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ESTIMATION OF GENETIC DIVERGENCE AMONG CHENCH (*CORCHORUS ACUTANGULUS* LAM.) GENOTYPES

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ABSTRACT

An investigation was carried out with 25 chench (*Corchorus acutangulus* Lam.) genotypes to identify diverse genotypes. On the basis of D^2 values the genotypes were grouped into five clusters. Cluster V was the largest containing 11 genotypes followed by cluster I with 7 genotypes. The maximum inter-cluster distance was recorded between clusters II and III (8.375) and the maximum intra cluster distance was shown by cluster I (3.666) followed by cluster V (3.251), cluster II (3.063), cluster III (2.911) and cluster IV (0.003). The characters like test weight contributes highest (58.99%), fibre content (16.90 %), duration of the crop (15.10 %), plant height (6.83 %) and leaf stem ratio (1.43 %) contributed maximum towards genetic diversity. Hence these characters could be given due importance for selection of genotypes for further crop improvement programme.

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INTRODUCTION

Chench (*Corchorus acutangulus* Lam.) is one of the unexploited and underutilized leafy vegetable and also know as vegetable jute in India. In Chhattisgarh, it is popularly known as *Chench Bhaji and* belongs to the family Tiliaceae. It is valued for its good nutritive value and fast growth with high yield potential. It is a regular leafy vegetable of the poor farmers of the Chhattisgarh and is commonly consumed along with *roti* and rice. Hence, it has the potential to become an important leafy vegetable of this region. The plant is said to possess anticancer, antipyretic, anticonvulsant, stomachic and digitalis glycoside like action whereas, leaves and arial parts of *Corchorus acutangulus* Lam. possess antibacterial potential (Patel, 2011). Moreover, *Corchorus* is known to contain high levels ofiron and folate which are useful for the prevention of anaemia (Steyn et al., 2001). Traditionally, genetic diversity studies are based on differences in morphological characters and qualitative traits. It has been used as a powerful tool in the classification of cultivars and also to study taxonomic status. Morphological traits continue to be the first step in the studies of genetic relationships in most of the breeding programmes (Van Bueningen *et al.*, 1997). The D^2 analysis proposed by Mahalanobis (1936) has been reported to be an effective tool to assess the genetic divergence among the types. The D^2 analysis has been established by several investigators like Shobha and Dharmatti (2004) in vegetable mesta, Rana *et al.*(2005) in grain amaranthus, Anuja and Mohideen (2007) in vegetable amaranthus for measuring the degree of divergence and for ascertaining the relative contribution of different characters to the total divergence. In the present investigation, therefore, the genotypes were subjected to D^2 analysis to findout nature and extent of genetic diversity present in 25 genotypes of chench for genetic improvement.

MATERIALS AND METHODS

The experimental material for the study comprised of 25 genotypes collected from three agroclimatic zones of Chhattisgarh and laid in randomized complete block design (RBCD) with three replications at the Horticultural Instructional and Research Farm, Department of Horticulture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) lies between 21°16′ N latitude and 81°36′ E longitude with an altitude of 289.56 meters above the mean sea level. The experiment was conducted during *Rabi* season 2014-15. The soil properties like organic carbon (%) 0.60, Available N (kg ha-1) 275.00, Available P (kg ha-1) 16.75 and Available K (kg ha-1) 303.00 Soil Reaction pH 7.09 and Electrical conductivity (n mh cm-1) 0.19 was observed in the site of experiment. The seeds were sown in 20 cm apart between rows and 15 cm within the row. Standard agronomic practices and plant protection measures were taken as per schedule. Test weight was recorded before sowing of crop. Observations were recorded on five randomly selected plants per replication for plant height, number of leaves per plant, leaf length, leaf width, petiole length, stem girth, number of branch per plant, root weight, root length, fresh weight of plant, dry weight of plant, internodal length, dry matter percentage of plant, leaf yield kg per plot, harvest index, leaf stem ratio, fibre content, were recorded at 60 days after sowing while days to 50% flowering, duration of crop were recorded periodically. The analysis of variance was carried out for all the characters and then data was analyzed following multivariate analysis of Mahalanobis (1936) and genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The genetic divergence existing in twenty five chench genotypes was studied by employing D^2 analysis for twenty quantitativecharacters. On the basis of D^2 analysis, twenty five genotypes were grouped into five clusters (Table 1). Maximum number of genotypes were grouped into cluster V (IGCB-6, IGCB-7, IGCB-8, IGCB-9, IGCB-10, IGCB-12, IGCB-13, IGCB-15, IGCB-18, IGCB-20, IGCB-21) included eleven genotypes whereas, cluster I (IGCB-4, IGCB-5, IGCB-11, IGCB-17, IGCB-19, IGCB-22) included seven genotypes and cluster II (IGCB-2, IGCB-3, IGCB-14, IGCB-16) included four genotypes, cluster III (IGCB-1, IGCB-25) included two genotypes and cluster I (IGCB-23) included only one genotype in cluster.The intra-cluster distance varied from 0.003 to 3.666 (Table 2). The maximum intra cluster distance was shown by cluster I (3.666) followed by cluster V (3.251), cluster II (3.063), cluster III (2.911) and cluster IV (0.003), which indicates distance within the cluster. These results are in general agreement with the findings of Anuja and Mohideen (2007) in vegetable amaranthus. An examination of average intra and inter cluster distance indicated that genotypes within cluster had little divergence from eachother with respect to aggregate of effects of 20 characters understudy. Therefore, thechance of obtaining recombinants in segregating generations by crossing the members of same cluster are very low. It is therefore, suggested that crosses should be attempted between the genotypes belonging to cluster separated by large inter cluster distances. To realize much variability and high heterotic effect, recommended that parents should be selected from two clusters having wider inter cluster distance (Thomas and Lal, 2012). Raman and Singh (1987) suggested that genotypes belonging to clusters separated by high genetic distance maybe used in hybridization program to obtain a wide spectrum of variation among the segregates and in the present study similar suggestion had been made.

Table 1: Composition of cluster

Cluster number	Number of genotypes included	Name of genotypes
I	7	IGCB-4,IGCB-5,IGCB-11,IGCB-17,IGCB-19,IGCB-22,IGCB-24
II	4	IGCB-2,IGCB-3,IGCB-14,IGCB-16
III	2	IGCB-1, IGCB-25
IVIV	1	IGCB-23
V	11	IGCB-6, IGCB-7, IGCB-8, IGCB-9, IGCB-10, IGCB-12, IGCB-13, IGCB-15, IGCB-18, IGCB-20, IGCB-21

Table 2: Intra (bold) and inter cluster distance values in chench

Cluster number	I	II	III	IV	V
I	**3.666**				
II	4.964	**3.063**			
III	5.772	6.161	**2.911**		
IV	7.607	6.951	8.375	0.003	
V	3.172	4.379	6.023	8.340	**3.251**

Table 3: Mean performance of genotypes in individual cluster for yield and its components

Character		Plant height (cm)	No. of leaves per plant	leaf length (cm)	leaf width (cm)	Petiole length (cm)	Stem girth (mm)	No. of branches per plant	Root Weight (g)	Root length (g)	fresh weight of plant (g)
Cluster											
I	7	31.4	12.86	6.27	2.09	2.04	3.67	7.64	0.51	10.11	7.46
II	4	43.41	16.07	6.85	3.12	2.59	4.44	12.18	0.42	10.26	6.76
III	2	39.75	24.5	7.61	2.52	1.8	3.53	14.87	0.47	14.12	5.99
IV	1	41.14	15.93	5.24	3.05	2.13	4.53	3.4	0.45	10.87	10.84
V	11	35.54	12.61	7.12	2.46	1.93	3.83	9.31	0.45	9.93	4.32

Character		Dry weight of plant (g)	Internodal length (cm)	Dry matter %	Days to 50 % flowering	Yield kg per plot	Harvest index (%)	leaf stem ratio	Fibre content %	Test weight (g)	Duration
Cluster											
I	7	1.01	10.33	18.24	59.19	1.57	0.55	1.42	10.24	2.4	33.43
II	4	1.19	20.91	18.58	60.17	1.98	0.55	1.23	10.59	3.03	33.33
III	2	1.09	12.23	16.57	48.17	2.02	0.31	1.08	8.92	2.16	32.83
IV	1	1.11	26.51	19.35	45.67	3.2	0.61	0.82	3.94	1.97	46
V	11	0.56	13.36	16.41	61.36	1.47	0.52	1.39	11.87	3.05	39.39

Table 4: Contribution of each character to divergence

Character	Plant height (cm)	No. of leaves / plant	leaf length (cm)	leaf width (cm)	Petiole length cm	Stem girth (mm)	No. of branches /plant	Root Weight (g)	Root length (g)	fresh weight of plant (g)
Number of times appearing first time	19	0	0	0	0	0	0	0	0	0
Percent contribution	6.83	0	0	0	0	0	0	0	0	0

Character plant (g)	Dry weight of (g)	Internodal length (cm)	Dry matter %	Days to 50 % flowering	Yield kg per plot	Harvest index (%)	leaf stem ratio	Fibre content %	Test weight (g)	Duration of the crop	Total
Number of times appearing first time	0	0	0	1	0	1	4	47	164	42	278
Percent contribution	0	0	0	0.35	0	0.35	1.43	16.9	58.99	15.1	100

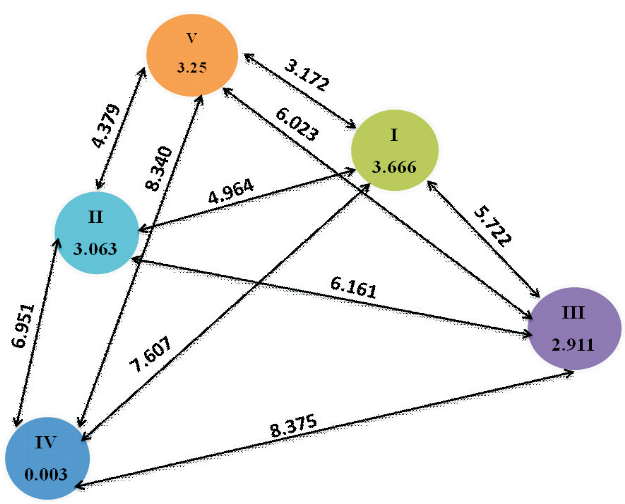

Figure 1: Cluster diagram of chench (*Corchorus acutangulus* Lam.) (Values inside circle is intra cluster distance)

The genotypes included in thediverse clusters namely, II, III, and I hold good promise asparents for obtaining potential hybrids and thereby creating greater variability of these characters to improve the yield.

The cluster mean values showed a wide range of variationsfor all the characters undertaken in the study (Table 3). The cluster mean for various traits showed that different cluster respond differentially for various traits.Cluster II expressed highest mean value for plant height, leaf width, petiole length and dry weight of plant. Cluster III showed highest mean performance for number of leaves per plant, leaf length, number of branches per plant and root length. Cluster IV showed highest mean value for stem girth, fresh weight of plant, internodal length, dry matter %, yield kg per plot and duration of the crop. Cluster V showed highest mean value for days to 50 % flowering, fibre content and test weight. Whereas, Cluster I showed highest mean value for root weight and leaf stem ratio.

In the contribution of each character to divergence presented in Table 4which showed test weight contributes highest (58.99%) to divergence followed by fibre content (16.90 %), duration of the crop (15.10 %), plant height (6.83 %), leaf stem ratio (1.43 %) whereas days to 50 % flowering (0.35 %) and harvest index (0.35 %) contribute lowest to divergence.

The results of the present study were close agreement with fiidings Ahammed *et al.* (2013) in amaranthus, Sandhya *et al.* (2015) in rice and Kumari and Singh (2015) in finger millet.

The inter-cluster distances in present investigation were higher than the intra cluster distance reflecting the wider diversity among the breeding lines of the distant group. Hence, it is suggested that intercrossing of genotypes from diverse clusters showing high mean performance will be helpful in obtaining better recombinants with higher genetic variability.

This implied that there was no parallelism between genetic divergence and geographical divergence. This has been observed that diverse the parents within its overall limits of fitness, the greater are the chances of heterotic expression in F_1's and a broad spectrum of variability in segregating generations. In this study, group constellation showed that cluster V (IGCB-6, IGCB-7, IGCB-8, IGCB-9, IGCB-10, IGCB-13, IGCB-15, IGCB-18, IGCB-19, IGCB-20, IGCB-21) were highly divergent from all other genotypes and may be used as parents in transgenic breeding programme and may directly be used as a pure line variety for leaf yield and it's component characters in chench (*Corchorus acutangulus* Lam.) for Chhattisgarh conditions.

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