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Genetic diversity study in red amaranths (*Amaranthus tricolor* L.)

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Abstract
Mahalanobis D^2 statistics was used to study genetic divergence for 11 characters in a collection of 20 genotypes of Red Amaranths. These genotypes were grouped into six clusters on the basis of relative magnitude of D^2 values. The genotypes included in cluster VI are a good source of plant height (cm), no of leaves per plant, no of branches per plant, leaves length (cm), plant fresh weight (gm), dry plant weight (gm) and foliage yield. Maximum 95.79% contribution towards genetic divergence was shown by characters days of first harvest, petiole length (cm), plant height (cm), no of branches per plant, plant fresh weight (gm), leaves width (cm), leaves length (cm) and dry plant weight (gm). Therefore, these characters should be considered while selecting the parents for hybridization programmes. The maximum inter cluster distance indicated that genotypes of cluster VI (Amar-03) and I (Amar-01, Amar-06, Amar-14, Amar-04, Amar-19) are highly divergent. The genotypes grouped in these clusters can be used in breeding programme to get a wide spectrum of variability and transgressive segregants.

Keywords: Amaranthus, Amaranthus spp., diversity genetic, divergence, D2 analysis, cluster analysis

Introduction
Red amaranths is the one of the most popular and important leafy vegetables of India. Amaranthus (*Amaranthus spp*.), popular known as "Chaulai". The edible and cooking amaranths belong to the family of Amaranthaceae. It is a unique leafy vegetable grown in a wide range of agro-climate condition and different cropping system. It is a hardy and an early growing crops with high yielding potential, easy to grow and suitable to fits in crop rotations in both homestead nutrition gardens and commercial cultivation. Generally diverse plants are expected to give higher hybrid vigour (Harrington, 1940) [5]. Hence it is necessary to study the genetic divergence among the existing variety and germplasm collection for identification of plants for the hybridization programme. The information on genetic divergence of various yield and quality contributing traits that would be the most useful in planning of the breeding programme. D^2 statistic developed by Mahalanobis (1952) provides a measure magnitude for divergence between two genotypes under comparison. Grouping of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding. This study is useful in selection of parents for hybridization to recover superior transgressive segregants.

Materials and Methods
Twenty genotypes of amaranths were grown in a randomized block design with three replications during *Rabi* 2020-21 at Pt. KLS College of Horticulture and Research Station, Rajnandgaon (Chhattisgarh). The seed are sowing in direct field at the distance 15 cm for row to row and 5 centimeter for plant-plant was maintained and the plot size was 1 m^2. Recommended dose of fertilizers, and other cultural packages of practice were adopted for raising good crop. Five competitive plants were selected randomizing from each plots to record observations on various characters. The mean values were used for D^2 statistic to know the genetic divergence (Mahalanobis 1936) [7] and genotype were grouped into various clusters by Tochers method as described by Rao (1952) [11].

Results and Discussion
In the present investigation based on D^2 value, 20 genotypes of red amaranths were grouped into 6 clusters (Table 1). Cluster IV was the largest, comprising of 07 genotypes followed by cluster I with 05 genotypes, cluster V with 04 genotypes, cluster II with 2 genotypes while cluster III and VI are solitary.

This indicated that quite a large number of genotypes were genetically close to each other. The clustering pattern of these genotypes under study suggested that geographic diversity may not be necessarily related with genetic diversity (Patil and Bhapkar, 1987) [10].

Table 1: Clustering pattern of 20 genotypes of red amaranths.

Cluster Number	Number of genotypes	Name of genotypes and geographical origin
Cluster-01	05	Amar-01 (Balodabazar), Amar-06 (Bemetara), Amar-14 (Bacheli), Amar-04 (Raipur), Amar-19 (Bilaspur)
Cluster-02	02	Amar-05 (Raigarh), Amar-18 (Berla)
Cluster-03	01	Amar-02 (Rajnandgaon)
Cluster-04	07	Amar-08 (Raipur), Amar-10 (Mungeli), Amar-09 (Bilaspur), Amar-11 (Rajnandgaon), Amar-12 (Kanker), Amar-15 (Janjgir), Amar-17 (Raipur)
Cluster-05	04	Amar-13 (Rajnandgaon), Amar-16 (Kawardha), Amar-07 (Bangalore), Amar-20 (Check Pusa Lal Chaulai)
Cluster-06	01	Amar-03 (Delhi)

The comparison of cluster means for different characters (Table 2) indicated that the genotypes included in cluster VI are a good source of plant height (cm), no of leaves per plant, no of branches per plant, leaves length (cm), plant fresh weight (gm), dry plant weight (gm) and foliage yield. The cluster V exhibited maximum leaves width (cm) whereas days of first harvest showed maximum mean in cluster number I. Thus, cluster VI, cluster V and cluster I hold great promise to create further variability for these characters and to select the recombinants. A wide variation has been confirmed from one cluster to another in respect of cluster mean from the above observation, which pointed out that genotypes having distinct mean performance for various characters were separated into different clusters. Similar findings were also observed by Ogbangwor (2014) [8] and Agadi (2019) [1].

Table 2: ANOVA and cluster means of different morphological characters in red amaranths.

	Plant height (cm)	No of leaves per plant	No of branches per plant	Leaves length (cm)	Leaves width (cm)	Petiole length (cm)	Plant fresh weight (gm)	Dry plant weight (gm)	Days of first harvest	Foliage yield (kg per plot)
1 Cluster	15.392	6.367	2.626	3.876	3.650	3.079	2.928	0.328	30.733	4.099
2 Cluster	15.891	6.705	2.766	4.000	3.655	3.200	2.872	0.343	28.917	4.246
3 Cluster	14.968	6.443	2.690	3.848	3.536	2.996	3.122	0.329	27.583	4.202
4 Cluster	15.488	6.530	2.759	3.971	3.642	2.919	2.962	0.326	29.869	4.157
5 Cluster	16.419	6.844	3.143	4.296	3.910	3.206	3.338	0.388	26.875	4.562
6 Cluster	16.659	7.371	3.619	4.396	3.890	3.423	3.624	0.465	23.667	4.802
Mean	15.723	6.607	2.843	4.030	3.706	3.074	3.061	0.348	28.967	4.267
Treat MSS	1.458	0.394	0.427	0.198	0.093	0.133	0.286	0.009	22.939	0.288
Err MSS	0.067	0.013	0.006	0.008	0.005	0.007	0.009	0.000	0.594	0.010
F Ratio	21.626	29.386	67.306	23.661	17.836	19.427	30.965	51.963	38.591	29.959

The contribution of various characters towards genetic divergence indicated that days of first harvest (22.63%) followed by petiole length (cm) (19.47%), plant height (cm) (12.11%), no of branches per plant (10.53%), plant fresh weight (gm) (8.42%), leaves width (cm) (7.89%), leaves length(cm) (7.37%) and dry plant weight (gm) (7.37%) contributed nearly 95.79% of total divergence in the material (Table 3). Therefore, these characters should be considered while selecting the parents for hybridization programmes. Contribution of most of the characters towards genetic divergence were also reported by Bhoya *et al.* (2017) [4] and Joshi & Rana (1995b) [6].

Table 3: Wilks test ranking and contribution of characters

S. No.	Source	Times ranked 1st	Contribution %
1.	Plant height (cm)	23	12.11%
2.	No of leaves per plant	6	3.16%
3.	No of branches per plant	20	10.53%
4.	Leaves length (cm)	14	7.37%
5.	Leaves width (cm)	15	7.89%
6.	Petiole length (cm)	37	19.47%
7.	Plant fresh weight (gm)	16	8.42%
8.	Dry plant weight (gm)	14	7.37%
9.	Days of first harvest	43	22.63%
10.	Foliage yield (kg per plot)	2	1.05%

The intra and inter cluster distances among six clusters are given in Table 4. The intra cluster distance ranged from 1.641 (cluster IV) to 0.00 (cluster III & VI). The inter cluster distances were greater than intra cluster distance revealing considerable amount of genetic diversity among the genotypes studied. Inter cluster distance is the main criterion for selection of genotypes using D^2 analysis. The maximum inter cluster distance was recorded between cluster I and cluster VI (20.551) followed by cluster V and cluster VI (17.549) whereas, the lowest inter cluster distance was observed between cluster I and II (1.937). The genotypes grouped in these clusters can be used in breeding programme

to get a wide spectrum of variability and transgressive segregants. Similar views were also expressed by Arunachalam and Bandyopadhyay (1984) [3], Verma et *al.* (2002) [12] and Joshi & Rana (1995) [6].

Table 4: Euclidean²: Average intra and inter cluster distance (D^2 value) among 6 clusters of 20 genotypes in Red amaranths.

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	(1.257)	1.937	3.667	1.871	7.107	20.551
2 Cluster		(0.347)	2.676	2.038	4.567	14.383
3 Cluster			(0.000)	2.738	5.456	14.051
4 Cluster				(1.154)	5.207	17.549
5 Cluster					(1.641)	6.296
6 Cluster						(0.000)

Note: Diagonal values red bold and italics are intra cluster distances while non diagonal values are inter cluster values. Values in parenthesis are the group distance ($\sqrt{D^2}$) to be used for cluster diagram.

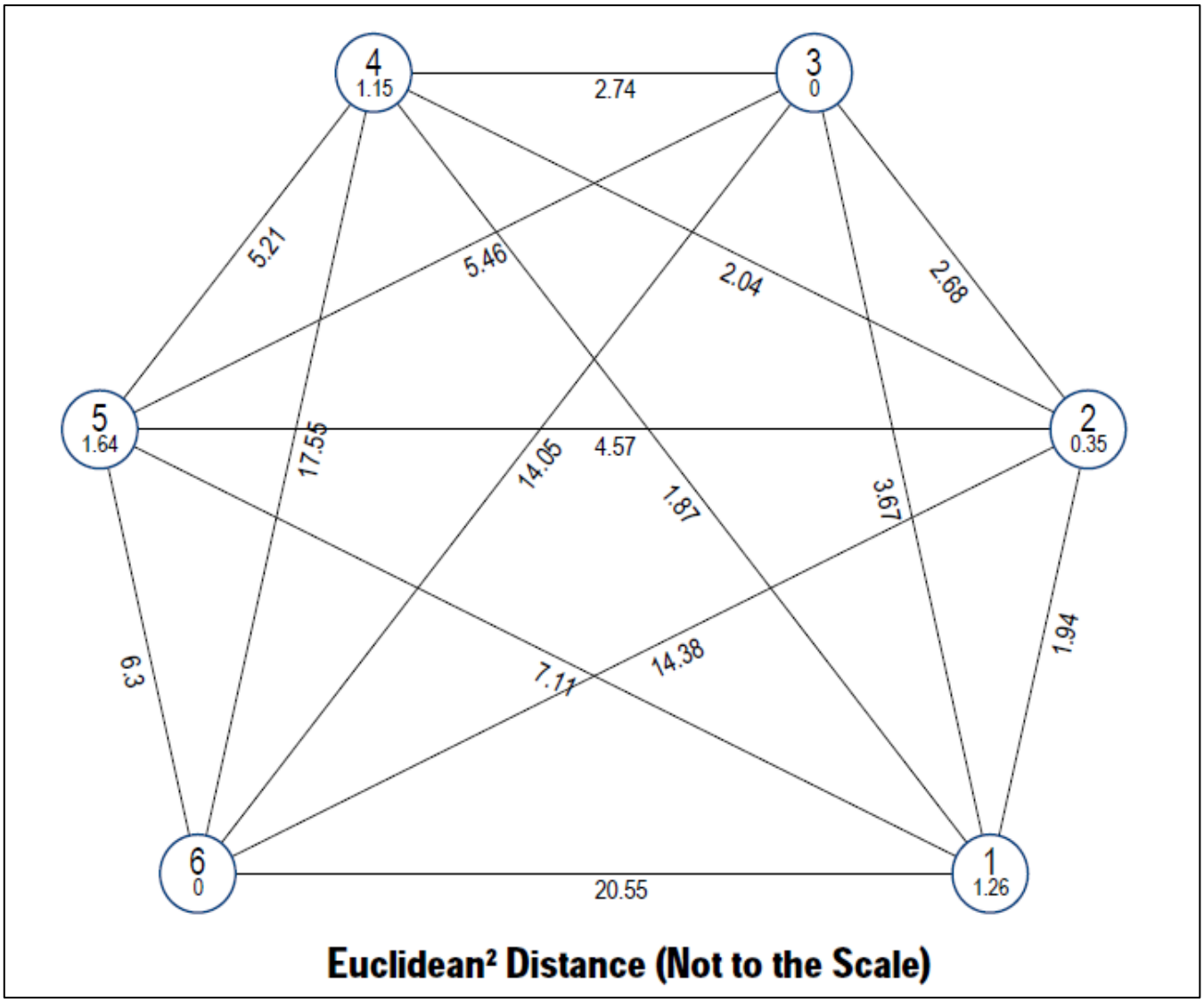

Fig 1: Diagrammatic representation of different inter and intra cluster distances of Amaranths. (Values inside circle is intra cluster distances)

Conclusion

D^2 study revealed that the genotypes included in cluster VI are a good source of plant height (cm), no of leaves per plant, no of branches per plant, leaves length (cm), plant fresh weight (gm), dry plant weight (gm) and foliage yield. Maximum 95.79% contribution towards genetic divergence was shown by characters days of first harvest, petiole length (cm), plant height (cm), no of branches per plant, plant fresh weight (gm), leaves width (cm), leaves length (cm) and dry plant weight (gm). Therefore, these characters should be considered while selecting the parents for hybridization programmes. The high inter cluster distance points that genotypes of cluster VI (Amar-03) and I (Amar-01, Amar-06, Amar-14, Amar-04, Amar-19) are highly divergent, permits heterotic recombinants in segregating generations, So it is suggested to perform cross between the genotype belonging to cluster's with higher divergence.

References

1. Agadi, Annapurna H. Genetic diversity studies in vegetable amaranthus (*Amaranthus tricolor* l.) for yield and its component traits. M. Sc. Thesis, University of

Agricultural & Horticultural Sciences, Shivamogga. 2019.
2. Akther CA, Hasan H, Raihan MS, Hossain MM, Mian MAK. Genetic Divergence in Stem Amaranth (*Amaranthus tricolor* L.). Genotypes for Yield & its Component Characters. The Agriculturists- A Scientific Journal of Krishi Foundation. 2013;11(1):82-88.
3. Arunachalam V, Bandyopadhyay A. Limits to genetic divergence of heterosis – experimental evidence from crop plants. Indian Journal of Genetics and Plant Breeding. 1984;49(3):548-554.
4. Bhoya RC, Jadhao AG, Sivasubbu S, Singh AR, Sabharwal A, Palande NV, et al. Genetic divergence analysis of amaranth (*Amaranthus hypochondriacus* L.). International Journal of Developmental Neuroscience. 2017;60:26-33.
5. Harrington JB. Yield capacity of wheat crosses as indicated by bulk hybrid tests. Canadian Journal Research. 1940;12(1):56-59.
6. Joshi BD, Rana JC. Genetic Diversity in grain amaranth (*Amaranthus hypochondriacus*). Indian Journal of Agricultural Sciences 1995b;65(8):605-607.
7. Mahalanobis PC. Studies on the generalized distance in statistics. Proc. Nat. Inst. Sci. India 1936;21:49-55.
8. Ogbangwor. Phenotypic, genotypic and environmental correlation, Biometrics 2014;17:474-480.
9. Panse VG, Sukhatme PV. Statistical methods for agricultural workers, Indian Council of Agricultural Research, New Delhi 1954, 361.
10. Patil RB, Bhapkar DG. Correlation studies in cowpea. Journal Maharashtra Agri. Univ 1987;12(1):56-59.
11. Rao CR. Advance Statistical Methods in Biometrical Research. John Wiley and Sons, New York 1952.
12. Verma PK, Gupta SN, Deen MK, Malik BPS. Genetic Divergence in grain amaranth. Annals of Biology 2002;18(1):35-38.