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RESEARCH

GENETIC VARIABILITY FOR VARIOUS ECONOMIC TRAITS IN CHILLI (*CAPSICUM ANNUUM* L.) GERMPLASM

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Abstract: India's chilli production, essential for both domestic and export markets, depends on genetic diversity. This study assessed the variability among 24 chilli genotypes. The analysis of variance revealed significant differences among all genotypes for various traits. Notably, parameters related to growth, yield and biochemical attributes displayed substantial Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), indicating considerable genetic diversity. Interestingly, PCV slightly exceeded GCV, suggesting a relatively lower impact of the environment on these traits. Crucially, high values of both phenotypic and genetic coefficients of variation highlighted significant potential for improvement through selective breeding. Traits exhibited high heritability, coupled with high to moderate genetic gains, except for the number of pickings. This indicated the prominence of additive gene action, emphasizing the effectiveness of selection processes. In essence, the study shows substantial potential for enhancing chilli genotypes via selection, due to the notable genetic diversity in crucial traits.

Keywords: Chilli, Genetic advance, Genetic variability, Heritability

INTRODUCTION

Chilli pepper or hot pepper (*Capsicum annuum* L.) commonly known as Mirchi is a member of the Solanaceae family with 2n=2x=24 chromosomes. It is believed to be originated in South and Central America (Bahurupe *et al*. 2013). In 1543, the term "*Capsicum*" was first suggested by the botanist Leonhart Fuchs, and later it was adopted by Carl Linnaeus in 1753 (Eich E, 2008). The genus *Capsicum* comprises a total of forty-three recognized species (Barboza *et al*., 2022). However, only five of these species, namely *C. annuum* L., *C. frutescens* L., *C. pubescens* Ruiz. & Pav., *C. baccatum* L., and *C. chinense* Jacq. are cultivated and are economically important (Perry *et al*., 2007). Fresh green chilli pepper is a nutritious food that provides a lot of vitamin C and A, as well as minerals such as folate, potassium, thiamine, molybdenum and manganese. It has more vitamin C (242mg/100g) than citrus fruits (70mg/100g) (Garcia *et al*., 1998; Marin *et al*., 2004) and is also called as capsule of vitamin C (Durust *et al*., 1997). The presence of capsaicin and capsanthin helps in fighting against infections, inflammation and cancer (Khan *et al*., 2014; Bosland *et al*., 2003).

Genetic variability arises from differences in the genetic makeup of individuals in a population or from changes in the environment. Selection is only feasible when the breeding material has a high degree of genetic variation among its individuals (Sumanth *et al*., 2017). Although the presence of high variability offers much scope for improvement of traits but it is more accurate when combined with genetic advance. Many workers have found genetic variability in chilli pepper to identify and utilize the germplasm for further selection or hybridization (Kumar *et al*., 2021; Ahmed *et al*., 2022; Lata *et al*., 2022; Baruah *et al*., 2023). Genotypic coefficient lower than phenotypic coefficient of variation indicated the high influence of environment on traits like days to first picking and number of fruits plant^{-1} (Hameedi *et al*., 2023). Further, the high heritability for fruit length, capsaicin content, fruit girth, fruit yield, flowering time and number of fruits plant^{-1} was observed in one hundred twenty chilli genotypes (Baruah *et al*., 2023). Utilization of available variability in the germplasm through selection or hybridization is the continuous process. Breeders always try to develop new genotypes to replace the old ones that are affected by various biotic and abiotic changes with time. Therefore, the present study was planned to estimate the various genetic variability components for further improvement in chilli crop.

Genetic variability stemming from differences in individuals genetic makeup or environmental changes, is vital for selection in breeding programs. A significant degree of genetic variation is necessary

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for effective selection (Sumanth *et al.*, 2017). Researchers have identified genetic variability in chilli peppers, crucial for germplasm selection and hybridization (Kumar *et al.*, 2021; Ahmed *et al.* 2022; Lata *et al.*, 2022; Baruah *et al.*, 2023). Environmental impact on traits like days to first picking and fruits per plant is evident through genotypic coefficients being lower than phenotypic coefficients (Hameedi *et al.*, 2023). High heritability in traits such as fruit length, capsaicin content, yield and flowering time was observed in 120 chilli genotypes (Baruah *et al.*, 2023). Breeders continually strive to create novel genotypes to replace outdated ones that become susceptible to evolving biotic and abiotic factors over time. Continuous utilization of germplasm variability through selection and hybridization is essential. This study aims to assess genetic variability components for further enhancing chilli crop improvement strategies.

MATERIALS AND METHODS

Genetic material and experimental site

Twenty-four chili pepper genotypes were acquired from different sources, as indicated in Table 1. The study was carried out at the Vegetable Research Farm, P.G Department of Agriculture, Khalsa College, Amritsar, Punjab, India, in the year 2022-23.

Field experiments and observations recorded

Seedlings aged one month were transplanted to raised rows under plastic-covered low tunnels in the month of November during the year 2022-23. The seedlings were spaced 75 cm apart on the rows and 45 cm apart within the rows. The experiment was laid out in Randomized Complete Block Design with three replications. A total of twenty seedlings of each genotype per replication was grown. Data was recorded for twenty-seven attributes i.e., plant height (cm), plant spread (N-S) (cm), plant spread (E-W) (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, leaf area (cm^2), days to first flowering, days to 50% flowering, days to first harvest, fruit length (cm), fruit diameter (mm), pericarp thickness (mm), fruit weight (g), fruit pedicel length (cm), number of pickings, number of fruits plant^{-1}, number of seeds plant^{-1}, thousand seed weight (g), harvesting duration (days), yield plant^{-1} (g), ascorbic acid (mg/100g FW), capsaicin content (%), colouring matter (ASTA units), oleoresin (%), total chlorophyll (mg/100g FW), total carotenoids (mg/100g FW) and total phenols (mg/100g FW). The ascorbic acid content was determined using the "2,6 dichlorophenol-indophenol visual titration method," as outlined by Ranganna (1979). Capsaicin content was measured following the procedure described by Bajaj and Kaur (1979). Colouring matter was assessed according to the method presented by Rosebrook *et al.* (1968). Oleoresin extraction was performed in a Soxhlet apparatus utilizing acetone as a solvent, following the method by Wesolowska *et al.* (2011). Chlorophyll and carotenoid levels were determined using the method detailed by Barnes *et al.* (1992). Total phenols were quantified using the modified Folin-Ciocalteu (FC) reagent method based on the approach of Swain and Hillis (1959). Standard agricultural practices as outlined in the Package and Practices for Vegetable Crops book by Punjab Agricultural University, Ludhiana, were adhered for optimal crop management (Anon., 2021).

Statistical analysis

An analysis of variance (ANOVA) was conducted for various traits following the methods outlined in Panse and Sukhatme (1984). Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) were calculated using the approach described by Burton and De Vane (1953). The PCV and GCV values were then classified as low (0-10%), moderate (10-20%) or high (20% and above) based on the criteria established by Burton and De Vane (1953) and Sivasubramanian and Madhavamenon (1973). Broad sense heritability, genetic advance (GA) and genetic advance as a percentage of the mean (GAM) were estimated following the methods outlined in Burton and De Vane (1953) and Johnson *et al.* (1955). The heritability values (h^2_{bs}) were categorized as Low (0-30%), Moderate (30-60%) and High (60% and above) based on the guidelines provided by Johnson *et al.* (1955). The range of genetic advance as a percentage was classified as low (0-10%), moderate (10-20%) or high (20% and above) as suggested by Johnson *et al.* (1955).

RESULTS

Analysis of variance (ANOVA)

The results of the analysis of variance showed that all the measured traits had significant differences among the assessions at 1% and 5% levels of significance (Table 2). This indicated that there was a lot of variation in the performance of the chilli pepper assessions, which can be used for further improvement.

Estimation of parameters of variability

Phenotypic coefficient of variation (PCV)

As mentioned in Table 3 range of phenotypic coefficient of variation was 9.00 % for days to first harvesting to 66.69% for yield plant^{-1}. High PCV existed for yield plant^{-1} (66.69%), number of fruits plant^{-1} (56.76%), average fruit weight (56.56%), leaf area (37.69%), number of seeds fruit^{-1} (35.40%), plant height (34.10%), plant spread (N-S) (30.56%), pericarp thickness (30.50%), plant spread (E-W) (30.26%), capsaicin in powder (28.40%), colouring matter (27.12%), carotenoids (26.42%), total phenols (26.12%), oleoresin content (25.92%), fruit length (25.38%), fruit diameter (24.60%), number of secondary branches plant^{-1} (24.31%), fruit pedicel length (22.89%), number of primary branches plant^{-1} (21.51%), number of pickings (21.36%), thousand seed weight (21.14%) and ascorbic acid (20.08%).

Moderate PCV was exhibited for days to final harvesting (12.00%), total chlorophyll (10.96%) and days to first flowering (10.03%). Whereas, days to 50% flowering (9.92%) and days to first harvest (9.00%) showed low PCV.

Genotypic coefficient of variation (GCV)

The extensive range of genotypic variability was observed for the characters under study ranging from 8.88% for days to first harvest to 66.02% for yield^{-1}. High genotypic coefficient of variation was found in parameters explicitly yield plant^{-1} (66.02%), average fruit weight (56.43%), number of fruits plant^{-1} (56.22%), leaf area (37.67%), number of seeds fruit^{-1} (35.33%), plant height (34.03%), pericarp thickness (30.38%), plant spread (N-S) (30.20%), plant spread (E-W) (29.94%), capsaicin in powder (28.18%), colouring matter (27.11%), carotenoids (26.41%), total phenols (25.93%), oleoresin content (25.76%), fruit length (25.31%), fruit diameter (24.49%), number of secondary branches plant^{-1} (24.06%), fruit pedicel length (22.40%), number of primary branches plant^{-1} (20.81%), thousand seed weight (21.04%) and ascorbic acid (20.03%). Moderate GCV was exhibited for number of pickings (14.95%), days to final harvesting (11.84%) and total chlorophyll (10.96%) whereas days to first flowering (9.90%), days to 50% flowering (9.84%) and days to first harvest (8.88%) showed low GCV.

Estimation of Heritability (h^2_{bs})

In present investigation, the assessment of heritability for various characters ranged from 48.98% for number of pickings to 99.94% for total carotenoids and high evaluations were attained for most of the characters (Table 3). High heritability estimates existed for total carotenoids (99.94%), leaf area (99.88%), colouring matter (99.88%), number of seeds fruit^{-1} (99.58%), average fruit weight (99.55%), plant height (99.54%), fruit length (99.45%), ascorbic acid (99.45%), pericarp thickness (99.25%), fruit diameter (99.10%), thousand seed weight (99.03%), oleoresin content (98.75%), total phenols (98.49%), days to 50% flowering (98.47%), capsaicin in powder (98.40%), number of fruits plant^{-1} (98.12%), yield plant^{-1} (98.00%), number of secondary branches plant^{-1} (97.92%), plant spread (E-W) (97.89%), plant spread (N-S) (97.66%), days to first flowering (97.43%), days to first harvest (97.40%), days to final harvesting (97.24%), total chlorophyll (95.93%), fruit pedicel length (95.76%) and number of primary branches plant^{-1} (93.61%). Moderate estimation of heritability observed for number of pickings (48.98%).

Estimation of genetic advance (GA)

In present study, genetic advance for various traits ranges from 0.19% for total chlorophyll to 1222.67% for yield plant^{-1}. Eleven traits i.e., yield plant^{-1} (1222.67%), number of fruits plant^{-1} (272.81%), total carotenoids (187.79%), colouring matter (82.23%), plant height (44.12%), ascorbic acid (41.27%), number of seeds fruit^{-1} (36.66%), plant spread (N-S) (34.24%), plant spread (E-W) (33.32%), harvesting duration (20.53%) and days to first harvest (20.13%) showed high genetic advance. Four traits i.e., days to 50% flowering (19.93%), leaf area (19.38%), days to first flowering (18.08%) and total phenols (15.47%) showed moderate genetic advance. While, twelve traits like number of secondary branches plant^{-1} (7.17%), oleoresin content (5.3%), fruit diameter (4.92%), average fruit weight (4.52%), fruit length (4.03%), number of primary branches plant^{-1} (3.04%), thousand seed weight (2.02%), fruit pedicel length (1.61%), number of pickings (1.34%), pericarp thickness (0.61%), capsaicin in powder (0.37 %) and total chlorophyll (0.19%) showed low genetic advance.

Estimation of genetic advance as percent of the mean (GAM)

In the current study, high genetic advance as percent of mean was revealed for yield plant^{-1} (134.64%), average fruit weight (115.98%), number of fruits plant^{-1} (114.72%), leaf area (77.55%), number of seeds fruit^{-1} (72.62%), plant height (69.93%), pericarp thickness (62.35%), plant spread (N-S) (61.48%), plant spread (E-W) (61.02%), capsaicin in powder (57.57%), colouring matter (55.81%), carotenoids (54.38%), total phenols (53.00%), oleoresin content (52.73%), fruit length (51.99%), fruit diameter (50.23%), number of secondary branches plant^{-1} (49.04%), fruit pedicel length (45.16%), thousand seed weight (43.12%), number of primary branches plant^{-1} (41.48%) and ascorbic acid (41.14%). Moderate genetic advance was noted in current study for days to final harvesting (24.04%), total chlorophyll (21.66%), number of pickings (21.55%), days to first flowering (20.13%), days to 50% flowering (20.12%). Whereas, days to first harvest (18.06%) showed moderate genetic advance as per cent mean.

DISCUSSION

Fisher (1919) pioneered the study of genetic variability, introducing the concepts of genotypic and phenotypic variations to predict genetic responses. The degree of genetic diversity within a germplasm pool is a key determinant of a crop's potential for enhancement. When identifying superior genotypes, it is crucial to dissect the overall diversity into phenotypic and genotypic components. Variability plays a pivotal role in the outcomes of selection efforts. Genetic variation arises from the plant's inherent genetic makeup, while environmental variation is attributable to external factors. The plant's observable traits or phenotype, result from the intricate interplay between its genes and the surrounding environment. Therefore, understanding and measuring phenotypic variation in yield and related traits are vital. Subsequently, numerous researchers have delved into estimating genotypic and phenotypic variations in various chilli crop traits,

aiming to enhance their quality and productivity (Nahak et al 2018; Kumar *et al*. 2021; Ahmed *et al*. 2022; Baruah *et al*. 2023). In the present investigation, the information demonstrated that higher PCV value is recorded for some traits in current study viz., yield plant^{-1}, number of fruits plant^{-1}, average fruit weight, leaf area, number of seeds fruit^{-1}, plant height, plant spread (N-S), pericarp thickness, plant spread (E-W), capsaicin in powder, colouring matter, carotenoids, total phenols, oleoresin content, fruit length, fruit diameter, number of secondary branches plant^{-1}, fruit pedicel length, number of primary branches plant^{-1}, number of pickings, thousand seed weight and ascorbic acid. This suggests that the traits are minimally influenced by environmental factors, allowing for direct selection in early segregating populations to focus on these characteristics. Similar findings were observed for yield in high estimates of PCV by number of fruits plant^{-1}, average fruit weight, number of seeds fruit^{-1} (Hameedi *et al*. 2023), for plant height (Saisupriya *et al*. 2022), yield plant^{-1} (Hemlata *et al*. 2022), although maximum PCV for quality traits particularly for capsaicin in powder are correspondingly approved with the earlier findings by Singh *et al*. (2022); Sran *et al*. (2019), leaf area (Kumar *et al*. 2019), for pericarp thickness (Sran *et al*. 2019), fruit diameter (Farwah *et al*. 2020), fruit length (Ahmed *et al*. 2022) and (Nahak *et al*. 2018), and higher PCV for growth traits specially for number of primary branches plant^{-1} and number of primary branches plant^{-1} was also discovered by earlier worker (Elahi *et al*. 2017). The moderate PCV values noticed for various characters like, days to final harvesting, total chlorophyll and days to first flowering which indicated the presence of lesser variation among the genotypes. Suggestion should be provided for improvement of these characters, by improve the base population through intercrossing in F_2 generation followed by recurrent selection. The similar findings for quality character that moderate PCV was detected for total chlorophyll by Saisupriya *et al*. (2022) and days to first flowering by Chowdhury *et al*. (2023) and Kumar *et al*. (2020). The evaluation of low PCV was noted for days to 50% flowering and days to first harvest which indicated the small genetic variation and does not need any improvement and can also be utilized in hybridization program. These outcomes were similar to the previous findings by Kumar *et al*. (2020).

The data showed that some traits in the current study, including yield plant^{-1}, number of fruits plant^{-1}, average fruit weight, leaf area, number of seeds fruit^{-1}, plant height, plant spread (N-S), pericarp thickness, plant spread (E-W), capsaicin in powder, colouring matter, carotenoids, total phenols, oleoresin content, fruit length, fruit diameter, number of secondary branches plant^{-1}, fruit pedicel length, number of primary branches plant^{-1}, number of pickings, thousand seed weight and ascorbic acid, had higher GCV values which indicating that the environment had little effect. As a result, direct selection could be used to improve these traits in an early segregating population. These results are in consonance with the earlier conclusions of various researchers for yield characters specially for yield plant^{-1}, average fruit weight, number of fruits plant^{-1}, plant height, fruit length, fruit diameter, number of seeds fruit^{-1} namely, Chowdhury *et al*. (2023) and Hameedi *et al*. (2023) who exhibited maximum percentage of GCV whereas pericarp thickness and capsaicin in powder for higher GCV was revealed by Sran *et al*. (2019), for ascorbic acid Saisupriya *et al*. (2022) and for number of branches plant^{-1} by Farwah *et al*. (2020). The moderate GCV values observed for certain traits, including days to final harvesting, total chlorophyll and days to first flowering which confirmed that there was less variation across genotypes. The base population should be improved by intercrossing in F_2 generation, followed by recurrent selection, in order to improve these traits. The evaluations of low GCV were found which indicating that there is small genetic variation and does not need any improvement. These results can be utilized in hybridization programs. These results were similar for days to first flowering and days to 50% flowering by Hameedi *et al*. (2023) and Hemlata *et al*. (2022).

In the current study, maximum heritability was observed for all the traits except the number of pickings. This high heritability suggests that these traits are primarily influenced by genetic factors, making them reliable for selection based on observed phenotypic performance. Heritability serves as a crucial parameter in breeding programs as it indicates the proportion of observed trait variation that is due to genetic differences. When heritability is high, as observed in this study, it implies that the traits are relatively stable across generations and less affected by environmental factors. The reliance on phenotypic performance for selection is justified in such scenarios, as it provides a dependable basis for identifying superior lines. Additionally, high heritability facilitates the selection of superior lines from homozygous populations. This implies that when traits have a strong genetic basis, selecting plants based on their observable characteristics can lead to the development of more desirable and stable lines over successive generations. Therefore, considering both heritability and phenotypic performance is crucial in ensuring the success and effectiveness of plant breeding programs. Earlier workers estimated the maximum heritability for growth and yield parameters mainly for plant height, average fruit weight and number of seeds fruit^{-1} executed by (Chowdhury *et al*., 2023) whereas for the days to 50% flowering and days to first harvest was observed by (Hemlata *et al*., 2022), for fruit length and fruit diameter (Singh *et al*., 2022), for capsaicin content and ascorbic acid (Farwah *et al*., 2020), total chlorophyll (Kumar *et al*., 2020), pedicel

length (Kumar *et al*., 2019), pericarp thickness, oleoresin content and colouring matter (Sran *et al*., 2019), for plant spread (E-W) and plant spread (N-S) (Nahak *et al*., 2018), for harvesting duration (Chakrabarty *et al*., 2017), thousand seed weight and number of seeds fruit^{-1} (Pandiyaraj *et al*., 2017). While, number of pickings characters showed moderate heritability which was influenced by environmental effects and the genetic improvement through selection will be difficult. The result was found similar to earlier researcher (Sahu *et al*., 2016). Analyzing both genotypic coefficient of variance (GCV) and heritability is crucial. While GCV alone doesn't show inheritance, combining it with heritability indicates how genetic traits pass to the next generation. High heritability means traits are strongly inherited, aiding better selection. This comprehensive approach guides effective trait selection.

The high genetic advance coupled with high heritability was observed in yield plant^{-1}, number of fruits plant^{-1}, total carotenoids. The selection of top 5% of the genotypes with the highest yield as parents in hybridization program the new generation may like lead to increase in yield plant^{-1} up to 1222.67gm. Likewise, a much higher number of fruits plant^{-1} will rise from 237.80 to 510.61. Similarly, total carotenoids will elevate from 345.30 (mg/100g FW) to 533.09 (mg/100g FW) (Table 1). In present study high heritability along with high genetic advance as mean percent was observed for yield plant^{-1}, average fruit weight, number of fruits plant^{-1}, leaf area, number of seeds fruit^{-1}, plant height, pericarp thickness, plant spread (N-S), plant spread (E-W), capsaicin in powder, colouring matter, carotenoids, total phenols, oleoresin content, fruit length, fruit diameter, number of secondary branches plant^{-1}, fruit pedicel length, thousand seed weight, number of primary branches plant^{-1} and ascorbic acid which might be dispensed to additive gene effect effect by governing their inheritance and phenotypic selection for their improvement. Similar findings of higher genetic advance for yield chiefly for yield plant^{-1} have been reported by (Saisupriya *et al*., 2022) for average fruit weight similar findings are also observed by Chowdhury *et al*. (2023), Farwah *et al*. (2022) and Saisupriya *et al*. (2022). Meanwhile, higher genetic advance was also reported for growth and yield characters particularly for plant height by Hemlata *et al*. (2022), number of primary and secondary branches plant^{-1} Hemlata *et al*. (2022), Semba *et al*. (2022) and Chakrabarty *et al*. (2017), fruit length, fruit diameter and plant spread Farwah *et al*. (2022) and Nahak *et al*. (2018), number of fruits plant^{-1}, number of seeds fruit^{-1} and thousand seed weight by Singh *et al*. (2022) although higher genetic advance for quality traits have been recorded mainly for ascorbic acid and capsaicin in powder by Saisupriya *et al*. (2022), colouring matter and pericarp thickness by Sran *et al*. (2019). Therefore, selection of next generation based on these traits will be beneficial for further crop improvement. According to Johnson *et al*. (1955), relying solely on heritability as an indicator for selection response might be misleading. Both heritability and genetic advance offer more accurate insights into the potential outcomes of selection processes. This is because heritability values can be high due to various types of gene actions. When high heritability coincides with substantial genetic advance, it suggests that genes are acting additively, meaning their effects are predictable and cumulative, as noted by Panse (1957). Conversely, when high heritability is paired with low genetic advance, it implies non-additive gene actions, such as dominance and epistasis, where gene interactions are more complex and less predictable. This information, provided by Liang and Walter (1968), highlights that the observed traits are influenced by intricate genetic relationships, making their expression less straightforward and more susceptible to external factors.

CONCLUSION

In the study, the chilli genotypes analysed exhibited significant genetic diversity. Notably, most traits displayed higher phenotypic coefficient of variation (PCV) values compared to genotypic coefficient of variation (GCV) values. This discrepancy suggests that direct selection could be applied effectively, highlighting its relevance in hybridization programs. Furthermore, several traits exhibited substantial genetic variability indicating their potential for selection and improvement. These traits encompassed various aspects of plant morphology, such as plant height, plant spread both in the north-south (N-S) and east-west (E-W) directions, the number of secondary branches per plant, leaf area, as well as key fruit characteristics including length, diameter, thickness of the pericarp, weight and pedicel length. Moreover, significant variability was also observed in traits related to harvest, including the number of pickings, fruits per plant, seeds per plant, thousand seed weight and the overall duration of harvesting. Additionally, essential nutritional factors such as ascorbic acid content and colour intensity (colouring matter) exhibited notable genetic variability. This diversity was primarily influenced by additive genes, indicating that these traits expression could be enhanced through phenotypic selection methods. The complex interplay of these genetic factors underscores the intricate nature of chilli pepper traits, presenting both challenges and opportunities for breeding programs aiming to enhance these characteristics.

Table 1. Detail of chilli accessions under evaluation

Sr.no.	Accessions	Source
1.	IC-264788	*ICAR- National Bureau of Plant Genetic Resources Regional Station, Bhowali, Uttarakhand
2.	IC-264803	-do-
3.	IC-264841	-do-
4.	IC-264861	-do-
5.	IC-264865	-do-
6.	IC-264867	-do-
7.	IC-264878	-do-
8.	IC-264929	-do-
9.	Kashi Anmol	*ICAR-Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
10.	Kashi Abha	-do-
11.	Kashi Ratna	-do-
12.	Arka Khyati	*ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka
13.	Arka Harita	-do-
14.	Arka Meghana	-do-
15.	Arka Gagan	-do-
16.	Fzr-Longi	Ferozepur, Punjab
17.	Fzr-Acchari	-do-
18.	LHC-4409	Laxmi Inputs
19.	Sahiba	Vegetable N Rice Seeds
20.	Rahela	A Division of Dhana Crop Sciences Limited Seeds
21.	Surajmukhi	Durga Seeds
22.	CH-2	Welcome Seeds
23.	CH-1	Punjab Agricultural University, Ludhiana, Punjab
24.	CH-27	-do-

Where, *ICAR- Indian Council of Agricultural Research

Table 2 Analysis of variance (ANOVA) for various attributes in twenty-four assessions of chilli

Sr. no.	Source of variation / Traits	Mean sum of square		
		Replication	Genotypes	Error
	Degree of freedom	**2**	**23**	**46**
1.	Plant height (cm)	4.56	1384.63***	2.15
2.	Plant spread (N-S) (cm)	12.76	855.17***	6.76
3.	Plant spread (E-W) (cm)	12.24	807.31***	5.75
4.	Number of primary branches plant^{-1}	0.24	7.11***	0.15
5.	Number of secondary branches plant^{-1}	0.22	37.41***	0.26

6.	Leaf area (cm^2)	0.23	265.81***	0.10
7.	Days to first flowering	0.57	239.38***	2.80
8.	Days to 50% flowering	14.29	286.53***	1.48
9.	Days to first harvest	4.80	296.69***	2.62
10.	Fruit length (cm)	0.013	11.57***	0.021
11.	Fruit diameter (mm)	0.044	17.29***	0.052
12.	Pericarp thickness (mm)	0.002	0.26***	0.0006
13.	Average fruit weight (g)	0.007	14.53***	0.022
14.	Fruit pedicel length (cm)	0.044	1.93***	0.028
15.	Number of pickings	2.26	3.49***	0.90
16.	Number of fruits $plant^{-1}$	2287	53967***	343
17.	Number of seeds $fruit^{-1}$	3.17	955.56***	1.34
18.	Thousand seed weight (g)	0.00009	2.93***	0.00958
19.	Yield $plant^{-1}$ (g)	54011	1085729***	7334
20.	Harvesting Duration (days)	6.22	309.44***	2.90
21.	Ascorbic acid (mg/100g FW)	1.34	1212.81***	2.25
22.	Capsaicin in powder (%)	0.003	0.09***	0.0005
23.	Colouring matter (ASTA)	9.0	4787.5***	1.9
24.	Oleoresin content (%)	0.36	20.19***	0.08
25.	Total chlorophyll (mg/100g FW)	0.00006	0.02***	0.0003
26.	Total carotenoids (mg/100g FW)	4.8	24950.2***	4.8
27.	Total phenols (mg/100g FW)	1.73	168.26***	0.83

*Significant at $p \leq 0.05$; ** High significant at $p \leq 0.01$ and ***Highly significant at $p \leq 0.001$

Table 3 Assessment of PCV, GCV, h^2_{bs}, GA, GAM, Range and Mean for yield and related traits in twenty- four chilli accessions.

Sr. no.	Source of variation / Traits	PCV	GCV	h^2_{bs}	GA	GAM	Range	Mean
1.	Plant height (cm)	34.10	34.03	99.54	44.12	69.93	31.33-108.53	63.09
2.	Plant spread (N-S) (cm)	30.56	30.20	97.66	34.24	61.48	30.93-90.73	55.68
3.	Plant spread (E-W) (cm)	30.26	29.94	97.89	33.32	61.02	30.80-87.20	54.59
4.	Number of primary branches $plant^{-1}$	21.51	20.81	93.61	3.04	41.48	4.33-10.13	7.31
5.	Number of secondary branches $plant^{-1}$	24.31	24.06	97.92	7.17	49.04	9.26-20.33	14.62
6.	Leaf area (cm^2)	37.69	37.67	99.88	19.38	77.55	13.26-46.20	24.98
7.	Days to first flowering	10.03	9.90	97.43	18.08	20.13	71.20-115.13	89.83
8.	Days to 50% flowering	9.92	9.84	98.47	19.93	20.12	79.66-129.00	99.04
9.	Days to first harvest	9.00	8.88	97.40	20.13	18.06	92.26-140.86	111.44
10.	Fruit length (cm)	25.38	25.31	99.45	4.03	51.99	3.57-12.34	7.75
11.	Fruit diameter (mm)	24.60	24.49	99.10	4.92	50.23	5.25-16.09	9.78
12.	Pericarp thickness (mm)	30.50	30.38	99.25	0.61	62.35	0.58-1.86	0.97
13.	Average fruit weight (g)	56.56	56.43	99.55	4.52	115.98	1.19-13.00	3.89
14.	Fruit pedicel length (cm)	22.89	22.40	95.76	1.61	45.16	2.22-5.61	3.56
15.	Number of pickings	21.36	14.95	48.98	1.34	21.55	3.3-7.6	6.0
16.	Number of fruits $plant^{-1}$	56.76	56.22	98.12	272.81	114.72	58.73-576.40	237.80
17.	Number of seeds $fruit^{-1}$	35.40	35.33	99.58	36.66	72.62	27.86-111.26	50.48
18.	Thousand seed weight (g)	21.14	21.04	99.03	2.02	43.12	2.48-7.83	4.62
19.	Yield $plant^{-1}$ (g)	66.69	66.02	98.00	1222.67	134.64	197.13-2317.73	908.08
20.	Harvesting duration (days)	12.00	11.84	97.24	20.53	24.04	54.00-103.33	85.40
21.	Ascorbic acid (mg/100g FW)	20.08	20.03	99.45	41.27	41.14	62.40-134.64	100.29

22.	Capsaicin in powder (%)	28.40	28.18	98.40	0.37	57.57	0.38-1.04	0.63
23.	Colouring matter (ASTA)	27.12	27.11	99.88	82.23	55.81	80.01-230.73	147.35
24.	Oleoresin content (%)	25.92	25.76	98.75	5.30	52.73	5.59-14.37	10.05
25.	Total chlorophyll (mg/100g FW)	10.96	10.73	95.93	0.19	21.66	0.71-1.08	0.88
26.	Total carotenoids (mg/100g FW)	26.42	26.41	99.94	187.79	54.38	195.94-513.16	345.30
27.	Total phenols (mg/100g FW)	26.12	25.93	98.49	15.47	53.00	20.47-41.52	28.67

Where, PCV=Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h^2_{bs}=heritability in broad sense, GA= Genetic advance, GAM= Genetic advance as percent of the mean

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Data availability

All data generated for this study are included in the manuscript.

Ethical approval

The present study does not include results of studies involving animals or humans.

REFERENCES

Ahmed, I., Nawab, N.N., Kabir, R., Muhammad, F., Intikhab, A., Rehman, A.U., Farid, M.Z., Jellani, G, Nadeem, S., Quresh, W., Ali, M., Hussain, M.M. and Ali, I. (2022). Genetic diversity for production traits in hot chilli (*Capsicum annuum* L.). *Pak J Bot*., **54**:2157-2166. http://dx.doi.org/10.30848/PJB2022-6(10)

Google Scholar

Anonymous (2021). Package of Practices for Cultivation of Vegetable. Pp. 50-56. Punjab Agricultural University, Ludhiana, Punjab, India.

Google Scholar

Bahurupe, J.V., Sakhare, S.B., Kulwal, P.L., Akhare, A.A. and Pawar, B.D. (2013) Genetic diversity analysis in chilli (*Capsicum annuum* L.) using RAPD markers. *Bioscan*, **8**:915-918.

Google Scholar

Bajaj, K.L. and Kaur, G (1979). Colorimetric determination of capsaicin in capsicum fruits with the Folin-Ciocalteu reagent. *Mikrochim Acta*, **71**:81-86. https://doi.org/10.1007/BF01197523

Google Scholar

Barboza, GE., Carrizo García, C., de Bem Bianchetti, L., Romero, M.V. and Scaldaferro, M. (2022). Monograph of wild and cultivated chilli peppers (*Capsicum* L., Solanaceae). *Phyto Keys*, **200**:1-423. https://doi.org/10.3897/phytokeys.200.71667

Google Scholar

Barnes, J.D., Balaguer, L., Manrique, E., Elvira, S. and Davison, A.W. (1992). A reappraisal of the use of DMSO for the extraction and determination of chlorophylls a and b in lichens and higher plants. *Environ Exp Bot*., **32**: 85-100. https://doi.org/10.1016/0098-8472(92)90034-Y

Google Scholar

Baruah, J., Munda, S., Sarma, N., Begum, T., Pandey, S.K., Chanda, S.K., Sastry, GN. and Lal, M. (2023). Estimation of genetic variation in yield, its contributing characters and capsaicin content of *Capsicum chinense* Jacq. (Ghost pepper) germplasm from Northeast India. *Peer J* ,**11**: e15521. https://doi.org/10.7717/peerj.15521

Google Scholar

Bosland, P.W. and Votava, F.J. (2003). Peppers, Vegetable and Spice Capsicums. Pp. 204-233. CABI Publishing. Wallingford, UK.

Google Scholar

Burton, GW. (1952). Quantitative inheritance in grasses. In: Proceedings of 6th International Grassland Congress, **1**:277-283.

Google Scholar

Burton, GN. and De Vane, E.M. (1953). Estimating Heritability in Fall Fescue (Festuca arundiancea L.) from Replicated Clonal Materials. *Agronomy Journal*, **45**: 478-481. http://dx.doi.org/10.2134/agronj1953.00021962004500100005x

Google Scholar

Chakrabarty, S. and Islam, AKMA (2017). Selection criteria for improving yield in chilli (*Capsicum annuum*). *Adv Agric*., 2017:1-9. https://doi.org/10.1155/2017/5437870

Google Scholar

Chowdhury, MFN, Rafii, M.Y., Ismail, S.I., Ramlee, S.I., Hosen, M., Karim, KMR and Yusuff, O. (2023). Genetic analysis of anthracnose resistant and heat tolerant chilli inbreed lines based on morpho-physiological characteristics. *Chil J Agric Res*., **83**:168-180. http://dx.doi.org/10.4067/s0718-58392023000200168
Google Scholar

Durust, N., Sumengen, D. and Durust, Y. (1997). Ascorbic acid and element contents of Trabzon (Turkey). *J Agric Food Chem*., **45**:2085-2087. https://doi.org/10.1021/jf9606159
Google Scholar

Eich, E. (2008). Solanaceae and Convolvulaceae: Secondary Metabolites. Springer Berlin Heidelberg http://dx.doi.org/10.1007/978-3-540-74541-9
Google Scholar

Elahi, Z., Nawab, N.N., Ramzan, A., Noor, T., Qasim, M.U., Khan, T.N. and Batool, N. (2017). Hybrid performance and analysis of genetic variability in green chillies (*Capsicum annuum* L.). *Pak J Bot*., **49**:2221-2225.
Google Scholar

Farwah, S., Hussain, K., Rizvi, S., Hussain, S.M., Rashid, M. and Saleem, S. (2020). Genetic variability, heritability and genetic advance studies in chilli (*Capsicum annuum* L.) genotypes. *Int J Chem Stud*., **8**:1328-1331. https://doi.org/10.22271/chemi.2020.v8.i3r.9383
Google Scholar

Fisher, R.A. (1919). The correlation between relatives on the supposition of Mendelian inheritance. *Earth Environ Sci Trans R Soc Edinb*., **52**:399-433. https://doi.org/10.1017/S0080456800012163
Google Scholar

Garcia, J.A., Wall, M.W. and Waddell, C.A. (1998). Endogenous levels of tocopherols and ascorbic acid during fruits ripening of New Mexican-type chilli (*Capsicum annuum* L.) cultivars. *J Agric Food Chem*., **46**:5093-5096. https://doi.org/10.1021/jf980588h
Google Scholar

Hameedi, A., Kumar, S., Samnotra, R.K., Rai, S.K., Sharma, M.K. and Abrol, V. (2023). Genetic variability studies for growth, yield and quality traits in chilli (*Capsicum annuum* L.) Germplasm under Sub Tropical conditions of Jammu. *Biol Forum*, **15**:243-247.
Google Scholar

Hussain, F. andAbid, M. (2011). Pests and diseases of chilli crop in pakistan: a review. *Int J Biol Biotech*., **8**:325-332.
Google Scholar

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimate of genetic and environmental variability in soybean. *J Agron*., **47**:314-318. https://doi.org/10.2134/agronj1955.00021962004700070009x
Google Scholar

Khan, M.A., Asghar, M.A., Iqbal, J., Ahmed, A. and Shamsuddin, Z.A. (2014). Aflatoxins contamination and prevention in red chillies (*Capsicum annuum* L.) in Pakistan. *Food Addit Contam Part B Surveill*, **7**:1-6. https://doi.org/10.1080/19393210.2013.825330
Google Scholar

Kumar, P.J., Paramaguru, P., Arumugam, T., Boopathi, N.M. and Venkatesan, K. (2021). Genetic divergence among Ramnad mundu chilli (*Capsicum annuum* L.) genotypes for yield and quality. *Electron J Plant Breed*, **12**:228-234. https://dx.doi.org/10.37992/2021.1201.034
Google Scholar

Kumar, S.C., Sahu, GS., Tripathy, P., Pradhan, B. and Dash, S.K. (2019). Studies on genetic variability in chilli (*Capsicum annuum* L.) Germplasm. *J Pharmacogn Phytochem*, **8**:1992-1994.
Google Scholar

Lata, H. and Sharma, A. (2022). Evaluation, genetic variability, correlation and path analysis studies in chilli (*Capsicum annuum* L.) genotypes. *Himachal J Agric Res*., **48**:56-64.
Google Scholar

Liang, GHL and Walter, T.L. (1968). Heritability estimates and gene effects for agronomic traits in grain sorghum. *Crop Sci*., **8**:77-80. https://doi.org/10.2135/cropsci1968.0011183X0008000010022x
Google Scholar

Marín, A., Ferreres, F., Tomás-Barberán, F.A. and Gil, M.I. (2004). Characterization and quantitation of antioxidant constituents of sweet pepper (*Capsicum annuum* L.). *J Agric Food Chem*., **52**:3861-3869. https://doi.org/10.1021/jf0497915
Google Scholar

Nahak, S.C., Nandi, A., Sahu, GS., Tripathy, P., Dash, S.K., Patnaik, A. and Pradhan, S.R. (2018). Studies on variability, heritability and genetic advance for yield and yield contributing characters in chilli (*Capsicum annuum* L.). *J Pharmacogn Phytochem*., **7**:2506-2510.
Google Scholar

Pandiyaraj, P., Saraladevi, D., Juliet, H.S. and Das, A. (2017). Genetic variability, heritability and genetic advance for quantitative and qualitative traits in chilli (*Capsicum annuum* L.). *Int J Agric Sci*., **9**:4081-4083.
Google Scholar

Panse, V.G and Sukhatme, P.V. (1984). Statistical Methods for Agricultural Workers, 4th edn. Pp. 349. Indian Council of Agricultural Research, New Delhi.
Google Scholar

Perry, L., Dickau, R., Zarillo, S., Holst, I., Pearsall, D.M., Piperno, D.R. and Berman, M.J. (2007). Starch fossils and the domestication and dispersal of Chilli Peppers (*Capsicum* spp.) in the America. *Sci*., **315**:986-988. https://doi.org/10.1126/science.1136914
Google Scholar

Ranganna, S. (1979). Manual of analysis of fruit and vegetable production. Tata McGraw Hill Co. Ltd., New Delhi.

Google Scholar

Rosebrook, D.O., Prozle, C.C. and Barney, J.E. (1968). Improved method for determination of extractable colour in Capsicum species. *Assoc Official Chemists*., **51**:637-643.

Google Scholar

Sahu, L., Trivedi, J. and Sharma, D. (2016). Genetic variability, heritability and divergence analysis in chilli (*Capsicum annuum* L.). *Plant Arch*., **16**:445-448.

Google Scholar

Saisupriya, P., Saidaiah, P. and Pandravada, S.R. (2022). Analysis of genetic variability, heritability and genetic advance for yield and yield related traits in chilli (*Capsicum annuum* L.). *Int J Bio-resour Stress Manag*., **13**:387-393. http://dx.doi.org/10.23910/1.2022.2583

Google Scholar

Singh, S., Joshi, A.K., Vikram, A., Kansal, S. and Singh, S. (2022). Studies on genetic variability and character association in chilli genotypes (*Capsicum annuum* L.). *Int J Econ Plants*, **9**:323-327. HTTPS://DOI.ORG/10.23910/2/2022.0494

Google Scholar

Sivasubramanian, J. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agric J*., **12**:15-16.

Google Scholar

Sran, T.S. and Jindal, S.K. (2019). Genetic variability and character association analysis in chilli pepper (*Capsicum annuum* L.). *Agric Res J*., **56**:24-32. http://dx.doi.org/10.5958/2395-146X.2019.00004.8

Google Scholar

Sumanth, V., Suresh, B.G, Ram, B.J. and Srujana, G. (2017). Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). *J pharmacogn phytochem*., **6**:1437-1439.

Google Scholar

Swain, T. and Hillis, W.E. (1959). The Phenolic Constituents of Prunus domestica. I-The Quantitative Analysis of Phenolic Constituents. *J Sci Food Agric*., **10**:63-68. https://doi.org/10.1002/jsfa.2740100110

Google Scholar

Wesolowska, A., Jadczak, D. and Grzeszczuk, M. (2011). Chemical composition of the pepper fruit extracts of hot cultivars *Capsicum annuum* L. *Acta Sci Pol Hortorum Cultus*., **10**:171-184.

Google Scholar