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Genetic divergence analysis in amaranthus (*Amaranthus spp.*) genotypes for yield and its component characters

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Abstract
An experiment was carried out to identify the extent of genetic divergence that exist for the yield and yield contributing characters of 25 genotypes of Amaranthus (*Amaranthus spp.*) using statistics as proposed by Mahalanobis (1936) D^2 analysis. Analysis of variance showed significant difference among the genotypes for most of the characters studied. The genotypes under study fell into 5 clusters. The distribution pattern indicated that the distribution pattern indicated that the maximum numbers of six genotypes each were included in cluster-IV and cluster-V each followed by five genotypes in cluster-II and cluster-III and three genotypes in cluster-I. The intra cluster D^2 values ranged from 1.849 (cluster III) to 2.345 (cluster V). The intra cluster distance was observed highest in cluster V (2.345) followed by cluster IV (2.284), cluster I (2.050), cluster II (1.954) and was recorded the lowest in cluster III (1.849), which indicate distance within the cluster. However, the inter-cluster D^2 values varied from clusters II and V (2.523) to clusters II and III (6.370). The maximum inter-cluster distance was observed between the clusters II and III (6.370) followed by cluster III and IV (6.272), cluster I and IV (5.314) cluster III and V (4.795), cluster I and III (4.625), cluster I and II (4.278), cluster I and V (3.818), cluster II and IV (2.880), cluster IV and V (2.800), and the minimum inter-cluster observed between cluster II and V (2.523). Above finding indicated that high inter-cluster distance were the main causes of diversity in composition of cluster and hence, can be exploited in hybridization programme.

Keywords: Amaranthus, *Amaranthus spp.*, diversity genetic, divergence, D^2 analysis, cluster analysis

Introduction
Amaranthus is one of the important and popular leafy vegetable of India. Amaranthus (*Amaranthus spp.*), popularly known as "Chaulai". The edible amaranth belongs to the family Amaranthaceae, subfamily Amaranthoideae, and genus Amaranthus.
Amaranth uses the C4 cycle photosynthetic pathway. It has a high rate of photosynthesis and excellent water use efficiency at high temperatures and high radiation intensity. The small seeds of the leafy amaranths are usually very shiny and dark brown to black in colour.
Amaranthus is a rich source of nutrients it serves as an alternative source of nutrition for people in developing countries. (Prakash and Pal, 1991 and Shukla *et al*., 2003) [7, 10, 13, 14]. Tender stems and leaves contains moisture (85.70%), protein (4.0 g), fat (0.50 g), carbohydrates (6.30 g), calcium (397.0 mg), iron (25.5mg), phosphorus (83.0 mg), vitamin A (9200IU), and vitamin C (99 mg), (Rai and Yadav, 2005) [11]. It is also a good source of dietery fiber.
Existence of wide variability in various traits was documented in Amaranthus. Though, some improved varieties have been developed in India but many good local types often found in different regions. Critical evaluation of the available germplasm and selection of the improved types with high yield potential and good quality is, therefore, always has a good promise. Amaranthus is a frequent interspecific and intervarietal hybridization have resulted in wide genotypic variation. Amaranthus also exhibit tremendous diversity. However, identifying the correct genotype is important to evaluate the genetic diversity of local Amaranthus. Identifying and preserving germplasm are necessary for maintaining genetic diversity, studying local genetic material, and choosing ecotypes with high nutritional value in their place of origin.
Vegetable Amaranthus remains a subsidiary under exploited crop for vegetable purposes. Inspite of immense nutritional qualities, not much work has been done for its genetic improvement (Shukla *et al.,* 2003, 2004a) [13, 14]. Leafy vegetables play a major role in nutritional requirement of the tribal and local population in remote parts of the Chhattisgarh. Leafy vegetable not only provide food quantity but also make significant contribution to the population nutrition throughout the year (Chauhan *et al.,* 2014) [3].

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Traditionally, genetic diversity studies are based on differences in morphological characters and qualitative traits. It has been used as a powerful tool in the classification of cultivars and also to study taxonomic status. Morphological traits continue to be the first step in the studies of genetic relationships in most of the breeding programmes (Van Bueningen et al., 1997) [17].

Among several statistical methods developed for measuring divergence between populations, multivariate analysis of D^2 statistics has been effectively used for quantitative estimation of genetic variability according to Mahalanobis (1936) [4] D^2 statistics, which can be effectively used for assessing the genetic divergence between populations and helping in selection of desirable parents for crossing programme. McGrath and Quiros (1992) [6] reported that Genetic diversity among crop types (with the exception of turnip) was similar to diversity estimates of geographical regions, implying that crops used for similar purposes (i.e., oilseed or leafy vegetable) are derived from geographically differentiated populations.

The D2 analysis has been established by several investigators like – Chan ánd Sun (2013) [2] reported that genetic diversity and relationships of 23 cultivated and wild *Amaranthus* species were examined. Mandal and Das (2002) [5] evaluated genetic diversity of three grain amaranthus species *Amaranthus hypo-chondriacus, A. caudatus* and *A. cruentus* comprising a total of 17 accessions. Anuja *et al*. (2012) [1] reported that the genetic diversity in 100 amaranthus species including *Amaranthus tricolor, A. blitum* and *A. dubius* was determined using the Mahalanobis D^2 analysis. The genotypes grouped into 10 clusters. Pandey and Singh (2011) [9] reported that genetic divergence for 14 characters among 98 genotypes of grain amaranth (*Amaranthus hypochondriacus* L.) were determined for the purpose of identifying more diverse parents which are expected to engender maximum variability. Pandey and Singh (2011) [9] reported that genetic diversity of twenty six accessions of grain Amaranth (*Amaranthus hypochondriacus* L.) were evaluated for salient biochemical and quantitative traits chlorophyll a, chlorophyll b, total chlorophyll and phenol content. Shobha and Dharmatti (2004) [13] in vegetable Mesta, Rana *et al.,* (2005) [13] in grain amaranthus, Anuja and Mohideen (2007) in vegetable amaranthus for measuring the degree of divergence and for ascertaining the relative contribution of different characters to the total divergence. In the present investigation, therefore, the genotypes were subjected to D2 analysis to find out nature and extent of genetic diversity present in 25 genotypes of Amaranthus (*Amaranthus spp.*) for genetic improvement.

Materials and Methods
The experimental material for the study comprised of 25 genotypes are IGA-2013-1, IGA-2013-2, IGA-2013-3, IGA-2013-4, IGA-2013-5, IGA-2013-6, IGA-2013-7, IGA-2013-8, IGA-2013-9, IGA-2013-10, IGA-2013-11, IGA-2013-12, IGA-2013-13, IGA-2013-14, IGA-2013-15, IGA-2013-16,

IGA-2013-17, IGA-2013-18, IGA-2013-19, IGA-2013-20), IGA-2013-21, IGA-2013-22, IGA-2013-23, IGA-2013-24, IGA-2013-25, collected from different part of Chhattisgarh and laid in randomized block design (RBD) with three replications at the Horticultural Instructional and Research Farm, Department of Horticulture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) lies between 21o16' N latitude and 81o36' E longitude with an altitude of 289.56 meters above the mean sea level.. The experiment was conducted during Rabi season 2014-15. Field was prepared for planting and was levelled with the help of '*Pata*'. The seeds were sown at the depth of 1-2 cm with a spacing of 20 cm (Row to row) X 20 cm (Plant to plant) on 14 th November, 2014. Fertilizers Nitrogen, Phosphorus and Potassium were applied for the growth and development of the Amaranthus crop. The field was irrigated at regular interval of 7-10 days. The observations on yield attributes were recorded on five randomly selected competitive plants of each plot from each replication. Observations were recorded for plant height (cm), number of leaves plant^{-1}, number of branches plant^{-1}, leaf length plant^{-1}, leaf breadth plant^{-1}, petiole length plant^{-1}, stem girth plant^{-1}, root length plant^{-1}, leaf yield plot^{-1}, leaf yield ha^{-1}, seed yield plot^{-1}, seed yield ha^{-1}, Fresh weight of plant (gm), Dry weight of plant (gm), dry matter per cent, Root weight (gm), test weight, Chlorophyll content, fibre content per cent, Fiber pulp ratio, Duration of crop (Days). The analysis of variance was carried out for all the characters and then data was analyzed following multivariate analysis of Mahalanobis (1936) [4] and genotypes were grouped into different clusters following Tocher's method (Rao, 1952) [12].

Results and Discussion
Genetic divergence
The genetic divergence was estimated by Mahalanobis D^2 statistics as described by Rao (1952) [12]. Based on D^2 values, the constellation of genotypes into clusters was done adopting Tocher's method (Rao, 1952) [12].
The reports available on this aspect in Amaranthus are rather, scanty. Therefore, the present investigation was aimed at ascertaining the nature and magnitude of genetic diversity among a set of Amaranthus genotypes. The findings of the present investigation are described under the following heads:

Group constellations
In Amaranthus, due to stagnate and pre-petuating nature of heterosis, parental selection is a crucial step in any breeding programme. Using statistics as proposed by Mahalonobis (1936) [4] D^2 value were calculated among twenty five Amaranthus genotypes in all possible combinations.
The study of genetic divergence among genotypes under study, analysis of co-variance was performed for all possible pair of character and as an outcome, twenty five genotypes grouped into five different clusters using Mahalanobis' D^2 statistics. The clustering pattern and genotypes are given in (Table 1).

Table 1: Clustering pattern of different genotypes of Amaranthus

Cluster number	Number of Genotypes included	Name of genotypes
I	3	IGA-2013-3, IGA-2013-18, IGA-2013-19
II	5	IGA-2013-12, IGA-2013-13, IGA-2013-14, IGA-2013-15, IGA-2013-16
III	5	IGA-2013-20, IGA-2013-21, IGA-2013-22, IGA-2013-23, IGA-2013-24,
IV	6	IGA-2013-1, IGA-2013-2, IGA-2013-5, IGA-2013-6, IGA-2013-7, IGA-2013-8
V	6	IGA-2013-4, IGA-2013-9, IGA-2013-10, IGA-2013-11, IGA-2013-17, IGA-2013-25

The maximum numbers of six genotypes each were included in cluster-IV and cluster-V each followed by five genotypes in cluster-II and cluster-III and three genotypes in cluster-I.

Intra and inter-cluster distances

The intra and inter-cluster distance of all clusters has been presented in (Table 2). The intra cluster D^2 values ranged from 1.849 (cluster III) to 2.345 (cluster V). The intra cluster distance was observed highest in cluster V (2.345) followed by cluster IV (2.284), cluster I (2.050), cluster II (1.954) and was recorded the lowest in cluster III (1.849).

However, the inter-cluster D^2 values varied from clusters II and V (2.523) to clusters II and III (6.370). The maximum inter-cluster distance was observed between the clusters II and III (6.370) followed by cluster III and IV (6.272), cluster I and IV (5.314) cluster III and V (4.795), cluster I and III (4.625), cluster I and II (4.278), cluster I and V (3.818), cluster II and IV (2.880), cluster IV and V (2.800), and the minimum inter-cluster observed between cluster II and V (2.523). Above finding indicated that high inter-cluster distance were the main causes of diversity in composition of cluster and hence, can be exploited in hybridization programme.

Table 2: Inter and intra cluster distances

Cluster Number	I	II	III	IV	V
I	2.050	4.278	4.625	5.314	3.818
II		1.954	6.370	2.880	2.523
III			1.849	6.272	4.795
IV				2.284	2.800
V					2.345

Diagonal bold values indicate intra cluster distances

Component of cluster mean

Divergence reflecting in the material was also evidenced by an appreciable amount of desirable variation among cluster mean for different characters as shown in the (Table 3).

The component of cluster mean for the plant height was highest in cluster-IV (31.37) which was followed by cluster-II (26.28), cluster-V (25.62), cluster-III (25.21), and cluster-I (19.58). As regards number of leaves plant^{-1}, cluster-IV possesses the highest average performance (29.61) and it was followed by cluster-III (20.32), cluster-V (19.71), cluster-II (16.97) and cluster-I (14.30). The highest mean for number of branches plant^{-1} was observed in cluster-V (4.19) which was followed by cluster-II (3.48), cluster-III (3.47), cluster-IV (3.45) and cluster-I (2.51).

Leaf yield plot^{-1} showed the highest mean performance for the cluster-IV (2.51 kg) followed by cluster-V (2.36 kg), cluster-II (2.24 kg) cluster-I (1.83 kg) and cluster-III (1.73 kg). The seed yield plot^{-1} exhibited highest cluster mean for cluster-IV (79.64 g) followed by cluster-V (66.75 g), cluster-II (63.92 g), cluster–I (52.68 g) and cluster-III (21.21 g). The test weight exhibited highest cluster mean for cluster-II (1.37 g) followed by cluster-IV (1.35 g), cluster-V (1.32 g), cluster–I (0.97 g) and cluster-III (0.68 g).

Dry matter per cent showed highest mean performance for cluster- III (24.78 per cent) followed by cluster-V (22.17 per cent), cluster-I (21.48 per cent), cluster-IV (19.78) and lowest for cluster-II (18.64 per cent). The highest fiber content mean was exhibited cluster-III (7.75 per cent) followed by cluster-II (7.55 per cent), cluster-IV (7.44 per cent), cluster-V (7.35 per cent) and cluster–I (6.30 per cent).

The highest cluster mean for root length was recorded in cluster-II (8.60) followed by cluster-I (8.22), cluster-V (7.98), cluster- IV (7.71) and the lowest for cluster- III (6.93). As regards leaf length the highest cluster mean was observed in cluster-II (7.37) followed by cluster-IV (6.84), cluster- V (5.59), cluster-I (5.18) and the lowest for cluster- III (3.73).

The highest mean for leaf breadth was observed in cluster-II (4.52) followed by cluster-IV (4.12), cluster-V (3.55), cluster-I (3.53) and for lowest for cluster-III (2.12). The highest petiole length was observed in cluster-IV (4.89) followed by cluster-II (4.82), cluster-V (4.31), cluster- I (3.59) and for lowest for cluster- III (2.18). The highest cluster mean for stem girth was recorded in cluster-II (3.53) followed by cluster- IV (3.17), cluster-V (2.93), cluster-I (2.47), and for lowest for cluster- III (1.70).

The above findings of path studies are in accordance with the findings of Anuja *et al.* (2012) [1] for number of leaves plant^{-1}, and leaf area, Pandey and Singh (2011) [9] for yield,

Desirable genotypes based on cluster performance

The better genotype selected for all the characters under consideration are presented in (Table 4). Among them, IGA-2013-5 included in cluster- IV possessed the highest leaf yield plot^{-1} (2.51 kg) whereas, the seed yield plot^{-1} was observed in genotype IGA-2013-6 (79.64 gm) included in cluster-IV.

The genotype IGA-2013-9 of cluster-V exhibited the highest mean value for number of branches plant^{-1} (4.19).

The genotype IGA-2013-2 of cluster-IV exhibited the highest mean value for plant height (31.37). Similarly, the genotype IGA-2013-6 of cluster- IV exhibited the highest mean value for number of leaves/plant (29.61). The genotype IGA-2013-5 of cluster-IV exhibited the highest mean value for leaf yield (kg)/plot (2.51). The genotype IGA-2013-6 of cluster-IV exhibited the highest mean value for seed yield (gm)/plot (79.64). The genotype IGA-2013-6 of cluster-IV exhibited the highest mean value for petiole length (4.89).

The genotype IGA-2013-23 of cluster- III exhibited the highest mean value for dry matter per cent (24.78). The genotype IGA-2013-20 of cluster- III exhibited the highest mean value for fiber content per cent (7.75).

The genotype IGA-2013-14 of cluster- II exhibited the highest mean value for root length (8.60). The genotype IGA-2013-13 of cluster- II exhibited the highest mean value for test weight (1.37). The genotype IGA-2013-16 of cluster- II exhibited the highest mean value for leaf length (7.37). The genotype IGA-2013-15 of cluster- II exhibited the highest mean value for leaf breadth (4.52). The genotype IGA-2013-12 of cluster- II exhibited the highest mean value for stem girth (3.53).

Further, selection of material from same origin or source for different economic characters may be contributed to divergence. Present findings suggest the existence of true genetic divergence in population of Amaranthus.

Based on the present findings on genetic divergence and its component analysis, it can be concluded that the maximum inter cluster distance was noted between the cluster-III (6.370) and cluster-IV (6.272). On cluster-III promising genotypes are IGA-2013-20, IGA-2013-21, IGA-2013-22, IGA-2013-23 and IGA-2013-24 were fond promising for more than one yield trials. Similarly in cluster-IV genotypes IGA-2013-1, IGA-2013-2, IGA-2013-5, IGA-2013-6 and IGA-2013-8 found promising moreover, desirable genotypes. Hence there genotypes may be utilised as parents in hybridization programme for getting superior hybrids and segregants suitable for Chhattisgarh.

Table 3: Mean performance of genotype in individual cluster for different yield traits in Amaranthus

Cluster No.	Entries	Characters												
		Plant height (cm)	Number of leaves/ plant	Number of branches/ plant	Leaf yield (kg)/plot	Seed yield (gm)/ plot	Dry matter per cent	Fiber content (%)	Root length (cm)	Test weight (gm)	Leaf length (cm)	Leaf breadth (cm)	Petiole length (cm)	Stem girth (cm)
I	3	19.58	14.30	2.51	1.83	52.68	21.48	6.30	8.22	0.97	5.18	3.53	3.59	2.47
II	5	26.28	16.97	3.48	2.24	63.92	18.64	7.55	8.60	1.37	7.37	4.52	4.82	3.53
III	5	25.21	20.32	3.47	1.73	21.21	24.78	7.75	6.93	0.68	3.73	2.12	2.18	1.70
IV	6	31.37	29.61	3.45	2.51	79.64	19.78	7.44	7.71	1.35	6.84	4.12	4.89	3.17
V	6	25.62	19.71	4.19	2.36	66.75	22.17	7.35	7.98	1.32	5.59	3.55	4.31	2.93

Table 4: Desirable genotypes for important traits of Amaranthus based on individual clusters

| S. N.	Characters	Cluster i	Cluster ii	Cluster iii	Cluster iv	Cluster v
1	Plant height (cm)	IGA-2013-18	IGA-2013-14	IGA-2013-24	IGA-2013-2	IGA-2013-4
2	Number of leaves/plant	IGA-2013-18	IGA-2013-15	IGA-2013-24	IGA-2013-6	IGA-2013-9
3	Number of branches/plant	IGA-2013-18	IGA-2013-13	IGA-2013-22 & 24	IGA-2013-8	IGA-2013-9
4	Leaf yield (kg)/plot	IGA-2013-19	IGA-2013-16	IGA-2013-22	IGA-2013-5	IGA-2013-10
5	Seed yield (gm)/plot	IGA-2013-3	IGA-2013-16	IGA-2013-21	IGA-2013-6	IGA-2013-10
6	Dry matter per cent	IGA-2013-19	IGA-2013-16	IGA-2013-23	IGA-2013-2	IGA-2013-10
7	Fiber content (%)	IGA-2013-19	IGA-2013-14	IGA-2013-20	IGA-2013-2	IGA-2013-10
8	Root length (cm)	IGA-2013-19	IGA-2013-14	IGA-2013-22	IGA-2013-1	IGA-2013-9
9	Test weight (gm)	IGA-2013-3	IGA-2013-13	IGA-2013-24	IGA-2013-1	IGA-2013-10
10	Leaf length (cm)	IGA-2013-18	IGA-2013-16	IGA-2013-20	IGA-2013-1	IGA-2013-11
11	Leaf breadth (cm)	IGA-2013-18	IGA-2013-15	IGA-2013-21	IGA-2013-5	IGA-2013-9
12	Petiole length (cm)	IGA-2013-3	IGA-2013-15	IGA-2013-24	IGA-2013-6	IGA-2013-10
13	Stem girth (cm)	IGA-2013-19	IGA-2013-12	IGA-2013-24	IGA-2013-8	IGA-2013-17
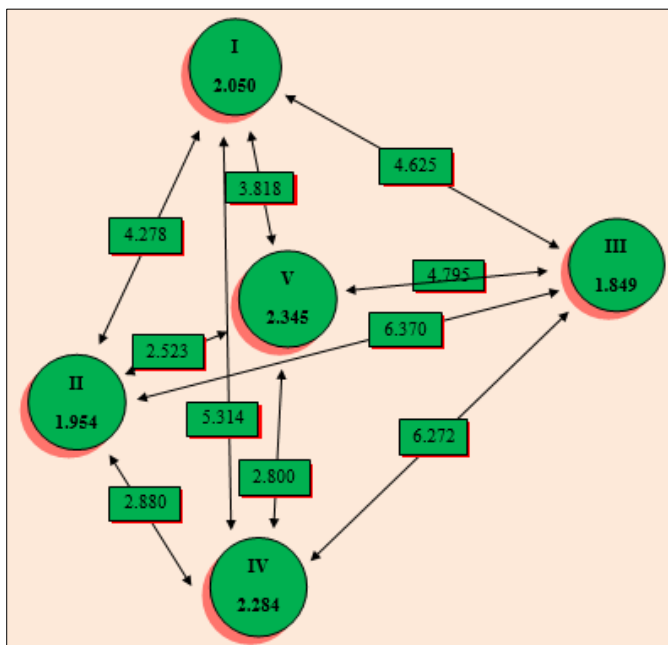
Fig 1: Diagrammatic representation of different inter and intra cluster distances of Amaranthus. (Values inside circle is intra cluster distances)

References

1. Anuja S. Evaluation of Amaranthus germplasm for green leaf yield (*Amaranthus* spp.). Advances in Plant Sciences. 2012; 25(2):463-466.
2. Chan KF, Sun M. Genetic diversity and relationships detected by isozyme and RAPD analysis of crop and wild species of Amaranthus. 2013; 8(19):2307-2311.
3. Chauhan D, Shrivastava AK, Patra S. Diversity of leafy vegetables used by tribal peoples of Chhattisgarh, India. Int. J Curr. Microbiol. App. Sci. 2014; 3(4):611-622.
4. Mahalanobis PC. Studies on the generalized distance in statistics. Proc. Nat. Inst. Sci. India. 1936; 21:49-55.
5. Mandal N, Das PK. Intra- and interspecific genetic diversity in grain Amaranthus using random amplified polymorphic DNA markers. Plant Tissue Cult. 2002; 12(1):49-56.
6. McGrath JM, Quiros CF. Genetic diversity at isozyme and RFLP loci in *Brassica campestris* as related to crop type and geographical origin. Theoretical-and-Applied-Genetics. 1992; 83(6-7):783-790.
7. Prakash D, Pal M. Nutritional and anti-nutritional composition of vegetable and grain amaranth leaves. J Sci. Food Agric. 1991; 57:573-583.
8. Prakash D, Nath P, Pal M. Composition, variation of nutritional contents in leaves, seed protein, fat and fatty acid profile of *Chenopodium* species. J Sci. Food Agric. 1993; 62:203-205.
9. Pandey RM, Singh R. Genetic divergence in grain amaranth (*Amaranthus hypochondriacus* L.). Genetika. 2011; 43(1):41-49.
10. Prakash D, Pal M. Nutritional and anti-nutritional composition of vegetable and grain amaranth leaves. Journal of Science of Food and Agriculture. 1991; 57:573-583.
11. Rai N, Yadav DS. Advances in vegetable production. Research co Book Centre New Delhi, 2005, 530-531.
12. Rao CR. Advance Statistical Methods in Biometrics Research. Hofaer Pub. Darion, 1952, 371-378.
13. Shobha S, Dharmatti PR. Genetic Divergence in Vegetable Mesta. Karnataka J Agri. Sci. 2004; 17(2):275-278.
14. Shukla S, Singh SP. Correlation and path analysis in grain amaranth (*Amaranthus* spp.). Indian Journal of Genetics and Pant Breeding. 2003; 63(2):163-174.
15. Shukla S, Pandey V, Pachauri G, Dixit BS, Banerji R, Singh SP. Nutritional contents of different foliage cuttings of vegetable amaranth. Pl. Food Hum. Nutr. 2003; 58:1-8.
16. Shukla S, Bhargava A, Chatterjee A, Singh SP. Estimates of genetic parameters to determine variability for foliage

yield and its different quantitative and qualitative traits in vegetable amaranth (*A. tricolor*). J Genet. Breed. 2004a; 58:169-176.

17. Van Beuningen LT, Busch RH. Genetic diversity among North American spring wheat cultivars, In: Analysis of the coefficient of parentage matrix. Crop Sci. 1997; 37:564-573.