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Genetic Divergence in Stem Amaranth (*Amaranthus tricolor* L.) Genotypes for Yield and its Component Characters

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Abstract

An investigation was carried out to identify the extent of genetic divergence that exist for the yield and yield contributing characters of seventeen genotypes of amaranth using Mahalanobis D^2 analysis. Analysis of variance showed significant difference among the genotypes for most of the characters studied. The genotypes under study fell into 4 clusters. The distribution pattern indicated that the maximum number of genotypes (6) was included in cluster (IV) followed by cluster III (5) and cluster II (5), and the minimum number was in cluster I (1). The inter cluster distance in most of the cases was higher than the intra cluster distance, which indicated wider genetic diversity among the accessions of different groups. The highest inter cluster distance was observed between IV and I, followed by the distance between cluster II and I showing wide diversity among the groups. The lowest inter-cluster distance was observed between clusters III and II suggesting a close relationship among the genotypes of these two clusters. The highest intra-cluster distance was observed for the cluster IV and the lowest for the cluster I. The positive values of vector I and vector 2 for stem weight and weight of leaf indicated that these two characters had the highest contribution towards the divergence among the stem amaranths. The genotypes of stem amaranth from cluster I and cluster IV may be selected as parents in future hybridization program.

***Keywords*: Stem amaranth, cluster, genetic divergence, D^2 statistics**

1. Introduction

The main type of amaranth, *Amaranthus tricolor* is a cross pollinated vegetable crop which is considered to be the native of India (Nath, 1976). Among the leafy types, *Amaranthus tricolor* L. occupies a predominant position in this subcontinent with different morphological forms in color and shape of leaves. Amaranth is highly nutritive vegetable containing high percentage of digestible protein along with carbohydrate and vitamins. It is also rich in minerals (Oke, 1980). The Bangladesh type has big fleshy stems, which are consumed with the leaves. The last documented area under this crop in Bangladesh is 4000 hectares with production of 18000 tons having yield of 4.5 t/ha only (Anonymous, 2007), which is very low. The low yield is attributed to the use of low yielding varieties & inefficient method of culture.

Through collection and selection program, a number of strains have been introduced and acclimatized in various parts of the world, but evaluation studies of yield and its contributing quantitative and qualitative traits are scarce

(Shukla, 2006). The multivariate analysis has been established by several investigators for measuring the degree of divergence and for ascertaining the relative contribution of different characters to the total divergence (Singh *et. al*., 2002). Such a study also permits to select the genetically divergent parents to obtain the desirable recombinants in the segregating generations. Moreover, precise information about the extent of genetic divergence and characters used for discrimination among the population is crucial in any crop improvement program (Ashana and Pandey, 1980; Pandey, 2009). Therefore, the present investigation was designed to provide information on genetic divergence of 17 stem amaranth genotypes.

2. Materials and Methods

Seventeen genotypes of stem amaranth collected from different sources (Table 1) were studied to measure the diversity among the genotypes at the Field Laboratory, Dept. of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur in 2008. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Data were recorded from randomly selected 10 plants from the plot of each replication on first flowering, plant height, leaf number, leaf length, weight of leaf, stem weight, stem diameter, dry weight with rind, dry weight without rind and marketable yield. The data were analyzed following Mahalanobis's D^2-statistics and principal component analysis (PCA) for assessment of genetic divergence among the genotypes of stem amaranth using GENSTAT 4.2b (Mahalanobis, 1936; Jager *et al.*, 1983 and Digby *et al*., 1989).

3. Results and Discussion

Analysis of variance revealed highly significant differences for all the characters among the 17 stem amaranth genotypes under study. The D^2-values varied widely and principal component scores also revealed a good degree of genetic diversity among the genotypes.

3.1. Non- hierarchical clustering

Non-Hierarchical clustering using covariance matrix grouped stem amaranth into four different clusters. The pattern of the distribution of genotype into various cluster is given in Table 2.

Table 1. List of genotypes and sources of stem amaranth

Sl. No.	Variety name	Source
G1	Rangpur1	Rangpur
G2	Green tower	East-West Seed Company
G3	Sureshawry1	Faridpur
G4	Vhutan	Jhenaidah
G5	Red tower	East-West Seed Company
G6	Baspata	Jessore
G7	Panna	East-West Seed Company
G8	Sarupa	Jessore
G9	Rangpur2	Rangpur
G10	Suresh danta	Faridpur
G11	Pryashi	Gazipur
G12	Aman (Red)	Jessore
G13	Vhutan (Jamboo)	Jessore
G14	Rupali	Gazipur
G15	Sureshawry2	Jessore
G16	BARI-1	BARI, Gazipur
G17	BARI-2	BARI, Gazipur

The distribution pattern indicated that the maximum number of genotypes (6) were included in cluster (IV) followed by cluster III (5), cluster II (5) and cluster I (1). Genetic diversity is generally associated with geographical diversity, but the former is not necessarily directly related with geographical distribution. The genotypes within the same clusters although formed specific clusters, but were collected from different places, which indicated the geographical distribution and genetic divergence and did not follow the same trend.

3.2. Canonical variate analysis

Canonical variate analysis was performed to obtain the inter-cluster distance (Mahalanobis's D^2- values). These values of inter-cluster distance (D^2) are presented in Table 3. Statistical distance presented the index of genetic diversity among the cluster. The inter-cluster distances suggested wider genetic diversity present among the genotypes of different groups. Pandey (2009) obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis in amaranth. The inter-cluster distance was maximum between IV and I (50.75) followed by the distance between cluster II and I (36.24) and so on (Table 3). The lowest inter-cluster distance 9.85 was found in between cluster III and II. The maximum values of inter-cluster distance indicated that the genotypes belonging to cluster I are far diverged from cluster IV. These relationships are also reflected in the scattered diagram (Fig. 1).

3.3. Construction of scatter diagram

Based on the values of principal components score 1 and 2 obtained from the principle component analysis, a two-dimensional scattered diagram (Z1-Z2) using component score 1 as X-axis and component score 2 as Y- axis was constructed, which has been represented in Figure 1. The position of the genotypes in the scatter diagram was apparently distributed into four groups, which indicated that there exists considerable diversity among the genotypes. The scattered diagram for the stem amaranth genotypes of different cluster revealed that the genotype number 4, 5, 11 and 15 were distantly located.

Table 2. Distribution pattern of 17 genotypes of stem amaranth in 4 different clusters

Cluster	Number of genotypes	Genotypes
1	1	4
II	5	1, 3, 5, 7, 12
III	5	2, 8, 9, 13, 15
IV	6	6, 10, 11, 14, 16, 17

Table 3. Average inter and intra cluster distance (D^2) of four clusters for stem amaranth genotypes

Cluster	I	II	III	IV
I	**0.00**			
II	36.24	**1.286**		
III	35.07	9.85	**0.860**	
IV	50.75	14.57	18.75	**1.537**

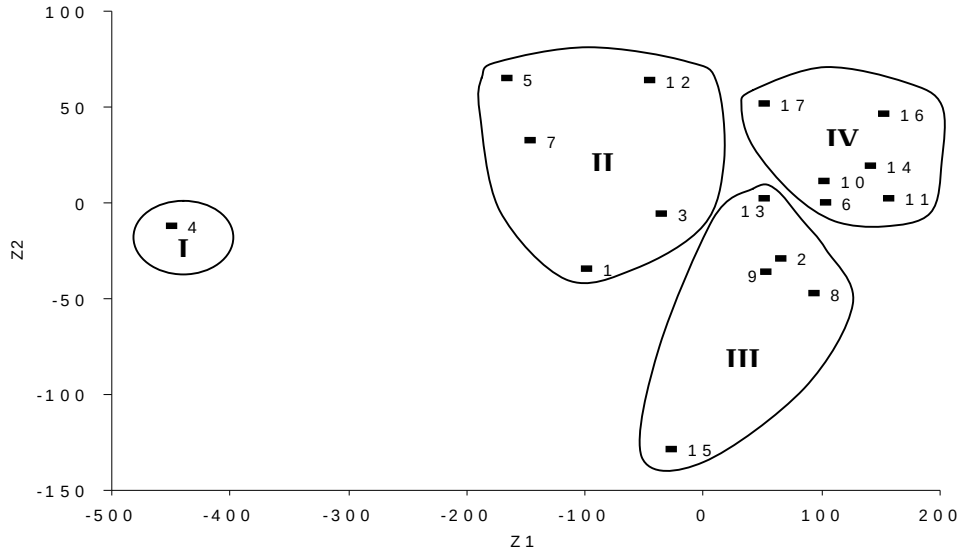

Fig. 1. Scattered distribution of 17 genotypes of stem amaranth based on their principal components analysis scores superimposed with clustering

3.4. Cluster mean values

Cluster mean for 13 characters are presented in Table 4. It was observed that marketable weight (g) had the highest inter-cluster mean (495.20) in cluster I followed by cluster II and III. The lowest inter cluster mean for this trait was observed in cluster IV. Dry weight with rind (g) had the highest group mean (33.15) in cluster I followed by II, III and IV. The lowest inter-cluster mean for this trait was in cluster IV. Dry weight without rind (g) had the highest group mean in cluster I (23.15) followed by II and III. The lowest cluster mean for this trait was in cluster IV (4.29). Stem weight (g) had the highest inter cluster mean in cluster I (450.37) followed by cluster II (233.38) and cluster III (124.23). The lowest cluster mean for this trait was in cluster IV (90.41). Stem diameter (mm) had the highest cluster mean in cluster I (31.40) followed by the cluster III (21.71), cluster II (20.25) and cluster IV (14.77). Plant height had the highest inter cluster mean (120.68) in cluster II followed by the cluster III (100.85) and cluster IV (100.51). The lowest cluster mean for this trait was in cluster I (99.50). Leaf number per plant had the highest inter cluster mean in cluster I (190.33) followed by cluster III (192.05) and cluster II (108.27). The lowest cluster mean for this trait was in cluster IV (64.45). Leaf length (cm) had the highest inter cluster mean in cluster I (26.80) followed by cluster III (21.02) and cluster II (19.79). The lowest cluster mean for this trait was in cluster IV (19.79). Leaf weight (g) had the highest inter cluster mean in cluster I (168.35) followed by cluster III (56.78) and cluster II (52.7). The lowest cluster mean for this trait was in cluster IV (23.05).

3.5. Contribution of characters towards diversity

The characters contributing maximum to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and the choice of parents for hybridization (Jagadev *et. al.*, 1991; Siddique, 2010).

Table 4. Cluster mean of 4 clusters for thirteen characters of stem amaranth

Parameters	Cluster			
	I	II	III	IV
Plant height (cm)	99.50	120.68	100.85	100.51
Leaf number	190.33	108.27	142.00	64.45
Leaf length (cm)	26.80	19.79	21.02	18.22
Leaf weight (g)	168.35	52.70	56.78	23.05
Leaf breath (cm)	8.62	7.22	9.28	7.19
Blade length (cm)	18.30	12.67	13.86	11.67
Petiole length (cm)	8.50	6.88	6.94	6.55
Stem weight (g)	450.37	233.38	124.23	90.41
Stem diameter (mm)	31.40	20.25	21.71	14.77
dry weight with rind (g)	33.15	20.76	17.03	10.23
Dry weight without rind (gm)	23.15	10.15	6.53	4.29
1000 seed wt. (g)	1.13	1.13	1.02	1.04
Marketable yield weight (g)	495.20	252.74	138.62	99.95

Table 5. Latent vectors (Eigen values) of 13 characters in 1st and 2nd principal components

Characters	Vector-I	Vector-II
Plant height (cm)	-0.095	0.112
Leaf number	0.142	-0.122
Leaf length (cm)	9.836	-6.128
Leaf weight (g)	0.203	0.127
Leaf breath (cm)	-1.048	0.375
Blade length (cm)	-10.825	6.372
Petiole length (cm)	-8.182	4.650
Stem weight (g)	0.657	0.091
Stem diameter (mm)	0.208	-0.359
dry weight with rind (g)	-0.181	0.218
Dry weight without rind (g)	1.869	-0.977
1000 seed weight (g)	-5.350	3.699
Marketable yield wt (g)	-0.664	-0.030

Contribution of characters towards divergence is presented in Table 5. The PCA revealed that both the vectors had positive values for stem and leaf weight. These results indicate that these two characters had the highest contribution towards the divergence among the stem amaranths. In vector I, the other important characters responsible for the genetic divergence in the major axis of differentiation were dry weight without rind; stem weight, stem diameter, leaf number, leaf length and leaf weight having positive vector values. While in vector II it was dry weight with rind, stem weight, plant height, leaf weight, leaf breadth, blade length, petiole length, and 1000 seed weight having positive vector values. Negative values in both vectors for marketable stem weight indicated that the character had lowest contribution to the divergence.

From the above results it appeared that contribution of stem weight and leaf weight was found prominent to the total divergence in stem amaranth. Pan *et al.* (2002) reported that about 87% of the genetic diversity present in the 45 genotypes occurred in the days to flowering, duration of harvest and total yield accounted for most of the variation present.

4. Conclusions

Genetic diversity was studied to detect the more diverse amaranth genotypes which might be used in hybridization program. Seventeen genotypes were grouped into four different clusters and the maximum number of genotypes (6) were included in cluster (IV). The highest inter cluster distance was observed between IV and I, while the highest intra-cluster distance was observed for the cluster IV. Stem and leaf weight had the highest contribution towards the divergence. The genotypes of stem amaranth from cluster I and cluster IV may therefore, be selected as parents in future hybridization program.

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