Genetic Divergence Analysis in Amaranth (*Amaranthus spp.*) by using Morpho-agronomic Traits in Western Uttar Pradesh, India

Abstract

The field experiment was conducted during 2021-22. During the study the analysis of variance for 19 diverse genotypes of Amaranthus were designed in randomized block design and revealed significant difference for all the 12 characters, this indicated the presence of wide spectrum of variability among the genotypes. The analysis of genetic divergence through Mahalanobis D^2 statistics revealed that a considerable genetic diversity was found among genotypes. 19 genotypes of Amaranthus were grouped into 5 clusters. Out of these 5 clusters, Cluster II contains maximum number of genotypes that is seven, followed by cluster I which comprising six genotypes, Cluster III comprising four genotypes, whereas cluster IV and V containing only one genotype each. All the desired combinations of traits should be considered, while breeding programme for selecting high yielding genotypes and suitable for breeders to achieving improved plant type.

Keywords

Genetic Diversity, Amaranthus, Morpho-agronomic Traits, breeding

Introduction

"Amaranthus is a genus belonging to the Amaranthaceae family that has originated in South America. This genus contains approximately 70 species and out of these most of them are cultivated as leafy vegetables, grains and ornamental plants in different parts of the world" (Espitia-Rangel 1994; Ebert et al. 2011). "There are three major grain producing Amaranthus species, A. caudatus, A. cruentus and A. hypochondriacus, all believed to originate from Central and South America; and three major leafy vegetable species, A. tricolor, A. dubius and A. blitum (A. lividus), of which A. tricolor is thought to originate from India or Southern China, A. blitum from Central Europe and A. dubius from Central America" (Grubben, 1993). "Amaranthus species are significant food crops that can withstand heat, drought, diseases, and pests" (Shukla et al. 2010). "It is one of those rare plants whose leaves are eaten as a vegetable while the seeds are used as cereals. Besides, it is also used as fodder, ornamental, organic red dye and for industrial purposes. It is high in protein, particularly in the amino acid, Lysine, which seeds is low in the cereal grains. Amaranth is one of the highest grains in fiber content. This makes Amaranth an effective agent against cancer and heart disease. Amaranth is also rich in many vitamins and minerals and it also does not contains gluten. They grow in a wide range of agroecological zones and are found in most tropical and subtropical areas” (Katiyar et al. 2000; Schippers 2000). In India it is cultivated in Jammu and Kashmir, Himachal Pradesh, Uttarakhand, Sikkim, Assam, Meghalaya, Arunachal Pradesh, Nagaland, Tripura, Jharkhand, Chhattisgarh, Maharashtra, Gujarat, Orissa, Karnataka, Kerala and Tamil Nadu both in hill and plain regions.

The grain Amaranthus are paleo-allote tetraploids. The multivariate analysis has been established by several investigators for measuring the degree of divergence and for ascertaining the relative contribution of different characters to the total divergence. Wide genotypic variation has been seen in Amaranthus as a result of frequent interspecific and intervarietal hybridization. Amaranthus also exhibit a tremendous level of diversity. To assess the genetic diversity of local Amaranthus, it is crucial to determine the proper genotype. Maintaining genetic variety, examining local genetic diversity, and selecting ecotypes with high nutritional value in their native environments all require the identification and preservation of germplasm. Amaranthus is still a minor crop that is not fully utilised for vegetable production. Despite having outstanding nutritional properties, little work has been done to improve its genetic profile.

Amaranthus shows a wide diversity in growth habit, leaf shape, colour and size, plant size and inflorescence characteristics. Among several statistical methods developed for measuring divergence between populations, multivariate analysis of D2 statistics has been effectively used for quantitative estimation of genetic variability according to Mahalanobis (1936) D2 statistics, which can be effectively used for assessing the genetic divergence between populations and helping in selection of desirable parents for crossing programme. Recent research indicates that “under cultivated conditions, Amaranth produces fresh leaf yields of up to 40 t/ha. The yield of grain amaranth is highly variable with 1000 kg/ha considered a good yield” [Shukla et al. (2010)]. The purpose of this research is to Genetic Divergence Analysis in Amaranth (Amaranthus spp.) by using Morpho-agronomic Traits in Western Uttar Pradesh, India.

Material and Methods

The experiment was conducted during 2021-22 at the Horticultural Research Center of the Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, using 19 diverse germplasm collected from IARI New Delhi as shown in Table 1. Randomized block design with three replications was used to conduct the experiment. The observations were recorded on randomly selected plants for the various characters i.e. days to germination, days to 50% flowering, days to maturity, plant height (cm), inflorescence length (cm), number of leaves per plant, number of branches per plant, fresh leaf weight (g), biological yield per plant (g), biological yield ton per hectare,seed yield per plant (g) and seed yield per hectare (kg/ha).

Table 1. List of cultivars/Germplasm included in the trial

S. No.	Notation	Germplasm	Source
1	T_1	Arun	Division of Vegetable Science, IARI, New Delhi
2	T_2	Arka Samraksha	IIHR, Bengaluru
3	T_3	Arka Suguma	IIHR, Bengaluru
4	T_4	CO-2	Coimbatore, Tamilnadu
5	T_5	CO-3	Coimbatore, Tamilnadu
6	T_6	CO-5	Coimbatore, Tamilnadu
7	T_7	Krishna Sree	Division of Vegetable Science, IARI, New Delhi
8	T_8	IC-151606	Division of Vegetable Science, IARI, New Delhi
9	T_9	IIHR-109-1	IIHR, Bengaluru
10	T_{10}	RNA-1	Division of Vegetable Science, IARI, New Delhi
11	T_{11}	Reni Sree	Division of Vegetable Science, IARI, New Delhi
12	T_{12}	Pusa Lal Chaulai	Division of Vegetable Science, IARI, New Delhi
13	T_{13}	Pusa Kiran	Division of Vegetable Science, IARI, New Delhi
14	T_{14}	Arka Arunima	IIHR, Bengaluru
15	T_{15}	Arka Verna	IIHR, Bengaluru
16	T_{16}	CO-4	Coimbatore, Tamilnadu
17	T_{17}	Kannara Local	Division of Vegetable Science, IARI, New Delhi
18	T_{18}	IIHR-109-4	IIHR, Bengaluru
19	T_{19}	IC-151608	Division of Vegetable Science, IARI, New Delhi

Statistical Analysis

All the statistical analysis to assess the genetic diversity in Amaranthus were performed by using standard formulas.

Results and Discussion

Significant differences were found for all the twelve characters in the analysis of variance for the 19 genotypes, revealing a wide range of variability among the genotypes.

All 19 genotypic sample of Amaranthus under research were divided into 5 clusters based on Mahalanobis D^2 values. The distributions of Amaranthus genotypes into five clusters are presented in Table 2. Cluster II contains maximum number of 07 genotypes comprising namely as Arun, Arka Samraksha, CO-2, CO-3, Krishna Sree, Reni Sree and Kannara Local, followed by cluster I which comprising 06 genotypes namely Arka Suguna, CO-5, IIHR-109-1, RNA-1, Arka Arunima and Pusa Kiran, Cluster III comprising 04 genotypes namely IC-151606, Arka Verna, CO-4 and IIHR-109-4,whereas cluster IV and V containing only 01 genotype in each, namely IC-151608 and Pusa Lal Chaulai respectively. The small variation in D^2 values makes it clear that the genotypes in the cluster do not differ significantly in terms of their relative genetic distance. Therefore, these genotypes that are genetically different can be used as promising genotypes for use as parents in hybridization.

Based on the statistically significant difference in cluster means for several parameters, diversity among the genotypes was also assessed. The cluster mean calculated for twelve characters under study have been presented in Table 3. Days to germination showed highest mean for cluster number IV (7.07) followed by cluster V (7.00), whereas lowest mean in cluster number I (6.11). 50 percent flowering revealed highest mean in cluster number IV (57.47) followed by cluster III (52.70) and lowest mean for cluster number I (46.18), Days to maturity exhibited highest mean in cluster number IV (104.93) and lowest mean in cluster number II (96.08). Plant height revealed highest mean in cluster number IV (71.21) and lowest mean in cluster number II (51.27). Inflorescence length showed highest mean in cluster number III (33.16) and lowest mean in cluster number V (25.93). Number of leaves per plant exhibited highest mean in cluster number IV (45.07) and lowest mean in cluster number III (36.09). Number of branches per plant revealed highest mean in cluster number IV (3.80) and lowest in cluster V (2.20). Fresh leaf weight exhibited highest mean in cluster number IV (6.05) and lowest mean in cluster number V (3.36). Biological yield per plant revealed highest mean in cluster number V (212.82) and lowest mean in cluster number II (123.00). Biological yield ton per ha exhibited highest mean in cluster number V (45.14) and lowest mean in cluster number II (16.85). Seed yield kg per ha showed highest mean in cluster number V (15.91) and lowest mean in cluster number III (5.61). Seed yield per plant revealed highest mean in cluster number V (184.70) and lowest mean in cluster number III (144.13). There was parallelism between genetic and geographical diversity. On the basis of cluster mean values for different characters it can be concluded that the varieties fall in different cluster for their respective character may be selected for hybridization programme. The viewpoint has been supported by the work of **Akther *et al.* (2013), Kumar *et al.* (2019) and Rana *et al.* (2005).**

The average intra and inter cluster D2 presented in Table 4. revealed maximum inter cluster D2 value (7.472), between cluster III and V followed by cluster IV and V (7.066), whereas the minimum inter cluster D2 value (2.959) was recorded between cluster I and II . The maximum intra cluster distance were found (2.511) for cluster III followed by cluster I (2.474), (2.180) for cluster II and (0.452) for cluster IV, whereas minimum intra cluster value was recorded in cluster V (0.00). "It is apparent therefore; the genotypes of cluster do not differ significantly with regards to their relative genetic distance as indicated from low variation of D^2 values. Crosses suggesting parent belonging to most divergence clusters would be expected to manifest maximum heterosis and also wide variability of genetic architecture. Thus, the crosses between the genetically diverse genotypes of cluster I and V based on genetic diversity and superiority with respect to any of traits the genotype may be identified and may be involve in crossing for obtaining high heterotic population, segregates and also may be exploited for development of hybrid" . [**Shukla *et al.* (2010), Arif *et al.*, (2013), Chattopadhyay *et al.* (2013), Gerrano *et al.* (2015) and Ngomuo *et al.*, (2017)].**

Significance of the study:

After assessing all the varieties and their characteristics it is suggested that Pusa Lal Chaulai and Pusa Kiran varieties shows better result in terms of yield attributing characters therefore these varieties can be used further in breeding improvement programmes.

Conclusion

The Amaranthus genotypes employed in this study can be successfully used for future breeding programmes, in accordance with the Mahalanobis D^2 analysis. For the majority of the examined traits, inter-crossing of genotypes exhibiting the greatest genetic divergence should produce superior heterotic hybrids and valued segregants in successive generations. It is anticipated that better performing variants will be developed to boost field Amaranthus yield.

The individual characters contributing maximum to the D^2 values have greater emphasis for deciding the cluster for the purpose of further breeding improvement programme. The maximum contribution percentage was found with days to germination contributes maximum towards total divergence and this was followed by days to maturity, inflorescence length, number of leaves per plant, number of branches per plant, 50 percent flowering, fresh leaf weight, biological yield ton per hec, seed yield kg per hec, plant height, seed yield per plant and biological yield per plant.

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Table 2. Number of genotypes in each cluster

Clusters	No of genotypes	Genotypes
I	6	Arka Suguna, CO-5, IIHR-109-1, RNA-1, Arka Arunima, Pusa Kiran
II	7	Arun, Arka Samraksha, CO-2, CO-3, Krishna Sree, Reni Sree, Kannara local
III	4	IC-151606, Arka Verna, CO-4, IIHR-109-4
IV	1	IC-151608
V	1	Pusa Lal Chaulai

Table 3. Cluster mean of 19 genotypes of Amaranth for 12 characters

Clusters		Days to Germination	50% Flowering	Days to maturity	Plant height (cm)	Inflorescence length (cm)	No. of leaf per plant	No. of branches per plant	Fresh leaf weight (g)	Biological yield per plant (g)	Biological yield ton/ha	Seed yield per ha (kg/ha.)	Seed yield per plant (g)
I	**Mean**	6.11	46.18	96.26	59.14	31.31	38.52	2.55	3.79	193.68	28.28	7.37	159.69
	± SE	0.43	3.96	4.92	6.94	1.19	5.18	0.28	0.53	6.66	3.12	1.99	8.63
II	**Mean**	6.50	47.13	96.08	51.27	30.26	42.93	2.73	3.66	123.00	16.85	8.78	160.15
	± SE	0.40	4.15	2.58	4.22	1.06	1.21	0.36	1.05	16.06	2.63	1.15	15.05
III	**Mean**	6.72	52.70	99.88	51.96	33.16	36.09	2.44	5.38	146.56	19.26	5.61	144.13
	± SE	0.52	3.83	3.30	4.85	1.84	3.15	0.16	1.64	44.27	5.72	0.92	9.97
IV	**Mean**	7.07	57.47	104.93	71.21	31.37	45.07	3.80	6.05	186.00	31.85	8.97	164.08
	± SE	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
V	**Mean**	7.00	49.53	96.27	61.50	25.93	39.20	2.20	3.36	212.82	45.14	15.91	184.70
	± SE	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Table 4. Average of inter and intra cluster distances

Clusters	I	II	III	IV	V
I	**2.474**				
II	2.959	**2.180**			
III	3.490	3.541	**2.511**		
IV	5.649	5.899	5.762	**0.452**	
V	5.477	6.126	7.472	7.066	**0.000**