

Studies on multivariate analysis in amaranthus

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ABSTRACT

Nature of genetic divergence in 74 genotypes of amaranthus which were collected from different localities and some high yielding popular cultivars was assessed using D^2 statistic based on six traits. The genotypes were grouped into 12 clusters of while cluster I was largest with 52 genotypes Based on the intra cluster values cluster XI and XII were identified as genetically more divergent. Based on mean performance of genotypes genetic distance and clustering pattern it was concluded that hybridization involving genotype from cluster XI XII may produce highly heterotic hybrids.

Key words: Genetic divergence, Geographical distribution, Clusters, Amaranthus, Growth and Yield characters.

INTRODUCTION

Any successful hybridization programme for varietal improvement depends mainly on the selection of the parents having wide genetic diversity. Thus, the genetic diversity in breeding for high yielding varieties has obvious importance as evidenced by earlier workers like Murthy and Arunachalam (1989) and Bhaumik *et al* (1993). The knowledge of genetic diversity is important for successful selection of parents for hybridization work. With this background, investigations for genetic diversity have been under taken on 74 amaranth's genotypes, which constituted some elite local collections and open pollinated varieties. Amaranthus being highly cross-pollinated crop, identification and selection of genotypes with under genetic diversity will be used as inbred and parental line for heterosis breeding programme to develop hybrids with high leaf yield nutritive values.

MATERIALS AND METHODS

The investigation was carried out at the experimental farm of college orchard, Department of Horticulture, Pandit Jawaharlal Nehru College and Research Institute, Karaikal during June – 2003 to January – 2004. Seventy-four genotypes of amaranthus were utilized for the study in randomized block design with two replications. A uniform population in each accession was ensured taking into account that five plants in each replication was pulled out randomly at 45 days after sowing for recording observation on quantitative characters. The data were subjected to multivariate analysis using Mahalanobis D^2 statistic. The original mean values were transformed to normalized variables and all possible D^2 values were calculated. For determining group constellations or clusters, relatively simple criteria Tocher's method was followed as described by Rao (1952). After establishing the cluster, intra – and inter cluster distances were worked out. The genetic distance between the clusters were arrived by taking the square root of the average D^2 values.

RESULTS AND DISCUSSION

Over all mean of six characteristics studied for divergence analysis of seventy-four genotypes is presented in the table1. The results of D^2 analysis are furnished in table 2. The inter and intra cluster D^2 values are presented in table3. The seventy-four genotypes are grouped into 12 clusters as follows.

Cluster XI and XII were monogenotypic containing only one genotype in each while the other cluster had more than one genotype. The clustering pattern of the genotypes revealed that cluster I was found to include genotypes from different states of India. Cluster I had the genotypes from germplasm lines and released cultivars viz., CO1 and CO3. Similarly in the cluster II to X two germplasm and varieties were grouped together. Thus the clustering pattern reveals that the genotypes did not resolve according to their geographical distribution.

Sl No.	Clusters	Genotypes
1.	Cluster I	A1 to A 39, A 41 to A 52 (C01), A 54 (C03), A 60,A 64 and A69
2.	Cluster II	A 40 & A 53 (C02)
3.	Cluster III	A 68 (Arun), A 72
4.	Cluster IV	A 61, A 62
5.	Cluster V	A 65, A 74 (Kannara local)
6.	Cluster VI	A 59, A 70 (Arka suguna)
7.	Cluster VII	A 60, A71 (Arka arunima)
8.	Cluster VIII	A 54, A 57
9.	Cluster IX	A 63, A 67
10.	Cluster X	A 58, A 73
11.	Cluster XI	A 55 (C04)
12.	Cluster XII	A 56 (C05)

Such a clustering pattern failed to indicate any relationship between genetic diversity and geographical distribution (Rani, 1995).It is therefore indicated that genetic diversity is not related to geographical origin and this may be due to free exchange of seed materials among different regions for breeding purpose. Hence, the character constellations that might be associated with a particular region in nature lose their individuality under human interference. Hence, geographical diversity is not adequate as an index of genetic diversity of amaranthus. Mishra *et al.* (1996) and Reena Susan *et al.* (1997) reported that the unidirectional selection for a particular trait practiced in several places produce a similar phenotypic and result in aggregation of genotypes irrespective of their geographical origin.

In the present investigation of seventy four genotypes were grouped into twelve cluster and fifty four out of seventy four representing 80 per cent of total genotypes studied were gathered in the cluster I. This suggests that the expression of diversity among different genotypes is restricted in amaranthus.

Cluster II to X, which had two genotypes, recorded the least intra cluster distance and this shows the closeness of the genotypes included in the clusters. The limited gene exchange between genotypes of the cluster may be the reason for highest intra cluster distance. Further selection for diverse characters could be reason for such intra cluster divergence.

Due to high divergent nature, cluster II to X had two genotypes each. The pattern of group constellations proved that geographical diversity need not necessarily be related to the genetic diversity. This was in line with the results of Mishra *et al.* (1996), Reena Susan *et al.* (1997). This indicated that geographical diversity though important might not be the only factor in determining genetic divergence.

Acclimatization of genotypes of differing geographical background under single environment through their domestication