

**GENETIC VARIABILITY FOR PLANT GROWTH, FRUIT, SEED  
AND BIOCHEMICAL TRAITS IN BELL PEPPER BREEDING POPULATIONS  
UNDER NORTH INDIAN PLAINS**

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The present research aimed to estimate the plant growth, fruit yield, seed and biochemical traits among the seven pepper parental lines and their six BC<sub>2</sub>F<sub>1</sub> populations in order to generate information regarding the extent of genetic variability, heritability and genetic advance. The study was conducted using a randomized complete block design (RCBD) with three replications at the Vegetable Research Farm of Punjab Agricultural University, Ludhiana, India. The analysis of variance (ANOVA) showed significant mean squares due to parents and BC<sub>2</sub>F<sub>1</sub> populations for almost all the studied traits, it indicating the presence of a sufficient amount of inherent variability among the parental line and developed populations which could be exploited via selection. The plant height, fruit weight, fruit width, number of lobes fruit<sup>-1</sup>, chlorophyll b, total chlorophyll, chlorophyll a and total fruit yield plant<sup>-1</sup> were recorded high GCV and PCV among the parental lines and developed populations BC<sub>2</sub>F<sub>1</sub>, indicating higher extent of variability for these traits in the evaluated genotypes. The results revealed that traits with high GCV and PCV offer a better scope for improvement through simple selection. High heritability and high estimates of genetic advance were determined for the traits viz., plant height, fruit weight, ascorbic acid content and total fruit yield plant<sup>-1</sup>, in both parents and populations. Based on these results, we can conclude that these traits are under the additive gene effects and that above mentioned characters could be considered as a good selection indices in bell pepper.

*Keywords:* Bell pepper, BC<sub>2</sub>F<sub>1</sub> populations, genetic variability, heritability, horticultural traits

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## INTRODUCTION

Bell pepper (*Capsicum annuum* L. var. *grossum* Sendt.) is one of the most vital vegetable crop grown worldwide, belonging to the family Solanaceae, and genus *Capsicum*, which comprises an incredible diversity. The genus originated from Central and South America (BARBOZA *et al.*, 2019), and comprises 43 species, five of which are cultivated: *Capsicum annuum* L., *Capsicum frutescens* L. (tabasco pepper), *Capsicum chinense* Jacq. (habanero pepper), *Capsicum pubescens* Ruiz Pavon (rocoto pepper), and *Capsicum baccatum* L. (aji or peruvian pepper) (BARBOZA *et al.*, 2022). The great diversity in fruit traits offers opportunity for breeders to collect, characterize, evaluate, and to select *Capsicum* species accessions with different fruit traits (RANI *et al.*, 2021a). Among these five cultivated species *Capsicum annuum* L. (comprising both hot pepper and bell pepper) is the leading one. It is cultivated in both tropical as well as temperate area in the world and is the main subject of the breeding program for commercial cultivation (MEENA *et al.*, 2020).

Bell pepper is an important worldwide cultivated vegetable crop for its delicate taste, good flavor and color, and widely used as a vegetable, for stuffing, or for salads in the immature and green fruit stage. Its fruits contain appreciable quantities of ascorbic acid, pro-vitamin A ( $\beta$ -carotene), vitamins B6, B9, and other carotenoid pigments such as lycopene and zeaxanthin which are powerful antioxidants for prevention of cancer and cardiovascular human diseases (GHASEMNEZHAD *et al.*, 2011). Bell peppers play a crucial role in neutralizing free radicals in the body that can cause cells to experience serious damage. Often they act as an anti-inflammatory and alleviate pain and inflammatory conditions (CHO *et al.*, 2020). Bell pepper is an important temperate countries' greenhouse crop. In India bell pepper is a mid-hill commercial crop. If improved production technology (greenhouse, agro-net, and poly-tunnel) is introduced in north-Indian plains, it can be highly profitable. Bell pepper sells at a high price in urban markets, mainly due to the increasing demand. Indian production of bell pepper surpassed 496 thousand tonnes of green fruit harvested on 34 thousand hectares in 2019. In Punjab on over 0.36 thousand hectares is grown, producing 5.71 thousand tonnes of bell pepper (ANONYMOUS, 2019). Recently, the bell pepper production scenario has changed with the increasing popularity of commercially grown hybrids.

To improve bell pepper yield efficiency, systematic breeding approach is required. For the ongoing and prospective agronomic and genetic improvement of this crop, systematic analysis and evaluation of bell pepper genotypes under polynet house conditions is of great concern. In addition, the assessment of genotypes is necessary in attempt to comprehend the genetic background and the breeding potential of the accessible genotypes, if an improvement programme is to be carried out (KAUR *et al.*, 2017). In any crop improvement programme the extent of genetic variability for yield and yield components (BAHADUR *et al.*, 2016) determine the effectiveness of selection as a breeding process. Any quantitative trait's genetic variance is composed of additive (heritable) and non-additive variance and includes dominance and epistasis (non-allelic interaction). Therefore, splitting the observed phenotypic variability into heritable and non-heritable components with appropriate parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance becomes essential. In genetic studies, characters with high genotypic coefficient of variation indicate the potential for an effective selection. Determining the components of yield variability allows us to know the degree of

environmental effects on yield, taking into account the fact that yield and components are quantitative characters that affect the environment (AHMED *et al.*, 2007). The applications of heritability in quantitative traits genetic studies is its predictive role, which aids in determining the reliability of phenotypic value as a guide to breeding value (MAGAR *et al.*, 2021). High heritability suggests that the observed variance has less environmental impact (SONGSRI *et al.*, 2008). Heritability value alone is unable to provide knowledge about the amount of genetic advancement that would result from selection of best individuals.

JOHNSON *et al.* (1955) reported that heritability projections would be more accurate in predicting the efficacy of choosing the best individuals, along with genetic advances. A significant parameter that guides the breeder in choosing a selection programme is the genetic advance which estimates the degree of gain in a trait obtained under a given selection pressure (TERFA and GURMU, 2020). High heritability and high genetic advancement for a given phenotype suggest that it is regulated by additive gene action and thus provides the most successful selection condition (NWOSU *et al.*, 2014). So proper genetic resource assessment is important to recognize and estimate genetic diversity and heritability. Studies on genetic parameters provide information on the predicted selection response of different characters and will help to improve optimum breeding procedures. Keeping in view of this, an attempt was made to find out the nature and magnitude of genetic variability existing for plant growth, fruit yield, seed and biochemical traits in the parental lines and BC<sub>2</sub>F<sub>1</sub> populations of bell pepper.

## MATERIALS AND METHODS

### *Experimental site and design*

The plant material comprised of seven parent lines namely 'MS-12' (hot pepper, *Capsicum annuum* var. *longum*), PAU SM-1, PAU SM-2, PAU SM-3, PAU SM-9, PAU SM-17 and PAU SM-21 (heat tolerant bell pepper, *Capsicum annuum* var. *grossum*) and six BC<sub>2</sub>F<sub>1</sub> populations *viz.*, MSSM-1, MSSM-2, MSSM-3, MSSM-9, MSSM-17 and MSSM-21 of bell pepper. The materials were planted in a randomized complete block design (RCBD) with three replications under polynet house at the Vegetable Research Farm, Punjab Agricultural University (PAU), Ludhiana, India. The farm is situated at 30°54' N, 70°45' E, and 247 m above sea level.

### *Establishment of pepper parental lines and BC<sub>2</sub>F<sub>1</sub> populations under polynet house conditions*

The F<sub>1</sub> hybrids were generated by crossing between a hot pepper genetic male sterile (GMS) line namely 'MS-12' and heat-tolerant bell pepper testers in line × tester mating design to transfer GMS *ms10* gene into bell pepper inbreds. Thereafter, the F<sub>1</sub> individual plant was backcrossed (manually) with their respective recurrent parent to generate BC<sub>1</sub>F<sub>1</sub> populations. To evaluate the developed BC<sub>1</sub>F<sub>1</sub> populations for male sterility gene, plants were screened (foreground selection) by using SSR marker 'AVRDC-PP12'. The best individual heterozygous male fertile (*Ms10ms10*) plant in each BC<sub>1</sub>F<sub>1</sub> population was selected and again backcrossed with their recurrent parents to generate BC<sub>2</sub>F<sub>1</sub> populations (RANI *et al.*, 2021b). The developed six BC<sub>2</sub>F<sub>1</sub> populations were evaluated with their parental lines for genetic variability parameters.

During the year 2019-20, all plant materials were transplanted under polynet house conditions with spacing of 30 cm between the plants and 100 cm between the rows. The cultivation protocol ensured optimal growing conditions throughout the crop season, applying the standard recommended dose of fertilizer (125 kg nitrogen, 75 kg phosphorus and 65 kg potash per hectare), irrigation (using drip irrigation system), weeding, mulching, canopy training and pruning. Special attention was given to the check-out of insect-pests and diseases under polynet house condition (ANONYMOUS, 2015). During the crop cultivation, fertilization was regularly applied in a form of foliar spraying with  $3\text{g.L}^{-1}$  of water soluble fertilizer containing N:P:K 19:19:19 (IFFCO- Indian Farmers Fertiliser Cooperative Limited, New Delhi, India).

#### *Data collected*

The data were recorded from seven plants from each genotype in each replication. Mean data were used for statistical analysis for nineteen diverse traits *viz.*, plant height (cm), plant spread (cm), number of primary branches  $\text{plant}^{-1}$ , fruit weight (g), fruit length (cm), fruit width (cm), pericarp thickness (mm), number of lobes  $\text{fruit}^{-1}$ , number of fruits  $\text{plant}^{-1}$ , number of seed  $\text{fruit}^{-1}$ , 1000 seed fresh weight (g), 1000 seed dry weight (g), dry matter content (%), ascorbic acid ( $\text{mg.100g}^{-1}$ ), capsaicin content (%), chlorophyll a ( $\text{mg.100g}^{-1}$ ), chlorophyll b ( $\text{mg.100g}^{-1}$ ), total chlorophyll ( $\text{mg.100g}^{-1}$ ) and total fruit yield  $\text{plant}^{-1}$  (g).

#### *Data analysis*

Analysis of variance was carried out by the method suggested by PANSE and SUKHATME (1985). The genotypic and phenotypic coefficients of variation were calculated using the formula of BURTON and DE VANE (1953). Heritability and genetic advance were calculated according to ALLARD (1960) and genetic advance as percent of mean was estimated using the method of JOHNSON *et al.* (1955). All the statistical analyses were performed using computer software program WINDOSTAT 9.1 developed by INDOSTAT services Ltd. Hyderabad, India.

## RESULTS AND DISCUSSION

#### *Analysis of variance (ANOVA)*

The ANOVA showed significant mean squares (MS) due to parents for all the studied 19 traits, it indicating the presence of a sufficient amount of inherent variability among the parents which could be exploited via selection. The MS of developed  $\text{BC}_2\text{F}_1$  populations were non-significant for plant spread, 1000 seed fresh weight and chlorophyll-a content, and significant for rest of the traits studied, which depicted the differential response of different  $\text{BC}_2\text{F}_1$  population to studied traits (data not shown). This is in agreement with the finding of CONSTANTINO *et al.* (2020).

#### *Assessment of genetic variability parameters*

The extent of crop improvement depends on the variability in primary raw material (base material) that exists. In the absence of this, there will be no selection response, and ultimately no crop improvement. The increase of harvestable fruit yield is one of the major breeding goals in all the agricultural crops including bell pepper (GHOLIPOOR and NADALI, 2019).

Therefore, variability for the fruit traits such as fruit weight, fruit length, number of fruits plant<sup>-1</sup>, etc. is essential in addition to yield. Data of the genetic variation in the population is a pre-requirement for starting any crop breeding program. Genetic variability in a population is important for biodiversity because without variability, it becomes difficult for a population to adapt to the environmental changes, and therefore makes it more prone to extinction and genetic variation and mode of inheritance of quantitative and qualitative traits are of prime importance in planning the breeding program (TERFA and GURMU, 2020; KARIM *et al.*, 2022). Measurement of the genotypic and phenotypic coefficients of variance is useful in measuring the amount of heterogeneity present in the accessions. High variability presence provides much scope for improvement and helps breeders to recognize the most promising genotype. For 19 observed traits in present study, the genotypic variance, phenotypic variance, coefficient of variability (genotypic coefficient of variation and phenotypic coefficient of variation), broad sense heritability ( $h^2_{bs}$ ), genetic advance and genetic gain were calculated for parents and BC<sub>2</sub>F<sub>1</sub> populations and presented in Table 1 and 2, respectively.

Table 1. Estimate of heritability, genotypic, and phenotypic coefficients of variance, and genetic advance for 19 traits in bell pepper parents

Traits	GV	PV	GCV (%)	PCV (%)	$h^2_{bs}$ (%)	GA (5%)	Genetic gain (5%)
Plant height (cm)	832.74	929.42	31.54	33.32	0.90	56.27	61.50
Plant spread (cm)	29.95	61.14	9.87	14.10	0.49	7.89	14.23
Number of primary branches plant <sup>-1</sup>	0.41	0.54	16.47	18.99	0.75	1.14	29.43
Fruit weight (cm)	779.45	817.39	51.11	52.34	0.95	56.16	102.81
Fruit length (cm)	1.81	2.02	23.95	25.30	0.90	2.62	46.72
Fruit width (cm)	3.18	3.45	36.34	37.86	0.92	3.53	71.86
Pericarp thickness (mm)	1.67	1.76	35.51	36.46	0.95	2.60	71.26
Number of lobes fruit <sup>-1</sup>	1.47	1.54	44.40	45.51	0.95	2.44	89.22
Number of fruits plant <sup>-1</sup>	5469.4	5594.59	127.96	129.42	0.98	150.63	260.64
Number of seed fruit <sup>-1</sup>	69.76	100.23	13.95	16.72	0.70	14.35	23.97
1000 seed fresh weight (g)	3.42	4.84	16.94	20.15	0.71	3.21	29.34
1000 seed dry weight (g)	1.38	1.57	15.76	16.81	0.88	2.27	30.43
Dry matter content (%)	30.53	30.97	59.30	59.73	0.99	11.30	121.27
Ascorbic acid content (mg.100g <sup>-1</sup> )	621.50	640.38	27.99	28.41	0.97	50.59	56.80
Capsaicin content (%)	0.02	0.02	43.57	43.97	0.98	0.26	88.92
Chlorophyll a (mg.100g <sup>-1</sup> )	0.01	0.01	29.48	30.01	0.97	0.19	59.66
Chlorophyll b (mg.100g <sup>-1</sup> )	0.01	0.01	41.13	41.42	0.99	0.20	84.10
Total chlorophyll (mg.100g <sup>-1</sup> )	0.01	0.01	30.69	30.88	0.99	0.18	63.03
Total fruit yield plant <sup>-1</sup> (g)	297630.09	305672.16	39.28	39.80	0.97	1108.96	79.84

Table 2. Estimates of genetic parameters for 19 horticultural traits in  $BC_2F_1$  population of bell pepper

Traits	GV	PV	GCV (%)	PCV (%)	$h^2$ (bs)(%)	GA (5%)	Genetic gain (5%)
Plant height (cm)	310.08	370.59	22.47	24.57	0.84	33.18	42.35
Plant spread (cm)	11.37	47.57	5.90	12.06	0.24	3.40	5.94
Number of primary branches plant <sup>-1</sup>	0.46	0.59	16.17	18.17	0.79	1.25	29.63
Fruit weight (cm)	318.63	351.23	33.75	35.44	0.91	35.02	66.22
Fruit length (cm)	0.33	0.70	8.71	12.58	0.48	0.82	12.41
Fruit width (cm)	1.37	1.53	24.73	26.13	0.90	2.29	48.24
Pericarp thickness (mm)	0.07	0.12	7.13	9.58	0.55	0.4	10.92
Number of lobes fruit <sup>-1</sup>	0.34	0.42	21.09	23.66	0.80	1.06	38.74
Number of fruits plant <sup>-1</sup>	9.36	19.18	9.35	13.39	0.49	4.40	13.45
Number of seed fruit <sup>-1</sup>	42.14	67.26	12.31	15.55	0.63	10.58	20.07
1000 seed fresh weight (g)	1.80	2.67	13.71	16.68	0.68	2.27	23.22
1000 seed dry weight (g)	0.22	0.54	6.42	10.05	0.41	0.62	8.45
Dry matter content (%)	0.78	1.37	10.86	14.50	0.56	1.36	16.75
Ascorbic acid content (mg.100g <sup>-1</sup> )	156.65	185.96	13.44	14.64	0.84	23.66	25.40
Capsaicin content (%)	0.004	0.004	19.33	19.91	0.94	0.12	38.66
Chlorophyll a (mg.100g <sup>-1</sup> )	0.003	0.003	24.09	26.24	0.84	0.10	45.54
Chlorophyll b (mg.100g <sup>-1</sup> )	0.005	0.006	40.68	42.88	0.90	0.14	79.49
Total chlorophyll (mg.100g <sup>-1</sup> )	0.004	0.004	30.31	31.77	0.91	0.12	59.56
Total fruit yield plant <sup>-1</sup> (g)	256326.98	275530.84	33.52	34.75	0.93	1005.95	66.60

#### Genotypic variance and phenotypic variance of parents and $BC_2F_1$ populations

In the present research, the genotypic variance ( $\sigma^2_g$ ; GV) ranged from 0.01 to 297630.09, and phenotypic variance ( $\sigma^2_p$ ; PV) varied from 0.01 to 305672.16 for parental lines. High GV and PV, respectively were recorded for total fruit yield plant<sup>-1</sup> (297630.09 and 305672.16) followed by a number of fruit plant<sup>-1</sup> (5469.40 and 5594.59), plant height (832.74 and 929.42), fruit weight (779.45 and 817.39), ascorbic acid (621.50 and 640.38), number of seed fruit<sup>-1</sup> (69.76 and 100.23), dry matter content (30.53 and 30.97), and plant spread (29.95 and 61.14); whereas, the lower extents were observed for chlorophyll a, chlorophyll b and total chlorophyll (0.01 and 0.01 for all three traits) followed by capsaicin content (0.02 and 0.02), number of primary branches plant<sup>-1</sup> (0.41 and 0.54), 1000 seed dry weight (1.38 and 1.57), number of lobes fruit<sup>-1</sup> (1.47 and 1.54), pericarp thickness (1.67 and 1.76), fruit length (1.81 and 2.02), fruit width (3.18 and 3.45), and 1000 seed fresh weight (3.42 and 4.84).

In the BC<sub>2</sub>F<sub>1</sub> populations, the lowest and highest GV values were estimate for chlorophyll a (0.003) and total fruit yield plant<sup>-1</sup> (256326.98), while PV values ranged from 0.003 (chlorophyll a) to 275530.84 (total fruit yield plant<sup>-1</sup>). Furthermore, maximum GV and PV, respectively were observed for total fruit yield plant<sup>-1</sup> (256326.98 and 275530.84) followed by fruit weight (318.63 and 351.23), plant height (310.08 and 370.59), ascorbic acid (156.65 and 185.96), and number of seed fruit<sup>-1</sup> (42.14 and 67.26). The moderate GV was found in one trait namely plant spread (11.37), while, high and moderate extent of PV was noticed for plant spread (47.57) and number of fruits plant<sup>-1</sup> (19.18), respectively. The lowest GV and PV were recorded for chlorophyll a (0.003 and 0.003) followed by capsaicin content and total chlorophyll (0.004 and 0.004 for both), chlorophyll b (0.005 and 0.006), pericarp thickness (0.07 and 0.12), number of lobes fruit<sup>-1</sup> (0.34 and 0.42), fruit length (0.33 and 0.70), number of primary branches plant<sup>-1</sup> (0.46 and 0.59), 1000 seed fresh weight (1.80 and 2.67), fruit width (1.37 and 1.53), 1000 seed dry weight (0.22 and 0.54), and dry matter content (0.78 and 1.37). High GV values indicates more contribution of a genetic component for the total variation, therefore the traits would be considered and exploited for selection purposes. On the other hand, high PV indicates the strong influence of environmental factors during the growth and reproductive periods for their expression. There were also analogous findings documented by BASEERAT *et al.* (2013), PANDEY *et al.* (2013), ISHAYA *et al.* (2020).

#### *Estimation of genotypic and phenotypic coefficient of variance in the parental lines and the BC<sub>2</sub>F<sub>1</sub> populations*

A better idea can be gained by comparing the relative amount of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for the actual strength of variability. The perusal of data of table 1 revealed that among the parents, GCV was ranged from 9.87 (plant spread) to 127.96 (number of fruit plant<sup>-1</sup>), although, PCV was varied from 14.10 (plant spread) to 129.42 (number of fruit plant<sup>-1</sup>). The number of fruit plant<sup>-1</sup> (127.96 and 129.42) followed by dry matter content (59.30 and 59.73), fruit weight (51.11 and 52.34), number of lobes fruit<sup>-1</sup> (44.40 and 45.51), capsaicin content (43.57 and 43.97), chlorophyll b (41.13 and 41.42), fruit width (36.34 and 37.86), pericarp thickness (35.51 and 36.46), plant height (31.54 and 33.32), total chlorophyll (30.69 and 30.88), chlorophyll a (29.48 and 30.01), ascorbic acid (27.99 and 28.41), fruit length (23.95 and 25.30), and total fruit yield plant<sup>-1</sup> (39.28 and 39.80) were recorded high GCV and PCV, respectively among parental lines, indicating higher extent of variability for these traits in the evaluated genotypes.

In the developed BC<sub>2</sub>F<sub>1</sub> populations, the GCV varied from 5.90 for plant spread to 40.68 for chlorophyll b and the range of PCV varied from 9.48 in pericarp thickness to 42.88 in chlorophyll b. Overall the highest GCV and PCV, respectively were found for chlorophyll b (40.68 and 42.88) followed by fruit weight (33.75 and 35.44), total fruit yield plant<sup>-1</sup> (33.52 and 34.75), total chlorophyll (30.31 and 31.77), fruit width (24.73 and 26.13), chlorophyll a (24.09 and 26.24), plant height (22.47 and 24.57), and a number of lobes fruit<sup>-1</sup> (21.09 and 23.66). High values of GCV and PCV were an indication of high genetic variability among the developed BC<sub>2</sub>F<sub>1</sub> populations thus there is scope for improvement of these characteristics through simple selection. BASEERAT *et al.* (2013), PANDEY *et al.* (2013), USMAN *et al.* (2014), and ISHAYA *et al.* (2020) recorded similar findings for studied characteristics as well.

Moderate amount of GCV and PCV, respectively were observed for the traits such as the number of primary branches plant<sup>-1</sup> (16.47 and 18.99), 1000 seed dry weight (15.76 and 16.81), and number of seed fruits<sup>-1</sup> (13.95 and 16.72) in the parental lines, simultaneously, for the capsaicin content (19.33 and 19.91), number of primary branches plant<sup>-1</sup> (16.17 and 18.17), 1000 seed fresh weight (13.71 and 16.68), ascorbic acid content (13.44 and 14.64), number of seed fruit<sup>-1</sup> (12.31 and 15.55), and dry matter content (10.86 and 14.50) in BC<sub>2</sub>F<sub>1</sub> populations. Moderate rates of the GCV and the PCV are indication of ample scope for improvement via simple selection. Such observations are also consistent with previous studies, such as SOOD *et al.* (2011), AHMED *et al.* (2012), BASEERAT *et al.* (2013), PANDEY *et al.* (2013), and ISHAYA *et al.* (2020).

In the current study, it was observed that magnitude of PCV were almost higher than the corresponding GCV for all the traits under study. This indicated that the apparent variation is not only due to germplasm but also due to the influence of the environment in the expression of the traits. Further, it was observed that the variation between values of GCV and PCV was smaller for all 19 studied traits. It means that these traits were less influenced by the environment and hence, they could be improved by following different phenotypic selections like disruptive, directional, and stabilized to improve the bell pepper breeding programme.

#### *Estimation of heritability ( $h^2$ in a broad sense) among the parental lines and BC<sub>2</sub>F<sub>1</sub> populations*

The overall genetic variance is measured by the genotypic coefficient of variation, while heritability tests the proportion to which the variability of a trait is transmitted to offspring (LUSH, 1949). BURTON and DE VANE (1953) proposed that along with heritability figures, genetic coefficients of variation would provide a credible indicator of expected degree of change through selection. Thus, heritability is a parameter of great importance to breeders as its magnitude indicates the accuracy with which it's phenotypic will classify a genotype. Estimates of heritability vary not only with the environment but also with the nature of the test populations (MEENA, 2017). Heritability estimate helps breeders to distribute resources effectively to select targeted traits and to accomplish highest genetic gain with less time and resources (MAGAR *et al.*, 2021).

Among the parental lines, the range of heritability (percentage) estimates varied from 49% in plant spread to 99% in three traits namely, dry matter content, chlorophyll b, and total chlorophyll. Except for plant spread (49%), all of the nineteen studied traits have high broad sense heritability. The highest amount of  $h^2_{bs}$  was observed for chlorophyll b, total chlorophyll and dry matter content (99% for each) followed by capsaicin content and number of fruits plant<sup>-1</sup> (98%), chlorophyll a, total fruit yield plant<sup>-1</sup> and ascorbic acid content (97%), fruit weight, pericarp thickness and number of lobes fruit<sup>-1</sup> (95%), fruit width (92%), fruit length and plant height (90%), and 1000 seed dry weight (88%). Similarly, in BC<sub>2</sub>F<sub>1</sub> populations, high heritability was noticed for capsaicin content (94%) followed by total fruit yield plant<sup>-1</sup> (93%), total chlorophyll and fruit weight (91%), chlorophyll b and fruit width (90%), chlorophyll a, plant height and ascorbic acid (84%), and a number of lobes fruit<sup>-1</sup> (80%), indicating that these characters are controlled by additive gene action. High heritability suggested that the traits were less influenced by the environment and a major part of the phenotypic variability was contributed by additive gene effects. Therefore, the improvement could be made by simple



selection. Such results are in line with the findings of SOOD *et al.* (2011), BASEERAT *et al.* (2013), ISHAYA *et al.* (2020). On the contrary, moderate heritability was recorded for dry matter content (56%) followed by pericarp thickness (55%), number of fruits plant<sup>-1</sup> (49%), fruit length (48%), and 1000 seed dry weight (41%), and the low heritability was noticed for plant spread (24%). The selection would be virtually impractical or considerably difficult for a character coupled with low heritability because of the masking effect of the environment on the genotypic effects. Genetic improvement of these traits would require growing of large populations over locations and years to reliably make selections on a phenotypic basis (MEENA, 2017).

#### *Estimation of genetic advance in parents and BC<sub>2</sub>F<sub>1</sub> populations*

Unaccompanied heritability provides no hint of the degree of genetic change that will arise from choosing individual genotypes. The consciousness of genetic development combined with heritability is thus most useful. Genetic development is an increase in the mean number of selected families over the base population (LUSH, 1949; JOHNSON *et al.*, 1955). It is also expressed as the change in gene frequency on the exercise of selection pressure towards the superior side. A character with high heritability may not automatically offer substantial genetic advancement. JOHNSON *et al.* (1955) proposed that, when computed together, heritability and genetic advancement would prove more useful in predicting the resulting effect of selection on phenotypic expression.

Estimates of genetic advance among the parental lines for 19 studied traits showed a wide range from 0.18 for total chlorophyll to 1108.96 for total fruit yield plant<sup>-1</sup> and in the BC<sub>2</sub>F<sub>1</sub> populations, it was varied from 0.10 for chlorophyll a to 1005.95 for total fruit yield plant<sup>-1</sup>. In parental lines, the highest genetic advance was recorded for total fruit yield plant<sup>-1</sup> (1108.96), number of fruit plant<sup>-1</sup> (150.63), plant height (56.27), fruit weight, (58.21), and ascorbic acid content (50.59). Two traits namely the number of seed fruit<sup>-1</sup> (14.35) and dry matter content (11.30) showed moderate genetic advance estimates. The lowest genetic advance was recorded for total chlorophyll (0.18) followed by chlorophyll a (0.19), chlorophyll b (0.20), capsaicin content (0.26), number primary branches plant<sup>-1</sup> (1.14), 1000 seed dry weight (2.27), number of lobes fruit<sup>-1</sup> (2.44), pericarp thickness (2.60), fruit length (2.62), 1000 seed fresh weight (3.21), fruit width (3.53), and plant spread (7.89).

In BC<sub>2</sub>F<sub>1</sub> populations, the maximum genetic advance was reported for total fruit yield plant<sup>-1</sup> (1005.95), fruit weight (35.02), plant height (33.18), and ascorbic acid (23.66). This is indicated that additive genes control such traits, and selection would be beneficial for improving these traits (ISHAYA *et al.*, 2020). Moderate genetic advance was reported for a single trait, number of seed fruit<sup>-1</sup> (10.58). Low genetic advance was noticed in chlorophyll a (0.10) followed by total chlorophyll and capsaicin content (0.12), chlorophyll b (0.14), pericarp thickness (0.40), fruit length (0.82), 1000 seed dry weight (0.62), number of lobes fruit<sup>-1</sup> (1.06), number of primary branches plant<sup>-1</sup> (1.25), dry matter content (1.36), 1000 seed fresh weight (2.27), fruit width (2.29), plant spread (3.40), and number of fruits plant<sup>-1</sup> (4.40). It can be due to the results of the non-additive gene, and these traits can be strengthened by hybridization and utilizing hybrid vigor. AHMED *et al.* (2012), USMAN *et al.* (2014), and ISHAYA *et al.* (2020) reported similar findings.

Heritability coupled with genetic advance is more effective and reliable in predicting the results and the effect of selection. In the present study, among parental lines, high heritability and high estimates of genetic advance were noted for total fruit yield plant<sup>-1</sup> (97 and 1108.96, respectively) followed by a number of fruit plant<sup>-1</sup> (98 and 150.63), ascorbic acid content (97 and 50.59), fruit weight (95 and 56.16) and plant height (90 and 56.27). On the contrary, in the BC<sub>2</sub>F<sub>1</sub> populations, high heritability along with high genetic advance were observed for total fruit yield plant<sup>-1</sup> (93 and 1005.95), ascorbic acid content (84 and 23.66), fruit weight (91 and 35.02) and plant height (84 and 33.18). It suggested that these traits are under the additive gene effects and that above mentioned characters could be regarded as accurate indices for selection and higher responses from a selection of these traits could be predicted. Many researchers also found high heritability and high genetic advance for total fruit yield plant<sup>-1</sup>, for fruit weight, and for a number of fruits plant<sup>-1</sup> (SREELATHAKUMARY and RAJAMONY, 2002). High heritability along with moderate genetic advance in parental lines was noted for two traits namely dry matter content (99 and 11.30) and number of seed fruit<sup>-1</sup> (63 and 10.58), while for number of seed fruit<sup>-1</sup> (63 and 10.58) in BC<sub>2</sub>F<sub>1</sub> populations. High heritability and low genetic advance were observed for number of primary branches plant<sup>-1</sup> followed by fruit length, fruit width, pericarp thickness, number of lobes fruit<sup>-1</sup>, 1000 seed fresh weight, 1000 seed dry weight, capsaicin content, chlorophyll a, chlorophyll b, and total chlorophyll content in parental lines. On the other hand, high heritability and low genetic advance were observed for number of primary branches plant<sup>-1</sup> followed by fruit width, number of lobes fruit<sup>-1</sup>, 1000 seed fresh weight, capsaicin content, chlorophyll a, chlorophyll b, and total chlorophyll content in BC<sub>2</sub>F<sub>1</sub> populations. Since these traits are controlled by non-additive gene actions and direct selection may not be possible, therefore mentioned traits could be improved through hybridization followed by selection (ARA *et al.*, 2009).

#### *Estimation of genetic gain in parental lines and BC<sub>2</sub>F<sub>1</sub> populations*

Though assessments of high heritability are effective in giving the basis for transmissible genes from parental lines to off-springs, more accurate conclusions are drawn when considering heritability along with genetic gain. In the present study, all the nineteen studied traits expressed high genetic gain (genetic advance expressed as percent of population mean) except for plant spread, and ranged from 14.23 (plant spread) to 260.64 (number of fruits plant<sup>-1</sup>) in the parental lines. The number of fruits plant<sup>-1</sup> (260.64) showed highest genetic gain than the other traits under the study such as dry matter content (121.27), fruit weight (102.81), number of lobes fruit<sup>-1</sup> (89.22), capsaicin content (88.92), chlorophyll b (84.10), total fruit yield plant<sup>-1</sup> (79.84), fruit width (71.86), pericarp thickness (71.26), total chlorophyll (62.03), plant height (61.50), chlorophyll a (59.66), and ascorbic acid (56.80). Moderate genetic gain was noted only for plant spread (14.23). Similarly, in BC<sub>2</sub>F<sub>1</sub> populations, low to high genetic gain was recorded for traits studied and varied from 5.94 (plant spread) to 79.49 (chlorophyll b). The high genetic gain was recorded for chlorophyll b (79.49) followed by fruit weight (66.22), total fruit yield plant<sup>-1</sup> (66.60), total chlorophyll (59.56), fruit width (48.24), chlorophyll a (45.54), plant height (42.35), number of lobes fruit<sup>-1</sup> (38.74), capsaicin content (38.66), number of primary branches plant<sup>-1</sup> (29.63), ascorbic acid content (25.40), 1000 seed fresh weight (23.22), and number of seed fruit<sup>-1</sup> (20.07). Moderate values were observed for the traits *viz.*, dry matter

content (16.75) followed by number of fruits plant<sup>-1</sup> (13.45), fruit length (12.41) and pericarp thickness (10.92). The lowest genetic gain of 5.94% was observed for plant spread and 8.45% for 1000 seed dry weight. AHMED *et al.* (2012) recorded analogous findings for different characteristics under their study.

JOHANSON *et al.* (1955) stated that for successful selection, high estimates of heritability coupled with high genetic gain were better than heritage alone. Among the parental lines, high inheritability coupled with a high genetic gain was found for all the studied traits except for plant spread. However, in the BC<sub>2</sub>F<sub>1</sub> populations, the high heritability with a high genetic gain was reported for capsaicin content followed by total fruit yield plant<sup>-1</sup>, total chlorophyll, fruit weight, chlorophyll b, fruit width, chlorophyll a, plant height, ascorbic acid, number of lobes fruit<sup>-1</sup>, number of primary branches plant<sup>-1</sup>, 1000 seed fresh weight and number of seed fruit<sup>-1</sup>. It indicates that these traits were under the strong influence of additive gene action; therefore simple selection based on a phenotypic output of these characteristics would be more successful. It also suggested the possibility of selecting high yielding genetic male sterile line from the developed backcross series (BC<sub>2</sub>F<sub>1</sub>). Such results concur with SOOD *et al.* (2009). Moderate heritability associated with low genetic gain has been determined for 1000 seed fresh weight in BC<sub>2</sub>F<sub>1</sub> populations. This showed that the non-additive gene effects are strongly regulated by certain traits. Improvement in this trait can be accomplished by further partitioning the genetic variation and allowing selection in segregating generations for the appropriate types.

#### Genetic association analysis among parental lines and BC<sub>2</sub>F<sub>1</sub> populations

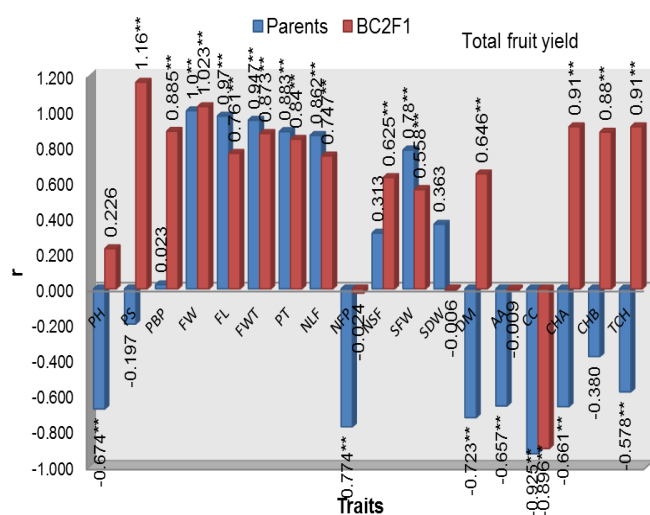


Figure 1. Estimates of genotypic correlation of different horticultural traits with total yield plant<sup>-1</sup> in parental lines and BC<sub>2</sub>F<sub>1</sub> generation of bell pepper

abbreviations used: PH (plant height), PS (plant spread), PBP (primary branches plant<sup>-1</sup>), FW (fruit weight), FL (fruit length), FWT (fruit width), PT (pericarp thickness), NLF (number of lobes fruit<sup>-1</sup>), NFP (number of fruits plant<sup>-1</sup>), NSF (number of seed fruit<sup>-1</sup>), SFW (1000 seed fresh weight), SDW (1000 seed dry weight), DM (dry matter content), AA (ascorbic acid), CC (capsaicin content), CHA (chlorophyll a), CHB (chlorophyll b), TCH (total chlorophyll)

Among the parental lines and BC<sub>2</sub>F<sub>1</sub> populations, total fruit yield plant<sup>-1</sup> was positively associated with fruit weight, fruit length, fruit width, pericarp thickness, number of lobes fruit<sup>-1</sup> and seed fresh weight, suggested that these traits are most important for selection view point to getting high fruit yield in bell pepper (Figure 1). The experimental results conducted on chilli pepper by AISWARYA *et al.* (2020) showed similar results.

### CONCLUSION

The analysis of genetic variation help plant breeder to decide the proper breeding strategy and selection criteria to be used for the improvement of the target characters. The current research study furnishes a step forward in comprehension of the genetic variability in bell pepper. Heritability, genetic gain, GCV, and PCV together could be provided the best picture of the amount of advance to be expected from selection. High  $h^2_{bs}$ , genetic gain, GCV and PCV was recorded for the traits namely, plant height, fruit weight, fruit width, number of lobes fruit<sup>-1</sup>, chlorophyll a, chlorophyll b, total chlorophyll, and total fruit yield plant<sup>-1</sup> in both parents and BC<sub>2</sub>F<sub>1</sub> populations. The observation indicated that above mentioned traits are under additive gene effects and more reliable for effective selection.

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### REFERENCES

- AHMED, N., A., MUHAMMAD, I., KHALIQ, M., MASAHIKO (2007): The inheritance of yield and yield components of five wheat hybrid populations under drought conditions. *Indones. J. Agric. Sci.*, 8: 53-59.
- AHMED, N., S.R., SINGH, S., LAL, K.A., MIR (2012): Genetic variability in bell pepper (*Capsicum annuum* L.) under high altitude temperate environment. *Indian J. Plant Genet. Resour.*, 25: 304-306.
- AISWARYA, C.S., S., VIJETH, I., SREELATHAKUMARY, P., KAUSHIK (2020): Diallel analysis of chilli pepper (*Capsicum annuum* L.) genotypes for morphological and fruit biochemical traits. *Plants*, 9: 1.
- ALLARD, R.W. (1960): Principles of plant breeding. Wiley and Sons, New York.
- ANONYMOUS (2015): Sweet Pepper. In: Package of Practices for Cultivation of Vegetables. Punjab Agricultural University, Ludhiana. pp 53-55.
- ANONYMOUS (2019): Area of bell pepper (ha) and production quantity (tonnes) in 2018-19. In: Third Advance Estimate of Area and Production of Horticulture Crops. [www.nhb.gov.in](http://www.nhb.gov.in).
- ARA, A., N., RAJ, A., NAZEER, S.H., KHAN (2009): Genetic variability and selection parameters for yield and quality attributes in tomato. *Indian J. Hort.*, 66: 73-78.
- BAHADUR, V., V., YESHUDAS, O.P., MEENA (2016): Nature and magnitude of genetic variability and diversity analysis of Indian turmeric accessions using agro-morphological descriptors. *Can. J. Plant Sci.*, 96: 371-381.
- BARBOZA, G.E., C., CARRIZO GARCÍA, L., DE BEM BIANCHETTI, M.V., ROMERO, M., SCALDAFERRO (2022): Monograph of wild and cultivated chili peppers (*Capsicum* L., Solanaceae). *PhytoKeys*, 200: 1-423.
- BARBOZA, G.E., C., CARRIZO GARCIA, S., LEIVA GONZALEZ, M., SCALDAFERRO X., REYES (2019): Four new species of *Capsicum* (Solanaceae) from the tropical Andes and an update on the phylogeny of the genus. *PLoS ONE*, 14: e0209792.
- BASEERAT, A., S.H., KHAN, F., MUSHTAQ, K., HUSSAIN, A., NABI (2013): Variability and correlation studies in sweet pepper (*Capsicum annuum* L.). *Prog. Hort.*, 45: 209-213.
- BURTON, G.W., E.H., DE VANE (1953): Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, 45: 478-481.

- CHO, S.Y., H.W., KIM, M.K., LEE, H.J., KIM, J.B., KIM, J.S., CHOE, Y.M., LEE, H.H., JANG (2020): Antioxidant and anti-inflammatory activities in relation to the flavonoids composition of pepper (*Capsicum annuum* L.). *Antioxidants*, 9: 986.
- CONSTANTINO, L.V., A.Y., SUZUKI FUKUJ, D.M., ZECCA, V.Y., BABA, L.E.D., CORTE, R.M., GIACOMIN, J.T.V., RESENDE, L.S.A., GONÇALVES (2020): Genetic variability in peppers accessions based on morphological, biochemical and molecular traits. *Bragantia*, 79: 558-571.
- GHASEMNEZHAD, M., M., SHERAFATI, G.A., PAYVAST (2011): Variation in phenolic compounds, ascorbic acid and antioxidant activity of five coloured bell pepper (*Capsicum annuum*) fruits at two different harvest times. *J. Funct. Foods*, 3: 44-49.
- GHOLOPOORA, M., F., NADALI (2019): Fruit yield prediction of pepper using artificial neural network. *Sci. Hortic.*, 250: 249-253.
- ISHAYA, E.B., A.S., GANA, D.A., AYELEKE, O.O., OBOGUN, M.O., AKINYELE, G.A., IDOWU (2020): Genetic variability, heritability and cluster analysis in some accessions of pepper (*Capsicum* spp). *WJIR*, 8: 34-41
- JOHNSON, H.W., H.F., ROBINSON, R.E., COMSTOCK (1955): Estimates of genetic and environmental variability in soybean. *Agron. J.*, 47: 314-318.
- KARIM, K.M.R.; M.Y., RAFII, A., MISRAN, M.F., ISMAIL, A.R., HARUN, R., RIDZUAN, M.F.N., CHOWDHURY, M., HOSEN, O., YUSUFF, M.A., HAQUE (2022): Genetic diversity analysis among *Capsicum annuum* mutants based on morpho-physiological and yield traits. *Agron.*, 12: 2436.
- KAUR, S., S.K., JINDAL, M.S., DHAILWAL, N., CHAWLA, O.P., MEENA (2017): Genetic diversity analysis in elite lines of tomato (*Solanum lycopersicum* L.) for growth, yield and quality parameters. *Genetika*, 49: 329-344.
- LUSH, J.L. (1949): Heritability of quantitative traits in farm animals. *Proc 8<sup>th</sup> Inst Cong Genetics, Heredes*, pp 336-357.
- MAGAR, B.T., S., ACHARYA, B., GYAWALI, K., TIMLSENA, J., UPADHAYAYA, J., SHRESTHA (2021): Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. *Heliyon*, 7: e07939.
- MEENA, O.P. (2017): *Evaluation of Cytoplasmic Male Sterile Lines of Chilli Pepper (Capsicum annuum L.) and Their Utilization in Heterosis Breeding*, Ph.D. Thesis, Punjab Agricultural University, Ludhiana, India.
- MEENA, O.P., M.S., DHALIWAL, S.K., JINDAL (2020): Heterosis breeding in chilli pepper by using cytoplasmic male sterile lines for high-yield production with special reference to seed and bioactive compound content under temperature stress regimes. *Sci. Hortic.*, 262: 109036.
- NWOSU, D.J., O.A., ONAKOYA, A.U., OKERE, A.O., BABATUNDE, A.F., POPOOLA (2014): Genetic variability and correlations in rainfed tomato (*Solanum* spp.) accessions in Ibadan, Nigeria. *Greener J. Agric. Sci.*, 4: 211-219.
- PANDEY, V., A., CHURA, M., ARYA, Z., AHMED (2013): Variability parameters for quantitative and qualitative traits in sweet pepper in mid hills of western Himalaya. *Veg. Sci.*, 40: 37-39.
- PANSE, V.G., P.V., SUKHATME (1985): *Statistical methods for agricultural workers* (2nd ed), Indian Council of Agricultural Research, New Delhi. pp 381.
- RANI, M., S.K., JINDAL, O.P., MEENA (2021a): Exploitation of heterosis among phenotypically diverse *Capsicum* parents for important fruit traits. *Braz. Arch. Biol. Technol.*, 64: e21200597.
- RANI, M., S.K., JINDAL, Y., VIKAL, O.P., MEENA (2021b): Genetic male sterility breeding in heat tolerant bell pepper: Introgression of *ms10* gene from hot pepper through marker assisted backcrossing. *Sci. Hortic.*, 285: 110172.
- SONGSRI, P., S., JOGLLOY, T., KESMALA, N., VORASOOT, C.P.A., AKKASAENG, C., HOLBROOK (2008): Heritability of drought resistant traits and correlation of drought resistance and agronomic traits in peanut. *Crop Sci.*, 48: 2245-2253.
- SOOD, S., K., NAVEEN, K.S., CHANDEL, S., PARVEEN (2011): Determination of genetic variation for morphological and yield traits in bell pepper (*Capsicum annuum* var. *grossum*). *Indian J. Agric. Sci.*, 81: 590-594.

- SOOD, S., R., SOOD, V., SAGAR, K.C., SHARMA (2009): Genetic variation and association analysis for fruit yield, agronomic and quality characters in bell pepper. *Int. J. Veg. Sci.*, 15: 272-284.
- SREELATHAKUMARY, I., L., RAJAMONY (2002): Variability, heritability and correlation studies in chilli (*Capsicum annuum* L.) under shade. *Indian J. Hort.*, 59: 77-83.
- TERFA, G.N., G.N., GURMU (2020): Genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L) genotypes for seed yield and other agronomic traits. *Oil Crop Sci.*, 5: 156-160.
- USMAN, M.G., M.Y., RAFII, M.R., ISMAIL, M.A., MALEK, M., ABDUL LATIF (2014): Heritability and genetic advance among chilli pepper genotypes for heat tolerance and morphophysiological characteristics. *Sci. World J.*, 2014: 308042.

## **GENETIČKA VARIJABILNOST ZA RAST BILJAKA, PLODOVA, SEME I BIOHEMIJSKE OSOBINE U OPLEMENJIVAČKIM POPULACIJAMA PAPRIKA U RAVNICAMA SEVERNE INDIJE**

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### Izvod

Ovo istraživanje je imalo za cilj da proceni rast biljaka, prinos plodova, semena i biohemijske osobine između sedam roditeljskih linija paprike i njihovih šest BC2F1 populacija kako bi se generisale informacije o stepenu genetske varijabilnosti, naslednosti i genetskom napretku. Studija je sprovedena korišćenjem randomiziranog kompletnog blok dizajna (RCBD) sa tri replikacije na farmi za istraživanje povrća na Poljoprivrednom univerzitetu Punjab, Ludijana, Indija. Analiza varijanse (ANOVA) je pokazala značajne srednje kvadrate roditelja i populacije BC2F1 za skoro sve proučavane osobine, što ukazuje na prisustvo dovoljne količine nasledne varijabilnosti među roditeljskim linijama i razvijenim populacijama koje bi se mogle iskoristiti selekcijom. Visina biljke, težina ploda, širina ploda, broj plodova po biljci, hlorofil b, ukupni hlorofil, hlorofil a i ukupan prinos po biljci su zabeležili visoki GCV i PCV među roditeljskim linijama i razvijenim populacijama BC2F1, što ukazuje na veći stepen varijabilnosti ovih osobina kod procenjenih genotipova. Rezultati su otkrili da osobine sa visokim GCV i PCV nude veće mogućnosti za poboljšanje jednostavnim odabirom. Visoka heritabilnost i visoke procene genetskog poboljšanja utvrđene su za osobine kao što su visina biljke, težina ploda, sadržaj askorbinske kiseline i ukupni prinos ploda po biljci, i kod roditelja i kod populacija. Na osnovu dobijenih rezultata možemo zaključiti da su ove osobine pod uticajem aditivnih gena i da bi se mogle smatrati dobrim selekcijskim indeksima kod paprike.

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