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Short communication

Assessment of genetic diversity in chilli genotypes using multivariate analysis

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ABSTRACT

Assessment of divergence for a set of characters utilizing different multivariate analyses has been effectively utilized in vegetable crops with diverse breeding system. Therefore, a study was carried out for determination of genetic divergence of 22 chilli genotypes. All the studied genotypes could meaningfully be grouped into six-clusters. Cluster I had the maximum of 14 genotypes, while clusters I & III comprised of two genotypes each, while clusters V and VI had one genotype each. The intra- and inter-cluster distance among 20 genotypes revealed that cluster I showed the maximum intra-cluster value (5.868) indicating that genotypes belonging to this cluster were diverse. Hybridization between genotypes belonging to cluster VI or IV and cluster II can be used to combine higher productivity with early maturity that can fit well in the multiple cropping systems. The top three traits, which contributed most towards the genetic divergence were number of primary branches/ plant (13.44%) followed by days to 50% fruiting (12.20%) and fruit length (12.14%). These traits may be used in selecting the genetically diverse parents for hybridization programme to exploit either maximum heterosis or to execute efficient selection in the segregating generation.

Key words: Chilli, genetic diversity, multivariate analysis.

INTRODUCTION

Chilli (*Capsicum annuum*), one of the most important horticultural crops belongs to the genus *Capsicum* in the Solanaceae family. Chilli is used in many forms, such as fresh or as cooked vegetables, as herbs or spices, and as various kinds of processed products (Hazra *et al*., 5). In spite of its high nutritive values, well acceptability among growers and consumers and wide range of available genetic variability, India is still lagging behind to attain the optimum productivity in chilli owing to use of local unimproved cultivars and heavy infestations of insect-pest and diseases particularly viral diseases (Kumar *et al*., 7). Therefore, much concentrated efforts are necessary to improve its yield, quality and host plant resistance against viral diseases. Hence, evaluation of the potentialities of the indigenous germplasm is essential because promise for further improvement programme depends on the genetic diversity of the crop. The magnitude of heritable and more particularly its genetic components, is clearly the most important aspect of the genetic constitution of the breeding material, which has a close bearing on its response to selection.

MATERIALS AND METHODS

The investigation was carried out at Research Farm of BCKV, Nadia, West Bengal under All India Coordinated Research Project on Vegetable Crops, situated at 23.5^0 N latitude and 89^0 E longitude of 9.75 m above mean sea level. The field experiments were undertaken in autumn-winter season starting from September, 2012 to March, 2014. The soil texture of the farm is sandy loam having neutral in reaction. The genotypes were grown in two consecutive years during autumn-winter season of 2012-13 and 2013-14 in Randomized block design with three replications. Each plot consisted of 20 plants spaced by 50 cm × 50 cm. Standard crop management practices and plant protection measures were taken from time to time. Observations were recorded on days to 50 per cent flowering, days to 50 per cent fruiting, plant height, number of primary branches per plant, number of fruits per plant, fruit length, fruit weight, fruit diameter, test weight, number of seeds per fruit and green fruit yield per plant from five randomly selected competitive plants in each genotypes of a replication. The data on different parameters were analysed by using SAS statistical software version 9.2. Mahalanobis's generalized distance (D^2) was used for assessing the genetic divergence between populations. The criterion used in clustering was done according to Tocher's method (Rao, 10).

RESULTS AND DISCUSSION

The investigation presents the range of variation for ten traits of growth, fruit and yield. Mean sum

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of square for the above mentioned characters and their significance are presented in the Table 1. The traits under study showed highly significant variation among the genotypes indicating their importance in the study of genetic variability. Significant variations in the mentioned traits were also reported by earlier workers (Chattopadhyay *et al.*, 2; Chaudhary *et al.*, 3; Arunkumar *et al.*, 1). Co-efficient of variation were low to moderate ranging from 5.79 to 14.93% for all the characters studied revealing less influence of environment for the expression of these characters.

Estimates for the co-efficient of phenotypic and genotypic variation (PCV and GCV respectively), heritability in broad sense (H), and GA as per cent of mean for these characters are presented in the Table 2. The genotypic co-efficient of variation measures the range of genetic variability shown by the plant characters and helps to compare the genetic variability present in various characters (Sanghi *et al.*,12), close estimates of GCV and PCV were recorded for all the traits except number of primary branches/ plant, number of seeds/ fruit. Close estimates of GCV and PCV were also recorded for most of the characters by Datta and Das (4). It implies that contribution towards final phenotypic expression of these traits were mostly by genetic makeup of these varieties rather than the environmental factors. This suggested that selection could be effective on the basis of phenotypic trait alone with equal probability of success in these traits. For correct estimation of the genetic makeup and its contribution to phenotypic expression of the trait, it is necessary that analysis of that trait should be conducted in terms of different locations and different seasons. The highest GCV value was recorded for the traits number of fruits/ plant, (45.25%) followed by fruit yield/ plant (44.16%) and the lowest value for days to 50% fruiting (9.31%). In the present investigation, number of fruits/ plant, fruit yield/ plant, number of primary branches/ plant, plants height, fruit width, and number of seeds/ fruit, exhibited high GCV and this finding corroborates the earlier observations of Manju and Sreelathakumary (7) and Chattopadhyay *et al*. (2). This shows prevalence of greater genetic variability among the genotypes, which offers good opportunities for crop improvement through selection.

Table 1. Analysis of variance for ten traits in chilli genotypes.

Source	d.f.	PH	NPB	D50F	D50FR	FL	FG	NFPP	NSPF	TWS	FYPP
Replication	2	345.648	0.197	10.968	207.37	1.305	13.504	85.273	401.23	0.00115	661.43
Genotype	21	630.96**	10.27**	477.28**	197.41**	7.56**	33.54**	1231.57**	351.98**	0.041**	12224.32**
Error	42	102.889	5.43	13.985	51.569	1.748	2.016	206.08	296.639	0.0054	2457.727
CD at 5%		23.67	5.432	8.720	16.754	3.085	3.313	33.479	40.203	0.172	115.727
CV (%)		14.28	14.78	5.79	6.67	14.90	13.51	14.70	13.27	14.80	14.93

**Significant at 1% level of significance

PH = Plant height (cm), NPB = No. of primary branches, D50F = Days to 50% flowering, D50FR = Days to 50% fruting, FL = Fruit length (cm), FG = Fruit girth (cm), NFPP = No. of fruits per plant, NSPF = No. of seeds per fruit, TWS = Test weight of seed (g), FYPP = Fruit yield per plant (g)

Table 2. Mean Range and Estimates of genetic variability of ten traits in chilli genotypes.

Trait	Mean	Range	GCV (%)	PCV (%)	GCV : PCV	Heritability (%) in b.s.	Genetic advance as (%) of mean
Plant height (cm)	47.65	32.30 to 80.00	35.05	27.84	79.42	63.10	45.56
No. of pr. branches / plant	6.51	3.67 to 10.30	40.75	19.50	47.85	22.90	19.20
Days to 50% flowering	64.54	46.67 to 97.67	20.11	19.25	95.72	91.70	37.97
Days to 50% fruiting	107.53	93.67 to 123.30	9.31	6.48	69.60	48.50	9.30
Fruit length (cm)	6.50	3.49 to 10.31	29.14	21.13	72.51	52.60	32.00
Fruit width (cm)	10.50	6.03 to 16.30	33.69	30.86	91.59	83.90	58.28
No. of fruits/ plant	51.72	32.00 to 108.30	45.25	43.74	96.66	86.40	58.15
No. of seeds/ fruit	52.72	37.33 to 73.30	33.67	8.15	24.20	5.90	4.06
Test wt. of seed (g)	0.49	0.34 to 0.75	26.63	22.07	82.80	68.70	38.77
Green fruit yield/ plant (g)	171.17	39.99 to 313.07	44.16	33.33	75.47	57.00	51.83

Multivariate analysis is a powerful tool in quantifying the degree of divergence between biological populations (genetic distance) and to assess the relative contribution of different components to the total divergence. Based on the degree of divergence (D^2 values) between any two genotypes, a logical grouping of the genotypes with low D^2 value could be arrived at by Tocher's method. Based on the determination of D^2 values, all the 22 genotypes could meaningfully be grouped into six clusters (Table 3). Cluster I had the maximum of 14 genotypes, cluster II, III, and IV comprised of two genotypes each, while cluster V and VI had one genotype each. In general, the pattern of distribution of genotypes from diverse geographical region into different clusters was random. It might be due to free and frequent exchange of genetic materials among the farmers and breeders of different regions (Kalloo *et al.*, 6). Differential selection pressure according to regional preference also produced greater uniformity in the germplasm. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin such as exchange of genetic stock, genetic drift, spontaneous mutation, natural and artificial selection are responsible for genetic diversity. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. Environmental influence on the composition of cluster was also recorded earlier in different self-pollinated crops like cowpea (Hazra *et al*., 5; Peter and Rai, 9) tomato.

The intra- cluster and inter-cluster distance represent the index of genetic diversity among clusters. The intra- and inter-cluster distance among 22 genotypes revealed that cluster I showed the maximum intra-cluster value (5.868) indicating that genotypes belonging in this cluster are diverse (Table 4). On the other hand, cluster VI had the minimum intra-cluster value (0.010). At the inter-cluster level, the minimum value was observed between cluster I and II (7.539) indicating close relationship among the genotypes included in these clusters. The maximum inter-cluster value was observed between clusters III and V (17.715) followed by 14.315 between cluster III and VI, which indicated that the genotypes included in these clusters had the maximum divergence. Hence, intermating between the genotypes included in these clusters was expected to give transgressive segregates in the advanced generation. Kalloo *et al.* (6) suggested that the crosses between selected varieties from widely separated clusters were most likely to give desirable recombinants. The top three characters, which contributed most towards the genetic divergence (Table 5) were number of primary branches/ plant (13.44%) followed by days to 50% fruiting (12.20%) and fruit length (12.14%). These traits may be used in selecting genetically diverse parents for hybridization programme to exploit either maximum heterosis or to execute efficient selection in the segregating generation.

Genotypes belonging to clusters VI, IV and II could be regarded as useful sources of gene for improving fruit yield of chilli. On the other hand, genotypes belonging to cluster II had taken the earliest days to reaching first flowering and 50% fruiting, which could be helpful for breeding an

Table 4. Inter- and intra-cluster distances amongst 22 chilli genotypes.

Cluster No.	I	II	III	IV	V	VI
I	5.868	7.539	11.289	7.946	9.473	9.761
II		4.199	13.501	9.577	7.956	9.618
III			3.847	14.225	17.715	14.315
IV				5.769	10.995	9.372
V					0.020	10.571
VI						0.010

Table 3. Cluster classification and source of collection of chilli genotypes.

Cluster No.	Name of the genotype / Source
I (14)	Siti (W.B.), Cob-12 (W.B.), HP-27 (W.B.), Kashi Anmol (U.P.), Jhal Lanka (W.B.), HP-31 (H.P.), BSS-1 (W.B.), Suli (W.B.), KDCS-810 (Gujarat), J. Mukta (W.B.), Cob-1 (W.B.), BSS-2 (W.B.), Samrat (Gujarat), Cob-8 (W.B.)
II (2)	BCCH Sel-4 (W.B.), Midnapur Local (W.B.)
III (2)	AC-575 (A.P.), Nadia Local (W.B.)
IV (2)	HP-33 (H.P.), Chaitali (W.B.)
V (1)	BCC-5 (W.B.)
VI (1)	BCC-1 (W.B.)

Table 5. Contribution of different traits (%) towards divergence.

Trait	(%) Contribution
Plant height (cm)	11.09
No. of primary branches /plant	13.44
Days to 50% flowering	7.35
Days to 50% fruiting	12.20
Fruit length (cm)	12.14
Fruit girth (cm)	8.48
No.of fruits/ plant	9.28
No. of seeds/ fruit	10.20
Test weight of seed (g)	6.49
Fruit yield per plant	9.33

early plant type. Hybridization between genotypes belonging to clusters VI or IV and cluster II could combine higher productivity with early maturity that can be fitted well in multiple cropping systems. For crop improvement in chilli, inter-crossing among genotypes with outstanding mean performance was suggested by previous workers (Roy and Sharma, 11). The results of present study are thus useful as it gives information regarding the traits that influence genetic diversity, which could be well utilized for selection of breeding methods for improvement of chilli crop.

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