistent. The value extended from -53.29 % to 13.52 % under E1, -36.97 % to 4.05 % under E2 and 48.16 % to 5-.05 % under E3 conditions. Only one hybrid in E1 successfully exhibited significant positive standard heterosis, demonstrating limited superiority of hybrids over the commercial check. Among the crosses, P4 × P7 recorded the highest value in E1 (13.52 %), while in E2 and E3, the same cross continued to perform relatively better, though with much lower magnitudes (4.05 % and restrained values in E3). The pooled analysis confirmed this trend, with P4 × P7 showing only marginal superiority (0.06 %) over the standard check (Table 11). Oleoresin build-up is a result of enhanced accumulation and biosynthesis of carotenoids, capsaicinoids and other lipid-soluble secondary metabolites during the stage of fruit ripening (10). The relatively low expression of economic heterosis indicates that although certain hybrids outperform their parents, transforming this advantage into commercially superior genotypes remains challenging for oleoresin content. Hybrids showing consistently high oleoresin across locations are valuable for the food colour, spice and oleoresin extraction industries (57). Earlier researchers (53, 58–60) have also conveyed similar patterns of heterotic response for oleoresin content, which are in accordance with present findings.

Table 11. Estimation of heterobeltiosis (BP) and standard heterosis (SH) for oleoresin (%)

Sl. No.	[a]Genotype	Better Parent (BP %)				Standard Heterosis (SH %)			
		E1	E2	E3	Pooled	E1	E2	E3	Pooled
1	P1× P2	-28.96 *	13.30 *	3.08	-3.32	-53.29 *	-22.60 *	-30.74 *	-35.46 *
2	P1× P3	-1.21	-7.73 *	-22.71 *	-10.58 *	-36.05 *	-36.97 *	-48.07 *	-40.30 *
3	P1× P4	-9.96 *	-9.35 *	-24.05 *	-14.34 *	-24.00 *	-27.50 *	-38.46 *	-29.93 *
4	P1× P5	-2.86	-3.14	-19.33 *	-8.32 *	-27.67 *	-27.59 *	-40.38 *	-31.81 *
5	P1× P6	4.75	3.43	-13.48 *	-0.86	-29.74 *	-29.35 *	-41.87 *	-33.58 *
6	P1× P7	-12.02 *	3.37	3.68	-1.64	-12.02 *	3.37	3.68	-1.64
7	P2 × P3	-2.74	-5.26	-20.59 *	-9.40 *	-36.05 *	-36.68 *	-48.16 *	-40.23 *
8	P2 × P4	-11.46 *	-6.52 *	-23.60 *	-13.76 *	-25.26 *	-25.24 *	-38.10 *	-29.46 *
9	P2 × P5	-22.75 *	-5.88	-3.54	-10.72 *	-42.48 *	-29.64 *	-28.70 *	-33.59 *
10	P2 × P6	6.09 *	2.6	-11.03 *	-0.65	-28.84 *	-30.52 *	-41.14 *	-33.44 *
11	P2 × P7	-45.81 *	-13.81 *	5.05	-18.25 *	-45.81 *	-13.81 *	5.05	-18.25 *
12	P3 × P4	-10.25 *	-5.06	-21.99 *	-12.34 *	-24.24 *	-24.07 *	-36.79 *	-28.30 *
13	P3 × P5	-10.73 *	-10.20 *	-26.24 *	-15.60 *	-33.52 *	-32.86 *	-45.48 *	-37.22 *
14	P3 × P6	-23.51 *	-6.49	-2.48	-10.85 *	-48.69 *	-36.68 *	-35.48 *	-40.27 *
15	P3 × P7	-25.17 *	-25.24 *	-37.94 *	-29.38 *	-25.17 *	-25.24 *	-37.94 *	-29.38 *
16	P4 × P5	19.43 *	25.66 *	8.14	17.83 *	0.81	0.5	-12.37 *	-3.62
17	P4 × P6	17.05 *	3.85	24.95 *	15.23 *	-1.2	-16.95 *	1.25	-5.75 *
18	P4 × P7	13.52 *	4.05	-17.70 *	0.06	13.52 *	4.05	-17.70 *	0.06
19	P5 × P6	-8.19 *	-7.84 *	-23.82 *	-13.16 *	-31.63 *	-31.11 *	-43.69 *	-35.41 *
20	P5 × P7	-8.05 *	-9.12 *	-20.58 *	-12.52 *	-8.05 *	-9.12 *	-20.58 *	-12.52 *
21	P6 × P7	-28.93 *	-29.05 *	-41.20 *	-32.99 *	-28.93 *	-29.05 *	-41.20 *	-32.99 *
	Number of significant crosses in desirable direction	04	02	01	02	01	00	00	00
	SE ±	0.37	0.40	0.26	0.29	0.37	0.40	0.26	0.29

* Significant at 5 % level of significance where, E1 = UHF, Nauni, E2 = RHR&TS, DhaulaKuan and E3 = RHR&TS, Bajaura. [a]Genotype acronyms given in Table 1.

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Total soluble solids (°B)

The heterotic response for total soluble solids (TSS) indicated significant variation across all the three locations, representing differential expression of this quality trait under shifting conditions. Under E1 conditions, the heterobeltiosis range extended from -34.04 % (P2 × P6) to 30.15 % (P1 × P7). Under E2 conditions, the variation was moderately narrower, ranging from -19.43 % (P3 × P7) to 21.86 % (P1× P7), while under E3 conditions, the range expanded again from -30.68 % (P3 × P6) to 38.64 % (P6 × P7). Only a few hybrids exhibited significant positive better-parent heterosis, with 2 hybrids each in E1, E2 and E3. Under E1 conditions, P1 × P7 (30.15 %) emerged as the superior hybrid, followed by P1 × P2 (16.33 %) and P5 × P7 (10.16 %). Likewise, the superior hybrids under E2 conditions are P1 × P7 (21.86 %) and P6 × P7 (16.37 %). But under E3 conditions, significant improvements were displayed by hybrid P6 × P7 (38.64 %), indicating a shift in hybrid performance across environments. When the data were pooled, heterobeltiosis varied from -21.93 % to 18.88 %. The cross P1× P7 (18.88 %) maintained its superiority, followed closely by P6 × P7 (17.86 %) (Fig. 3). The superior TSS of hybrids P1 × P7 and P6 × P7 may be correlated with favourable parental complementary distribution for photosynthetic carbohydrate production, effective sugar transport and enhanced carbohydrate buildup during fruit development. Sugar buildup in chilli is largely influenced by genotype and different fruit ripening stages and also glucose and fructose constitute the major soluble sugars at the fruit maturity stage (61). The consistency of these combinations suggests that parent P7 may act as a favourable parent for developing TSS, although the rate of improvement remains moderate.

In contrast to heterobeltiosis, standard heterosis for TSS was more pronounced and widely expressed. In E1, values ranged from -18.79 % to 55.78 %, while in E2 they varied from 6.05 % to 40.00 % and in E3 from -18.96 % to 44.55 %. Most of the hybrids revealed significant positive economic heterosis, with 15 hybrids each under E1 and E2 conditions and 10 hybrids under E3 conditions. Under E1 conditions, P5 × P7 (55.78 %) and P2 × P3 (49.25 %) were the most promising hybrids. Under E2 conditions, hybrids viz. P3 × P6 (40.00 %) and P2 × P3 (37.21 %) outperformed other crosses, while under E3 conditions, P6 × P7 (44.55 %) presented the highest superiority over the check (Fig. 4). Pooled analysis further defined the advantage of superior cross combinations, with P2 × P3 (34.37 %) exhibiting the maximum economic heterosis, followed by P1 × P5 (26.50 %) (Table 12). Total soluble solids are a complex quantitative trait in which numerous metabolic pathways are involved in the synthesis, transport and accumulation of sugar. In chilli fruits, sugar concentration is strongly influenced by genotype, fruit developmental stage and environmental factors and therefore only specific parental genotypes involving favourable complementary genes can outshine the better parent for this character (61). Additionally, increased fruit number and size may create larger sink demand, leading to dilution of soluble sugars during fruit development and therefore reducing the expression of TSS heterosis after having superior yield performance (51). Diverse environmental conditions viz., temperature, radiation and water availability further affect fruit water content and carbohydrate buildup inside fruits, which results in variable expression of heterosis across tested locations for TSS (15). However, the comparatively better magnitude and frequency of standard heterosis with heterobeltiosis suggest that several crosses outperformed the commercial check variety even when their advantage over the better parent is limited. The study findings are in conformity with some earlier studies (15, 16, 35, 59, 60, 62) where similar heterotic expression was recorded for TSS in chilli.

The differences in heterosis estimations under different Himalayan agroclimatic zones may be due to the environmental alteration of non-additive gene action and the changing degrees of adaptation exhibited by genotypes under different ecological conditions. Significant changes in hybrid performance and heterosis across environments were previously observed by researchers (42) under wet-temperate North-Western Himalayan conditions and by others (63) under high-rainfall conditions. The heterotic expression in chilli genotypes assessed under different circumstances has also been found to be influenced by several environmental factors like temperature and rainfall. Fruit yield is a complex trait controlled by different growth- and yield-related characteristics. Thus, the environment has a significant impact on the expression of heterosis for fruit production in chilli (15). It has also been revealed that, under multi-environment conditions, fruit diameter and length exhibit variable heterotic expression. Previous studies reported that fruit width showed both positive and negative heterosis depending on parental combinations and growing conditions, whereas most chilli hybrids exhibited significant positive heterosis for fruit length (26). Changes in temperature during fruit development and growth stages can also considerably affect fruit thickness and size, leading to inconsistent heterotic performance across environments (15). Moreover, factors like temperature and moisture have a significant impact on biochemical production in chilli fruits as well as quality characteristics including oleoresin and total soluble solids (TSS), which are particularly sensitive to environmental differences. High temperature and more sunshine enhanced oleoresin content in chilli fruits and enhanced heterosis for bioactive chemicals, as reported by previous researchers (15). Likewise, high temperatures during fruit growth raised the concentration of oleoresin and capsaicin, indicating that environmental factors have a direct impact on the accumulation of metabolites in genotypes. Thus, genotype × environment interaction affecting physiological growth, assimilate partitioning and biochemical synthesis in chilli hybrids may be a primary factor in the different heterosis responses for yield, plant spread, fruit and quality traits across

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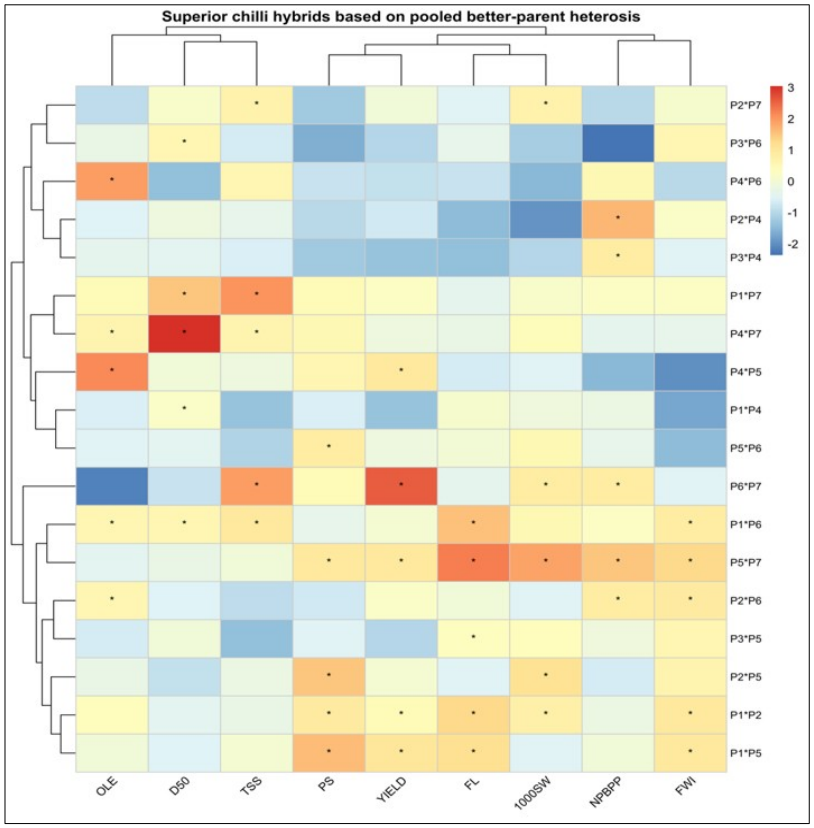
Himalayan agroclimatic zones. These findings highlight the necessity of a multi-location study in developing and evaluating stable hybrids with broad adaptability and consistent quality performance under various Himalayan agroclimatic circumstances. The top 5 crosses selected for each trait are depicted in Fig. 5 and the pooled mean performance of genotypes for red ripe fruit yield per plant is depicted in Fig. 6.

Table 12. Estimation of heterobeltiosis (BP) and standard heterosis (SH) for TSS (°B)

Sl. No.	[a]Genotype	Better Parent (BP %)				Standard Heterosis (SH %)			
		E1	E2	E3	Pooled	E1	E2	E3	Pooled
1	P1 × P2	16.33 *	-3.7	-29.05 *	-5.35	43.22 *	8.84	-18.96 *	10.4
2	P1 × P3	-23.19 *	-10.6	-24.37 *	-19.33 *	6.53	17.67 *	0	8.16
3	P1 × P4	-22.54 *	-4.82	-22.18 *	-16.39 *	-5.03	10.23	-11.85	-2.08
4	P1 × P5	-3.34	-4.71	2.24	-2.08	36.68 *	22.33 *	21.14 *	26.50 *
5	P1 × P6	11.95	9.73	1.09	7.65	27.14 *	15.35 *	5.4	15.74 *
6	P1 × P7	30.15 *	21.86 *	5.21	18.88 *	30.15 *	21.86 *	5.21	18.88 *
7	P2 × P3	7.61	4.24	-11.18 *	0.21	49.25 *	37.21 *	17.44 *	34.37 *
8	P2 × P4	-3.67	-3.61	-11.62 *	-5.87	18.59 *	11.63	0.95	10.24
9	P2 × P5	-10.45 *	-0.72	-2.56	-4.68	26.63 *	27.44 *	15.45 *	23.14 *
10	P2 × P6	-34.04 *	10.29	-12.86 *	-12.26 *	-18.79 *	24.65 *	-0.47	2.34
11	P2 × P7	1.63	-1.23	13.78 *	4.69	25.13 *	11.63	29.95 *	22.11 *
12	P3 × P4	-10.51 *	-3.18	-12.80 *	-8.79	24.12 *	27.44 *	15.31 *	22.29 *
13	P3 × P5	-31.41 *	-8.69	-12.47 *	-16.99 *	-3.02	20.19 *	15.73 *	11.3
14	P3 × P6	-3.26	6.36	-30.68 *	-9.14	34.17 *	40.00 *	-8.34	21.82 *
15	P3 × P7	-24.78 *	-19.43 *	-21.65 *	-21.93 *	4.32	6.05	3.6	4.67
16	P4 × P5	-3.34	-5.8	-2.72	-3.99	36.68 *	20.93 *	15.26 *	24.03 *
17	P4 × P6	0.74	8.84	0.42	3.39	23.52 *	26.05 *	13.74 *	21.09 *
18	P4 × P7	1.23	9.24	1.67	4.1	24.12 *	26.51 *	15.17 *	21.92 *
19	P5 × P6	-17.91 *	-11.96 *	-10.96 *	-13.72 *	16.08 *	13.02	5.5	11.46
20	P5 × P7	10.16	-3.99	-16.48 *	-2.92	55.78 *	23.26 *	-1.04	25.41 *
21	P6 × P7	-0.88	16.37 *	38.64 *	17.86 *	12.56	22.33 *	44.55 *	26.72 *
	Number of significant crosses in desirable direction	02	02	02	02	15	15	10	13
	SE ±	0.32	0.33	0.30	0.28	0.32	0.33	0.30	0.28

* Significant at 5 % level of significance where, E1 = UHF, Nauni, E2 = RHR&TS, DhaulaKuan and E3 = RHR&TS, Bajaura. aGenotype acronyms given in Table 1.



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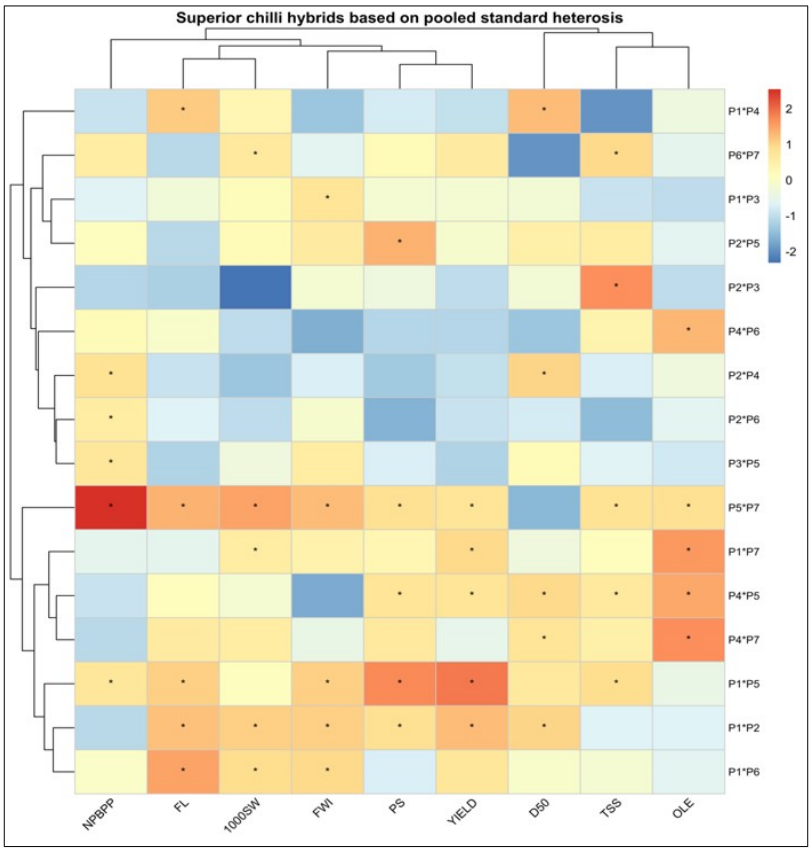

Fig. 5. Superior crosses for better parent heterosis and standard heterosis based on data pooled over locations. *Indicates the genotype among the top 5 crosses for each trait. D50: days to 50 % flowering; PS: plant spread; NPBPP: number of primary branches per plant; FL: fruit length; FW: fruit width; 1000SW: thousand seed weight; TSS: total soluble solids; OLE: oleoresin.

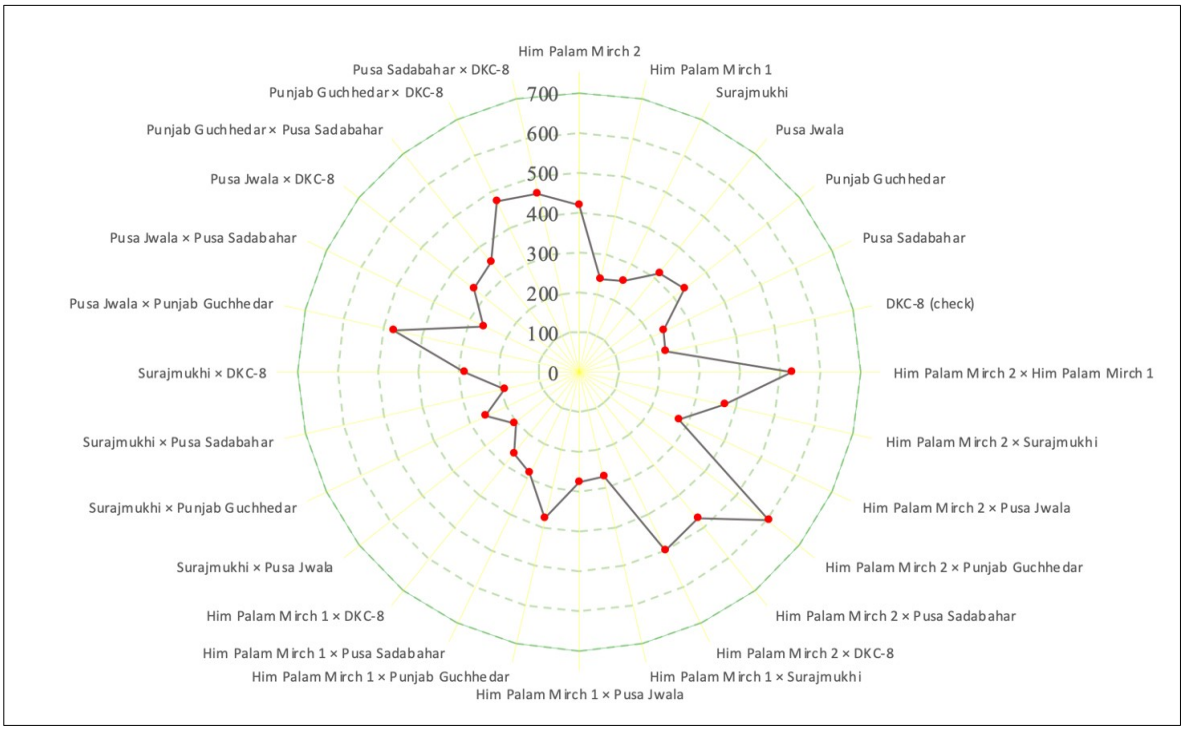

Fig. 6. Pooled mean performance of parents, hybrids and check.

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4. Conclusion

The research successfully evaluated the quantitative and qualitative traits of *Capsicum annuum* L., for various hybrid combinations significantly across multiple locations. The hybrids exhibited highly significant variation for all the characters across locations, with a strong influence of the environment on the traits examined. Hybrid combinations like Him Palam Mirch 2 × Punjab Guchhedar, Him Palam Mirch 2 × Him Palam Mirch 1, Him Palam Mirch 2 × Pusa Jwala came as emerging genotypes across all the environments. Broadly, the results advance strategic crosses development in chilli. The analytical methods adopted during the experiment showed a valuable framework for developing and adopting the best performing hybrids in chilli. Advanced hybrids can be used for future breeding purpose to enhance earliness, growth, yield and quality, specifically based on their performance at their respective locations.

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Authors' contributions

HDS and AC jointly conceptualised the research, contributed to data curation, methodology development and project administration. VS and AC conducted the formal analysis. HDS was solely responsible for funding acquisition, while HDS, AC and AS provided the necessary resources. AC, VS, M, AS and US contributed to writing and reviewing the manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest

Authors do not have any conflict of interests to declare.

Ethical issues

None

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