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The Magnitude of Variability for Different Quantitative Characters and Genetic Variation in Chilli (*Capsicum annuum* L.)

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Abstract The present investigation was conducted during *rabi* 2013-2014 with 33 chilli genotypes in a randomized block design with three replications to estimate the genetic variability, heritability and genetic advance for eight quantitative traits. The higher magnitude of genotypic as well as phenotypic coefficient of variation was recorded for number of green fruit weight and seed weight per fruit suggesting presence of sufficient variability in the gene pool. This offers ample scope for genetic improvement through selection of these traits. The magnitude of PCV was higher than GCV for all the traits which may due to higher degree of interaction of genotypes with the environment.All the characters showed high values of heritability. Among these traits number of seed weight per fruit showed highest followed by fruit length and fruit diameter. High heritability coupled with high genetic advance was exhibited by number of seeds per fruit and dry weight per plant. These characters were showing additive gene action and could be used as selection indices in yield improvement.

Keywords PCV, GCV, Variability, Quantitative characters, Heritability.

Introduction

Chilli (*Capsicum annuum* L.) is one of the most important vegetable-cum-spice crops valued for its aroma, taste, flavor and pungency. India contributes one-fourth of the world production of chilli with an average annual production of 1304000 tonnes from an area of 794000 hectares with a productivity of 1.6 MT/HA [1]. India being the largest chilli producer has vast potentiality to increase the production in order to promote export besides meeting its domestic requirements. However, despite continuous efforts at various levels, the chilli productivity did not gain momentum. This could be attributed to low genetic variability in germplasm lines, varieties and hybrids. Furthermore, the success in crop Improvement program depends chiefly on the availability of genetic variability in the crop. Therefore plant breeder needs adequate knowledge on variability, genetic divergence, character association and the extent of contribution of each character to fruit yield. To develop such breeding programs, there is a need of evaluating the available germplasm for variability and divergence.

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According to Burton [2], large spectrum genetic variability in segregating populations depending on the level of genetic diversity among genotypes offers better scope for selection. Selection of high yielding varieties based on grain yield will not be much effective unless adequate information on genetic parameters is available to formulate hybridization and selection program for further improvement because the estimate of the mean serves as a basis for eliminating the undesirable genotypes, whereas genetic variability (Genotypic Coefficient of Variation, GCV and Phenotypic Coefficient of Variation, PCV) help to choose the potential genotypes. Estimates of GCV, PCV, heritability and genetic advance will play an important role in exploiting future research projections of chilli improvement. In other words, for the improvement in any crop species, the knowledge of genetic variability for characters of economic importance and their heritability and genetic advance is of utmost importance in planning future breeding programs.

Heritability and genetic advance are other important selection parameters. Heritability along with genetic advance may provide a clearer picture for selection of particular trait. The estimates of heritability help the plant breeder in determining the character for which selection would be rewarding. The breeders are interested in selection of superior genotypes based on their phenotypic expression. The major function of heritability estimates is to provide information on transmission of characters from the parents to the progeny. Heritability estimates can anticipate improvement by selection of useful characters [3].

Similarly, genetic advance is also considered important because genetic advance shows the degree of the gain obtained in a character from one cycle of selection. High genetic advance coupled with high heritability estimates offers the most suitable condition to decide the criteria of selection [4–6]. In view of these, the present study was done with the objectives to assess genetic variability, heritability and genetic advance of thirty three chilli pepper genotypes.

Materials and Methods

The experiment was laid out with 33 chilli genotypes (Table 1) in a randomized block design with three replications at Vegetable Breeding Station, Indo-American Hybrid Seeds Ltd, Bangalore, Karnataka during *rabi,* 2014. The 8 quantitative traits studied werte fruit length (FL), fruit diameter (FD), green fruit weight (GFW), seed number per fruit (SNPF), stalk length (SL), dry weight per fruit (DWPF), seed weight per fruit (SWPF), and dry yield per plant (DYP).

Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse and Sukhatme [7]. PCV and GCV were calculated by the formula given by Burton and De Vane [8], heritability by Lush [9] and Hanson et al. [10] and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson et al. [11] in order to estimate the genetic variation in 33 chilli genotypes.

Results and Discussion

Table 1. List of genotypes with accession number used for genetic variability.

Sl. No.	Accession No.	Sl. No.	Accession No.	Sl. No.	Accession No.
1	HK 13R003	12	HK13R019	23	1-67
2	HK 13R005	13	HK13R023	24	HR12R012
3	HK13R008	14	HK13R024	25	HR12R040
4	ARUNIMA	15	HK13R030	26	HR12R044
5	HK13R010	16	INDUS-145	27	US-341
6	HK13R012	17	HK12R002	28	HR12R047
7	I-648	18	HK12R021	29	HR12R049
8	HK13R016	19	HK12R027	30	HR12R050
9	HK13R017	20	HK12R084	31	LALIMA
10	HK13R018	21	HK12R089	32	HR12R073
11	1-5	22	HK12R048	33	HR12R074

Table 2. Mean performance of 8 quantitative characters of 33 genotypes of chilli. Legends : VE = Environmental variance, VG=Genotypic variance, VP=Phenotypic variance, GCV = Genotypic coefficient of variation, h2 = Heritability, PCV = Phenotypic coefficient of variation, GA= Genetic advance, GAM = GA as percent of mean, FL = Fruit length, FD = Fruit diameter, GFW= Green fruit weight, SNPF= Seed weight per fruit SL = Stalk length, DWPF=Dry weight per fruit, SWPF= Seed weight per fruit, DYP=Dry yield per plant.

Sl. No.	Characters	VE	VG	VP	GCV (%)	PCV (%)	h2 %	GA	GAM
1	FL	0.45	1.56	2.02	16.26	18.48	77.50	2.26	29.49
2	FD	0.03	0.01	0.05	12.07	20.17	35.80	0.17	14.87
3	GFW	0.61	1.84	2.45	32.00	36.92	75.10	2.42	57.12
4	SNPF	37.43	110.64	148.08	15.15	17.52	74.70	18.73	26.98
5	SL	0.09	0.19	0.29	16.47	20.13	67.00	0.74	27.78
6	DWPF	0.12	0.13	0.25	23.63	32.78	51.90	0.53	35.08
7	SWPF	0.00	0.04	0.04	29.64	31.13	90.50	0.39	58.02
8	DYP	223.03	440.76	663.80	24.44	30.00	66.40	35.24	41.03

Genetic variability estimates including genotype means, range, genotypic, phenotypic and environmental variance, PCV, GCV, heritability, genetic advance and genetic advance as per cent mean for different characters are presented in Table 2.

Fruit length (FL)

The environmental, genotypic and phenotypic variances observed for fruit length were 0.45, 1.56 and 2.02 respectively while the PCV and GCV were 18.48% 16.26% respectively. High heritability (77.50%) was observed with high genetic advance (2.26%) and genetic advance as percent of mean (29.49%).

Fruit diameter (FD)

The environmental, genotypic and phenotypic variance observed for fruit diameter were 0.03, 0.01 and 0.05 respectively. The phenotypic coefficient of variation observed was 20.17% while genotypic coefficient of variation was 12.07%. Moderate heritability of 35.80% was observed with a high genetic advance of 0.17%. Genetic advance as percent of mean was observed to be 14.87%.

Green fruit weight (GFW)

The environmental, genotypic and phenotypic variances observed for green fruit weight were 0.61, 1.84 and 2.45, respectively. Moderate PCV (36.92), GCV (32.00), heritability (75.10%), genetic advance (2.42%) and genetic advance as percent of mean (57.12%) were observed.

Seed number per fruit (SNPF)

The components of variance viz., genotypic, environmental and phenotypic observed for seed number per fruit were 37.43, 110.64 and 148.08 respectively. High phenotypic coefficient of variation (17.52%) and genotypic coefficient of variation (15.15%) along with high genetic heritability (74.70%), genetic advance (18.73%) and genetic advance as percent of mean (26.98%) were observed for this character.

Stalk length (SL)

The environmental, genotypic and phenotypic variances observed for stalk length were 0.09, 0.19 and 0.29, respectively. Moderate PCV (20.13), GCV (16.47), heritability (67.00%), genetic advance (0.74%) and genetic advance as percent of mean (27.78%) were observed.

Dry weight per fruit (DWPF)

The environmental, genotypic and phenotypic variances observed for dry fruit weight were 0.12, 0.13 and 0.25 respectively. High PCV (32.78%) and GCV (23.63%) along with moderate heritability (51.50%) coupled with moderate genetic advance (53.80%) and genetic advance as percent of mean (35.08%) were obtained for dry fruit weight.

Seed weight per fruit (SWPF)

The environmental variance value observed for seed weight per fruit was 0.00, and that of genotypic and phenotypic variances were 0.04 and 0.04 respectively. GCV and PCV were 29.61 and 31.13 which were high. High heritability (90.50%) coupled with high genetic advance (0.39%) and genetic advance as percent of mean (58.02%) were obtained for this parameter.

Dry yield per plant (DYP)

The environmental, genotypic and phenotypic variances observed for dry fruit weight were 223.03, 440.76 and 663.80 respectively. For this character a high PCV (30.00%) and GCV (24.44%) along with high heritability (66.40%) coupled with moderate genetic advance (35.24%) and genetic advance as percent of mean (41.03%) was obtained.

In the present investigation, it is inferred from Table 2 that estimates of PCV were found higher than their corresponding GCV, indicating that there is little influence of environment on the expression of these characters. The present observations were in accordance to the earlier reports of Burton [2] who also stated that there is no significant influence of environment on the expression of characters. The genotypic coefficient of variation is most important and useful in the measurement of range and to compare the genetic variability of quantitative traits. The high genotypic coefficient accompanied with high phenotypic coefficient of variation for dry fruit yield per plant suggests that an enough genetic variability is present for these traits. Therefore, selection will be more effective is isolating the superior genotypes.

Johnson et al. [11] suggested that heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression. They opined that without genetic advance the estimation of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability.

Analysis of variance revealed significant differences among the genotypes for all the traits indicating the presence of sufficient genetic variability in the genotypes and considerable scope for their improvement. Sufficient genetic variability for many of the horticultural traits studied in chilli had also been reported by earlier workers [12–14].

Mishra et al. [15] also reported high phenotypic and genotypic co efficient of variations for fruit yield per plant, number of fruits per plant and fruit length, respectively. The heritability of the high magnitude was noticed for fruit yield per plant. Thus, it indicated that larger proportion of phenotypic variance has been attributed to genotypic variance and reliable selection could be made for almost all the traits on the basis of phenotypic expression.

Similar reports have been published earlier for high heritability estimates for fruit yield per plant, average fruit weight [16], number of fruits per plant [17], fruit length heritability and high genetic advance [18], fruit yield per plant [18], for average fruit weight [19] and number of fruits per plant [17]. High heritability along with moderate to low genetic advance was observed for average fruit weight, fruit length and fruit diameter. The results are in consonance with the findings of Ibrahim et al. [20] for fruit length and Manna and Paul [21] for fruit weight.

All genotypes were significantly different from each othe for all the characters under study. Dry yield per plant was found to be positively and significantly correlated with fruit length, fruit diameter, green fruit weight, seed number per fruit, stalk length, dry weight per fruit and seeds weight per fruit.

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