RESEARCH PAPER

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D^2 analysis in vegetable amaranthus

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Presence of wide genetic diversity among the genotypes was revealed by Mahalonobis D^2 analysis. 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 VII and clusters IX 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 member of leaves and leaf weight contributed the maximum genetic divergence.

Key words : Genetic diversity, Amaranthus, Greenyield.

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INTRODUCTION

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 D^2 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 of amaranthus.

RESEARCH METHODOLOGY

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 July - September, 2007. Observations were recorded on 10 random plants for green yield and its contributing characters at 30 days after sowing. (Evaluation stage – 4) Mahalanobis's D^2 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.

RESULTS AND ANALYSIS

The 100 genotypes were grouped into 9 clusters by the application of clustering technique (Table 1). It was observed that cluster I had maximum of 65 genotypes of diverse origin. This was followed by cluster II and IV with 7 genotypes, cluster V and VIII with 5 genotypes each, cluster IV with four genotypes each, cluster VI and VII with 3 genotypes each and cluster IX with one 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 absence of relationship between genetic 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 (14.73 per cent) towards the yield of greens