

Genetic diversity for green yield characteristics in vegetable amaranthus (*Amaranthus* spp.)

S. ANUJA AND M. KADER MOHIDEEN

See end of article for authors' affiliations

Correspondence to :
S. Anuja
Department of Horticulture,
Faculty of Agriculture,
Annamalai University,
ANNAMALAINAGAR (T.N.)
INDIA

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ABSTRACT

Presence of wide genetic diversity among the genotypes was revealed by Mahalanobis D² analysis. The 100 genotypes selected for the present investigation formed as many as ten clusters. The types chosen from the same eco-geographical origin were found scattered in different clusters. The clustering of types from different eco-geographic regions in one cluster was also observed. Among the clusters, the clusters IX and cluster X showed high genetic divergence, hence the crossing between the types of these two clusters may result in the development of useful progenies. Among the different characters, number of leaves and leaf area contributed the maximum genetic divergence.

Key words: Genetic diversity, Amaranthus

Amaranth (*Amaranthus* sp.) occupies a prominent position among tropical leafy vegetables all over the world. Though majority of Indian population are vegetarian, the per capita intake of vegetables is estimated to be only about 135 g as against the requirement of about 285 g, among which leafy vegetables constitute 80 g for a balanced diet (Pandey, 1993). The D² analysis proposed by Mahalanobis (1936) has been reported to be an effective tool to assess the genetic divergence among the types. Such an attempt eventually help to choose desirable parents for recombination breeding and thus results in the development of superior varieties. The present investigation has been undertaken to assess the genetic divergence among the genotypes and also the contribution of each character to the total diversity among the 100 genotypes of amaranthus.

MATERIALS AND METHODS

The hundred genotypes of amaranthus belonging to *A. tricolor*, *A. blitum*, *A. tricolor* var. *tristis*, *A. dubius* from diverse sources chosen from the germplasm maintained at the Department of Horticulture, Faculty of Agriculture, Annamalai University was raised in randomized block design with three replications in the year March – May, 2002. Observations were recorded on 10 random plants for green yield and its contributing characters at 30 days after sowing. Mahalanobis's D² analysis as suggested by Rao (1952) was used for estimating the genetic divergence among the 100 genotypes. For determining the group constellations, a relatively simple criteria suggested by Tocher (Rao, 1952) was followed.

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RESULTS AND DISCUSSION

The 100 genotypes were grouped into 12 clusters by the application of clustering technique (Table 1). It was observed that cluster-I had a maximum of 44 genotypes of diverse origin. This was followed by cluster-II with 15 genotypes, cluster-III with nine genotypes, cluster-V and VII with six genotypes each, cluster-IV with five genotypes, cluster-VI, VIII and IX with four genotypes each and cluster X with three genotypes.

In general, genotypes belonging to different species clustered together. The grouping pattern of the genotypes indicated that the clusters were heterogenous for geographical origin of genotypes. From a close observation of the distribution of genotypes among the clusters no relationship could be established between clustering and eco-geographical origin (Patil and Bhapkar, 1987). The absense of relationship between genetic diversity and geographical diversity indicated that forces other than geographical origin such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection may be responsible for genetic diversity as reported by Nagarajan and Prasad (1980). The character number of leaves contributed maximum (16.24 %) towards the yield of greens followed by leaf area (13.19 %) and leaf weight (10.44 %). The contribution of petiole length was minimum (3.43 %) (Table 2).

The intra-cluster generalized distance ranged from 3.456 to 18.836 (Table 3). Cluster-II showed minimum intra-cluster distance (3.456) and maximum intra-cluster distance (18.836) was exhibited by the cluster-IX. Minimum inter-cluster distance was found to exist between cluster-II and III (7.701), while maximum inter-cluster distance was observed between cluster-IX and X (32.387) followed