# Genetic diversity of quantitative traits in grain amaranth (Amaranthus hypchondriacus L)

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#### **ABSTRACT**

Investigations on genetic divergence in twenty six genotypes of grain amaranth (*Amaranthus hypchondriacus* L) were conducted at the research farm of Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during rabi season 2017-2018. All genotypes were grouped into five clusters indicating wide diversity in the experimental material. Cluster III was the largest comprising 11 genotypes while cluster II was solitary with only one genotype. The inter-cluster distance was maximum between clusters II and V followed by IV, III and I. The diverse clusters derived could be used in hybridization programmes to evolve high yielding varieties of grain amaranth.

Keywords: Clusters; diversity; grain amaranth; genotypes; quantitative traits

### INTRODUCTION

Grain amaranth is dicotyledonous belonging to genus Amaranthus and family Amaranthaceae. It is still an underutilized crop due to lack of popularity and poor yield. The precise details on acreage and productivity of grain amaranth are still unknown. However it is reported that it covers 40-50 thousand hectares area with 1,200 kg/ha productivity in India (Dua et al 2009) and 2,000 kg/ha production in plain zone of Chhattisgarh (Yadav 2016). It has 14-16 per cent protein with lysine content (5.5%) more than the other cereals. Amaranth is an ancient grain that is loaded with healthy nutrients. Amaranth is considered as a 'Superfood' because it contains high nutraceutical values. Divergence analysis is a powerful tool to formulate suitable breeding methods and superior parents for crossing to increase grain yield. Therefore the present study was undertaken to estimate the genetic diversity for 13 quantitative characters in the germplasm of grain amaranth.

#### MATERIAL and METHODS

Twenty six genotypes along with three checks viz CG Rajgira-1, RMA-7 and Suvarna of grain amaranth were grown in RBD with three replications

at the research farm of Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during rabi season 2017-2018. Seed material was obtained from different coordinating centres of potential crops. The rows were 3 metres long and 45 cm apart. Whole package of practices was followed to raise the crop. Phenotypic observations were recorded for 13 quantitative characters. Statistical analysis was computed on the mean basis across the genotypes following Mahalanobis (1936) to measure the genetic divergence.

#### RESULTS and DISCUSSION

Based on divergence analysis, 26 genotypes were grouped into 5 clusters (Table 1). Maximum number of genotypes were included in cluster III (11) followed by cluster I (6), cluster V (5) and cluster IV (3). Only 1 genotype was grouped in cluster II due to natural selection. Intra- and inter-cluster distance D² values among 26 genotypes of grain amaranth are given in Table 2. The intra-cluster distance in cluster IV (8,329.67) was maximum followed by cluster I (1,920.13) and cluster III (1,765.43). It indicated considerable diversity. The minimum and negligible intra-cluster distance exhibited by clusters V (841.04) and II (0.00) indicated limited diversity among the

constituents of genotypes. Inter-cluster distance was maximum between clusters II and V (24,779.20) followed by clusters IV (18,141.58), III (4,245.44) and I (2,666.61). It shows that diversity was much between each other. Therefore it would be logical to incorporate genotypes from these clusters in further breeding programmes. Highest cluster mean value was recorded in cluster II (Table 3) for most of the characters viz panicle length, dry weight of panicles, harvest index, 1,000-grain weight and grain yield per plant, in cluster IV for stem girth and in cluster III for panicle width.

These observations are similar to the findings reported by Erum et al (2012).

It means crossing between genotypes of these 3 clusters may appear to be most promising. Earliness to days to 50 per cent flowering and dwarf stature of cluster III; early maturity and low biological yield per plant in cluster II; low dry weight of stem and leaves in cluster I may be included in hybridization programmes for development of high yielding varieties in grain amaranth.

Table 1. Genotypes included in different clusters based on D<sup>2</sup> analysis in grain amaranth

Cluster	Number of genotypes	Genotypes			
I	6	IC-95430, RGA-8, SKPGA-96, BGA-7, RMA-7, IC-81698-13			
II	1	RGA-10			
III	11	RGA-6, CG Rajgira-1, SKPGA-52, BUGA-30, IC98957, BGA-10, BAUGA 78-2, BAUGA 47-1, BGA 10-1, SKNA 1207, RMA-6			
IV	3	SKPGA 102, IC 35615, Suvarna			
V	5	BAUGA-13, BAUGA-17, BGA-2, SKPGA-101, SKPGA-70			

Table 2. Intra- and inter-cluster distance D<sup>2</sup> values among 26 genotypes of grain amaranth

Cluster	I	II	III	IV	V
I II III IV V	1,920.13	22,403.67 0.00	5,210.79 41,505.00 1,765.43	17,190.00 8,917.89 32,275.27 8,329.67	2,666.61 24,779.20 4,245.44 18,141.58 841.04

Table 3. Cluster means for grain yield and its components in 26 genotypes of grain amaranth

Character		Cluster number					
	I	II	III	IV	V		
Days to 50% flowering	52.47	46.88	48.94	51.33	48.57		
Days to maturity	142.76	128.44	148.17	143.19	148.14		
Plant height (cm)	131.45	153.88	125.33	137.98	134.02		
Stem girth (cm)	9.78	9.03	6.39	10.44	6.20		
Panicle length (cm)	58.50	68.88	41.29	47.83	48.31		
Panicle width (cm)	29.51	29.72	30.41	29.10	29.71		
Dry weight of leaves (g)	2.68	3.56	2.30	2.06	2.20		
Dry weight of panicles (g)	76.19	147.28	45.23	124.05	65.64		
Dry weight of stem (g)	36.11	65.31	37.57	68.49	59.62		
Biological yield/plant (g)	114.44	207.50	81.56	191.45	125.49		
1,000-grain weight (g)	1.05	1.25	1.03	0.98	1.02		
Harvest index (%)	26.22	77.84	15.04	18.69	17.21		
Grain yield/plant (g)	21.15	38.37	17.84	10.45	13.84		

Number of genotypes- Cluster I: 6, Cluster II: 1, Cluster III: 11, Cluster IV: 3, Cluster V: 5

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