*Short Communication*

# Analysis of genetic diversity in grain amaranth (*Amaranthus* spp.)

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**Abstract**

**The genetic divergence in 100 genotypes and germplasm lines of grain amaranth (*Amaranthus spp.*) was assessed by using non-hierarchical Euclidean cluster analysis. The genotypes were grouped into 15 distinct clusters revealing wide diversity in the experimental material. Cluster XV was largest with 18 followed by cluster XIV with 15 and cluster VIII with 11 genotypes, while cluster VI was solitary. Clustering pattern of genotypes showed lack of any relationship between geographic origin and genetic diversity. Intra cluster values ranged from 0.00 to 23.81 and cluster VII was the most diverse group. The inter cluster values ranged from 22.30 to 133.55. Maximum divergence was noticed between clusters VI and XIII (133.55) followed by clusters I and IV (132.74). The diverse clusters derived could be used in hybridization programme to develop high yielding grain amaranth varieties.**

**Key words**:    Grain amaranth, genetic divergence, non hierarchical Euclidian cluster

Grain amaranth is a protein rich pseudo cereal contains 14-16% quality protein with higher lysine content [1]. Hence, grain amaranth holds high promise for supplementing nutritive food and amelioration of protein deficiency strictly in the vegetarian diet people [2]. Inspite of its high nutritive value it is still a underutilized crop due to lack of popularity and low yield. Assessment of genetic diversity in the available germplasm is very essential to formulate effective breeding programme through selection of diversed and superior parents for hybridization to increase the yield *per se*. The present study is aimed to assess the genetic diversity in 100 germplasm lines of grain amaranth using non hierarchical Euclidian Cluster analysis for 15 quantitative and qualitative traits including grain yield and protein content.

One hundred germplasm lines of grain amaranth were assessed in a field experiment carried out at the Main Research Station, Hebbal, University of Agricultural Sciences Bangalore during *kharif* 2011-12 under protective irrigation. Fifty out of 100 lines were obtained from Sardar Krushinagar Dantiwada Agricultural University (SDAU), Gujarat and other fifty from National Bureau of Plant Genetic Resources (NBPGR) Regional Station, Akola, Maharashtra. Varieties Suvarna, BGA-2 and GA-2 were used as checks. The experiment was laid out in an augmented design with 10 Compact Blocks. Phenotypic observations on 15 traits including grain yield and protein content were recorded. Crude protein content was estimated following Micro Kjeldhal Distillation method and the percent nitrogen calculated was multiplied by a factor 6.25 and protein content expressed in percentage. Non-hierarchical Euclidean cluster analysis was used to assess the genetic divergence existing in the germplasm accessions.

Based on Euclidian distance analysis, 100 genotypes were grouped into 15 clusters (Table 1). Clustering pattern showed appreciable amount of divergence among the genotypes. Maximum number of genotypes were included in cluster XV and was considered to be the largest cluster, followed by

**Table 1.**  Grouping of 100 grain amaranth genotypes into different clusters

| Clusters | No. of genotypes | Name of the genotypes |
|---|---|---|
| I | 3 | SKGPA-61, SKGPA-62, SKGPA-63 |
| II | 5 | SKGPA-70, SKGPA-80, SKGPA-103, IC035702,   IC035717 |
| III | 9 | SKGPA-106, SKGPA-108, IC032190, IC032195, IC095251, IC095389,IC120670, IC120689,IC432086 |
| IV | 6 | SKGPA-109, SKGPA-110, IC021938, IC032186, IC120621, IC120649 |
| V | 3 | SKGPA-96, SKGPA-99, IC035633 |
| VI | 1 | IC035615 |
| VII | 7 | SKGPA-64, SKGPA-71, SKGPA-79, SKGPA-82, SKGPA-84, IC095406, IC095498 |
| VIII | 11 | SKGPA-66, SKGPA-67, SKGPA-68, SKGPA-69,   SKGPA-72, SKGPA-75, SKGPA-85, SKGPA-86, SKGPA-91, SKGPA-94, IC035661 |
| IX | 6 | SKGPA-89, SKGPA-90, SKGPA-93, SKGPA-95, SKGPA-98, SKGPA-100 |
| X | 2 | SKGPA-88, SKGPA-92 |
| XI | 4 | SKGPA-107, IC032193, IC035642, IC035701 |
| XII | 2 | SKGPA-97, IC035635 |
| XIII | 8 | IC035638, IC035651, IC035716, IC035719, IC035742, IC095204, IC095391, IC120668 |
| XIV | 15 | SKGPA-102, SKGPA-104, SKGPA-105, IC035415, IC035711, IC081698-B, IC094654, IC094661, IC095244, IC095248, IC095371, IC095382-B, IC095430, IC095510, IC095556 |
| XV | 18 | SKGPA-65, SKGPA-73, SKGPA-74, SKGPA-76, SKGPA-77, SKGPA-78, SKGPA-81, SKGPA-83, SKGPA-87, SKGPA-101, IC 021803-A, IC021937, IC035404, IC035665, IC035713, IC035735, IC095383 |

Clusters XIV and VII .The formation of solitary cluster with only one or two (clusters X and XII) accessions may be due to total isolation preventing the gene flow or intensive natural or human selection for diverse adaptive complexes. The intra-cluster distance value ranged from 0 to 23.81. Of the fifteen clusters formed (Table 2) genotypes grouped in the same cluster presumably diverge little from one another as aggregates of characters measured. Theoretically, crossing of genotypes belonging to the same cluster may not yield superior hybrids or desirable segregants. However, a general notion in theory exists that the larger is the divergence between the genotypes, higher will be the heterosis. Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses and desirable segregants. Further, heterosis can not be exploited in a highly self-fertilized crop like grain amaranth. In this context, inter-cluster distance was worked out considering ten characters and these distances ranged from 22.30 to 133.55. The inter-cluster distance was maximum of 133.55 between cluster VI and XIII followed by 132.74 between cluster I and IV. Therefore, clusters XIII and VII were

considered to be strictly more diverse from rest of the clusters. Those genotypes included in clusters with maximum inter-cluster distance are obviously genetically more divergent. Hence, it would be logical to incorporate genotypes from these clusters in further breeding programmes. The minimum inter-cluster distance was observed between cluster III and IV indicating close genetic association between the genotypes of these two clusters.

It was observed that the genotypes in Cluster I may be chosen for hybridization programme as it recorded highest cluster mean values (Table 3) for most of the yield contributing traits *viz.*, stem girth, number of leaves per plant, panicle length, seed weight and it also includes the best grain yielding genotypes [3]. In addition, clusters I and III were more divergent for grain yield and seed weight. Hence, crossing between genotypes of these two Clusters may appear to be most promising to combine considerable grain yield with high protein content. Hence, it is suggested to consider these genotypes belonging to distant clusters which were confirmed through their higher inter-cluster distance. Earliness and dwarf statured

**Table 2**. Estimates of average intra and inter-cluster distances for the fifteen clusters in grain amaranth

| Clusters | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | **9.44** | 47.07 | 118.01 | 132.74 | 91.70 | 71.90 | 96.69 | 30.65 | 69.08 | 45.39 | 95.89 | 60.36 | 114.31 | 115.31 | 75.17 |
| II | | **18.03** | 87.27 | 97.55 | 64.84 | 88.77 | 54.91 | 26.34 | 48.97 | 47.48 | 55.20 | 31.12 | 68.39 | 76.54 | 34.17 |
| III | | | **23.61** | 22.30 | 36.56 | 100.72 | 73.34 | 88.85 | 50.12 | 85.76 | 69.14 | 70.06 | 69.41 | 33.40 | 65.48 |
| IV | | | | **20.72** | 52.53 | 120.98 | 70.84 | 103.29 | 67.50 | 104.21 | 70.24 | 83.89 | 63.33 | 29.04 | 70.61 |
| V | | | | | **20.50** | 75.54 | 63.61 | 62.35 | 28.83 | 62.66 | 51.07 | 41.58 | 67.41 | 39.49 | 49.35 |
| VI | | | | | | **0.00** | 120.53 | 64.32 | 61.69 | 52.39 | 110.94 | 73.47 | 133.55 | 112.71 | 97.87 |
| VII | | | | | | | **23.81** | 71.96 | 65.93 | 91.68 | 25.99 | 60.86 | 28.35 | 45.97 | 25.49 |
| VIII | | | | | | | | **18.66** | 40.78 | 30.51 | 69.00 | 32.59 | 87.68 | 85.31 | 48.22 |
| IX | | | | | | | | | **19.21** | 40.02 | 60.78 | 33.34 | 75.41 | 56.26 | 43.71 |
| X | | | | | | | | | | **13.09** | 85.67 | 38.81 | 100.92 | 91.90 | 66.65 |
| XI | | | | | | | | | | | **18.29** | 49.96 | 32.65 | 41.63 | 30.27 |
| XII | | | | | | | | | | | | **9.89** | 68.16 | 63.71 | 39.21 |
| XIII | | | | | | | | | | | | | **20.08** | 40.07 | 42.10 |
| IX | | | | | | | | | | | | | | **18.72** | 47.33 |
| XV | | | | | | | | | | | | | | | **21.08** |

**Table 3.** Cluster mean values for ten characters in grain amaranth germplasm lines

| Clusters | Days to 50 % flowering | Days to maturity | Stem girth (cm) | No. of leaves/ plant | Plant height (cm) | Panicle length (cm) | Panicle width (cm) | Seed weight (g/10 ml) | Grain protein (%) | Grain yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 43.52 | 83.29 | 3.63 | 120.84 | 166.72 | 56.49 | 11.07 | 10.61 | 12.06 | 41.17 |
| II | 39.58 | 75.85 | 3.02 | 115.68 | 125.87 | 36.53 | 11.82 | 7.97 | 13.20 | 33.87 |
| III | 42.61 | 75.88 | 2.45 | 38.24 | 89.95 | 33.24 | 11.80 | 7.25 | 11.65 | 16.38 |
| IV | 39.61 | 75.12 | 2.47 | 38.92 | 67.99 | 33.34 | 10.19 | 7.46 | 12.07 | 17.84 |
| V | 54.88 | 93.49 | 3.03 | 59.29 | 109.73 | 29.33 | 11.62 | 7.83 | 13.77 | 20.97 |
| VI | 59.08 | 106.87 | 2.21 | 59.90 | 178.78 | 56.33 | 8.89 | 8.00 | 13.78 | 18.89 |
| VII | 45.16 | 84.56 | 2.85 | 107.11 | 72.91 | 40.67 | 11.42 | 7.98 | 11.42 | 30.79 |
| VIII | 44.93 | 84.27 | 3.34 | 104.67 | 144.49 | 47.19 | 9.50 | 8.71 | 12.42 | 31.51 |
| IX | 44.37 | 82.88 | 2.95 | 69.46 | 126.24 | 44.41 | 10.43 | 7.31 | 12.97 | 22.74 |
| X | 39.03 | 75.99 | 3.02 | 85.40 | 160.89 | 36.94 | 12.79 | 8.27 | 15.62 | 23.72 |
| XI | 57.96 | 94.02 | 3.43 | 101.70 | 81.89 | 25.01 | 11.00 | 7.92 | 14.34 | 23.17 |
| XII | 44.64 | 88.12 | 3.21 | 93.35 | 128.78 | 22.07 | 10.66 | 8.56 | 13.28 | 25.27 |
| XIII | 41.44 | 74.28 | 3.05 | 100.41 | 62.68 | 19.86 | 11.61 | 7.74 | 13.53 | 20.95 |
| IX | 45.45 | 85.29 | 2.82 | 64.53 | 72.78 | 28.28 | 10.48 | 7.23 | 12.19 | 18.77 |
| XV | 43.27 | 81.45 | 3.13 | 101.64 | 97.01 | 42.35 | 10.30 | 8.06 | 12.85 | 26.35 |

genotypes may be desirable in grain amaranth for multiple cropping system and hence, genotypes from cluster XIII may be included in hybridization programme to achieve this objective. The genotype from the solitary cluster VI which showed highest mean plant height may be considered in present breeding programme to improve plant height which has positive association with grain yield. Quality traits like protein are given more importance in the present breeding programme. Considering the mean protein content, cluster X and XI having high protein content hence genotypes from these clusters may be utilized in the hybridization to improve the protein content in grain amaranth. Hybridization between genotypes of divergent clusters will lead to accumulation of favorable genes in single variety and also it may suggest creating of variability for developing the varieties involving a large number of divergent lines instead of closely related ones [4]. Grain Amaranth being a nutritionally potential crop and neglected crop in genetic improvement. The results of the present study suggest that crosses may be effected among the genotypes of the said cluster for improving more than one economic character to obtain potential segregants and which may lead to develop high yielding cultivars in grain amaranth.

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