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EXPLORING GENETIC DIVERSITY AND HERITABILITY IN NEWLY BRED INDUSTRIALLY VALUED ELITE CHILLI (*CAPSICUM ANNUUM* L.) GENOTYPES

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ABSTRACT

The present investigation in order to evaluate the performance of twenty elite genotypes of chilli (*Capsicum annuum* L.) for dry fruit yield and its component traits was carried out at Horticultural Research and Extension Centre, Haveri (Devihosur) during 2020-21 *kharif* season. The experiment with 20 genotypes was laid out in randomized complete block design with three replications. Analysis of variance revealed that the genotypes differed significantly for all the growth, yield and quality parameters. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were higher for number of fruits per plant, fruit length, average dry fruit weight and capsaicin. High heritability and high GAM were observed for number of fruits per plant, fruit length, colour value, capsaicin and oleoresin content.

Key words : *Capsicum annuum*, Heritability, Yield, GAM, GCV, PCV, Capsaicin and Oleoresin.

Introduction

Chilli (*Capsicum annuum* L.) is one of the most important vegetable and spice crops cultivated worldwide. Commonly known as hot pepper, it belongs to the family Solanaceae and the genus Capsicum, possessing a diploid chromosome number of 2n = 24. The crop is native to South America and was introduced into India by the Portuguese in 1584 from Brazil (Dhaliwal *et al*., 2014). Chilli is cultivated under tropical, subtropical and temperate climates for multiple purposes as a vegetable (green chilli), spice (dry chilli), condiment and as a raw material for sauces and pickles (Chattopadhyay *et al*., 2011).

Chilli is a major commercial crop in India, cultivated both for fresh consumption and value-added products. Its distinctive pungency is attributed to the presence of capsaicinoids, a group of alkaloid compounds primarily capsaicin (8-methyl-N-vanillyl-6-enamide) and dihydrocapsaicin which together account for about 80–90% of the total capsaicinoids. These compounds are not only responsible for the characteristic heat of chilli but also possess significant pharmaceutical properties, including antioxidant, anti-obesity, anti-arthritic, analgesic, antimicrobial and anticancer activities (Harish *et al.*, 2020).

Furthermore, the vibrant colour of chilli fruits is primarily due to the presence of carotenoid pigments such as capsanthin, capsorubin, cryptoxanthin and zeaxanthin. These natural pigments are widely extracted and utilized in the food processing industry as natural colourants, enhancing the visual appeal and nutritional quality of a wide range of food products. India stands as the world's largest producer, consumer and exporter of chillies, contributing over 36.57% of the global dry chilli production (Geetha *et al.*, 2017). The crop is cultivated across an estimated 364 thousand hectares, yielding about 3.72 million tonnes annually (Anonymous, 2019). During the financial year 2020, India exported approximately 484 thousand metric tonnes of chilli and its processed products, valued at around ` 6,222 crores, accounting for nearly 38% of the total global production (Anonymous, 2020). Within India, the major chilli-producing states include Andhra Pradesh, Telangana, Tamil Nadu, Karnataka and Madhya Pradesh. To meet the higher demand of chilli due to increased population, necessary efforts should be made in order to increase the production and productivity. Increased chilli growing area is one key to increase production but one should consider alternate solution for increasing productivity of the crop instead *viz*., cultivation of local adopted and high yielding cultivars. Although the crop is available throughout the year, the demand of chilli is further increasing with the expanding population. A wide range of variability reportedly exists in this crop with respect to growth and yield attributes. Therefore, the present study was aimed at comparison of different advanced elite chilli genotypes to screen for growth, yield and quality parameters.

A comprehensive understanding of the nature and magnitude of genetic variability within a germplasm collection is one of the most essential prerequisites for developing effective and sustainable breeding strategies (Krishna *et al.*, 2007). The success of any crop improvement programme largely depends on the extent of genetic variation available among the existing genotypes. Greater variability within a population provides a broader genetic base, thereby enhancing the chances of identifying and selecting superior individuals with desirable attributes (Vavilov, 1951).

The portion of phenotypic variation that is transmitted from parent to offspring is termed heritability and it reflects the degree to which a trait is genetically determined. High heritability indicates that selection for that trait is likely to be more effective, as a greater proportion of the observed variation is due to genetic rather than environmental factors. Thus, heritability estimates are crucial in distinguishing whether the observed phenotypic differences are governed by genotypic effects or environmental influences. However, heritability alone does not provide a complete picture of the potential for genetic improvement. The combination of heritability estimates with genetic advance offers a more reliable prediction of the expected genetic gain from selection (Johnson *et al*., 1955).

Given the challenges in improving complex quantitative traits influenced by both genetic and environmental factors, there is a pressing need to identify superior genotypes that exhibit high productivity and desirable quality attributes. In the case of chilli (*Capsicum annuum* L.), identifying genotypes with high dry fruit yield and superior quality is crucial for enhancing both state and national productivity. Furthermore, distinguishing consumer-preferred types for domestic use and industrial applications is vital for meeting market demands. Therefore, the characterization of chilli cultivars using both morphological and molecular markers is indispensable for the precise identification and differentiation of genotypes possessing economically important traits.

In this context, the present investigation was undertaken to assess the extent of genetic variability, heritability and genetic advance for sixteen important quantitative and qualitative traits in a set of chilli genotypes. The findings of this study are expected to aid in the identification of promising lines with high yield potential and superior quality traits, which can be effectively utilized in future chilli improvement programmes.

Materials and Methods

The experiment was carried out at the Horticultural Research and Extension Centre (HREC), Devihosur, Haveri, under the jurisdiction of the University of Horticultural Sciences, Bagalkot, during the kharif season of 2020-21. The chemical properties of the experimental soil are presented in Appendix I. The experimental site, Haveri, is located in the Northern Transitional Agro-Climatic Zone (Zone VIII) of Karnataka, at 14°47' N latitude, 75°21' E longitude and an altitude of 563 meters above mean sea level (MSL). This region benefits from both the South-West and North-East monsoon systems, with a mean annual rainfall of approximately 728 mm. The meteorological data recorded during the crop period at the observatory of HREC, Haveri, are provided in Appendix II. The experimental material comprised 20 chilli genotypes, including five mutant lines exhibiting deciduous red ripening fruits with non-persistent calyx characteristics. The trial was laid out in a Randomized Complete Block Design (RCBD) with three replications. Seeds were sown on raised nursery beds on May 22, 2020 and healthy seedlings were transplanted to the main field at a spacing of 75 cm × 45 cm when they were 38 days old. For data collection, five plants were randomly selected from each genotype in each replication to record observations on various quantitative and qualitative traits. The morphological characterization of the chilli genotypes was carried out using the standard descriptors for Capsicum species.

Estimation of quality parameters

Capsaicin (SHU)

The approach proposed by Palacio (1977) was used to quantify capsaicin in red wet stages of fruits, as stated below. 2 g ground dried chilies, sieved at No. 40 (0.42 mm) and placed in a 100 ml volumetric flask to extract, dilute with ethyl acetate to a level of 10 mL and leave for 4 hours. Just before reading, dilute 1 ml of extract in 5 ml ethyl acetate, then add 0.5 ml vanadium oxytrichloride ($VoCl_3$) solution (0.5 percent VoCl3in ethyl acetate) and mix. Read at 720 nm, deduct the reading from 0.5 mL Vanadium oxytrichloride added to ethylacetate, and compare to the pure capsaicin reference curve.

$$\text{Capsaicin } \% = \frac{\left(\mu_g \text{ capsaicin} \times 100 \times 100\right)}{1000 \times 1000 \times 1 \times 2}$$

SHU= capsaicin (g/g) × 1.6 × 10^7

Oleoresin (%)

Soxhlet apparatus, created by Soxhlet in 1879, is used to extract chilli oleoresin. In a thimble, 10 gramme of chilli is placed, and 1:10 acetone is poured over it, then heated at reflux. As the water boils, the fumes rise to the surface and are condensed by a condenser. The thimble is then filled with the condensed solvent. It automatically syphons back down into the container once it has filled with enough solvent. This process is continued until all of the oleoresin has been extracted to organic acid, and the solvent is then allowed to evaporate, usually using a rotary evaporator. The formulae are used to calculate the amount of oleoresin extracted.

$$\text{Oleoresin } (\%) = \frac{W_3 - W_2}{W_1} \times 100$$

Where,

W_1 – Weight of sample taken W_2 – Weight of porcelain dish

W_3 – weight of porcelain dish + sample extract after drying

Colour value (ASTA)

The absorbance of acetone extract of powdered chilli fruit at 450 nm was used to estimate the extractable colour value in dry chilli fruits. 50 ml pure acetone was used to extract 50 mg of chilli powder. This solution was maintained at room temperature in a dark place for sixteen hours. When taking spectrophotometer readings, pure acetone is used as a blank.

The absorbance of standard $K_2Cr_2O_7$ (potassium dichromate) solution at 450 nm is used to calculate the colour value. 50 mg of $K_2Cr_2O_7$ is dissolved in 100 mL of distilled water to make the standard $K_2Cr_2O_7$ solution. The following formulae are used to determine the colour value,

$$\text{Colour value (ASTA units)} = \frac{\text{O.D of sample} \times 200}{\text{mg/ml of sample} \times \text{O.D of Standard solution} \times 2}$$

Results and Discussion

Genetic variability for growth parameters

The plants height varied between 57.85 cm (NPC-2) and 85.96 cm (NPC-3), with a mean measurement of 63.29 cm (Table 1, Figs. 1 and 2). Heritability (81.61%) and genetic advance above the mean were also validated for this attribute, along with low estimates of genotypic coefficient of variation (19.32 %) and moderate estimates of PCV (21.38%) and GAM (35.95%). The plant spread ranges from 33.65 cm (NPC-4) to 53.28 cm (GCS 94/68), with a mean of 38.98 cm. The GV and PV values were 37.63 and 50.44, respectively, with reasonable estimates for heritability, PCV and genotypic mean advance. The average number of primary branches per plant was 2.36 and the range was 2.34 (GCS 94/68 and Byadgi Kaddi) to 3.64. (NPC-2). The estimates for the GCV and PCV were average (19.28% and 21.41%, respectively). With 81.11 per cent of heritability and 35.77 per cent of GAM, respectively, this trait had a moderate heritability and GAM. However, the secondary branches per plant had a range from 4.72 (NPC-1) to 6.74, with an average of 4.85 (NPC-2). The coefficients of variation for the genotype and phenotype were moderate (17.97% and 20.05%, respectively). However, the GAM and heritability for this characteristic were found to be moderate (80.34% and 33.19%, respectively). According to Surya Kumari *et al.* (2014) and Meena *et al.* (2016), all the growth traits plant height, plant spread, primary branches per plant and secondary branches per plant resulted in moderate estimates of GCV, PCV, moderate heritability and GAM. The non-additive genes are responsible for the modest GCV, PCV, heritability and GAM. As a result, there is less opportunity for selection to improve growth-related traits as these characters are greatly influenced by the environment.

Genetic variability for yield parameters

After transplanting, the days to first flowering ranged from 25.00 (NPC-5) to 34.00 (DCA-234) days, with a

Table 1 : Estimates of genetic parameters for growth, yield and quality parameters in chilli genotypes.

Characters	Range		Mean	GV	PV	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
	Min.	Max.								
Plant height (cm)	57.85	85.96	63.29	149.47	183.14	19.32	21.38	81.61	22.75	35.95
Plant spread (cm)	33.65	53.28	38.98	37.63	50.44	15.74	18.22	74.61	10.92	28.00
Number of primary branches	2.34	3.64	2.36	0.21	0.26	19.28	21.41	81.11	0.85	35.77
Number of secondary branches	4.72	6.74	4.85	0.76	0.95	17.97	20.05	80.34	1.61	33.19
Days to first flowering	25.00	34.00	29.63	2.37	10.90	5.20	11.14	21.74	1.48	4.99
Days to red fruit harvest	49.54	62.52	56.74	9.22	37.65	5.35	10.81	24.48	3.09	5.45
Number of fruits/plant	39.82	76.45	44.05	442.19	458.29	47.74	48.60	96.49	42.55	96.60
Fruit length (cm)	7.95	17.74	9.08	13.82	14.55	40.93	42.00	94.96	7.46	82.17
Fruit width (cm)	0.74	2.11	1.17	0.09	0.11	26.19	28.25	87.23	0.39	50.76
Average red fruit weight (g)	2.13	3.70	2.38	0.52	0.59	30.46	32.31	88.87	1.41	59.15
Average dry fruit weight (g)	0.64	2.27	0.98	0.25	0.26	51.31	52.42	95.84	1.01	103.48
Green chilli yield / Plant (g)	540.48	944.82	552.08	29676.15	31950.28	31.20	32.38	92.88	342.01	61.95
Dry chilli yield / Plant (g)	48.63	74.46	50.07	134.03	157.30	23.12	25.05	85.21	22.01	43.97
Capsaicin (SHU)	6286.39	97343.67	21662.78	697407721.9	697777733.7	121.91	121.94	99.95	54387.04	251.06
Oleoresin (%)	7.63	17.32	11.98	6.81	6.92	21.78	21.95	98.45	5.33	44.51
Colour value (ASTA)	87.51	196.41	127.96	1150.18	1161.83	26.50	26.64	99.00	69.51	54.32

GV – Genetic Variance PV – Phenotypic Variance GCV – Genotypic coefficient of Variation PCV – Phenotypic coefficient of Variation
h^2– Broad Sense Heritability GA– Genetic Advance GAM– Genetic Advance Over Mean.

mean of 29.63 days (Table 1, Figs. 1 and 2). The respective GV and PV values were 2.37 and 10.90. However, the observed values for GCV, PCV, heritability and GAM were 5.20%, 11.14%, 21.74% and 4.99%, respectively. The time taken for harvesting the first ripening fruit ranged from 49.54 (NPC-3) to 62.52 (DCA-88) days after transplanting, with a mean time of 56.74 days, with 9.22% and 37.65% the GV and PV values, respectively. The average number of fruits produced by a plant is 44.05. Fruit production per plant ranges from 39.82 (NPC-1) to 76.45. (NPC-5). The estimates for GCV and PCV, 47.74% and 48.60%, respectively, were also high. Heritability and GAM estimates for this characteristic were both high (96.49% and 96.60%, respectively).

The range of fruit length is between 7.95 cm (NPC-4) and 17.74 cm (SRS-2) with an average fruit length of 9.08. GV and PV had values of 13.82 and 14.55, respectively. The estimated GCV and PCV percentages were moderate, with 40.93 and 42.00%, respectively, for each trait, the GAM (82.17%) and moderate heritability (94.96%) were noted. The fruit width noted an average of 1.17 cm, varied from 0.74 cm (NPC-3) to 2.11 cm (Byadgi Dabbi). The GV and PV were respectively 0.09 and 0.11. The estimations for this characteristic were moderate, with 26.19% GCV, 28.25% PCV, 87.23% heritability and 50.76% GAM being observed.

The mean fruit weight was 2.38 g, with the average wet fruit weight ranging from 2.13 g in NPC-4 to 3.70 g in Byadgi Dabbi. The character's GV and PV were 0.52 and 0.59, respectively. Along with high heritability (88.87%) and GAM, moderate GCV and PCV (30.46 % and 32.31%, respectively) were detected (59.15%). Five dry fruits were weighed on average, with weights ranging from 0.64 (SRS-2) to 2.27 g (DCA-161) and a weight of 0.98 g being recorded as the average. With the GCV (51.31%), PCV (52.42%), heritability (95.84%) and GAM (103.48%) values, the GV and PV were respectively 0.25 and 0.26. The values of green yield per plant obtained from 540.48 g to 944.82 g with a norm yield of 552.08 g.

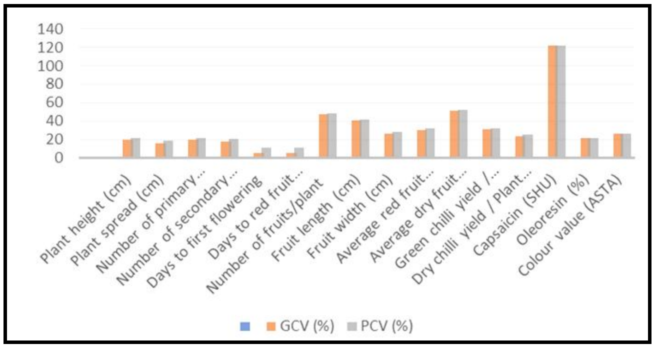

Fig. 1 : Estimates of GCV and PCV for growth, yield and quality parameters in chilli genotypes.

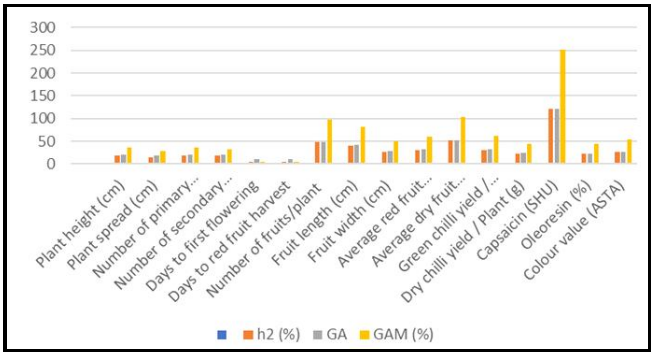

Fig. 2 : Estimates of h^2, GA and GAM for growth, yield and quality parameters in chilli genotypes.

With more heritability (92.88%) and GAM, GCV and PCV estimations were moderate, at 31.20 and 32.38 per cent, respectively (61.95%). Dry yield values per plant range from 48.63 g to 74.46 g, with a mean yield of 50.07 g. GCV and PCV estimates were moderate with 23.12 per cent and 25.05 per cent respectively with high heritability (85.21%) and GAM (43.97%). In the current study, the characteristics number of fruits per plant and fruit production per plant showed high PCV and GCV (>20%) together with high heritability (>60%) and GAM (>20%). It shows that additive gene activity predominates. Consequently, selection based on phenotype would be advantageous for the enhancement of these qualities (Choudhary and Samadia 2004; Amit *et al*., 2014; Maurya *et al*., 2015 and Abhinaya *et al*., 2016). The high level of GCV, PCV, heritability and genetic advance observed which indicated the preponderance of both additive and non-additive gene action for traits like a number of fruits fruit length, fruit width and average fruit weight and similar results were also reported by Maurya *et al.* (2015). Therefore, selection and hybridization can be used to increase these traits.

Genetic variability for quality parameters

The capsaicin content of fruit had a range between 6286.39 and 97343.67 with a mean 21662.78 heat units (Table 1, Figs. 1 and 2). The GCV, PCV, heritability and GAM were 121.91%, 121.94%, 99.39% and 251.06%, respectively. Fruit has an oleoresin concentration that ranges from 7.63 to 17.32%, with 11.8% being the average. The estimates for the trait's GCV (21.78%), PCV (21.95%), heritability (98.45%) and GAM (44.51%) were high. With a mean value of 127.96 ASTA units, the colour value ranged from 87.51 to 196.41 ASTA units. With high heritability (99.00%) and GAM, GCV and PCV estimates were moderate with 26.50 and 26.64%, respectively (54.32%). Capsaicin and colour value, two quality variables, had high levels of GCV, PCV, heritability and GAM, but oleoresin had modest values. As a result, it suggests that selecting genotypes with higher-quality features may be successful in enhancing these qualities and expanding their scope (Surya Kumari *et al.,* 2014).

Conclusion

The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for the growth parameters, namely plant spread, number of primary branches per plant and number of secondary branches per plant, were found to be moderate (11-20%). This indicates the presence of limited variability among the genotypes for these traits, suggesting that the scope for improvement through selection is relatively restricted, as these characters are likely governed by non-additive gene action. Conversely, low estimates of both GCV and PCV were recorded for days to 50% flowering, implying that phenotypic selection for this trait would be ineffective due to its low genetic variability. In contrast, high GCV and PCV values (>20%), coupled with high heritability (>60%), were observed for fruit length, fruit width, fruit weight, number of fruits per plant, fruit yield per plant, colour value, capsaicin content and oleoresin content. These results indicate a predominance of additive gene action, suggesting that selection based on phenotype would be highly effective in improving these traits. Furthermore, traits such as plant height, plant spread, number of primary and secondary branches and oleoresin content exhibited high heritability along with high genetic advance as a percentage of mean (GAM), despite showing moderate GCV and PCV estimates. This pattern suggests the involvement of additive genes, whose expression might be partially influenced or suppressed by environmental factors. Therefore, it may still be possible to achieve genetic improvement through selection for these traits under appropriate environmental conditions.

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