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GENETIC DIVERGENCE ANALYSIS OF 38 GRAIN AMARANTH (*Amaranthus hypochondriacus* L.) GENOTYPES USING D² STATISTICS UNDER SEMI-ARID GUJARAT CONDITIONS

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ABSTRACT

Genetic divergence was evaluated in 38 grain amaranth genotypes to assess the variability and identify diverse parents for hybridization programmes. The experiment was conducted during the *rabiseason* of 2024-25 at the Centre for Crop Improvement, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. Twelve quantitative characters were assessed using Mahalanobis D² statistics. The genotypes were grouped into ten distinct clusters following Tocher's method. Cluster I was the largest (15 genotypes), while Clusters III, IV, V, VIII, and X were solitary. The maximum inter-cluster distance was observed between Cluster V and Cluster IX (24.27), indicating high genetic diversity. Cluster VIII exhibited the highest mean values for grain yield per plant (29.09 g), harvest index, and test weight. Cluster VI recorded the highest protein and lysine content. Days to 80% maturity (39.26%) and biological yield per plant (24.47%) contributed maximally to the total divergence. The evaluation of these genotypes suggests that crossing diverse parents from distant clusters could effectively improve yield and quality in grain amaranth.

Keywords : *Amaranthus*, Genetic divergence, Mahalanobis D², Cluster analysis, Tocher's method.

Introduction

Grain amaranth (*Amaranthus hypochondriacus* L.) is a C₄ pseudocereal crop with high photosynthetic efficiency and adaptability to drought and high-temperature conditions, making it well suited for cultivation in the semi-arid regions of Gujarat (Rastogi and Shukla, 2013). Amaranth belongs to *Amaranthaceae* family, *Caryophyllales* order, and *Amaranthus* genus (Wolosik and Markowska, 2019). The genus *Amaranthus* is dibasic with (x = 16, 17) chromosomes, almost equally distributed in section amaranth. Among 30 species, four species have 2n = 32, while all others have 2n = 34. Out of these, only 3 species viz., *Amaranthus caudatus* L. (2n = 32), *A. cruentus* L. (2n = 34) and *A. hypochondriacus* L. (2n = 32) are domesticated species with *A. caudatus* L. being drooping type and rest two are erect type (Grant,

1959). Grain amaranth (*Amaranthus hypochondriacus* L.) is a highly nutritious pseudo-cereal, often referred to as a "crop of the future" due to its exceptional protein quality and high lysine content (Prakash *et al.*, 2021; Bashyal *et al.*, 2022). Despite its nutritional superiority, the crop has not received adequate attention in terms of systematic breeding, leading to limited genetic improvement (Kumar and Murthy, 2017). The success of any hybridization program is largely determined by the selection of parents, which in turn depends on the magnitude of genetic divergence present in the gene pool (Rao, 1952). Evaluating genetic divergence is therefore a prerequisite for identifying parents that can produce high heterosis and wide variability in segregating generations (Shrivastav *et al.*, 2017).

Multivariate analysis, particularly Mahalanobis's D² statistic, is a robust tool for assessing genetic diversity (Mahalanobis, 1936). It considers the inter-correlations between multiple traits simultaneously and groups genotypes into clusters, allowing breeders to visualize genetic relationships (Singh and Chaudhary, 1985). The D² statistic groups a set of potential parents based on genetic divergence with the assumption that the best parent may be those showing genetic divergence (Yadav, 2021). The present investigation was undertaken to evaluate the genetic divergence among 38 grain amaranth genotypes using D² statistics to select suitable parents for future breeding programs.

Material and Methods

The experimental material comprised 38 genotypes of grain amaranth obtained from Centre for Crop Improvement, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat. The experiment was conducted during the *rabi* 2024-25 at Centre for Crop Improvement, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The climate of this region is a sub-tropical type and comes under semi-arid region, in general, the monsoon is warm and moderately humid, winter is cold and dry, while summer is largely hot and dry. The soil of the experimental site was having sandy loam texture with a pH of 7.3 to 7.6.

The genotypes were sown in a Randomized Block Design (RBD) with three replications. Standard

agronomic practices were followed to raise a healthy crop. Twelve quantitative characters were recorded on five randomly selected competitive plants per genotype: days to 50% flowering, days to 80% maturity, length of inflorescence (cm), width of inflorescence (cm), plant height (cm), stem girth (cm), biological yield per plant (g), harvest index (%), test weight (g/10ml), protein content (%), lysine content (%) and grain yield per plant (g).

Genetic divergence was evaluated using Mahalanobis's (1936) generalized distance (D²) statistic. The genotypes were grouped into clusters using Tocher's method (Rao, 1952). The relative contribution of each character towards divergence was estimated using the method suggested by Singh and Chaudhary (1985). Statistical analysis was performed using INDOSTAT software.

Results and Discussion

Genetic Divergence and Grouping of Genotypes

The evaluation of genetic divergence using Mahalanobis D² statistics revealed considerable genetic diversity among the 38 grain amaranth genotypes for the twelve characters studied. Based on Tocher's method as suggested by Rao (1952), the genotypes were grouped into ten distinct clusters indicating the presence of considerable genetic diversity among the studied material. Dendrogram showing distribution of 38 grain amaranth genotypes into 10 clusters illustrated in Fig. 1.

Table 1: The distribution of 38 grain amaranth genotypes to different clusters

Cluster	No. of genotypes	Genotypes
I	15	BGA 07, BGA 10, SKNA 2007, SKNA 2009, SKNA 2208, RMA 31, AGR 23.1, SKNA 2202, GA 6, BGA 29, CGA 18-1, SKNA 2203, SKNA 2005, SKNA 2105, SKNA 2103
II	8	SKNA 2104, RGAG 14-2, GA 1, GA 7, SKNA 1803, SKNA 903, SKNA 1902, CGA 18-2
III	1	VL 44
IV	1	Suvarna
V	1	SKNA 2205
VI	3	GA 2, GA 3, SKNA 2003
VII	3	GA 4, PRA 1, SKNA 1906
VIII	1	SKNA 1804
IX	4	GA 5, SKNA 2010, GA 9, GA 8
X	1	SKNA 2011

Cluster I was the largest, comprising 15 genotypes, followed by Cluster II with 8 genotypes, Cluster IX with 4 genotypes, and Clusters VI and VII with 3 genotypes each. The remaining Clusters III, IV,

V, VIII and X were solitary clusters, each containing only one genotype: VL 44, Suvarna, SKNA 2205, SKNA 1804 and SKNA 2011, respectively. The presence of solitary clusters suggested that the

genotypes included in these clusters were highly divergent from the remaining genotypes and could be utilized in hybridization programmes to obtain desirable segregants. These findings are in close agreement with the results of Kumar and Murthy (2017), Shrivastav *et al.* (2017) and Tiwari *et al.* (2018), who also reported substantial genetic diversity and the formation of solitary clusters in grain amaranth.

Intra and Inter-Cluster Distances

The estimates of intra-cluster distance (Table 2) ranged from 0.00 to 10.76. Cluster diagram showing interrelationship among twelve clusters using D² analysis is shown in fig 2. The highest intra-cluster distance was recorded in Cluster VI (10.76) followed by Cluster IX (10.59), Cluster II (10.53) and Cluster VII (10.21), indicating the presence of considerable genetic divergence among the genotypes within these clusters. Cluster I recorded an intra-cluster distance of 8.54. However, clusters III, IV, V, VIII and X exhibited zero intra-cluster distance due to the presence of only one genotype in each cluster.

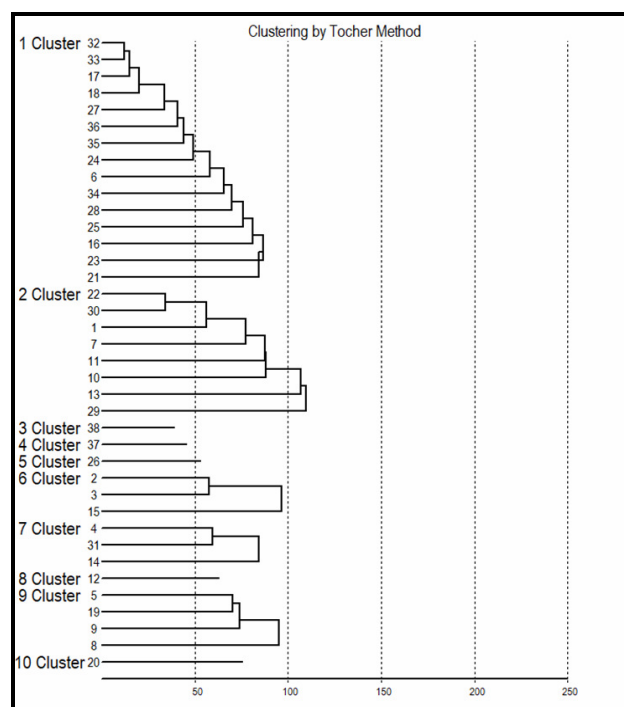


Fig. 1: Dendrogram showing distribution of 38 grain amaranth genotypes into 10 clusters

Table 2: Average intra-cluster (bold diagonal) and inter-cluster distances (D²) among 38 grain amaranth genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	8.54	14.30	16.79	11.38	16.38	16.96	13.35	11.26	18.44	20.49
II		10.53	12.20	15.29	11.87	13.83	17.28	14.12	17.83	12.40
III			0.00	18.84	14.18	16.79	16.61	17.49	17.35	12.02
IV				0.00	19.63	20.79	17.78	9.84	17.74	22.14
V					0.00	10.37	16.15	17.69	24.27	14.13
VI						10.76	15.99	20.70	24.14	15.84
VII							10.21	18.49	23.64	22.40
VIII								0.00	18.46	20.86
IX									10.59	18.13
X										0.00

The inter-cluster distance (Table 2) ranged from 9.84 to 24.27. The highest inter-cluster distance was observed between Cluster V and Cluster IX (24.27) followed by Cluster VI and Cluster IX (24.14) and Cluster VII and Cluster IX (23.64), indicating wider genetic divergence among genotypes belonging to these clusters. Therefore, hybridization among genotypes from these clusters may result in greater heterosis and desirable segregants. The lowest inter-cluster distance was observed between Cluster IV and Cluster VIII (9.84), followed by Cluster V and Cluster VI (10.37), indicating close genetic relationship among the genotypes of these clusters.

The higher inter-cluster distances observed in the present study suggested the existence of substantial genetic diversity among the evaluated genotypes, which could be effectively utilized in hybridization programmes for the development of superior grain amaranth varieties. Similar findings were reported by Kumar and Murthy (2017), Shrivastav *et al.* (2017), Tiwari *et al.* (2018), Kumar *et al.* (2019), Rani *et al.* (2020), Yadav (2021) and Bashyal *et al.* (2022), who also reported considerable inter and intra-cluster distances among grain amaranth genotypes.

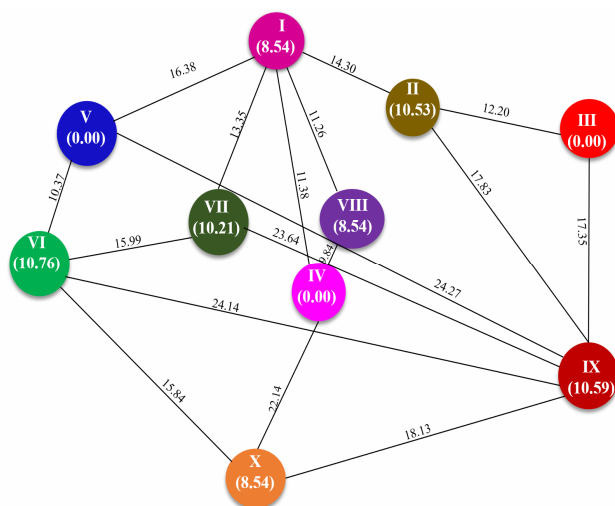


Fig. 2 : Cluster diagram showing interrelationship among twelve clusters using D² analysis (not to scale)

Cluster Means for Traits

The cluster mean values for twelve characters among the ten clusters were presented in Table 3. Considerable variation was observed among the clusters for all the characters studied.

Cluster X recorded the minimum mean values for days to 50% flowering (58.00 days) and days to 80% maturity (91.00 days), indicating earliness among the genotypes grouped under this cluster. Cluster VIII exhibited the highest mean values for length of inflorescence (61.07 cm), harvest index (38.47%), test weight (8.06 g) and grain yield per plant (29.09 g).

Cluster III recorded the highest mean value for stem girth (4.76 cm) and width of inflorescence (18.33 cm). Cluster V showed the minimum mean value for plant height (111.87 cm), while Cluster IX recorded the highest mean value for biological yield per plant (171.23 g). Cluster VI exhibited the highest mean values for protein content (14.76%) and lysine content

(5.94%). The genotypes grouped under clusters possessing desirable mean values for important yield and quality traits may be utilized in selection programmes as well as hybridization programmes for the development of superior grain amaranth genotypes. Similar findings on cluster mean performance were reported by Prakash *et al.* (2021), Bashyal *et al.* (2022), Yadav (2022), Kamini *et al.* (2023), Dhanalakshmi *et al.* (2024) and Sefasi *et al.* (2025), who also observed considerable variation among cluster means for different yield and related traits in grain amaranth genotypes.

Contribution of Individual Character towards Divergence

The per cent contribution of individual characters towards genetic divergence among 38 grain amaranth genotypes is presented in Table 4. Among the twelve characters studied, days to 80% maturity contributed the highest towards total genetic divergence (39.26%) by ranking first 276 times, followed by biological yield per plant (24.47%) with 172 times ranking first. Length of inflorescence also contributed considerably towards divergence with 8.82%, followed by days to 50% flowering (7.11%) and width of inflorescence (6.26%).

Moderate contribution towards divergence was observed for protein content (4.55%), harvest index (4.13%) and lysine content (3.41%). However, stem girth (1.28%), grain yield per plant (0.57%) and plant height (0.14%) contributed very little towards total divergence. Test weight did not contribute towards genetic divergence as it ranked first zero times. The results indicated that days to 80% maturity and biological yield per plant were the major contributors towards genetic divergence and should be given due importance while selecting diverse parents for hybridization programmes in grain amaranth improvement.

Table 3: Cluster means for twelve characters in 38 genotypes of grain amaranth (Torcher's method)

Cluster	Days to 50% flowering	Days to 80% maturity	Length of inflorescence (cm)	Width of inflorescence (cm)	Plant height (cm)	Stem girth (cm)	Biological yield per plant (g)	Harvest index (%)	Test weight (g/10ml)	Protein content (%)	Lysine content (%)	Grain yield per plant (g)
I	62.36	116.24	50.04	15.77	129.75	3.92	81.59	22.83	7.73	13.94	5.41	17.74
II	62.46	101.96	52.64	16.97	129.23	4.14	79.25	31.31	7.82	13.55	5.60	22.96
III	62.00	101.67	47.87	18.33	129.07	4.76	91.93	17.99	7.61	11.53	5.36	16.47
IV	73.33	117.00	45.80	18.07	136.20	3.77	89.33	30.24	7.98	13.50	5.73	27.00
V	60.67	97.67	50.47	16.20	111.87	3.03	46.60	25.13	7.21	14.52	5.11	13.80
VI	59.44	99.56	44.80	14.16	119.89	3.98	47.13	31.12	7.81	14.76	5.94	13.58
VII	60.67	116.00	36.09	12.46	115.51	3.39	50.67	24.58	7.30	12.57	5.56	12.08
VIII	62.33	115.33	61.07	18.07	119.53	3.90	75.67	38.47	8.06	13.04	5.13	29.09
IX	64.08	108.67	55.17	16.87	134.35	4.01	171.23	16.11	7.99	13.20	5.58	27.46
X	58.00	91.00	53.80	16.80	144.67	4.45	112.80	23.08	7.50	14.50	5.09	25.73

Table 4: Per cent contribution of different characters to total divergence

Sr. No.	Character	Number of times ranked first	Per cent contribution
1	Days to 50% flowering	50	7.11
2	Days to 80% maturity	276	39.26
3	Length of inflorescence (cm)	62	8.82
4	Width of inflorescence (cm)	44	6.26
5	Plant height (cm)	1	0.14
6	Stem girth (cm)	9	1.28
7	Biological yield (g)	172	24.47
8	Harvest index (%)	29	4.13
9	Test weight (g/10 ml)	0	0.0
10	Protein content (%)	32	4.55
11	Lysine content (%)	24	3.41
12	Grain yield per plant (g)	4	0.57
Total	-	703	100

Similar findings on the contribution of individual characters towards genetic divergence were reported by earlier researchers in grain amaranth. Pandey and Singh (2017) reported that grain yield per plant contributed the highest towards divergence (18.93%), followed by harvest index (13.57%). Shrivastav *et al.* (2017) observed maximum contribution from plant height (32.02%) followed by biological yield per plant (15.42%). Tiwari *et al.* (2018) also reported that plant height contributed maximum towards divergence (28.16%), followed by grain yield per plant (13.91%) and days to 50% flowering (5.03%). Sefasi *et al.* (2025) reported that grain yield per plant contributed the highest (19.77%) followed by inflorescence length (18.90%) towards total genetic divergence. The variation in contribution of different characters across studies may be attributed to differences in genetic material and environmental conditions.

The present study revealed considerable genetic diversity among 38 grain amaranth genotypes. Greater emphasis should be given to days to 80% maturity and biological yield per plant, as these traits contributed maximum towards total genetic divergence. The maximum inter-cluster distance was observed between Cluster V and Cluster IX, followed by Cluster VI and Cluster IX, indicating that the genotypes included in these clusters may be utilized as potential parents in hybridization programmes to obtain desirable transgressive segregants and broad genetic variability. Cluster VIII and Cluster VI were identified as promising sources for high grain yield and superior protein content, respectively.

References

- Bashyal, S., Upadhyay, A., Ayer, D. K., Dhakal, P., Bimochana, G. C. and Shrestha, J. (2022). Multivariate analysis of grain amaranth (*Amaranthus* spp.) accessions to quantify phenotypic diversity. *Heliyon*. **8**(10), e11202.
- Dhanalakshmi, T. N., Madhusudan, K., Ramesh, S., Rao, A. M., Reddy, K. M. S. and Anand, S.R. (2024). Unveiling genetic diversity in grain amaranth through k-means clustering and principal component analysis. *International Journal of Plant and Soil Science*. **36**(10), 611-620.
- Grant, W. F. (1959). Cytogenetic studies in *Amaranthus*. Chromosome numbers and phylogenetic aspects. *Canadian Journal of Genetics and Cytology*. **1**(4), 313-328.
- Kamini, K., Yadav, R. K. and Sandilya, V. K. (2023). Assessment of genetic diversity in grain amaranth (*Amaranthus hypochondriacus* L.). *The Pharma Innovation Journal*. **12**(7), 3033-3036.
- Kumar, L. B. and Murthy, N. (2017). Genetic variability and divergence studies for yield component traits in grain *Amaranth* spp. *International Journal of Current Microbiological Application Science*. **6**(12), 1276-1285.
- Kumar, Y., Prasad, R. and Chameli. (2019). Genetic divergence analysis in amaranthus (*Amaranthus* spp.) genotypes for yield and its component characters. *International Journal of Chemical Studies*. **7**(3), 2686-2689.
- Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings of the National Institute of Sciences of India*. **2**(1), 49-55.
- Pandey, S. and Singh, R. (2017). Genetic divergence in grain amaranth (*Amaranthus hypochondriacus* L.). *Journal of Plant Breeding and Genetics*. **5**(2), 57-62.
- Prakash, V., Ameen, G., Sandilya, V. K. and Tiwari, J. K. (2021). Variability, heritability and correlation studies for economic traits in grain amaranth (*Amaranthus* spp.). *Indian Journal of Plant Genetic Resources*. **37**(1), 80-89.
- Rani, R., Mahato, J., Prasad, K., Lal, H. C. and Raj, H. (2020). Studies on genetic divergence in amaranth genotypes (*Amaranthus hypochondriacus* L.). *International Journal of Current Microbiology and Applied Sciences*. Special Issue-10, 53-57.
- Rao, C. R. (1952). Advanced statistical methods in biometric research. New York, John Wiley and Sons. p. 390.
- Rastogi, A. and Shukla, S. (2013). Amaranth, A new millennium crop of nutraceutical values. *Critical Reviews in Food Science and Nutrition*, **53**(2), 109-125.
- Sefasi, A., Nyasulu, M., Kamanga, R. M., Yalaukani, L., Katengeza, S. P., Monjerezi, M., Malidadi, C. and

- Masamba, K. (2025). Phenotypic diversity and multivariate analyses of yield and yield-related traits in amaranth accessions from Malawi. *BMC Plant Biology*. **25**(1), 1145.
- Shrivastav, S., Yadav, C. B. and Singh, V. (2017). Genetic variability, divergence, correlation and path coefficient analysis for yield and its contributing traits in amaranthus. *Trends in Biosciences*. **10**(18), 3416-3420.
- Singh, R. K. and Chaudhary, B. D. (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi.
- Tiwari, S., Pant, N. C., Gupta, A., Dwivedi, U., Meena, J. K., Pandey, C. S., Singh, S. P. and Bhatt, A. (2018). Genetic variability and genetic divergence for seed yield and its components characters in grain amaranth (*Amaranthus hypochondriacus* L.) germplasm. *International Journal of Chemical Studies*. **6**(2), 3292-3297.
- Wolosik, K. and Markowska, A. (2019). *Amaranthus cruentus* taxonomy, botanical description, and review of its seed chemical composition. *Natural Product Communications*. **14**(5).
- Yadav, R. K. (2021). Path coefficient analysis for protein content in grain amaranth (*Amaranthus hypochondriacus* L.). *International Journal of Farm Sciences*. **11**(4), 31-31.