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EXPLORING GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN FRUIT QUALITY TRAITS WITHIN *CAPSICUM* GERmplASM LINES

Sahiini Ronald^{1*}, Madhavi Reddy Kambham² and Luwangshangbam James Singh¹

¹College of Horticulture, U.H.S., G.K.V.K., Bengaluru-560065, Karnataka, India.

²ICAR-Indian Institute of Horticultural Research, Hessaraghatta Lake Post, Bengaluru-560089, Karnataka, India.

*Corresponding author E-mail: ronaldsahiini@gmail.com

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ABSTRACT

Genetic variability estimates were conducted on twenty two *Capsicum* (*Capsicum annuum* L.) germplasm lines at the Research Farm of ICAR-Indian Institute of Horticultural Research, Bengaluru. Variance analysis and other genetic parameters revealed significant genetic variability across all traits among the genotypes studied. Phenotypic coefficient of variation exceeded genotypic coefficient of variation for all traits, indicating the influence of environmental factors on these characteristics. High genotypic and phenotypic coefficients of variation were observed for traits such as fruit length and width, placenta length and width, total soluble solids, fruit to seed ratio, seed number, and total capsaicinoids. Heritability was high for these traits, except for total soluble solids. Low to moderate genetic advance coupled with heritability was observed for fruit length and width, pericarp thickness, placenta length and width, and fruit to seed ratio. In contrast, seed number, total capsaicinoid content, and total soluble solids exhibited both high heritability and genetic advance, indicating that additive gene effects predominantly influence their expression.

Key words: Genetic variability, *Capsicum* germplasm, Phenotypic coefficient of variation, Genotypic coefficient of variation, Heritability.

Introduction

Chilli peppers, the vibrant fruits of the *Capsicum* genus, consist of over 200 different varieties across more than 30 species. Among these, five have been domesticated: *C. annuum* L., *C. baccatum* L., *C. chinense* Jacq., *C. frutescens* L., and *C. pubescens* (Bal *et al.*, 2022). Of these, *C. annuum* is the most well-known and economically significant, widely consumed both raw and cooked for its taste, colour, essential oils, and capsaicin content (Barboza *et al.*, 2019). This species plays a crucial role in the food industry, being a rich source of health-promoting compounds such as ascorbic acid (vitamin C), carotenoids (provitamin A), tocopherols (vitamin E), flavonoids, and capsaicinoids (Lu *et al.*, 2010). India is the leading producer and exporter of chillies, with major contributions from states such as Andhra Pradesh, Telangana, Madhya Pradesh, Karnataka, Orissa, Tamil Nadu, Assam, and Gujarat. These states together

account for approximately 86% of the total cultivation area and 90% of the country's production (Anonymous, 2022).

The significance of genetic variability within breeding materials cannot be over stated. It is essential not only for the selection of desirable traits but also for providing valuable insights into choosing diverse parent plants for hybridization programmes. Plant breeders must identify sources of favourable genes, integrate them into breeding populations, and aim to isolate productive genotypes and cultivars (Begna and Teresa, 2024). However, systematic breeding efforts for chillies have been lacking, making the improvement of this crop highly dependent on the availability of advantageous genetic diversity. The high variability in the chilli crops offers considerable potential for improvement. Hence, an effort has been made to assess genetic variability, heritability, and genetic advancements within a collection of twenty-two chilli

germplasm lines, focusing on traits that contribute to both yield and quality of chilli fruits.

Materials and Methods

The experiment was conducted at the Research Farm Vegetable Block VIII of the ICAR-Indian Institute of Horticultural Research (ICAR-IIHR) in Bengaluru. Bengaluru is located in the eastern dry zone of Karnataka

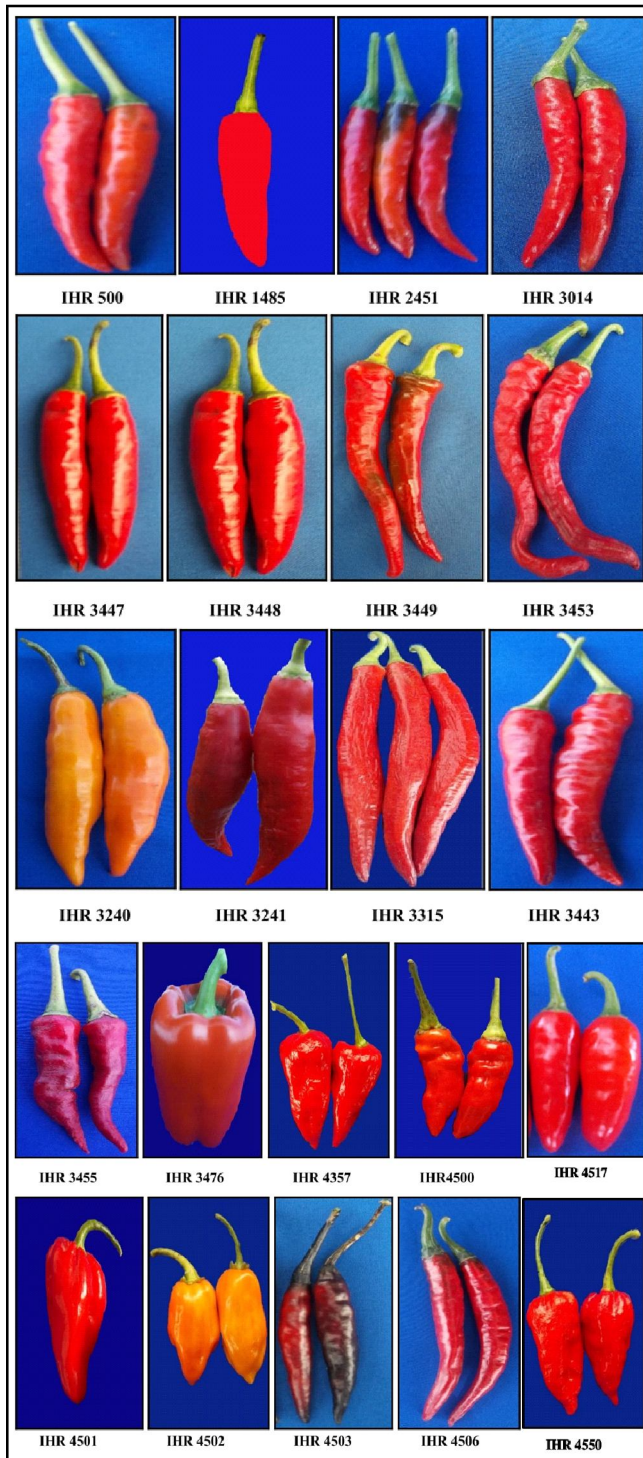


Fig. 1: Fruits of twenty-two germplasm line of *Capsicum species*.

Table 1: *Capsicum* germplasm lines used in the study.

S. No.	Accession No.	<i>Capsicum</i> species
1.	IHR 500	<i>Capsicum annuum</i>
2.	IHR 1485	<i>Capsicum annuum</i>
3.	IHR 2451	<i>Capsicum annuum</i>
4.	IHR 3014	<i>Capsicum annuum</i>
5.	IHR 3240	<i>Capsicum baccatum</i>
6.	IHR 3241	<i>Capsicum baccatum</i>
7.	IHR 3315	<i>Capsicum annuum</i>
8.	IHR 3443	<i>Capsicum annuum</i>
9.	IHR 3447	<i>Capsicum annuum</i>
10.	IHR 3448	<i>Capsicum annuum</i>
11.	IHR 3449	<i>Capsicum annuum</i>
12.	IHR 3453	Derivative of <i>Capsicum chinense</i>
13.	IHR 3455	<i>Capsicum annuum</i>
14.	IHR 3476	<i>Capsicum annuum</i>
15.	IHR 4357	<i>Capsicum chinense</i>
16.	IHR 4500	<i>Capsicum chinense</i>
17.	IHR 4501	Natural cross between <i>Capsicum chinense</i> and <i>Capsicum frutescens</i>
18.	IHR 4502	<i>Capsicum chinense</i>
19.	IHR 4503	<i>Capsicum annuum</i>
20.	IHR 4506	<i>Capsicum annuum</i>
21.	IHR 4517	<i>Capsicum annuum</i>
22.	IHR 4550	<i>Capsicum chinense</i>

state at 12° 58' north latitude and 77° 45' east longitude, with an altitude of 930 meters above mean sea level. This region, falling under zone-5 of region-3 within the agro-climatic zones of Karnataka, benefits from both south-west and north-east monsoons. The average annual rainfall is approximately 800 mm, distributed over a period of five to six months (May to October), with peaks in September.

In September seeds of *Capsicum* sp. germplasm lines were sown in separate plots, and seedlings emerged within nine to twelve days after sowing. The four-week-old seedlings of twenty-two capsicum germplasm lines (Table 1 and Fig. 1) were transplanted with a spacing of 60 cm × 20 cm between plants and rows, following a randomized complete block design with twenty-two treatments and three replications. Manures and fertilizers were applied according to recommended guidelines. Weed control was carried out as needed to maintain weed-free crops, and irrigation was provided as required.

Data on various parameters, such as fruit length (cm), fruit width (cm), pericarp thickness (mm), placenta length (cm), placenta width (cm), total soluble solids [TSS (°Brix)], fruit to seed ratio, seed number, and total capsaicinoids (SHU), were recorded on an individual plant basis from five randomly selected plants per plot.

Table 2: Analysis of variance (mean sum of squares) of fruit quality traits evaluated in twenty-two *Capsicum* genotypes.

S. No.	Characters	Sources of variation (df)		
		Replication (02)	Genotypes (22)**	Error (44)
1	Fruit length (cm)	0.04	29.91	0.622
2	Fruit Width (cm)	0.01	1.63	0.330
3	Pericarp thickness (mm)	0.006	0.37	0.0080
4	Placenta length (cm)	0.01	1.61	0.0238
5	Placenta Width (cm)	0.03	2.01	0.0119
6	TSS (°Brix)	0.49	23.71	0.204
7	Fruit to seed ratio	0.70	3.28	0.2301
8	Seed number	36.04	325.24	108.864
9	Total capsaicinoids (SHU)	214.93	1523.42	116.075

** Significant at P<0.01.

Statistical analysis of parameters

An analysis of variance (ANOVA) was performed on pooled data from two-year seasons to assess various characteristics, following the method outlined by Panse and Sukhatme (1985). Genetic variability for the different traits was determined according to the recommendations of Singh and Choudhary (1985). Genotypic and phenotypic coefficients of variation were computed using the methodology established by Burton and Devane (1953) and categorized as per the suggestions of Sivasubramanian and Menon (1973). Broad-sense heritability and genetic advance as percentage of mean were characterized as suggested by Johnson *et al.*, (1955) and calculated based on the formula provided by Allard (1960).

Results and Discussion

Analysis of variance showed significant differences among the genotypes for all nine fruit quality characters studied. Table 2 displays the mean sum of squares attributed to genotypes for these characters. The study revealed a substantial degree of diversity across all the considered characters, indicating potential for improving the population's performance, as suggested by Cherian (2000). Table 3 presents a comprehensive analysis of variability in terms of range, mean, and genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), heritability (h^2), and genetic advance GA (%) for the different characters. The data indicates a wide range of variability across nearly all the characters, providing ample opportunities for selecting desirable variations. The maximum range was observed in total capsaicinoids, ranging from 1394 to 340,917 SHU, followed by seed number (7.75-129.25), fruit length (2.85-14.15 cm), and TSS (5.90-15.80 °Brix), as shown in Table 3.

All traits examined showed greater PCV values than GCV values, suggesting that the variability in these traits is influenced by both genotypes and environmental factors. Similar results have been reported in previous studies (Jogi *et al.*, 2017; Sharma and Sood, 2018; Ain *et al.*, 2019; Patel *et al.*, 2022). However, close estimates of GCV and PCV were recorded for most characters, indicating that the genetic architecture of the genotypes largely contributes to the final phenotypic expression of these characters. These results suggest that selecting traits based on their phenotypic characteristics could enhance the chilli improvement programme, a conclusion also supported by Choudhary and Samadia (2004) and Patel *et al.*, (2022). Among the traits studied, the largest variation was observed between PCV and GCV Estimates for TSS, followed by seed number and total capsaicinoids. The highest GCV value was associated with total capsaicinoids (74.25%), followed by fruit to

Table 3: Range, mean, components of variance, heritability and genetic advance for different characters in twenty-two *Capsicum* germplasm lines.

Characters	Range		Mean	GCV (%)	PCV (%)	Heritability (h^2)	Genetic advance (%)
	Min.	Max.					
Fruit length(cm)	2.85	14.15	7.06	43.10	48.33	79.55	11.16
Fruit width(cm)	0.62	5.10	1.78	47.04	52.81	78.87	2.61
Pericarp thickness (mm)	1.57	3.20	2.16	20.79	23.36	78.75	1.68
Placenta length (cm)	0.70	5.20	1.77	42.19	47.60	79.00	2.60
Placenta width (cm)	0.60	3.80	1.59	56.48	60.36	65.42	2.43
TSS (°Brix)	5.90	15.80	10.37	34.01	78.56	58.42	80.55
Fruit to seed ratio	0.62	7.32	2.00	58.63	64.87	81.71	3.87
Seed number	7.75	129.25	74.74	41.14	49.38	69.42	96.20
TotalCapsaicinoids(SHU)	1394	340917	93170.13	74.25	82.46	79.35	80.66

seed ratio (58.63%) and placenta width (56.48 cm).

Heritability is a valuable indicator for the transmission of characters from parents to offspring (Falconer, 1989). Traits with high heritability are more responsible for improvement through direct selection, as they are less influenced by environmental factors. In our study, heritability values ranged from 58.42% (TSS) to 81.71% (fruit to seed ratio), with the exception of TSS, placenta width, and seed number, the remaining characters showed more than 70% heritability. Characters with high heritability facilitate more effective selection based on their phenotypic performance. The high heritability estimates for the mentioned characters likely result from additive gene effects (Narayana *et al.*, 1996), aiding in selecting individuals based on their phenotypic performance.

Genetic advance is a critical measure for assessing the progress achieved through selection, signifying an improvement in the average genotypic values of selected plants relative to the parental population. The effectiveness of genetic advance under selection depends on genetic variability, heritability, and the intensity of selection (Allard, 1960). High heritability alone is insufficient for substantial improvement through selection; it must be accompanied by high genetic advance (Shukla *et al.*, 2006). The most effective selection strategy involves combining high heritability values with substantial genetic advance as per cent of mean, rather than focusing on either alone (Johnson *et al.*, 1955; Gandhi *et al.*, 1964). Traits with high heritability and high genetic advance are governed by additive genes, whereas traits with high heritability but low genetic advance are typically influenced by non-additive genes (dominant and/or epistatic), limiting the potential for improvement through selection (Akbar *et al.*, 2003). Traits with high heritability and moderate to low genetic advance as per cent of mean, can be enhanced through multiple crosses and heterosis breeding rather than simple selection (Diwaker *et al.*, 2012; Meena *et al.*, 2016; Rosmaina *et al.*, 2016).

In this investigation, the genetic advance expressed as a per cent of mean was assessed across various traits in the chilli genotypes studied. These genetic advances ranged from 1.68% (pericarp thickness) to 96.20% (seed number). Notably, high heritability coupled with a high expected genetic advance as per cent of mean was observed for specific fruit-related attributes. For instance, seed number exhibited a heritability estimate of 69.42% and an expected genetic advance of 96.20%, while total capsaicinoids displayed a heritability estimate of 79.35% and an expected genetic advance of 80.66%. Similarly, TSS showed a heritability of 58.42% with an expected

genetic advance of 80.55%. Traits with high heritability and high genetic advances are reliable selection indices, suggesting a significant influence of additive gene effects in their expression. Our findings align with previous studies (Ukkund *et al.*, 2007; Diwaker *et al.*, 2012; Rajya Lakshmi and Vijayapadma, 2012; Agasimani and Kumar, 2013; Janaki *et al.*, 2015) and indicate a predominance of additive gene action in these traits, with minimal influence from environmental factors. This outcome implies the potential for improvement through selective breeding techniques. Our assessment of variability parameters pertaining to capsaicinoids content agrees with previous studies (Gupta and Yadav, 1984; Rani and Singh, 1996; Manju and Sreelathakumary, 2002; Khurana *et al.*, 2003; Krishna *et al.*, 2007; Singh *et al.*, 2009; Sonia *et al.*, 2009; Datta and Das, 2013). These findings contrast with Munshi *et al.*, (2010), who observed low values of PCV, GCV, heritability, and genetic advance for the capsaicin trait. Similar trends in traits such as number of fruits per plant, yield per plant, and primary branches per plant in chilli were observed by Datta and Das (2013).

In light of the preceding discussion, it is evident that significant variability exists within the various germplasm lines for most traits under scrutiny. Consequently, these diverse germplasm lines hold promise for incorporation into forthcoming breeding programs. Effective selection of germplasm may yield substantial benefits, particularly for traits characterized by high heritability and higher genetic advance as per cent of mean, such as high seed number, total capsaicinoids (SHU), and TSS ($^{\circ}$ Brix), which are primarily influenced by additive gene effects.

Conclusions

This study revealed substantial diversity across various fruit quality traits, providing valuable opportunities for population improvement. Traits with high heritability and genetic advance, such as seed number, total capsaicinoids, and TSS, showed strong potential for significant improvements through selective breeding. The observed diversity within germplasm lines holds promise for future breeding efforts, particularly for traits governed by additive gene effects. Overall, this research offers valuable insights for enhancing the performance of chilli genotypes.

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Declaration

The authors have declared that no competing interests exist.

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