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Genetic divergence in grain amaranth

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SUMMARY
Genetic divergence among sixty-four grain amaranth genotypes was assessed using Mahalanobis D^2 statistic. The genotypes were grouped into eleven clusters, which revealed wide diversity in the experimental material. Panicle fresh weight contributed maximum towards genetic divergence. The maximum inter cluster distance was observed between cluster III and XI followed by cluster VII and XI, cluster II and III. The highly diverse clusters could serve as potential sources of the accessions for their use in hybridization programme.

Key words : Grain amaranth, Genetic divergence, Cluster analysis, Diversity.

Grain amaranth (*Amaranthus sp*.) constitutes an important class of pseudocereals that were the principle food crop of ancient America. The crop is grown in India in the Sub-Himalayan ranges and in the Nilgiri hills of South India. It has a higher energy density than conventional grains, which may be of importance for dietary considerations. Success of crop improvement programme depends on the extent of genetic variability, choice of parents for hybridization and selection procedure adopted. The choice of genetically diverse parents is important in hybridization programme to create variation for selection of useful recombinants. For estimation of degree of genetic divergence in germplasm collection of various crops multivariate analysis using D^2 statistic has been found to be a potential biometrical tool, (Rao, 1952). The use of generalized distance (D^2) as a quantitative measure of genetic divergence was illustrated in crop plants and other biological populations. In this contact, an attempt was made to study the genetic diversity in grain amaranth genotypes.

MATERIALS AND METHODS

The material for the present study composed of 64 genotypes, including Annapurna as check were evaluated in 8 x 8 simple lattice design in four replications during kharif 2002, at Botany garden, University of Agricultural Sciences, Dharwad. Each genotype was raised in 2.5m row spaced at 60cm between rows and 20cm within the row. Five plants were selected randomly from each plot and observations were recorded on days to 50% flowering, days to maturity, stem girth at collar region, number of leaves, number of branches, plant height, panicle length, number of spikes per panicle, dry weight of panicle, dry weight of stem and harvest index. Genetic diversity was studied by analyzing the data using Mahalanobis (1936) D^2 statistic as described by Rao (1952). The genotypes were grouped into different clusters according to Tocher's method, Rao (1952) and inter and intra cluster distances were calculated as per Singh and Chaudhary. (1977).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the genotypes for all the 12 characters studied indicating sufficient scope for further improvement in these traits.

Sixty-four genotypes were grouped into 11 clusters, cluster I was the largest comprising 35 genotypes, cluster II with 9 genotypes. Cluster III with 3 genotypes and the remaining seven clusters each with one genotype only (Table 1). The genotypes grouped in the same cluster are expected to have little genetic divergence in respect of aggregate of the 13 characters studied and hybridization between members of the same cluster is not likely to produce desirable recombinants. The parental genotypes should be chosen on the basis of inter cluster distance which represents the index of genetic diversity among clusters (Joshi and Rana, 1995; Verma *et al*., 2002).

The average intra and inter cluster distance are presented in Table 2. The intra cluster D^2 values ranged from zero (cluster V to XI) to 64.254 (cluster II). The maximum inter cluster distance was observed between cluster III and cluster XI (397.178) followed by cluster VII and XI (324.433) and cluster II and III (320.899). Hence the hybridization between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement. The least inter cluster

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