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Diversity and Path Analysis of Chilli (*Capsicum spp.*) Based on Morphological Traits in Northern Region of Bangladesh

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A R T I C L E I N F O	A B S T R A C T
	Genetic variability, heritability, genetic advance, correlation coefficient analysis, path coefficient analysis and genetic divergence between yield and its contributing traits were estimated using fifteen (15) different chilli genotypes in northern region of Bangladesh. The aim of this study is to screen out suitable parents for next hybridization program. The phenotypic coefficient of variations was found slightly higher than the genotypic coefficient of variations for all characters studied, indicating that the apparent variation is not only genetic but also influenced by the growing environment in the expression of the traits. High genotypic and phenotypic coefficient of variation was observed in length of fruit (27.27% and 27.81%). High heritability coupled with high genetic advance in percent of mean in fruit yield per plant (71.23 and 39.38), number of fruits per plant (71.26 and 31.18), weight of individual fruit (88.52 and 43.80), length of fruit (96.13 and 70.59) and diameter of fruit (79.58 and 35.79) suggested that these characters would be considered for varietal selection. The correlation studies revealed that fruit yield per plant showed significant positive correlation with plant height (0.369), number of fruits per plant (0.587), weight of individual fruit (0.634) and length of fruit (0.450) which can be considered for selection of a good variety. Path analysis revealed weight of individual fruit (0.293), plant height (0.205), number of branches per plant (0.186), length of fruit (0.164), number of fruits per plant (0.132) and diameter of fruit (0.078) had direct positive effect on yield per plant, indicating these traits are the main contributors to fruit yield per plant. The divergence value for cluster analysis showed the highest inter-cluster distance between clusters II and IV which indicates that these genotypes may provide high heterosis in hybridization and expected to show wide variability in genetic architecture.

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Introduction

Chilli (Capsicum annuum L.) originated in South and Central America belongs to the family Solanaceae is a spice crop and also used as vegetable and widely cultivated throughout the world (Dias et al., 2013; Wahyuni et al., 2013). The constituents of chilli are important for its nutritional value, aroma, texture, color and it is also a good source of oleoresin which has diversified uses in process food, beverage industries and in pharmaceuticals (Osuna-Garcia et al., 1998; Marin et al., 2004). Chilli, of the genus Capsicum, has more than 25 commonly used species with four cultivars groups as Chinense group (West Indies chilli), Frutescens group (bird chilli), Annuum group (hot chilli) and sweet pepper group (Nsabiyera et al., 2013). Throughout the world, chilli is generally consumed either in fresh, dried or in powder (El-Ghoraba et al., 2013).

Generally chilli is grown as a cash crop but its commercial production and it is largely concentrated in Bogra, Rangpur, Comilla, Noakhali, Faridpur, Chittagong and Mymensingh district. In Bangladesh 434,757 acres land is under its cultivation and total production of green chilli was approximately 1,549,474 metric tons (BBS, 2014). Chilli is rich in proteins, lipids, carbohydrates, fibres, mineral salts (Ca, P, Fe) and in vitamins A, D_3, E, C, K, B2 and B_{12} (El-Ghoraba et al., 2013). The fruits are an excellent source of health-related phytochemical compounds, such as ascorbic acid, carotenoids, tocopherols (vitamin E), flavonoids, and capsaicinoids that are very important in preventing chronic diseases such as cancer, asthma, coughs, sore throats, diabetes (Wahyuni et al., 2013); The pharmaceutical application of capsaicinoid

is attributed to its antioxidant, anticancer, antiarthritic, and analgesic properties (Akbar et al., 2010). Moreover, the consumption of fresh fruits facilitates starchy food digestion in human body (Bhattacharya et al., 2010). It has antioxidant, antiutagenesis and hypocholesterolemic properties and also inhibits bacterial growth and platelet agglomeration (Wahyuni et al., 2013).

The systematic breeding works involved the several steps, like collecting of germplasm, assessing of genetic variability, creating of genetic variability, implementing of selection, and developing of selected genotypes to be released as commercial variety (Poehlman and Sleper, 1995 and Syukur et al., 2012). For efficient and effective breeding work, investigation and better understanding of the variability existing in a population base of crop is required so that it can be exploited by plant breeder for crop improvement. Moreover, the success of any crops improvement program depends not only on the amount of genetic variation present in a crop but also on magnitude of variation which is heritable from the parent to the progeny (Bello et al., 2014). A wide range of variability is available in chilli genotypes which provide great scope for improving fruit yield through systematic breeding. Estimation of genetic variability present in the germplasm of a crop is a pre-requisite for designing effective breeding programme (Parkash, 2012).

Several researchers observed that phenotypic coefficient of variation (PCV) to be higher than genotypic coefficient of variation (GCV) for all the studied traits (Kadwey et al., 2016; Gupta et al., 2009 and Bendale et al., 2006). Heritability was found to be very high for fruit yield per plant, seed yield per plant, fruit length, fruit weight of green chilli and fruit yield per hectare (Wilson and Philip, 2009 and Bharadwaj et al., 2007). In order to benefit transgressive segregation, the knowledge of genetic distance between parents is necessary (Lahbib et al., 2012 and Khodadadi et al., 2011). The information the degree of genetic divergence is essential for the breeder to choose the right type of parents for purposeful hybridization in heterosis breeding (Khodadabi et al., 2011 and Farhad et al., 2010). More diverse the parents within a reasonable range, better are the chances of improving economic characters in the offspring. The critical assessment of nature and magnitude of variability in the germplasm stock is one of the important pre-requisites for formulating effective breeding methods (Krishna et al., 2007). The choice of the most suitable breeding method for the rational improvement of yield and its components in any crop largely depends upon the genetic variability, correlations and association between qualitative and quantitative characters and heritability estimates.

Considering the entire situation, the present study was steered for genetic diversity analysis of chilli with the following specific objectives; to compare the yield contributing characters and yield potentiality of different chilli genotypes; the nature of association of traits, direct and indirect relation between yield contributing characters and yield of different chilli genotypes; to screen out the suitable parents group which are likely to provide superior segregates on hybridization and to assess the magnitude of genetic divergence in genotypes for identifying the genetically divergent parents to use them in future breeding program.

Materials and Method

Experimental Site

The experiment was conducted at the Northern Region of Bangladesh from November 2015 to April 2016 in rabi season. The experimental area was under the subtropical monsoon climate zone, which was characterized by heavy rainfall, high humidity, high temperature and relatively long day during the growing season. The soil was sandy loam in texture having pH 5.47-5.63. The mean temperature of the growing period was 26.43°C with average maximum and minimum being 36°C and 20.54°C, respectively.

Plant Materials

Fifteen genotypes of chilli were used in this study which was collected from Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka and Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur and Farmers' field of Northern districts of Bangladesh (Table 1).

Field Managements

All the fertilizers were applied as recommended dozes following appropriate application timing and method. The recommended dosage of Urea, TSP, MoP, Gypsum and Znic sulphate was applied in field at the rate of 210, 300, 200,100 and 15 Kg/ha respectively. Irrigation was applied once a week at emergence and every two weeks at flowering and fruit production. Chemical (Sevine, Marshal and deltanet) and cultural practices (hand picking and remove infected plant part) were applied to control insect pest. Tender fruits were harvested two times per week to estimate fruit yield while mature fruits were harvested when fruits turned to loss green color and dry fruit for seed yield parameter.

Data Collection and Analysis

Data for different plant parameters were recorded from 5 plants of each genotype. Genotypic and phenotypic variance was estimated by the formula used by Johnson et al. (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary, 1985. Cluster Analysis (CA) was done by using GENSTAT 5.13 and Microsoft Excel 2007 software. Data of ten characters were subjected to analysis of variance (ANOVA) using MSTATC software program to test the presence of significant differences among accessions for the traits measured. It was also measure of mean, range, CV, standard deviation by this software. Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (H^2) and expected genetic advance as percentage to mean (GAM) were computed. The phenotypic and genotypic correlation coefficients obtained from correlation study, were further partitioned into direct and indirect effects with the help of path coefficient analysis as suggested by Wright, 1921 and applied in plant breeding by Dewey and Lu, 1959. Diversity analysis was estimated from measured quantitative traits. Duncan's Multiple Range (DMRT) was employed to identify genotypes that are significantly different from each other. Descriptive statistic was used for qualitative traits data.

Table 1. Chili genotypes and their basic information's

Genotypes	Name of genotypes	Genotypes	Name of genotypes
G_1	Ca 001	G_9	SRCO 1
G_2	Ca 002	G_{10}	SRCO 2
G_3	Special chili of Bogra	G_{11}	SRCO 9
G_4	Surjamukhi IMP	G_{12}	SRC 13
G_5	Black Lady (local variety)	G_{13}	CO 613
G_6	Local 1 variety	G_{14}	SRCO 5
G_7	HP 1029	G_{15}	Hot Morich of Bogra
G_8	CO 610		

* G1 and G2 = Exotic cultivar; G7 – G14 = Farmer cultivars that collected from different districts of North Bengal of Bangladesh and Sher-e-Bangla Agricultural University (SAU), Bangladesh.

Table 2. Estimation of variance parameters for ten characters in chilli genotypes

Traits	GenMS	Min	Max	Mean	σ^2_g	σ^2_P	GCV	PCV	h^2_b	GA	GA^1
Days to 1st flowering	16.676*	42.67	53.67	46.73	3.23	10.22	3.85	6.84	31.60	2.67	5.71
Plant height (cm)	154.988**	64.36	84.57	73.10	40.73	73.52	8.73	11.73	55.41	12.54	17.16
Number of branches/plant	2.179**	6.33	9.07	7.7	0.50	1.17	9.12	13.94	42.83	1.22	15.76
Number of fruits/plant	314.398**	54.40	88.73	68.70	92.38	129.76	13.99	16.57	71.26	21.42	31.18
Weight of individual fruit (g)	2.365**	3.91	7.11	4.93	0.76	0.85	17.63	18.74	88.52	2.16	43.80
Length of fruit (cm)	9.376**	1.53	8.51	6.44	3.08	3.21	27.27	27.81	96.13	4.55	70.59
Diameter of fruit (mm)	3.921**	5.56	9.53	7.22	1.20	1.51	15.20	17.04	79.58	2.58	35.79
Number of seeds/fruit	136.799**	44.40	73.47	65.68	33.62	69.56	8.83	12.70	48.33	10.64	16.20
Weight of 1000 seeds (g)	59.028*	62.44	81.07	67.68	11.19	36.63	4.93	8.92	30.54	4.88	7.19
Yield/plant (g)	12037.511**	242..89	427.44	336.41	3536.30	4964.91	17.68	20.95	71.23	132.49	39.38

1: (% mean), ** Significant at 1%, * Significant at 5%

Results

The mean performance of the genotypes, estimated variability components viz. phenotypic and genotypic variance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as percent of means (GA%) for 10 characters are presented in Table 2. Days to 1st flowering refers to phenotypic variance (10.22) was higher than the genotypic variance (3.23) supported by high difference between phenotypic (6.84%) and genotypic (3.85%) co-efficient of variation with low heritability (31.60%) and moderate genetic advance in percentage of mean (5.71). Plant height refers to phenotypic variance (73.52) was higher than the genotypic variance (40.73) supported by moderate difference between phenotypic (8.73%) and genotypic (11.73%) co-efficient of variation with moderate heritability (55.41%) was observed in plant height attached with high genetic advance in percentage of mean (17.16). Number of branches/plant refers to phenotypic variance (1.17) was higher than the genotypic variance (0.50) supported by high difference between phenotypic (13.94%) and genotypic (9.12%) co-efficient of variation with moderate heritability (42.83%) and high genetic advance in percentage of mean (15.76). Number of fruits/plant refers to phenotypic variance (129.64) was higher than the genotypic variance (92.38) supported by high difference between phenotypic (16.57%) and genotypic (13.99%) co-efficient of variation with high heritability (71.26%) and high genetic advance in percentage of mean (31.18). Weight of individual fruit refers to phenotypic variance (0.85) was higher than the genotypic variance (0.76) supported by low difference between phenotypic (18.74%) and genotypic (17.63%) co-efficient of variation with high heritability (88.52%) and high genetic advance in percentage of mean (43.80). Length of fruit refers to phenotypic variance (3.31) was higher than the genotypic

variance (3.08) supported by low difference between phenotypic (27.81%) and genotypic (27.27%) co-efficient of variation with high heritability (96.13%) and high genetic advance in percentage of mean (70.59). Diameter of fruit refers to phenotypic variance (1.51) was higher than the genotypic variance (1.20) supported by low difference between phenotypic (17.04%) and genotypic (15.20%) co-efficient of variation with high heritability (79.58%) and high genetic advance in percentage of mean (35.79). Number of seeds per fruit refers to phenotypic variance (69.56) was higher than the genotypic variance (33.62) supported by high difference between phenotypic (12.70%) and genotypic (8.83%) co-efficient of variation with moderate heritability (48.33%) and high genetic advance in percentage of mean (16.20). Weight of 1000 seeds refers to phenotypic variance (36.63) was higher than the genotypic variance (11.19) supported by high difference between phenotypic (8.92%) and genotypic (4.93%) co-efficient of variation with low heritability (30.54%) and moderate genetic advance in percentage of mean (7.19). Yield/plant refers to phenotypic variance (4964.91) was higher than the genotypic variance (3536.30) supported by high difference between phenotypic (20.95%) and genotypic (17.68%) co-efficient of variation with high heritability (71.23%) and low genetic advance in percentage of mean (39.38).

Correlation coefficient was worked out to assist in selection procedure which suggests the association of traits with yield. The association among the component traits listed in Tables 3. In correlation study, highly significant positive association was recorded for days to 1st flowering of chilli genotypes with weight of individual fruit (0.446), whereas the non-significant positive association was recorded for plant height (0.142), number of branches/plant (0.158), length of fruit (0.032), diameter of fruit (0.273) and yield/plant (0.154).

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Table 3. Correlation matrix for yield attributes and yields of different chilli genotypes

Characters	DF	PH	NBP	NFP	WIF	LF	DF	NSF	WS	YP
DF	1									
PH	0.142	1								
NBP	0.158	0.365**	1							
NFP	-0.24	0.360*	0.229	1						
WIF	0.446**	0.145	-0.03	-0.245	1					
LF	0.032	0.161	-0.032	0.376**	0.191	1				
DF	0.273	0.065	-0.107	-0.353*	0.2	-0.329*	1			
NSF	-0.319*	-0.001	0.188	0.275	-0.205	-0.021	-0.175	1		
WS	-0.186	0.07	-0.027	-0.222	0.365**	-0.118	-0.062	-0.017	1	
YP	0.154	0.369**	0.149	0.587**	0.634**	0.450**	-0.119	0.048	0.119	1

DF: Days to 1st flowering, PH: Plant height (cm), NBP: Number of branches per plant, NFP: Number of fruits / plant, WIF: Weight of individual fruit (g), LF: Length of fruit (cm), DF: Diameter of fruit (mm), NSF: Number of seeds / fruit, WS: Weight of 1000 seeds (g), YP: Yield per plant, ** = Significant at 0.01 level of probability; * = Significant at 0.05 level of probability

Table 4. Path coefficients for yield attributes and yields of different chilli genotypes

Characters	DF	PH	NBP	NFP	WIF	LF	DF	NSF	WS	YP
DF	-0.148	0.379	0.234	-0.063	-0.211	0.136	-0.142	0.167	-0.198	0.154
PH	0.156	0.205	-0.102	-0.132	0.198	0.219	0.169	-0.267	-0.077	0.369
NBP	-0.231	0.123	0.186	0.208	-0.229	-0.289	0.125	0.165	0.091	0.149
NFP	0.176	-0.067	0.218	0.132	0.169	0.109	-0.157	0.045	-0.038	0.587
WIF	0.187	0.213	-0.029	-0.138	0.293	-0.084	0.125	-0.189	0.256	0.634
LF	-0.113	-0.158	0.228	0.073	-0.104	0.164	-0.072	0.19	0.242	0.45
DF	0.133	0.094	-0.188	-0.152	0.055	-0.212	0.078	0.055	0.018	-0.119
NSF	-0.152	0.073	0.097	0.128	0.038	0.131	0.133	-0.133	-0.267	0.048
WS	0.184	-0.109	-0.138	-0.055	0.289	-0.044	-0.105	0.308	-0.211	0.119
YP	0.154	0.369**	0.149	0.587**	0.634**	0.450**	-0.119	0.048	0.119	1

DF: Days to 1st flowering, PH: Plant height (cm), NBP: Number of branches per plant, NFP: Number of fruits / plant, WIF: Weight of individual fruit (g), LF: Length of fruit (cm), DF: Diameter of fruit (mm), NSF: Number of seeds / fruit, WS: Weight of 1000 seeds (g), YP: Yield per plant, Residual effect = 0.3803

Highly significant positive association was recorded for plant height of chilli genotypes with number of branches/plant (0.365), number of fruits/plant (0.360) and yield/plant (0.369), while the non-significant positive association was recorded for days to 1st flowering (0.142), weight of individual fruit (0.145), length of fruit (0.161), diameter of fruit (0.065) and weight of 1000 seeds (0.070). Highly significant positive association was recorded for number of branches per plant of chilli genotypes with plant height (0.365), while the non-significant positive association was recorded for days to 1st flowering (0.158), number of fruits/plant (0.229), number of seeds/fruit (0.188) and yield/plant (0.149). Highly significant positive association was recorded for number of fruits/plant of chilli genotypes with plant height (0.360), length of fruit (0.376) and yield/plant (0.587), while the non-significant positive association was recorded for number of branches/plant (0.229) and number of seeds/fruit (0.275) Highly significant positive association was recorded for weight of individual fruit of chilli genotypes with days to 1st flowering (0.446), weight of 1000 seeds (0.365) and yield/plant (0.634), whereas the non-significant positive association was recorded for days plant height (0.145), length of fruit (0.191) and diameter of fruit (0.200). Highly significant positive association was recorded for length of fruit of chilli genotypes with number of fruits/plant (0.376) and yield/plant (0.450), while the non-significant positive association was recorded for days to 1st flowering (0.032), plant height (0.161) and weight of individual fruit (0.191). Non-significant positive association was recorded for diameter of fruit with days to 1st flowering (0.273), plant

height (0.065) and weight of individual fruit (0.200). On the other hand, highly significant negative association was recorded for number of fruits/plant (-0.353) and length of fruit (-0.329). Non-significant positive association was recorded for number of seeds per fruit for number of branches per plant (0.188), number of fruits per plant (0.275) and yield per plant (0.048). Highly significant positive association was recorded for weight of 1000 seeds of chilli genotypes with weight of individual fruit (0.365), while the non-significant positive association was recorded for plant height (0.070) and yield/plant (0.119). Highly significant positive association was recorded for yield per plant of chilli genotypes with plant height (0.369), number of fruits/plant (0.587), weight of individual fruit (0.634) and length of fruit (0.450), while the non-significant positive association was recorded for days to 1st flowering (0.154), number of branches/plant (0.149), number of seeds/fruit (0.048) and weight of 1000 seeds (0.119).

The mutual relationship of component characters might vary both in magnitude and direction and the simple correlation coefficient may not provide the exact relationship between yield and yield attributes. Therefore, it is necessary to conduct path coefficient analysis which permits a critical examination of specific direct and indirect effects of characters and measures their relative intensity in determining the ultimate goal yield. Path coefficient analysis (Table 4) revealed that days to 1st flowering had negative direct effect (0.148), plant height had positive direct effect (0.205), number of branches/plant had positive direct effect (0.186), number of fruits/plant had positive direct effect (0.132), weight of individual fruit had positive

direct effect (0.293), length of fruit had positive direct effect (0.164), diameter of fruit had positive direct effect (0.078), number of seeds/fruit had negative direct effect (-0.133) and weight of 1000 seeds had negative direct effect (-0.211) on yield/plant.

The clustering pattern of all genotypes has been presented in (Table 5). The cluster I comprised eight genotypes including G2, G3, G4, G6, G8, G9, G11 and G13. Cluster II contained three genotypes namely, G7, G10 and G14. Cluster III consisted of three genotypes viz., G1, G5 and G15. Cluster IV was composed of single genotype G12

indicated that this genotype is totally different from other genotypes used in this study. The intra cluster (Bold) and inter cluster divergence (average D^2 values) of all clusters have been presented in Table 6. Intra cluster average D^2 values ranged from 0.00 to 0.6732. It recorded maximum (0.6732) in cluster IV with one genotype followed by 0.4765 in cluster III with three genotypes. Inter cluster average D^2 values were higher (12.541) between cluster II and cluster IV followed by 9.672 between cluster II and cluster III. The minimum inter cluster value for all the characters were as 4.023 between cluster I and cluster III.

Table 5. Distribution of 15 genotypes in different clusters

Cluster	Members	Chilli Genotypes	Name of genotypes
I	8	G_2, G_3, G_4, G_6, G_8, G_9, G_{11} and G_{13}	Ca 002, Special chilli of Bogra, Surjamukhi IMP, Local 1, CO 610, SRCO 1, SRCO 9 and CO 613
II	3	G_7, G_{10} and G_{14}	HP 1029, SRCO 2 and SRCO 5
III	3	G_1, G_5 and G_{15}	Ca 001, Black Lady and Hot Morich of Bogra
IV	1	G_{12}	SRC 13

Table 6. Intra (Bold) and inter cluster distances (D^2) for 15 genotypes

Cluster	I	II	III	IV
I	0.000			
II	5.452	0.1574		
III	4.023	9.672	0.4765	
IV	5.134	12.541	8.679	0.6732

Discussion

The analysis of variance revealed significant difference among the genotypes for all the characters (Table 2). The existence of high variability for different characters among chilli genotypes has earlier studied by Kumary and Rajmony (2004). The variation was highest for fruit yield per plant (242.89-427.44 g) and narrow range of variability was observed for number of branches per plant (6.33-9.07). The similar finding was also reported by Singh et al. (2013) and Kadwey et al. (2016). The highest phenotypic variances were calculated for fruit yield per plant (4964.91) followed by number of fruits per plant (129.76) and plant height (73.52) while the lowest value was recorded for weight of individual fruit (0.85) followed by number of branches per plant (1.17) and fruit diameter (1.51). The genotypic variance ranged from 0.01 (Number of branches per plant) to 3536.30 (fruit yield per plant). This suggested the scope for improvement of these characters through selection. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters studied. According to Sivasubramaniah and Meron (1973) PCV and GCV values greater than 20% are regarded as high, values between 10% and 20% to be medium whereas values less than 10% are considered to be low. Based on this delineation among all characters exhibiting high degree of genotypic and phenotypic coefficients of variation was in length of fruit (27.27% and 27.81%) and this closer magnitude of genotypic and phenotypic coefficients of variation indicated that a greater role was played by genotypes rather than environment. Moderate GCV and PCV were found in number of fruits per plant (13.99% and 16.57%) weight of individual fruit (17.63) and diameter of fruit (15.20% and 17.04%) (Table 2). Medium PCV and GCV value suggests that these characters are controlled more of by the genetic factors.

Hence, these characters amenable to selection for further improvement. The eminent scientist Johnson et al. (1955) suggested that high heritability combined with high genetic advance is indicative of additive gene action and selection based on these parameters would be more reliable. In the present investigation, high heritability estimates in conjunction with high genetic advances were observed for fruit yield per plant, number of fruits per plant, weight of individual fruit, length of fruit and diameter of fruit. Similar findings were also studied by Choudhary and Samadia (2004) and Ukkund et al. (2007) who reported high heritability and high genetic advance for fruits per plant and fruit weight.

Plant breeders always look for genetic variation among characters to select the desirable types which are highly correlated among themselves and with yield and the analysis of the relationship among these characters are vital for selection criteria. Fruit yield has shown positive and significant correlations with plant height (0.369), number of fruits per plant (0.587), weight of individual fruit (0.634) and length of fruit (0.450). Fruit yield per plant has also shown negatively and insignificantly correlated with diameter of fruit (-0.119). The findings of positive correlation are also confirmatory with Patel and Patel (2014), Yatung et al. (2014) and Dolkar et al. (2015), Patel et al. (2015), Sharma and Sridevi (2016), and Mamatha et al. (2016). In contrast, fruit yield showed positive and non-significant correlation with days to 1st flowering (0.154), number of branches per plant (0.149), number of seeds per plant (0.048) and weight of 1000 seeds (0.119).

The path coefficient analysis (Table 4) showed that, weight of individual fruit (0.293) had highest positive direct effects on fruit yield per plant followed by plant height (0.205), number of branches per plant (0.186),

length of fruit (0.164), number of fruits per plant (0.132) and diameter of fruit (0.078) which is in agreement with Yatung et al., (2014), Pandit and Adhikary (2014), Patel et al., (2015), Mamatha et al., (2016) and Sharma and Sridevi (2016). On the other hand, the direct negative effects were recorded for days to 1st flowering (-0.148), number of seeds per fruit (-0.133) and weight of thousand seeds (-0.211) on fruit yield per plant. Hence, direct selection for weight of individual fruit was suggested to improve yield.

All 15 genotypes grouped into four clusters on the basis of yield components studied. Clustering of genotypes on the basis of genetic diversity would help the breeder for selecting diverse plants for using in hybridization under further breeding program. Clustering pattern was not influenced by geographical distribution of genotypes. Karad et al. (2002), reported eight clusters with 40 genotypes. Manju and Sreelathakumary (2004) reported six clusters with 32 accessions. Senapati et al. (2003) reported six clusters in 20 diverse genotypes of chili and Amarul Junior et al. (2005) reported eight distinct grouped in 50 accessions of chili. Genotypes from these four clusters if involve in hybridization may occur a wide spectrum of segregating population as genetic diversity is very distinct among the groups. The selection of diverge genotype from cluster would produce a broad spectrum of variability for morphological and quality traits studied which may enable further selection and improvement.

Conclusion

Genetic advancement in chilli is possible through varietal selection exercised for the number of fruits per plant, weight of individual fruit, length of fruit, diameter of fruit and fruit yield per plant which showed high heritability coupled with high genetic advance. In our study, fruit yield has shown positive and significant correlations with plant height, number of fruits per plant, weight of individual fruit and length of fruit. Therefore, plant height, number of fruits per plant, weight of individual fruit and length of fruit were the most important traits for improving the genotypes for higher fruit yield and may be applied for selection in chilli productivity. Path analysis revealed that, the highest direct positive effect on fruit yield was exerted by weight of individual fruit, plant height, number of branches per plant, length of fruit, and number of fruits per plant and diameter of fruit. Thus, on the basis of current result, weight of individual fruit, plant height, number of branches per plant, length of fruit, and number of fruits per plant and diameter of fruit could be the most important yield component characters which might be selected for yield improvement. The hybrids of genotypes with maximum distance resulted in high yield and thus the cross between the genotypes from cluster II and IV can be used in chilli breeding to achieve maximum heterosis. Minimum distance was between the genotypes of cluster I and III which can be used for backcrossing programs.

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