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Original Research Article

Studies on Genetic Divergence in Amaranthus Genotypes (*Amaranthus hypochondriacus* L.)

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ABSTRACT

Keywords

Amaranthus,
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In the present investigation 67 germplasm including four checks of *amaranthus* (*Amaranthus hypochondriacus* L.) maintained in research plot of Department of Plant Breeding and Genetics at Birsa Agricultural University, Kanke. Genetic divergence studies revealed clustering of germplasm into twelve clusters, irrespective of their origin. Many genotypes based on cluster means & genetic diversity were identified as potential parents. Highest protein content was being shown by cluster XI followed by cluster VI and cluster X, highest seed yield /plant was found in cluster VI followed by cluster III and cluster II.

Introduction

Amaranthus, collectively known as amaranth is a cosmopolitan genus of annual or short-lived perennial plants. Some amaranth species are cultivated as leaf vegetables, pseudo-cereals, and ornamental plants. Most of the species from *Amaranthus* are summer annual weeds and are commonly referred to as pigweed. Amaranth originated in America and is one of the oldest food crops in the world, with evidence of its cultivation reaching back as far as 6700 BC. The nutritive value as per 100 gram of grain amaranth is energy-1,554 kJ (371 kcal), carbohydrates-65.25 g, fat-7.02g saturated fat-1.459g, protein-13.56g. Amaranth is not usually planted in South Africa but occurs as a volunteer crop after the first rains; it is harvested from the wild. Genetic divergence study helps to develop cultivars with increased yield, wider adaptation, desirable qualities, pest and disease resistance. Contribution of component traits to yield either through their direct effects or indirect effects cannot be differentiated from more correlation studies. Manggoel *et al.*, (2012) suggested that path coefficient analysis would be of great importance to a plant breeder as a flexible means of relating the correlations coefficients between variables in a multiple system to the functional relation among them.

Materials and Methods

The present investigation was carried out in the experimental area of Department of Plant Breeding & Genetics, Birsa Agricultural University, Ranchi. Sixty seven germplasm of grain amaranth were taken from Underutilized Crops research scheme of Plant Breeding and Genetics department along with seven check varieties in the present experiment. The parental material for the present study comprised of 60 germplasm along with **s**even checks varieties.

The data on twelve quantitative characters were recorded on randomly in each selected plant for characters like Plant Height (cm), Inflorescence length (cm), Leaf length (cm), Leaf width (cm), Petiole Length (cm), Days to 50% flowering, Number of branches per plant, Days to 80% Maturity, Seed weight (g/10 ml), Seed yield per plant (g), Oil Content (%), Protein Content (%). The mean value is used for statistical analysis. Analysis of variation was done for partitioning the total variation into variation due to treatments and replications. Heritability in broad sense was calculated by the formulae given by Lush (1949) and Johnson (1955). The genetic advance was obtained by the formulae given by Johnson (1955).

Results and Discussion

The analysis of variation was carried out among 67 genotypes including seven checks (GA-1, GA2, VL-44, Suvarna, GA-3, BGA-2, RMA-7), out of 12 character studied the analysis of variance revealed highly significant difference among the genotypes for the all the yield attributing traits which is shown in Table 1. Total sixty-seven genotypes were divided into 12 clusters, cluster five shows maximum intra-cluster distance (19.56), while cluster 11 and 12 showed maximum inter-cluster distance as shown in Table 2.

The minimum intra cluster distance (0.00) in VI, VII, IX, X ,XI. Intra cluster values ranged from 0.00 to 19.56 and cluster XII is the most diverse group as shown in Table 3. The diverse clusters derived could be used in hybridization programme to generate wide range of transgressive segregants in population to develop high yielding grain amaranth varieties. In present study protein content is responsible for contributing to maximum divergence. The similar results were found out by Joshi and Rana (1995).

All the sixty seven genotypes were grouped in to twelve clusters based on quantitative characters. Cluster IV was the largest which accommodated twenty four (24) genotypes followed by cluster V (12 genotypes), cluster I (8 genotypes), cluster II and III (7 genotypes), cluster VIII and XII accommodated two genotypes while clusters VI, VII, IX, X and XI accommodated one genotype in each. Cluster means of characters revealed that genotypes accommodated under cluster IV have most of the desirable characters.

Table.1 Analysis of variance of different characters in grain amaranth

Sources of variation	df	Plant height (cm)	Inflorscence length (cm)	Leaf length (cm)	Leaf width (cm)	Petiole length (cm)	Days to 50% flowering	Number of branches/ plant	Days To maturity	Seed weight (g/10ml)	Seed yield/ plant (g)	Oil content (%)	Protein content (%)
Treatment	66	1494.7**	116.6**	13.55**	3.861**	8.306**	209.60**	9.038**	253.68**	1.261*	93.622**	23.903**	31.349**
Replication	2	0.096	0.002	0.002	0.003	0.001	0.154	0.001	1.209	0.001	0.313	0.070	0.039
Error	132	9.571	4.070	0.617	0.236	0.248	9.442	0.227	27.294	0.408	93.622	0.163	0.034
*, ** Significant at 5% and 1% probability levels, respectively.													

Table.2 Composition of genotypes in different clusters based on yield components

Sl. No.	Cluster	No. of Genotype	Genotype(s)
1	Cluster I	8	SKGPA-65, SKGPA-68, SKGPA-67, BAUGA 33, IC- 35716, SKGPA-61, IC-81698-B, SKGPA-66
2	Cluster II	7	IC- 32195, IC- 35615, IC- 35661, IC-21803-A, IC- 35635, IC-21937,IC-432086
3	Cluster III	7	IC-35713,IC-95204,IC-35717,IC-35711,IC-95389,IC-21938,IC-35735
4	Cluster IV	24	BAUGA 78,BAUGA 76,SKGPA-63,SKGPA-73,BAUGA 5,BGA -2,BAUGA 10,BAUGA-90,BAUGA 9,BAUGA-69,BAUGA 49,IC-120649,SKGPA-62,BAUGA 47,IC-120670,SKGPA-69,IC-120689,SKGPA-70,SKGPA-71,BAUGA 35,BAUGA 38,BAUGA22,BAUGA 79,BAUGA 69
5	Cluster V	12	GA-3,IC-120668,BAUGA-81,BAUGA 28,BAUGA 58,IC-95406,BAUGA 6,BAUGA 75,IC-22186,GA-1,BAUGA 68,VL 44
6	Cluster VI	1	SKGPA-72
7	Cluster VII	1	GA- 2
8	Cluster VIII	2	IC-35404, BAUGA 42
9	Cluster IX	1	BAUGA 17
10	Cluster X	1	IC-94654
11	Cluster XI	1	IC-33193
12	Cluster XII	2	SUVARNA, RMA 7

Table.3 Intra-and inter-cluster (diagonal) distance of different genotypes in grain amaranth

Clusters	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**	**Cluster IX**	**Cluster X**	**Cluster XI**	**Cluster XII**
Cluster I	**13.37**	18.74	21.22	40.29	26.79	16.74	38.97	44.76	43.54	19.81	27.71	70.08
Cluster II		**14.18**	20.67	38.07	24.73	20.06	31.71	40.97	44.49	19.42	23.50	66.64
Cluster III			**15.46**	42.71	28.36	24.96	35.30	40.37	50.57	24.34	20.27	70.73
Cluster IV				**19.06**	25.47	47.86	28.73	27.83	24.15	42.51	51.79	36.14
Cluster V					**19.56**	34.30	26.40	28.67	32.33	30.06	36.14	50.76
Cluster VI						**0.00**	42.94	54.68	52.40	17.04	28.35	78.59
Cluster VII							**0.00**	28.07	43.71	31.99	41.90	47.87
Cluster VIII								**12.07**	38.26	47.12	46.54	39.02
Cluster IX									**0.00**	49.94	60.64	39.16
Cluster X										**0.00**	29.95	71.91
Cluster XI											**0.00**	78.68
Cluster XII												**16.06**

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