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Short Communication

Genotypic diversity in vegetable amaranth for antioxidant, nutrient and agronomic traits

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Abstract

In this investigation, magnitude of genetic divergence was studied in 25 vegetable amaranth using D^2 statistics. The genotypes were grouped into 5 clusters with the highest number of genotypes (10) in cluster V. High inter-cluster distance indicated that genotypes of cluster III were far diverged from the genotypes in cluster I, II and IV, respectively. The PCA indicated prominent contribution of protein, foliage yield, leaf area and Zn content towards total divergence. Cluster I and Cluster III could be considered for excellent antioxidant and nutrients and high foliage yield. Cluster II for nutrients, cluster IV for antioxidant and nutrients and cluster V for antioxidant, nutrients, and foliage yield. Based on inter-cluster distance, intra-cluster and scatter diagram, the genotypes AA28, AA15, AA19, AA26, AA9 and AA17 would be potential genotypes for generating transgressive segregants.

Key words: Ascorbic acid, beta carotene, multivariate analysis, D^2 statistics, clustering.

Vegetable amaranth (*Amaranthus tricolor*) leaves are good source of protein with critical amino acid (lysine and methionine), dietary fiber, dietary minerals, antioxidant like ascorbic acid and carotenoid (Venskutonis and Kraujalis 2013). Besides, it can grow successfully under a variety of soil and agro climatic conditions (Katiyar et al. 2000). Some metalloenzymes like catalase (Fe), super oxide dismutase (Mn and Zn) required Fe, Mn and Zn minerals for their antioxidant activity (Swaran 2009). Recently, the genus has been reported to have medicinal value including anticancer properties (Dusgupta and De 2007). Although vegetable amaranth is used as a cheap source of a variety of antioxidants, nutrient and the staple food crop in many parts of the world, little efforts have been made for its genetic improvement (Shukla et al. 2006). Genetic diversity assessment is very useful tools that help a breeder to identify diverse parental combinations for creation of segregating progenies with genetic variability. It also facilitates introgression of desirable genes from a diverse germplasm into the existing genetic base population (Thompson et al. 1998). However, reports on diversity analysis of *Amaranthus tricolor* are sparse (Shukla et al. 2010). Therefore, the present investigation was conducted to categorize the vegetable amaranth genotypes based on the contribution of antioxidant, nutrient content, and contributing agronomic traits towards divergence and to identify genotype for utilization in future breeding program.

Twenty five vegetable amaranth genotypes were investigated in the experimental field of BSMRAU for two successive years (2014 and 2015) in a completely randomized block design with three replications. The unit plot size of each genotype was $4m^2$ for foliage yield and $1m^2$ for antioxidant, nutrient and agronomic traits. The row-to-row distance was 25 cm and plant to plant 5 cm. Appropriate cultural practices were followed. Data were recorded at 30 DAS on 10 randomly

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selected plants in each replication for plant height (cm), leaves plant^{-1}, leaf area (cm^2), fiber (%) and stem diameter (cm), foliage yield, beta carotene (mg g^{-1}), ascorbic acid (mg 100 g^{-1}) Fe (mg kg^{-1}), Zn (mg kg^{-1}), Mn (mg kg^{-1}), protein (mg 100 g^{-1}), Ca (g 100 g^{-1}) K (g 100 g^{-1}), Mg (g 100 g^{-1}) and nickel (mg kg^{-1}). Protein was estimated as per the method of Lowry et al. (1951); the extraction and estimation of beta carotene as per Jensen (1978); the estimation of fibre content according to Watson (1994) and ascorbic acid was analyzed by the method given by Glick (1954). The analyses of variance (ANOVA) were done according to Singh and Chaudhary (1985). Data were subjected to principal component analysis using Mahalanobis (1936) D^2 values extended by Rao (1952) utilizing GENSTAT5 Computer software program.

Principal component analysis

The first two principal components (PCs) contributed 32.83% and the remaining seven PCs contributed 78.95% of the variability. Shukla et al. (2010) observed 68% of the total variation for first four PCs in vegetable amaranth. A two-dimensional scatter diagram (Z_1-Z_2) was constructed by computing principal component score 1 in X axis and component score 2 in the Y axis (Fig. 1). The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that there exists considerable diversity among the genotypes. The scattered diagram displayed the genotypes, AA28, AA15, AA19, AA26, AA9 and AA17 were distantly located in their respective clustering which suggesting more diverged from the rest of the genotypes.

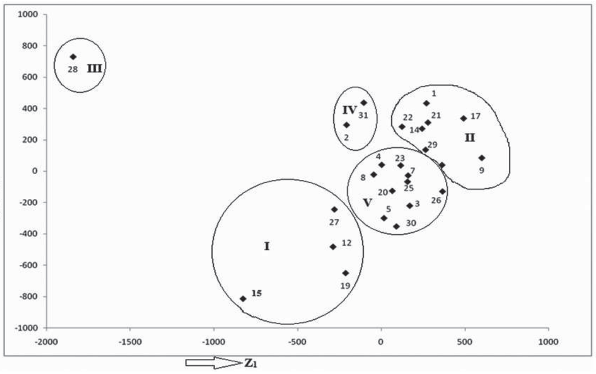

Fig. 1. Scatter diagram superimposed into nonhierarchical clustering based on component score 1 (Z_1) in X axis and component score 2 (Z_2) in Y axis

Non hierarchical clustering

Twenty five vegetable amaranth genotypes were grouped into 5 different clusters. Number of genotypes per cluster ranged from one (Cluster III) to ten (Cluster V) (Table 1). Cluster V was having 10 genotypes from different geographical sources displaying genetic divergence with no relationship with geographical divergence. It indicates that forces other than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection, are perhaps responsible for genetic diversity as has been observed earlier (Pandey and Singh, 2011). However, different trend was recorded in maize (Rezai and Frey 1990); and oat (Alika et al. 1993), where genetic diversity follows the geographical diversity. The distance between clusters was more than the intra cluster distances indicating that diversity in between clusters was more than within cluster (Table 2). The inter-cluster distances have also been presented in Table 2. The far diverged genotypes from cluster I, V, II and IV might be used for hybridization program to obtain a broad spectrum of variability or transgressive segregants. These relationships are also reflected in the scattered diagram (Fig. 1).

Table 1. Distribution of 25 vegetable amaranth genotypes in five different clusters.

Cluster	No. of genotypes	Inbred lines included in different clusters
I	4	AA12, AA15, AA19, AA27
II	8	AA1, AA9, AA10, AA14, AA17, AA21, AA22, AA29
III	1	AA28
IV	2	AA2, AA31
V	10	AA3, AA4, AA5, AA7, AA8, AA20, AA23, AA25, AA26, AA30

Table 2. Inter- and intra-cluster (bold phase) distance (D^2) for 25 vegetable amaranth genotypes

Cluster	I	II	III	IV	V
I	**9.94**				
II	13.23	**8.36**			
III	331.65	330.58	**0.00**		
IV	15.01	7.40	323.21	**11.16**	
V	5.38	7.88	331.61	11.00	**8.09**

Cluster mean

Genotypes of cluster I had a good source of antioxidant (high Fe, Zn, ascorbic acid, medium Mn and beta carotene), excellent source of nutrients (high Ca, Mg, Ni, protein and medium K), high foliage yield and could be selected as donor for these traits (Table 3). Genotypes of cluster II had medium antioxidant content, (medium Mn and beta carotene) excellent source of nutrients, (high Ca and Mg content and a good source of Ni and protein) and medium tall and thickness of plant with medium leaf size, number, dietary fiber, foliage yield and could be selected for these traits. Cluster III composed of single genotypes that exhibited as an excellent source of antioxidant (enrich of ascorbic acid, beta carotene, Fe, Mn and Zn content), excellent source of nutrients (enrich Ca, Mg, K, Ni and protein) and tall plant with medium leaf size and foliage yield. Cluster IV comprising two genotypes having antioxidant (high Zn, Mn, medium ascorbic acid), good source of nutrients (high Ca, medium Ni, Mg and medium protein), thick stem, medium leaves per plant with big leaf size, high dietary fiber content, foliage yield and could be considered as a donor parent parent in the hybridization program for these traits. Cluster V having ten genotypes exhibited good antioxidant content, (high beta carotene and medium Fe) enrich of nutrients, (moderate Ca, Mg, K, Ni and protein), tall plant with more leaves plant^{-1}, high dietary fiber, the highest foliage yield plot^{-1} and could be considered for these traits. The results of five clusters mean to suggest that selection could be performed based on individual trait or a combination of traits along with selection of genotypes from distant clusters for hybridization to obtain good amount of genetic variability for the improvement of vegetable amaranth.

Table 3. Cluster means for 16 antioxidant, nutrient, agronomic traits in 25 vegetable amaranth genotypes

Characters	Clusters				
	I	II	III	IV	V
Fe (mg kg^{-1})	1866.2	806.4	1625.9	974.2	1222.6
Zn (mg kg^{-1})	920.3	759.6	1582.87	1232.9	741.1
Ca (g 100 g^{-1})	1.7	1.7	1.9	1.7	1.6
Mn (mg kg^{-1})	118.5	116.3	197.6	133.2	106.1
Mg (g 100 g^{-1})	2.9	2.9	3.5	2.8	2.8
K (g 100 g^{-1})	3.9	3.7	9.2	3.8	4.0
Ni (mg kg^{-1})	243.1	218.7	274.2	211.4	214.3
Beta carotene (mg g^{-1})	0.8	0.8	1.0	0.7	0.9
Ascorbic acid (mg 100 g^{-1})	130.8	104.1	148.4	111.9	106.9
Protein (mg 100 g^{-1})	1.3	1.2	1.5	1.2	1.2
Plant height (cm)	18.5	22.6	24.5	20.4	24.9
Leaves plant^{-1}	9.5	9.6	4.9	9.2	10.7
Stem base diameter (cm)	6.0	6.8	6.1	8.0	6.0
Fiber (%)	7.7	8.1	6.7	8.6	8.4
Leaf area (cm^{2})	21.6	27.1	27.7	28.7	26.4
Foliage yield plot^{-1} (kg)	4.9	4.5	4.5	4.9	5.0

Contribution of traits towards divergence

The PCA revealed that both the vectors had positive values for protein content, foliage yield plot^{-1}, leaf area and Zn content. In vector I, the other important characters responsible for the genetic divergence in the major axis of differentiation were Ca, beta carotene, stem base diameter, fiber content, leaves plant^{-1} and Mn having positive vector values. Whereas, in vector II, plant height, K, ascorbic acid and iron had positive vector values. Usually the leaf size, grain yield plant^{-1}, harvest index and length of top lateral branches plant^{-1} are considered important traits contributing towards genetic divergence. A previous report on *Amaranthus* has also cited protein as a major contributing trait (Alba et al. 1996). Particular genotypes of a cluster having desirable genes for specific traits could be hybridized with other promising genotypes of different divergent clusters, which can facilitate the accumulation of suitable genes in hybrids. Thus the obtained hybrids may be fixed following recurrent selections of their selected transgressive segregants in advance generations, which may lead to the development of high-foliage-yielding varieties enrich with antioxidant nutrient components.

Authors' contribution

Conceptualization of research (US, MTI, MGR, SO); Designing of the experiments (US, MTI, MGR, SO); Contribution of experimental materials (US); Execution of field/ lab experiments and data collection (US, MTI, MGR); Analysis of data and interpretation (US); Preparation of manuscript (US, MTI, MGR, SO).

Declaration

The authors declare no conflict of interest.

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