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Genetic diversity of chilli (*Capsicum annuum* L.) genotypes of India based on morpho-chemical traits

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Abstract

Study on genetic diversity was conducted with 30 chilli (*Capsicum annuum* L.) genotypes of Indian origin at the research farm of Vegetable Science, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh, India during March-October 2011. Twelve quantitative characters *viz.* plant height (cm), number of primary branch per plant, days to first flowering, fruit length (cm), fruit diameter (cm), number of fruit per plant, average fruit weight (g), green fruit yield per plant (g), number of seed per fruit, ascorbic acid (mg/100g), capsaicin content (%) and chlorophyll content (mg/g) were taken into consideration. The analysis of variance revealed considerable variability among the genotypes for the character studied. Cluster analysis was used for grouping of 30 chilli genotypes under the study grouped into six clusters. Cluster III had maximum (14) and cluster IV and V had the minimum number (1) of genotypes. The highest (459.81) inter cluster distance was observed between cluster II and IV and the lowest (36.04) between cluster I and IV. Cluster III (D^2= 67.66) have exhibited highest intra cluster distance and the lowest was observed in cluster II (D^2=11.19). The characters capsaicin content and ascorbic acid contributed maximum towards divergence. Considering diversity pattern and other horticultural performance the genotypes CHFC-7 from cluster VI, genotype CHFC-27 from cluster II and CHFC-15 from cluster III may be taken into consideration as better parents for an efficient hybridization programme of chilli.

Keyword: *Capsicum annuum*, parent selection, genetic divergence, yield.
Abbreviations: CHFC_College of Horticulture and Forestry Chilli; g_gram; NEH_North Eastern Hill, ANOVA_Analysis of variance.

Introduction

A wide variability in chilli fruit morphology, pungency, bearing habit and crop duration is found throughout India (Asati and Yadav, 2004; Julia et al., 2012). Genetic resources of chilli landraces in north eastern India have not been well documented, but a few names mentioned include Naga Jolokia, Bhut Jolokia and Bih Jolokia. Chilli is grown in almost all the parts of NEH region and most of them are local cultivars or landraces. Landraces are variable plant populations adapted to local agro climatic conditions, which are locally named, selected and maintained by the traditional farmers to meet their social, economic, cultural and ecological needs (Teshome et al.,1997). The chilli landraces of north eastern region are heterogeneous and serve as a reservoir of genetic variability for chilli breeder. The chilli landraces have been selected by farmers for agronomic and horticultural traits important to them (e.g., fruit size, heat level, colour and early maturity) and as a result of natural selection, are well adapted to the specific environment to this region. Genetic divergence existing in the population helps in the selection of suitable parents for utilization in any crop breeding programme leading to reduction in the number of crosses (Guerra et al., 1999). Selection of parents depends on specific objective of the research programme and their performance. Various statistical analyses are available to select suitable parents. The information on the nature and degree of genetic divergence is essential for the breeder to choose the right type of parents for purposeful hybridization in heterosis breeding (Patel et al., 1989; Farhad et al., 2010; Khodadabi et al., 2011). In order to benefit transgressive segregation, the knowledge of genetic distance between parents is necessary (Joshi et al., 2004; Khodadadi et al., 2011). The standardization of variables is also essential towards determining the genetic distance so that all variables are of similar importance in determining the distance. Various methods have been used in studying of genetic diversity through cluster analysis of which Tocher's methods is the most popular approach. The cluster analysis is an appropriate method for determining family relationships (Mellingers, 1972). Euclidean distance can theoretically estimate the genetic distance between parents to maximize the transgressive segregation (Hoque and Rahman, 2006). The higher genetic distance between parents, the higher heterosis in progeny can be observed (Lahbib et al., 2012). In the present study 30 chilli genotypes from different regions of NEH and other parts of India were collected and cultivated with standard package of practices at Vegetable research farm, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh and analyzed for their genetic diversity based on morpho-chemical traits. The main objective of this study is to capture the potential genetic diversity between chilli genotypes grown in India by using cluster analysis and selection of suitable genotypes for future chilli hybridization programme.

Results

The analysis of variance exhibited significant differences among the genotypes for all the traits under study which indicated considerable amount of genetic variability and subjected for further analysis. The computation from covariance matrix gave non-hierarchical clustering based on Mahalanobis D^2 values among 30 chilli genotypes and

Table 1. Description of studied chilli genotypes.

Genotype	Pedigree/Source
CHFC-1	A land race of East Siang district of Arunachal Pradesh
CHFC-2	A land race of East Siang district of Arunachal Pradesh
CHFC-3	A land race of Bishnupur district of Manipur
CHFC-4	A land race of East Siang district of Arunachal Pradesh
CHFC-5	A land race of East Siang district of Arunachal Pradesh
CHFC-6	A land race of East Siang district of Arunachal Pradesh
CHFC-7	A land race of Sang district of Sikkim
CHFC-8	A land race of East Siang district of Arunachal Pradesh
CHFC-9	A land race of East Siang district of Arunachal Pradesh
CHFC-10	A land race of East Siang district of Arunachal Pradesh
CHFC-11	A land race of East Siang district of Arunachal Pradesh
CHFC-12	A land race of Lower Subansiri district of Arunachal Pradesh
CHFC-13	A land race of Khasi hill of Meghalaya
CHFC-14	A land race of East Siang district of Arunachal Pradesh
CHFC-15	A land race of East Siang district of Arunachal Pradesh
CHFC-16	A land race of Bishnupur district of Manipur
CHFC-17	A land race of East Siang district of Arunachal Pradesh
CHFC-18	A land race of East Siang district of Arunachal Pradesh
CHFC-19	A land race of East Khasi hill district of Meghalaya
CHFC-20	A land race of East Khasi hill district of Meghalaya
CHFC-21	A land race of East Siang district of Arunachal Pradesh
CHFC-22	A land race of East Siang district of Arunachal Pradesh
CHFC-23	A selection from local land race of Jaunpur, Uttar Pradesh
CHFC-24	A land race of East Khasi hill of Meghalaya
CHFC-25	A land race of Sang district of Sikkim
CHFC-26	A land race of East Siang district of Arunachal Pradesh
CHFC-27	A land race of East Siang district of Arunachal Pradesh
CHFC-28	A land race of East Siang district of Arunachal Pradesh
CHFC-29	A land race of East Siang district of Arunachal Pradesh
CHFC-30	A land race of Pun district of Maharashtra

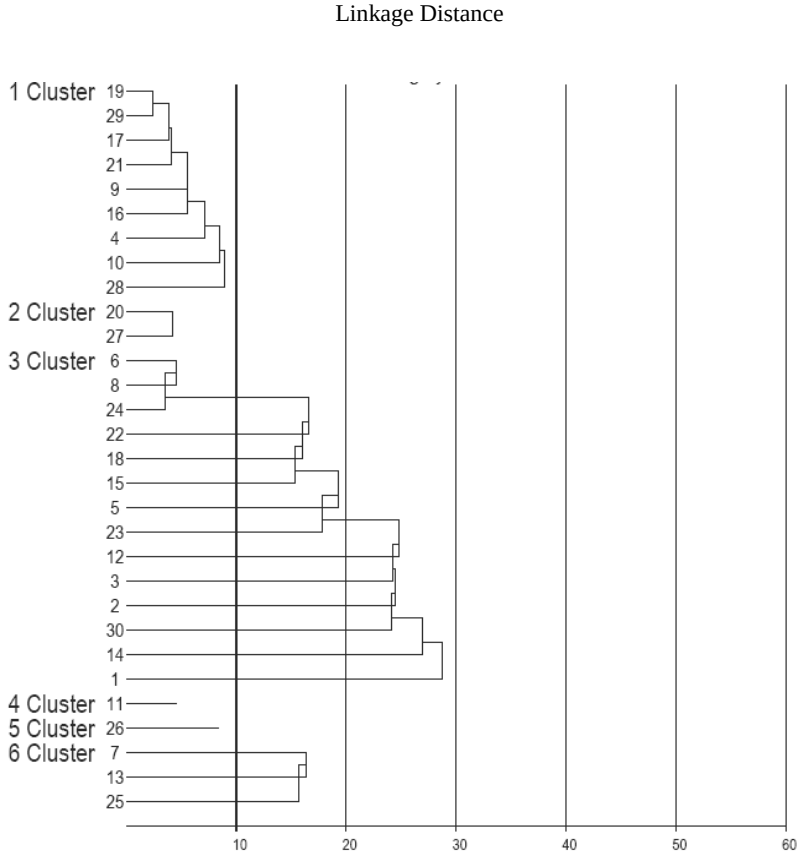

Fig 1. Tree diagram of 30 genotypes of chilli for 12 studied characters using hierarchical cluster analysis (Tocher's method).

grouped them into six clusters (Table 3). It explained that cluster III contained highest number of genotypes (14) followed by cluster I having 9 genotypes, cluster III having 3 genotypes, cluster II having 2 genotypes and cluster IV and V having 1 genotypes each. CHFC-4, CHFC-9, CHFC-10, CHFC-16, CHFC-17, CHFC-19, CHFC-21, CHFC-28 and CHFC-29 genotypes were classified in first cluster including 30.0% of the total genotypes. The average values of genotypes in this cluster for fruit length, number of seed per fruit and ascorbic acid content is higher than the mean of all genotypes (Table 5). CHFC-20 and CHFC-27 genotypes were classified in II cluster including 6.67% of the total genotypes. The average values for number of seed per fruit, number of fruit per plant, ascorbic acid content, chlorophyll content and green fruit yield per plant in this cluster was less than the total mean and for other traits was in the range of total mean (Table 5). The genotypes CHFC-2, CHFC-3, CHFC-5, CHFC-6, CHFC-8, CHFC-12, CHFC-14, CHFC-15, CHFC-28, CHFC-22, CHFC-23, CHFC-24 and CHFC-30 were classified in III cluster accounting for 46.67% of the total genotypes. Values of number of fruit per plant, green fruit yield per plant and plant height in cluster III were greater than the total mean (Table 5) and most of other traits were less than the total mean. Only one genotype CHFC-11 belonged to cluster IV accounting for 3.33% of the total genotypes. In this group mean of ascorbic acid content, days to first flower and fruit length was more than the average and for other traits were approximately less than the total average mean (Table 5). CHFC-26 genotype was classified in cluster V accounting for 3.33% of the total genotypes. There was positive differences for number of fruit per plant, green fruit yield per plant, plant height and number of primary branch per plant with the overall mean and other traits were approximately less than the total average mean (Table 5). The cluster VI consisted of genotypes CHFC-7, CHFC-13 and CHFC-25 accounting for 10.0% of the total genotypes. There was positive difference for green fruit yield per plant, number of fruit per plant and ascorbic acid content with overall mean and other traits were approximately less than or equal to the total average mean (Table 5). According to Mahalanobis's D^2 statistics, the intra and inter cluster distance (D^2) values are presented in Table 4. The inter cluster D^2 values were found range between 36.04 to 459.81. Minimum inter cluster distance between cluster I and IV (36.04) indicated that genotypes were genetically close to each other. Maximum inter cluster distance was observed between cluster II and IV (459.81) and indicated that genotypes are highly divergent. The intra cluster divergence varied from 11.19 to 67.66. Maximum intra cluster distance was achieved in cluster III (67.66) which comprised six genotypes while minimum divergence was observed in cluster II (11.19). Cluster IV and V showed zero intra cluster distance due to containing only one genotype. On the basis of cluster mean value (Table 5) it was observed that the genotypes in cluster I exhibited lowest plant height (57.03) while those in cluster V exhibited highest (71.68). Maximum number of primary branch per plant was observed in cluster V (6.23) and minimum number in cluster VI (3.80). Cluster II reported maximum days to first flowering (60.50) while cluster V exhibited minimum (36.07). Fruit length varied from 2.90 in cluster VI to 5.16 in cluster II. Similarly, maximum fruit diameter was in cluster II (1.97) and minimum in cluster III (0.83). Maximum number of seed per fruit was shown by cluster I (44.69) and minimum by cluster IV (31.48). Maximum number of fruit per plant was recorded in cluster V (427.95) and minimum in clusters II (44.24). Highest fruit weight was observed for cluster II (2.40) and lowest in cluster IV (1.01). Highest capsaicin content was recorded for cluster II (2.06) and lowest for cluster IV (0.42). Highest ascorbic acid content was recorded for cluster IV and V as exhibited by the values 328.26 and 175.23, respectively. Cluster V recorded highest chlorophyll content (0.59) while cluster IV recorded lowest (0.16). Maximum green fruit yield per plant was reported in cluster V (531.38) while cluster II reported minimum (106.04). Thus, CHFC-7 (cluster VI), CHFC-27 (cluster II) and CHFC-15 (cluster III) were identified as promising genotypes with respect to character like number of fruit, fruit yield, capsaicin content and ascorbic acid, respectively.

Discussion

The highest genetic distance was observed between the Cluster II and IV (459.81). According to Kumar et al., (2010), 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 IV (36.04) which can be used for backcrossing programmes. Similar to findings by Sundaram et al. (1980) reported that cluster analysis can prove useful for finding high yielding chilli genotypes. Further, many reports Indira (1994), Roy and Sorma (1996) and Mishra et al. (2004) also indicate the presence of a high genetic divergence among chilli genotypes in their respective experiments. Considering the main component for diversity; the capsaicin content contributed 32.41% towards diversity analysis in the present study. Cluster analysis allowed a natural grouping of the genotypes although grouping of different clusters indicates that no firm conclusion regarding relation between genetic divergence and geographical distance in chilli. Accordingly, the use of different measurement techniques can be appropriately used for genotypes grouping (Bauer et al., 2007; Karic et al., 2009). Evaluation of genetic diversity can be useful for the selection of efficient genotypes and if such efforts result in reduction of diversity; production of crop plants with higher uniformity may assure supply of nutrients to under nourished population of the world. Consequently, it is suggested that choosing parents for hybridization or in other crop improvement programmes need not necessarily be based on geographical distance. Some of the desirable genotypes identified by present study include CHFC-10, CHFC-28,CHFC-29 in cluster I, CHFC-20, CHFC-27 in cluster II, CHFC-1, CHFC-6, CHFC-8, CHFC-24 in cluster III, CHFC-11 in cluster IV, CHFC-20 in cluster V and CHFC-7, CHFC-13 and CHFC-25 in cluster VI. D^2 statistic has been found as a tool to estimate genetic divergence and being a numerical estimate, it has added advantage over other criteria permitting precise comparison among all possible pairs of population in any group. Crop improvement is made through generating variability in desired traits followed by selection. Continued success in crop improvement can only be realized when new substantial variability is found and used in a population. Divergence between any two parents expresses the allelic differences between them (Dias et al., 2003). The genotypes grouped into the same cluster presumably diverge very little from one another. Crossing of genotype belonging to the same cluster is not expected to yield desirable segregants. Consequently, a crossing progr-

Table 2. Analysis of variance, mean, coefficient of variation and least significant differences for studied traits in chilli genotypes.

Mean of Square													
S O V	DF	Plant height (cm)	Number of Primary Branch per plant	Days to first flowering	Fruit length (cm)	Fruit diameter (cm)	Number of Seed per fruit	Number of fruit per plant	Average fruit weight (g)	Capsaicin content (%)	Ascorbic acid (mg/100g)	Chlorophyll content (mg/g)	Green fruit yield per plant (g)
Replication	2	5.769^{ns}	0.007^{ns}	0.806^{ns}	0.099^{ns}	0.017^{ns}	3.729^{ns}	73.885^{ns}	0.001^{ns}	0.003^{ns}	54.652^{ns}	0.001^{ns}	118.925^{ns}
Genotype	29	307.401**	3.441**	252.467**	4.659**	0.483**	322.477**	29302.862**	0.514**	0.819**	11421.668**	0.053**	38282.418**
Error	58	38.026	0.458	24.357	0.449	0.042	38.524	1088.474	0.009	0.004	268.596	0.001	2496.103
Mean		60.12	4.55	44.32	4.26	1.01	40.54	164.49	1.22	0.73	278.93	0.49	189.67
CV %		10.26	14.86	11.13	15.73	20.25	15.31	20.06	7.77	9.03	5.88	8.34	26.34
CD (5%)		10.08	1.11	8.07	1.09	0.33	10.14	53.92	0.15	0.11	26.79	0.07	81.66

*, **and ns significant at P<0.05, P<0.01 and non-significant, respectively

Table 3. Percent contribution of twelve characters towards diversity in chilli.

Character	Times Ranked 1st	Contribution (%)
Plant height	4	0.92
Number of primary branch per plant	4	0.92
Days to first flowering	0	0.00
Fruit length	6	1.38
Fruit diameter	0	0.00
Number of seed per fruit	2	0.46
Number of fruit per plant	29	6.67
Average fruit weight	72	16.55
Capsaicin content	141	32.41
Ascorbic acid	92	21.15
Chlorophyll content	72	16.55
Green fruit yield per plant	13	2.99

Table 4. Clustering pattern of 30 chilli genotypes by Tocher's method

Cluster	Number of genotypes	Genotypes
Cluster I	9	CHFC-19, CHFC-29, CHFC-17, CHFC-21, CHFC-9, CHFC-16, CHFC-4, CHFC-10, CHFC-28
Cluster II	2	CHFC-20, CHFC-27
Cluster III	14	CHFC-6, CHFC-8, CHFC-24, CHFC-22, CHF-18, CHFC-15, CHFC-5, CHFC-23, CHFC-12, CHFC-3, CHFC-2, CHFC-30, CHFC-14, CHFC-1
Cluster IV	1	CHFC-11
Cluster V	1	CHFC-26
Cluster VI	3	CHFC-7, CHFC-13, CHFC-25

Table 5. Average inter and intra cluster distances (D^2) for 30 chilli genotypes

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**21.47**	329.13	53.72	**(36.04)**	130.95	161.85
Cluster II		**11.19**	390.93	**(459.81)**	433.77	150.17
Cluster III			**67.66**	90.70	93.32	160.39
Cluster IV				**0.00**	192.62	212.76
Cluster V					**0.00**	182.82
Cluster VI						**56.26**

(The value in the parthensis indicates D^2 value**)**

Table 6. The average of traits for each cluster (above number) and the difference between each cluster with the total mean (below number).

Cluster I	57.03	4.45	39.18	4.60	0.89	44.70	130.93	1.13	0.49	317.38	0.43	150.35
	-3.09	-0.10	-5.15	0.34	-0.12	4.16	-33.56	-0.09	-0.24	38.44	-0.06	-39.31
Cluster II	67.16	5.42	60.50	5.16	1.97	37.36	44.24	2.40	2.06	242.01	0.43	106.04
	7.05	0.86	16.18	0.90	0.95	-3.18	-120.26	1.18	1.33	-36.92	-0.06	-83.63
Cluster III	60.78	4.57	43.04	4.11	0.83	40.65	180.88	1.07	0.53	261.23	0.55	191.50
	0.67	0.02	-1.29	-0.16	-0.18	0.11	16.39	-0.15	-0.20	-17.71	0.06	1.83
Cluster IV	57.77	4.10	47.07	4.75	0.85	31.48	131.72	1.01	0.42	328.26	0.16	134.81
	-2.35	-0.45	2.74	0.49	-0.16	-9.06	-32.77	-0.21	-0.31	49.33	-0.34	-54.86
Cluster V	71.68	6.23	36.07	5.12	0.88	39.04	472.95	1.12	0.62	175.23	0.59	531.38
	11.57	1.68	-8.26	0.86	-0.13	-1.50	308.45	-0.10	-0.11	-103.70	0.10	341.71
Cluster VI	58.51	3.80	56.82	2.90	1.65	33.16	176.99	1.53	1.62	288.97	0.55	259.21
	-1.60	-0.75	12.50	-1.36	0.64	-7.37	12.49	0.31	0.90	10.03	0.05	69.54

amme should be conducted with putative parents belonging to different characters. Therefore, crosses between the members of clusters separated by inter-cluster distances are likely to be beneficial for further improvement.

Material and Methods

Plant materials

Thirty chilli (*Capsicum annuum* L.) genotypes (Table 1) were collected from different part of the India and cultivated in the research farm of department of Vegetable Science, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh, India during March-October, 2011.

Field experiment

The four weeks old seedlings were transplanted using 60.0 cm x 20.0 cm plant to plant and row to row on the basis of a randomized complete block design with three replications. Fertilizers (nitrogen, phosphorus and potash at rate of 90.0, 60.0 and 60.0 kg/ ha, respectively) were applied. The observations were recorded on five randomly selected plants of each genotype on plant height (cm), number of primary branch per plant, days to first flowering, fruit length (cm), fruit diameter (cm), number of fruit per plant, average fruit weight (g), green fruit yield per plant (g), number of seed per fruit, ascorbic acid (mg/100g), capsaicin content (%) and chlorophyll content (mg/g) were measured.

Statistical analysis

Five plants per plot were selected and the mean data points were used for statistical analysis. Analysis of variance, cluster analysis based on Tocher's method using squared Euclidean distance (Kumar et al., 2009) was performed using the statistical software Indostat and statistical package for agricultural research (SPAR) version 2.0 programme. The genetic divergence was calculated according to Mahalanobis D^2 statistics (1936).

Conclusion

The thirty genotypes of chilli (*Capsicum annuum* L.) under study were grouped into six clusters irrespective of their origin. Distant parents are able to exert high heterosis. Considering this theme and variability, diversity analysis of the genotypes CHFC-7 for number and fruit yield per plant, CHFC-27 for capsaicin content and CHFC-15 for ascorbic acid content were identified as promising genotypes. From this study, it may be concluded that a wide range of variation for almost all the economically important traits are present in this crop. This implies a great potential for breeding through hybridization programme or direct use as variety for successful chilli production in NEH region of India. Further, one or two promising genotypes from different clusters may be chosen for further genetic studies either by way of diallel or line x tester analysis.

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