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Genetic divergence studies in vegetable *Amaranthus* (*Amaranthus* spp. L.) genotypes

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Abstract

The study on estimation of genetic divergence in vegetable *Amaranthus* (*Amaranthus* spp. L.) genotypes was carried out during 2022-23 at Main Agricultural Research Station, University of Agricultural Sciences, Dharwad. In the present investigation forty-one genotypes including two checks were studied. Genetic divergence studies revealed clustering of germplasm into six clusters, irrespective of their origin. Many genotypes based on cluster means & genetic diversity were identified as potential parents. Among six clusters, cluster IV and V had the highest inter cluster distance (14.52) between genotypes, followed by cluster III and V (14.02) and cluster II and V (13.25). Whereas, cluster III and VI (6.11) had the lowest inter-cluster distance. Cluster III and VI consisted of genotypes which are having common characters such as early flowering, highly branching and small sized leaves. Genotypes with dwarf growth habit and high leaf: stem ratio were grouped in cluster IV. Whereas, cluster I and II consisted of majorly local and released genotypes having the characters of straight growing and less branching and genotype with quick growing and good leaf characters was grouped under cluster V.

Keywords: Cluster, genetic divergence, genotypes, vegetable *Amaranthus*

Introduction

Amaranthus (*Amaranthus* spp. L.) is a cosmopolitan genus of annual or short-lived perennial plants, belonging to Amaranthaceae family, and it originated from Central and South America. Since centuries *Amaranthus* species are being cultivated for grain and leaf purpose, characterized by a high degree of diversity having broad adaptability to different agro-ecological conditions (Snezana *et al.*, 2012) [1].

Almost universally, *Amaranthus* has been considered as poor people's resource (Akaneme and Ani, 2013) [2]. It substantially contributes to the nutritional well-being of rural people by providing the essential nutrients required for body growth and development and for prevention of diseases associated with nutritional deficiencies. It is a highly nutritious super food rich in protein, carbohydrates, dietary fibres, calcium, iron, manganese, zinc, vitamin-A, vitamin-C, vitamin-K, riboflavin, niacin, vitamin-B₆ and folate which enables it to combat mal-nutrition. Due to its nutritional superiority, *Amaranthus* has been suggested as an alternative source of rich protein leafy vegetable and cereal feeding those over populated and under nourished areas (Dhangra *et al.*, 2015) [3].

A comprehensive understanding of the magnitude of genetic diversity present in available germplasm for various traits, followed by effective selection adopting various breeding methodologies, is required to initiate the crop improvement programme. Genetic divergence study helps to develop cultivars with increased yield, wider adaptation, desirable qualities, pests and disease resistance. Several basic and applied genetic investigations on selected genotypes of *Amaranthus* species have been conducted while majority of the genotypes maintained are still remain untested (Pandey, 2005) [8]. Hence, there is a need to evaluate available germplasm for inclusive development of the crop. With this background, present investigation was undertaken to estimate genetic diversity among different genotypes of vegetable *Amaranthus*.

Material and methods

The experiment on genetic divergence studies in vegetable *Amaranthus* (*Amaranthus* spp. L.) genotypes was conducted during 2022-23 at Main Agricultural Research Station, University of Agricultural Sciences, Dharwad. The experiment was laid out in augmented block design (Federer, 1956) [4] with forty-one genotypes with three blocks and two checks replicated thrice. Genotypes were sown with spacing of 30 x 10 cm. From the five randomly selected plants, morphological traits and yield parameters were recorded. The observation's recorded includes, leaf length, leaf width, number of leaves plant⁻¹, leaf thickness, petiole length, leaf fresh and dry weight, chlorophyll content (SPAD unit). Plant height, number of branches plant⁻¹, number of nodes plant⁻¹, stem girth, stem fresh and dry weight, herbage yield and leaf: stem ratio. The mean data of parameters was subjected to ANOVA.

Hierarchical cluster analysis (Hierarchical clustering) is a general approach to cluster analysis, in which the objective is to group together objects or records that are "close" to one another. A key component of the analysis is repeated calculation of distance measures between objects, and between clusters once objects begin to be grouped into clusters. The outcome is represented graphically as a dendrogram. The initial data for the hierarchical cluster analysis of N objects is a set of N×(N-1)/2 object-to-object distances and a linkage function for computation of the cluster-to-cluster distances. Hierarchical cluster analysis for yield related traits was done by R software.

Results and Discussion

The selection of genetically dissimilar parents for hybridization is a basic need for the development of genotypes with desirable traits. Genetic diversity between genotypes indicates difference in the gene frequencies. Hierarchical clustering (Murtagh and Legendre, 2014) [6] is a method that groups related objects into groupings called clusters. The endpoint is a collection of clusters, each distinct from the others and the things within each cluster are broadly similar to one another. This is possible by clustering the entries based on Euclidean distance, as it represents the index of genetic diversity among the genotypes and clusters.

Hierarchical clustering of 41 vegetable *Amaranthus* genotypes based on phenotypic traits measured are represented in table 1 and figure 1. Cluster III was found to be largest comprising of 12 genotypes, followed by cluster IV and VI with 10 genotypes each, cluster I with five genotypes, cluster II with three genotypes and cluster V with only one genotype. Cluster III and VI consisted of genotypes which are having common characters such as early flowering, highly branching and small sized leaves. Genotypes with dwarf growth habit and high leaf: stem ratio

were grouped in cluster IV. Whereas, cluster I and II consisted of majorly local and released genotypes having the characters of straight growing and less branching and genotype with quick growing and good leaf characters was grouped under cluster V.

The average inter-cluster distance values for the six clusters are presented in table 2. Among six clusters, cluster IV and V had the highest inter cluster distance (14.52) between genotypes, followed by cluster III and V (14.02) and cluster II and V (13.25), indicated that the genotypes grouped in these clusters were genetically different. Whereas, cluster III and VI (6.11) had the lowest inter-cluster distance. Similar results were reported by Pandey and Singh (2011) [7]; Ahammed *et al.* (2013) [1]; Sarker *et al.* (2018) [10] and Tejaswini *et al.* (2018) [12]. There was a significant genetic difference between genotypes from different groups. Kallo *et al.* (1980) [5] proposed that the crosses between selected varieties from widely separated clusters were most likely to give desired recombinants.

The cluster means for yield and yield attributing traits in different clusters of vegetable *Amaranthus* genotypes are represented in table 3.

Results on cluster mean showed wide variations among the clusters for 16 traits. Invariably, the result showed cluster II revealed the highest herbage yield at 45 DAS (74.32 t ha⁻¹), leaf length at 20 (8.40 cm), 30 (13.06 cm) and 45 DAS (23.84 cm), leaf width at 45 DAS (15.32 cm), petiole length at 30 (3.55 cm) and 45 DAS (11.36 cm), leaf fresh weight at 45 DAS (75.02 g plant⁻¹), leaf dry weight at 45 DAS (17.26 g plant⁻¹), plant height at 45 DAS (90.00 cm), stem girth at 45 DAS (20.48 mm), stem fresh weight at 45 DAS (147.95 g plant⁻¹) and stem dry weight at 45 DAS (11.18 g plant⁻¹).

Regarding mean data of cluster V showed higher values for the traits *viz.*, herbage yield at 30 DAS (11.33 t ha⁻¹), leaf width at 20 (6.06 cm) and 30 DAS (9.22 cm), leaf thickness at 30 (1.2 mm) and 45 DAS (1.49 mm), leaf fresh weight at 30 DAS (17.98 g plant⁻¹), leaf dry weight at 30 DAS (3.46 g plant⁻¹), plant height at 30 DAS (33.8 cm), stem girth at 30 DAS (10.34 mm), stem fresh weight at 30 DAS (16.02 g plant⁻¹) and stem dry weight at 30 DAS (3.38 g plant⁻¹).

The cluster III showed higher mean values for the traits such as, number of leaves per plant at 45 DAS (105.53), chlorophyll content at 20 DAS (37.12), number of branches per plant at 45 DAS (11.86) and number of nodes per plant at 45 DAS (17.91). On the other hand cluster VI recorded the highest mean values with number of leaves per plant at 30 DAS (15.28), number of branches per plant at 30 DAS (7.98) and number of nodes per plant at 30 DAS (10.92). Whereas, cluster IV showed the highest mean values for leaf: stem ratio at 30 (1.39) 45 DAS (1.67). The results of present investigation on cluster means are in agreement with the findings of Ahammed *et al.* (2013) [1].

Table 1: Clustering of vegetable *Amaranthus* genotypes based on yield and yield attributing traits

Cluster	Number of genotypes	Genotypes
Cluster I	05	DAC- 01, DAC- 05, DAC-06, CO -2, Arka Suguna
Cluster II	03	DAC- 02, DAC- 04, CO - 1
Cluster III	12	DAC-03, NIC-22568, NIC-22570, IC-38174, IC-447684, IC-551459, IC- 551466, IC-551468, IC-551477, IC-551482, IC-551486, IC-551494
Cluster IV	10	DAC-07, DAC-08, Pusa Kiran, Arka Arunima, Renusree, Arun, Vaika, MSC-22-DWD-R-42, IC-582925, Pusa Lal Chulai
Cluster V	01	INDAM 1
Cluster VI	10	NIC-22569, IC-547515, IC-322041, IC-582922, IC-582928, IC-551462, IC-551483, IC-551492, IC-551506, IC-150202

Table 2: Average inter-cluster values in vegetable *Amaranthus* genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	0	8.85	7.37	7.68	11.17	7.57
Cluster II		0	11.34	11.46	13.25	11.45
Cluster III			0	6.84	14.02	6.11
Cluster IV				0	14.52	8.56
Cluster V					0	12.02
Cluster VI						0

Table 3: Mean of yield and yield attributing traits in different clusters of vegetable *Amaranthus* genotypes

Sl. No.	Clusters Characters		I(5)	II(3)	III(12)	IV(10)	V(1)	VI(10)
01.	Leaf length (cm)	20 DAS	6.56	8.40	6.32	5.38	5.60	6.06
		30 DAS	11.06	13.06	9.00	8.23	9.78	9.90
		45 DAS	19.80	23.84	14.81	14.50	19.82	18.02
02.	Leaf width(cm)	20 DAS	3.67	3.76	3.17	3.22	6.06	3.65
		30 DAS	6.28	6.28	4.03	4.80	9.22	4.60
		45 DAS	10.12	15.32	5.41	9.31	10.20	5.76
03.	Petiole length (cm)	30 DAS	2.94	3.55	2.21	1.94	3.38	2.77
		45 DAS	6.64	11.36	4.79	4.64	4.68	4.85
04.	Number of leaves plant ⁻¹	30 DAS	12.11	9.53	11.75	8.33	11.80	15.28
		45 DAS	70.42	31.60	105.53	51.51	57.00	102.92
05.	Leaf thickness (mm)	30 DAS	0.51	0.45	0.33	0.35	1.20	0.40
		45 DAS	0.79	1.09	0.40	0.68	1.49	0.48
06.	Chlorophyll content (SPAD unit)	20 DAS	31.72	31.57	37.12	30.88	32.82	36.88
07.	Leaf fresh weight (plant ⁻¹)	30 DAS	6.93	5.84	2.22	2.60	17.98	6.13
		45 DAS	58.44	75.02	21.34	38.17	49.37	25.38
08.	Leaf dry weight (plant ⁻¹)	30 DAS	1.20	1.06	0.42	0.47	3.46	1.10
		45 DAS	11.53	17.26	3.85	7.50	12.16	4.40
09.	Plant height (cm)	30 DAS	22.21	25.31	23.96	14.82	33.80	28.00
		45 DAS	55.86	90.00	59.83	35.77	63.00	59.68
10.	Number of branches plant ⁻¹	30 DAS	4.04	0.80	6.41	2.14	5.20	7.98
		45 DAS	10.66	7.13	11.86	8.69	9.60	11.58
11.	Number of nodes plant ⁻¹	30 DAS	8.48	7.33	9.41	6.47	7.80	10.92
		45 DAS	17.78	17.06	17.91	13.35	15.60	15.90
12.	Stem girth (mm)	30 DAS	4.81	4.65	4.50	2.85	10.34	6.01
		45 DAS	14.63	20.48	11.31	11.91	13.78	10.25
13.	Stem fresh weight (plant ⁻¹)	30 DAS	5.67	6.23	4.41	1.96	16.02	9.34
		45 DAS	57.59	147.95	44.10	25.56	64.63	43.95
14.	Stem dry weight (plant ⁻¹)	30 DAS	1.01	0.75	0.64	0.26	3.38	1.26
		45 DAS	5.46	11.18	3.91	2.76	4.14	5.22
15.	Herbage yield (t ha ⁻¹)	30 DAS	4.19	4.02	2.21	1.51	11.33	5.15
		45 DAS	38.67	74.32	21.81	21.23	38.00	23.11
16.	Leaf: Stem ratio	30 DAS	1.18	0.97	0.54	1.39	1.12	0.86
		45 DAS	1.17	0.50	0.50	1.67	0.76	0.62

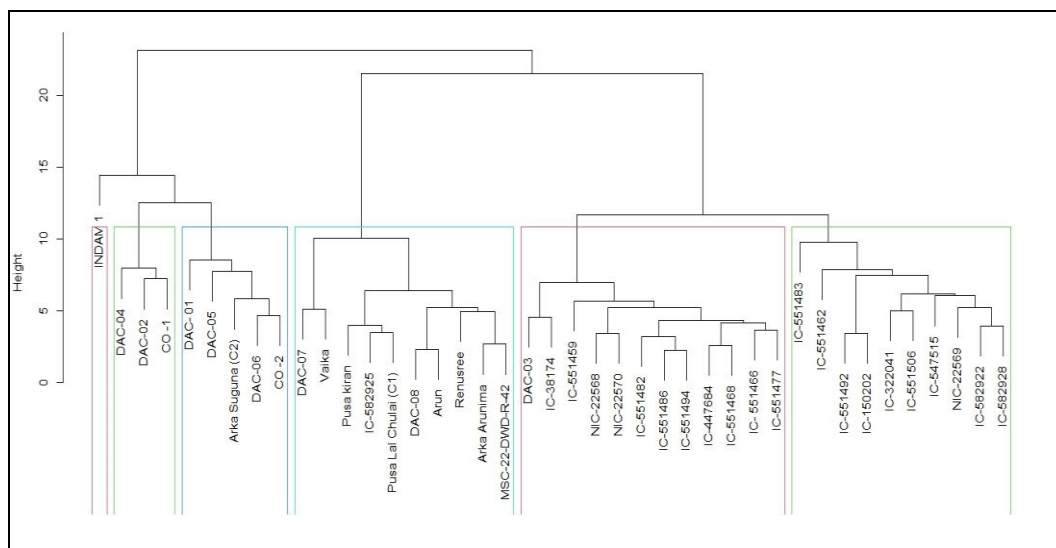


Fig 1: Dendrogram representing the hierarchical clustering of vegetable *Amaranthus* genotypes

Conclusion

From the present study, it may be concluded that, higher inter cluster distance between cluster IV and V and cluster III and V, indicated the genotypes grouped in these clusters were genetically different. Hence, inter-mating between the diverse genotypes superior for different combination of traits included in these clusters could be expected to give transgressive segregates in the advanced generations. The genotypes classified under cluster II could be considered for selecting as high yielding with good leaf characters and cluster IV could be considered for selecting the genotypes with better leaf: stem ratio.

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