

RESEARCH ARTICLE

Study on genetic diversity in Amaranthus (*Amaranthus hypochondriacus* L.)

■ B. H. Kale, S. B. Sarode, S. G. Gawai and S. L. Haloli

SUMMARY

Grain amaranth is a protein rich pseudocereal, assumes an important position in terms of quality breeding activities. Systematic characterization, evaluation and utilization of the potential genotype in the crop are prerequisite to any crop improvement. Genetic diversity study was conducted in one hundred fifty genotypes using Mahalanobis D² Statistics during *Kharif* 2017 at College of Agriculture Badnapur. Based on D² values, 150 genotypes were grouped into XII clusters. In the present investigation, the cluster II was with the highest number of genotypes (62) followed by cluster I (33), clusters VI (25), cluster VI (16), IX (3), X (3) and cluster III, V, VII, VIII, XI, XII had single genotype. The intra cluster distance (D) range from 4.74 to 48.64. The maximum inter cluster distance (D= 48.64) was observed between cluster XII and IX cluster, followed by cluster XI and IX (D= 46.25), cluster XI and cluster IV (D= 45.43), cluster IX and cluster VIII (D= 43.92), cluster IX and cluster II (D= 39.03) indicating that the genotypes falling in these clusters were highly divergent from each other implying large amount of diversity within and between groups, which could be exploited in breeding programmes. As crosses between genotypes belonging to the clusters with maximum inter cluster distance, may give high heterotic response resulting in better recombinants.

Key Words : Amaranthus, Cluster analysis, D² statistics, Inter cluster distance, Intra cluster distance

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Grain Amaranthus also known as rajgira or pigweed belongs to family Amaranthaceae trib Amaranthaceae subfamily Amaranthoideae

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suborder chenopodiaceae Goosefoot family chenopodiaceae and common name Rajgira or pigweed. It is a self-pollinated, tetraploid (2n = 36) crop. Grain Amaranthus are important pseudocereals that are widely cultivated in India in the sub-Himalayan ranges and in the Nilgiri Hills of South India. Amaranthus are one of the oldest food crops in the new world. It is an ancient food crop reported to have been cultivated in Mexico. The long history of cultivation of grain amaranthus in India under diverse agro-climatic conditions and the

associated human and natural selection has resulted in generation of large variability giving India the status of secondary centre of diversity. In India amaranth is cultivated in Jammu and Kashmir, Himachal Pradesh, Uttarakhand, Sikkim, Assam, Meghalaya, Arunachal Pradesh, Nagaland, Tripura, Jharkhand, Chhattisgarh, Maharashtra, Gujrat, Orissa, Karnataka, Kerala, and Tamil Nadu both in hills and plains. The exact information about the statistics on area and production in India is lacking. However, as a grain crop it is estimated to be grown in about 40-50 thousand ha. Hand harvested yields have been as high as 4000 kg/ha in Montana and 6000 kg/ha in Peru, between 2500 and 3300 kg/ha in southwest Germany, between 2100 and 2700 kg/ha in Slovak Republic and 1200 kg/ha in India.

The first advance estimation area, production and productivity in Maharashtra *Kharif* 2017-2018 total area 0.864 lakh ha, production 0.932 lakh tones and productivity 1078 kg/ha (Directorate of Agriculture, Government of Maharashtra).

The achievement in plant breeding programme largely depends upon the genetic variability available in breeding population and the efficiency of selection technique. The importance of genetic diversity in plant breeding is obvious from results obtained in different crops. The recognition and measurement of such diversity, its nature and magnitude are beneficial, perhaps crucial to any breeding programme. This is particularly important in a crop like *Amaranthus* where hybridization is difficult, there being limited scope for making large number of crosses by random mating and hence, the information regarding the nature of genetic diversity of the parents to be used in the hybridization, is of paramount importance to amaranthus breeder. Inclusion of diverse parents in hybridization helps in isolation of superior recombinants. Mahalanobis's D^2 statistics is a powerful tool in quantifying the degree of variability at the genotype level. The utility of multivariate analysis has greatly been emphasized (Murty and Arunachalam, 1966). Several workers studied the genetic diversity, clustering pattern, relative contribution of different characters towards divergence and effectiveness of selection (Venkateswarlu, 2001; Manivannan *et al.*, 2002 and Bisht *et al.*, 2005). The present study aims to find out the genetic diversity among 150 promising grain *Amaranthus* genotypes.

MATERIAL AND METHODS

The present investigation on grain *Amaranthus* for

genetic diversity analysis was conducted at College of Agriculture Badnapur, Section of Agricultural Botany, Badnapur, during *Kharif* season of 2017-18. The experimental materials used for study consisted of one hundred fifty (150) genotypes of grain *Amaranthus* including checks. Genotypes were obtained of 150 germplasm lines received from NBPGR, Akola. One hundred forty-sevengenotypes of *Amaranthus* along with three standard checks *viz.*, GA1, GA2 and Suvarna were evaluated in a Randomized Block Design (RBD) with two replications during *Kharif* season of 2017-18. Each genotype was sown in four rows of 3 m length with spacing of 45 cm between rows and 15 cm within plants. Data were calculated by Mahalanobis D^2 statistics (1936) and the genotypes were grouped into different clusters according to Tocher's method as described by Rao (1952). Contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1979). Grouping of variety into various clusters was done and average intra and inter cluster distance were estimated.

RESULTS AND DISCUSSION

Based on the D^2 values the 150 genotypes were grouped into twelve clusters (Table 1). The utility of D^2 analysis was enhanced by its application to estimate the relative contribution of the various plant characters to genetic divergence. The per cent contribution of ten characters studied, towards total divergence is presented in Table 2. It was observed that, thousand grain weight (62%) contributed highest for divergence. It was followed by plant height (38.87%), number of primary branches per plant (38%), inflorescence length (34.72%), flag leaf sheath width (0.53%), finger length (0.53%), finger number per panicle (0.49%), stem diameter (12%), days to 50% flowering (9.12%), days to maturity (7.79%), seed yield per plant (4.64%), protein content (2.54%), number of secondary branches per plant (1.22%). Similar results were observed for protein by Erum *et al.* (2012) and Srivastava and Roy (2012).

On the basis of D^2 values all the genotypes were grouped into the twelve clusters with varying number of genotypes in the clusters.

The clustering pattern of these genotypes does not follow the geographical distribution. The maximum genetic distance (D) of 48.64 was found between the clusters XII and cluster IX. Greater the divergence between the two clusters, wider is the genetic diversity in the

Table 1 : Composition of one hundred fifty grain Amaranthus genotypes into different clusters by Tocher's method

Cluster No.	No. of genotypes	Genotypes included in the cluster
I	33	IC-35616, IC-35783, IC-35719, IC-41988, IC-41985, IC-35726, IC-35720, IC-35701, IC-35702, IC-35614, IC-41989, IC-35710, IC-35609, IC-35711, IC-81706, IC-35731, IC-25668, IC-35754, IC-35774, IC-81707, IC-35687, IC-35682, IC-35611, IC-35771, IC-35641, IC-35749, IC-35716, IC-35741, IC-35736, IC-35753, IC-35779, IC-35491, IC-35652.
II	64	IC-35427, IC-35429, IC-35433, IC-35436, IC-35534, IC-35424, IC-35431, IC-35421, IC-35435, IC-35601, IC-35438, IC-35564, IC-35590, IC-35707, IC-35598, IC-35688, IC-35544, IC-35403, IC-35574, IC-35571, IC-35557, IC-35553, IC-35562, IC-35541, IC-35543, IC-35439, IC-35450, IC-35449, IC-35589, IC-35603, IC-35548, IC-35476, IC-35506, IC-35441, IC-35459, IC-35434, IC-35462, IC-35440, IC-35445, IC-35537, IC-35502, IC-35488, IC-35440, IC-35552, IC-35505, IC-35533, IC-35524, IC-35452, IC-35404, IC-35470, IC-35497, IC-35613, IC-35555, IC-35463, IC-35514, IC-35480, IC-35607, IC-35460, IC-35494, IC-35479, IC-35727, IC-35721, IC-25594, IC-35501.
III	1	IC-35729
IV	25	IC-35567, IC-35568, IC-35694, IC-35706, IC-35682, IC-35558, IC-35442, IC-35559, IC-35563, IC-35546, IC-35521, IC-35484, IC-35606, IC-35451, IC-35445, IC-35500, IC-35499, IC-35530, IC-35561, IC-35515, IC-35580, IC-35576, IC-35689, IC-35709, IC-35651.
V	1	IC-35732.
VI	16	IC-35481, IC-35483, IC-35618, IC-35550, IC-35492, IC-35635, IC-35708, IC-35742, IC-35714, IC-35493, IC-35471, IC-35495, IC-35770, IC-35498, IC-35453, IC-35666.
VII	1	IC-35681.
VIII	1	IC-35747
IX	3	GA2, Suvarna, GA1
X	3	IC-35703, IC-35722, IC-35596
XI	1	IC-35554
XII	1	IC-35713

Table 2 : Analysis of variance for ten characters in grain Amaranthus

Sr. No.	Characters	Mean sum of squares		
		Replication (d.f. 1)	Genotype (d.f. 149)	Error (d.f. 149)
1.	Days to 50% flowering	8.003**	50.00***	0.81
2.	Plant height (cm)	0.75	836.74***	3.60
3.	Number of primary branches per plant	3.00*	7.37***	0.58
4.	Number of secondary branches per plant	0.213	12.58***	0.522
5.	Stem diameter (cm)	0.34	0.37***	0.140
6.	Inflorescence length (cm)	2.083	138.08***	0.66
7.	Days to maturity	1.20	320.58***	4.57
8.	Thousand grain weight (g)	0.027	0.349***	0.032
9.	Seed yield per plant (g)	7.363*	54.17***	1.27
10.	Protein content (%)	5.16**	17.81***	0.49

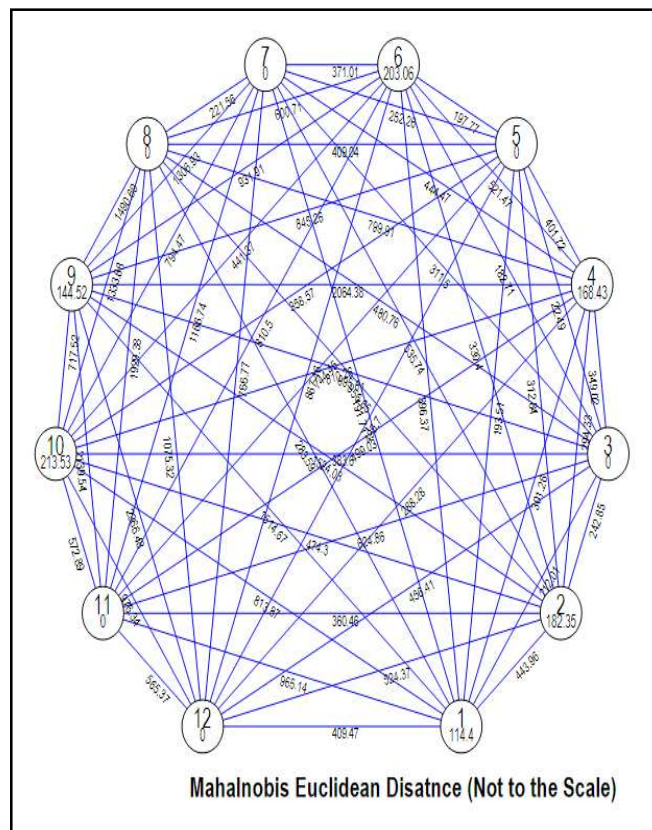


Fig. 1: Cluster diagram in grain *Amaranthus*

genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit

decrease in heterosis (Table 1). Therefore, while selecting the parents by considering the diversity, their performance and cluster mean for the characters also need due to consideration in the crop improvement programme (Fig. 1). In the present investigation, the cluster means for the ten characters studied are presented in Table 3. The cluster mean for days to 50 per cent flowering varied from 57.50 (XII) to 67.50 days (IX). The cluster means for plant height ranged between 120.50 (IX) to 208.50 cm (VIII). The cluster mean for primary branches per plant ranged between 4.50 (III) to 10.17 (IX). The cluster mean for secondary branches per plant ranged from 7.50 (III) and (VIII) to 14.50 (cluster XI). The cluster mean for stem diameter ranged between 0.75 (XI) and 1.82 (IX). The cluster mean for inflorescence length was maximum in cluster (VIII) 64.00 and it was minimum in cluster (XI) 18.50. The cluster mean for days to maturity was maximum in cluster (IX) 139.83 and minimum in case of cluster (VII) 94.00. The cluster mean for thousand grain weight was maximum in cluster (III) 2.88 and it was minimum in cluster (II) 12.32. The cluster mean for seed yield per plant was maximum in cluster (IX) 28.17 and it was minimum in cluster (XI) 8.50. The cluster mean for protein content was minimum in cluster (II) 9.64 and it was maximum in cluster (IX) 15.17.

Crossing between the genotypes belonging to the same clusters will not give desired improvement hence; the parents selected for crossing should be from different clusters.

Table 3 : Cluster means of different characters to genetic diversity in grain *Amaranthus*

Sr. No.	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (cm)	Inflorescence length (cm)	Days to maturity	Thousand grain weight (g)	Seed yield per plant (g)	Protein content (%)
I	63.42	198.48	6.95	10.21	1.44	47.32	118.14	2.72	16.08	14.32
II	59.63	167.54	5.74	7.51	1.19	35.86	101.15	2.32	10.25	9.64
III	58.50	172.50	4.50	7.50	0.85	45.50	123.50	2.88	13.50	14.84
IV	62.22	192..88	6.30	8.70	1.19	35.10	101.58	2.39	12.14	11.69
V	60.50	174.50	6.50	8.50	1.05	46.50	127.00	2.79	19.00	14.89
VI	63.03	161.31	5.03	8.13	1.34	47.66	107.16	2.61	12.56	10.61
VII	62.50	193.50	8.50	12.50	1.35	51.50	94.00	2.70	22.50	15.06
VIII	64.50	208.50	7.50	7.50	1.05	64.00	119.50	2.85	18.00	14.80
IX	67.50	120.50	10.17	14.50	1.82	55.67	139.83	2.48	28.17	15.17
X	63.50	138.50	6.50	10.50	1.42	34.83	116.50	2.46	24.67	12.78
XI	59.50	152.50	6.50	8.50	0.75	18.50	96.50	2.41	8.50	14.83
XII	57.50	205.50	5.50	11.50	1.45	29.50	134.00	2.74	16.50	15.00

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