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Genetic divergence for yield and quality traits in bathua (*Chenopodium album* L.)

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Abstract

An investigation was carried out with the twenty four genotypes of bathua to study the nature and magnitude of genetic divergence using Mahalanobis D^2 analysis. Analysis of variance showed significant difference among the genotypes for all the characters studied. The twenty four genotypes were grouped into four clusters depending on similarities of their D^2 values. The distribution pattern indicated that the maximum number of genotypes (18) was included in cluster (I) followed by cluster II (4) and the minimum number was in cluster III and cluster IV (1). The inter cluster distance in most of the cases was higher than the intra cluster distance, which indicated wider genetic diversity among the accessions of different groups. The highest inter cluster distance was observed between cluster II and IV, followed by the distance between cluster III and IV showing wide diversity among the groups. The lowest inter-cluster distance was observed between cluster I and III suggesting a close relationship among the genotypes of these two clusters. The highest intra cluster distance was observed for the cluster II and the lowest for the cluster III and IV. This suggested presence of considerable diversity among the groups of the genotypes.

Keywords: Genetic divergence, yield, quality traits, bathua (*Chenopodium album* L.)

1. Introduction

Bathua (*Chenopodium album* L.) is one of the most important leafy vegetables and used predominantly for edible green leaves. It is an annual herb and belongs to family Chenopodiaceae. It is considered to be the native of Europe and the major centers of distribution are West Indies, South America, North America, Africa, Australia, Oceania and India (Pandey, 2008) [6]. Bathua is highly nutritive vegetable containing high percentage of vitamins along with carbohydrate and protein. It is also rich in minerals. The bathua has fleshy leaves, which are consumed with the stem. The area and yield under this crop in India is very low. The low yield is attributed to the use of low yielding varieties and inefficient method of culture. In order to make it more productive and resistant to diseases and pests, breeders have to launch an intensive breeding programme for releasing wide range of variability in the population to ensure the assembly of a pool of variable germplasm.

The Mahalanobis's D^2 statistics gives an understanding of genetic diversity in the crop. Mahalanobis's (1936) [3] generalized distance, D^2 measures the degree of diversification and determines the relative proportion of each component traits to the total divergence. Such a study also permits to select the genetically divergent parents to obtain the desirable recombinants in the segregating generations. Moreover, precise information about the extent of genetic divergence and characters used for discrimination among the population is crucial in any crop improvement program (Pandey, 2009) [5]. Therefore, the present investigation was designed to provide information on genetic divergence of 24 bathua genotypes.

2. Material and Methods

Twenty four genotypes of bathua collected from different sources (Table 1) were studied to measure the diversity among the genotypes at the field and laboratory, Department of Vegetable Science, K. R. C. College of Horticulture, Arabhavi, in 2017. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Data were recorded from randomly selected 5 plants from the plot of each replication on Plant Height (cm), Plant spread E-W(cm), Plant spread N-S(cm), Number of leaves per plant, Number of branches per plant, Leaf area(cm), Stem girth (cm), Days to first flowering, Days to 50% flowering, Number of inflorescence per plant, Inflorescence length (cm), Inflorescence fresh weight(g), Inflorescence dry weight (g), Fresh weight of plant (g), Dry weight of plant (g), Foliage yield per plant (g), Foliage yield per plot(kg), Foliage yield per hectare (tonnes),

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Vitamin- A(mg), Vitamin -C(mg), Protein (mg), Calcium(mg), Magnesium (mg), Iron (mg), Zinc(mg), Oxalates (mg), Nitrates (mg), Total Phenols (mg). The data were analyzed following Mahalanobis's D^2 statistics for assessment of genetic divergence among the genotypes of bathua using INDOSTAT software.

3. Result

Twenty four bathua genotypes were evaluated for twenty eight traits to study the divergence and the obtained data was subjected to D^2 analysis. As many as four divergent clusters were grouped by using Tocher's method (Fig. 1 and 2)

3.1 Classification of bathua genotypes

By adopting the method suggested by Tocher's (Rao, 1952), twenty four genotype were grouped into four clusters by treating estimated D^2 values as the squares of generalized distances (Fig 1). The distribution pattern of genotypes into various clusters is given in Table 2.

Cluster I is the largest cluster having 18 genotypes, followed by cluster II with four genotypes, cluster III and cluster IV had one genotype each (Fig.2).

Intra and inter-cluster distance D^2 values are presented in Table 3. Among four clusters, cluster II with four genotypes showed maximum intra-cluster distance ($D^2 = 294.46$) followed by cluster I ($D^2 = 245.75$), it indicates that the genotypes grouped in cluster II and cluster I were diverse for most of the characters. Cluster III and cluster IV had no intra-cluster distance ($D^2 = 0.00$) as they possessed single genotype in each, it indicates that genotypes included in these clusters were less diverse from each other.

Based on distance between clusters *i.e.* inter-cluster distances in Table 3, the maximum distance was observed between cluster II and IV ($D^2 = 1585.98$), followed by cluster III and IV (1210.55), cluster II and III ($D^2 = 943.60$), cluster I and IV ($D^2 = 810.06$). The least inter cluster distance was observed between cluster I and II ($D^2 = 686.24$) followed by cluster I and III ($D^2 = 350.35$).

3.2 Mean performance of characters in clusters

Cluster mean in twenty eight characters are summarized in Table 4.

3.2.a Growth and flowering parameters

The highest mean for plant height at 30 DAS in bathua was observed in the cluster II (70.81) followed by cluster III (59.67). The lowest mean was observed in the cluster IV (48.33).

The highest mean for number of leaves per plant in bathua was observed in the cluster II (109.78) followed by cluster III (108.93). The lowest mean was observed in the cluster I (85.59). The highest mean for number of branches per plant in bathua was observed in the cluster III (11.40) followed by cluster II (11.27). The lowest mean was observed in the cluster IV (8.73).

The highest mean for leaf area in bathua was observed in the cluster II (73.56) followed by cluster III (68.70). The lowest mean was observed in the cluster I (53.33). The highest mean for stem girth in bathua was observed in the cluster III (2.37) and cluster IV (2.37) followed by cluster II (2.22). The lowest mean was observed in the cluster I (2.15).

The highest mean for plant spread E-W in bathua was observed in the cluster III (29.27) followed by cluster IV (24.87). The lowest mean was observed in the cluster II (24.37). The highest mean for plant spread N-S in bathua was

observed in the cluster IV (27.73) followed by cluster III (26.33). The lowest mean was observed in the cluster II (22.87).

The highest mean for days to first flowering in bathua was observed in the cluster III (40.34) followed by cluster I (39.37). The lowest mean was observed in the cluster II (38.78). The highest mean for days to 50% flowering in bathua was observed in the cluster I (43.35) followed by cluster III (43.00). The lowest mean was observed in the cluster IV (40.67).

The highest mean for inflorescence length in bathua was observed in the cluster IV (17.73) followed by cluster II (17.37). The lowest mean was observed in the cluster III (13.30).

The highest mean for inflorescence fresh weight in bathua was observed in the cluster IV (12.96) followed by cluster II (12.95). The lowest mean was observed in the cluster III (7.05). The highest mean for dry weight in bathua was observed in the cluster II (6.64) followed by cluster IV (6.33). The lowest mean was observed in the cluster III (4.27).

The highest mean for number of inflorescence per plant in bathua was observed in the cluster IV (11.33) followed by cluster I (10.75). The lowest mean was observed in the cluster III (7.80).

3.2.b Yield and quality parameters

The highest mean for fresh weight of the plant in bathua was observed in the cluster II (174.26) followed by cluster IV (127.53). The lowest mean was observed in the cluster III (89.06). The cluster II (23.87) showed highest cluster mean for dry weight of the plant, followed by cluster III (19.00). The lowest cluster mean was observed for the cluster I (13.74).

The highest mean for foliage yield per plant in bathua was observed in the cluster IV (266.95) followed by cluster I (262.40). The lowest mean was observed in the cluster II (236.76). The cluster mean for foliage yield per plot was highest in the cluster II (109.63) followed by cluster III (72.67). The lowest mean was observed in the cluster IV (43.13). The highest mean for foliage yield per hectare in bathua was observed in the cluster II (1.97) followed by cluster IV (1.37). The lowest mean was observed in the cluster I (1.21).

For vitamin-A content in bathua, the highest mean was observed for the cluster II (12.30) followed by cluster III (11.59). The lowest mean was observed in the cluster IV (7.31). The cluster II (478.04) showed highest cluster mean for vitamin-C content followed by cluster I (379.78). The lowest mean was observed for the cluster III (250.57).

The highest mean for protein content in bathua was observed in the cluster II (45.86) followed by cluster III (44.42). The lowest mean was observed in the cluster I (42.36). The cluster II (4.82) showed highest cluster mean for calcium content followed by cluster III (4.22). The lowest mean was observed for the cluster IV (3.85).

Magnesium content in bathua, the highest mean was observed for the cluster II (1429.83) followed by cluster I (1165.20). The lowest mean was observed in cluster III and IV (1079.83). The cluster II (1216.90) showed highest cluster mean for iron content followed by cluster I (487.57). The lowest cluster mean was observed for the cluster III (240.90).

For zinc content in bathua, the highest mean was observed for the cluster II (9.49) followed by cluster III (8.31). The lowest mean was observed in the cluster IV (2.96). The cluster II (0.14) showed highest cluster mean for oxalate content

followed by cluster III (0.12). The lowest mean was observed for the cluster IV (0.03).

The highest mean for nitrate content in bathua was observed in the cluster IV (390.84) followed by cluster I (389.27). The lowest mean was observed in the cluster II (346.14). The cluster I (305.46) showed highest cluster mean for total phenol content followed by cluster IV (300.73). The lowest mean was observed for the cluster II (257.32)

3.3 Relative contribution of different characters towards divergence

The character contributing maximum to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and the choice of parents for hybridization (Jagadev *et al.*, 1991; Siddique, 2010)^[2, 8]. The relative contribution of different characters for genetic parameters for genetic divergence (D^2) is given in the Table-5. Magnesium content (37.32%) contributed maximum to the total divergence among the genotypes followed by zinc (35.87%), iron (11.59%), vitamin-C (3.26%), total phenol (2.54%), nitrate (1.81%), inflorescence fresh weight (1.81%), days to first flowering (1.45%), inflorescence length (1.09%), foliage yield per hectare (1.09%), protein (1.09%), calcium (0.72%), and oxalate (0.36%). However, the traits like plant height, plant spread E-W, plant spread N-S, number of leaves per plant, number of branches per plant, leaf area, stem girth, days to first flowering, number of inflorescence per plant, inflorescence dry weight, fresh weight of plant, dry weight of plant, foliage yield per plant, foliage yield per plot, and vitamin-A content had no substantial contribution to total divergence.

4. Discussion

The importance of genetic diversity has been widely appreciated. Recognising and estimating such diversity has always been a difficult task. Multivariate analysis utilising the concept of statistical distance has been found to be a very powerful statistical tool in estimating diversity in biological populations. The D^2 analysis proposed by Mahalanobis (1936)^[3] has been reported to be effective tool to assess the genetic divergence. Such an analysis eventually helps to choose desirable parents for recombination breeding and the results in the development of superior varieties.

Ecological diversity has been regarded as a reasonable index of genetic diversity (Vavilov, 1926 and Moll *et al.*, 1962)^[10].

^{4]} Assuming this, the cultivars from widely separated localities have been included in the hybridisation programme by most of the plant breeders for recovering promising segregants. But Sachan and Sharma (1971)^[7] could not find and direct relationship between geographical distribution and genetic diversity in crops belonging to different breeding systems. The material for present study includes 24 bathua genotypes. The divergence analysis revealed considerable diversity was implied by the magnitude of all possible D^2 values, which ranged from 350.35 to 1585.98. Twenty four genotypes were grouped into four clusters which had considerable inter-cluster D^2 values (Table-3).

Studies on intra cluster distance revealed that, cluster II with four genotypes showed maximum intra-cluster distance ($D^2 = 294.46$) followed by cluster I ($D^2 = 245.75$) with eighteen genotypes it indicates more diversity present within the cluster and remaining cluster III and cluster IV had one genotypes and hence, the intra cluster distance was zero, it indicates very minimum diversity was found within the cluster.

Based on distance between clusters (inter-cluster distance), the maximum distance was observed between cluster II and cluster IV ($D^2 = 1585.98$) followed by cluster III and IV ($D^2 = 1210.55$), cluster II and III ($D^2 = 943.60$), cluster I and IV ($D^2 = 810.06$), cluster I and II ($D^2 = 686.24$). The cluster I revealed the least distance relationship with the cluster III ($D^2 = 350.35$).

The inter cluster distance between cluster II and IV (1585.98) were comparatively high for most of the yield and quality parameters. Therefore, it is desirable to attempt crosses between the genotypes belonging to these clusters to evolve desirable variety with high foliage yield, Vit-A, Vit-C, Protein, Ca, Mg, Fe, Zn content.

5. Conclusion

Genetic diversity was studied to detect the more diverse bathua genotypes which might be used in hybridization program. Twenty four genotypes were grouped into four different clusters and the maximum number of genotypes (14) were included in cluster (I). The highest inter cluster distance was observed between II and IV, while the highest intra-cluster distance was observed for the cluster II. The genotypes of bathua from cluster II and cluster IV may therefore, be selected as parents in future hybridization program.

Table 1: Details of bathua genotypes used in the study

Sl. No	Genotypes	Source
1.	HUB-1, HUB-2, HUB-3, HUB-4, HUB-5, HUB-6, HUB-7, HUB-8, HUB-9	Local collection from different parts of Karnataka
2.	IC-109235, NC-58616, NIC-22506, IC-243192, IC-341703, NIC-22517, IC-415477, IC-540842, IC-109249, IC-4152393, EC-359444, EC-359445, NIC-22492, IC-540831, NC-50229	NBPGR, New Delhi

Table 2: Distribution pattern of 24 genotypes of bathua in 4 different clusters

Cluster	Number of genotypes	Genotypes included in the cluster
I	18	HUB-5, IC-109235, NC-58616, NIC-22506, IC-243192, HUB-2, HUB-1, IC-341703, NIC-22517, IC-415477, HUB - 3, IC-540842, IC-109249, HUB-9, IC-4152393, EC-359444, EC-359445, NIC-22492
II	4	HUB-8, HUB-7, HUB-6, IC-540831
III	1	HUB-4
IV	1	NC-50229

Table 3: Average Intra cluster and inter cluster distance (D²) of four clusters for bathua genotypes

	I	II	III	IV
I	245.75	686.24	350.35	810.06
II		294.46	943.60	1585.98
III			0.00	1210.55
IV				0.00

Table 4: The cluster mean of 28 characters for four clusters in bathua genotypes

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
I	53.48	85.59	9.78	53.53	2.15	24.55	24.21	39.37	43.35	17.26	11.23	6.31	10.75	104.06	13.74	53.2	1.21	8.18	379.78	42.36	3.97	1165.2	487.57	5.52	0.11	389.27	305.46	262.4
II	70.81	109.78	11.27	73.56	2.22	24.37	22.87	38.78	42.42	17.37	12.95	6.64	10.1	174.26	23.87	109.63	1.97	12.3	478.04	45.86	4.82	1429.83	1216.9	9.49	0.14	346.14	257.32	236.76
III	59.67	108.93	11.4	68.7	2.37	29.27	26.33	40.34	43	13.3	7.05	4.27	7.8	89.06	19	72.67	1.26	11.59	250.57	44.42	4.22	1079.83	240.9	8.31	0.12	356.85	275.54	242.38
IV	48.33	95.8	8.73	64.48	2.37	24.87	27.73	39.32	40.67	17.73	12.96	6.33	11.33	127.53	15.87	43.13	1.37	7.31	341.33	43.52	3.85	1079.83	456.9	2.96	0.03	390.84	300.73	266.95

- | | | | |
|---------------------------------|------------------------------------|-------------------------------|-----------------------------|
| 1. Plant height | 8. Days to first flowering | 15. Dry weight of plant | 22. Magnesium |
| 2. Number of leaves per plant | 9. Days to 50% flowering | 16. Foliage yield per plot | 23. Iron |
| 3. Number of branches per plant | 10. Inflorescence length | 17. Foliage yield per hectare | 24. Zinc |
| 4. Leaf area | 11. Inflorescence fresh weight | 18. Vitamin- A | 25. Oxalate |
| 5. Stem girth | 12. Inflorescence dry weight | 19. Vitamin – C | 26. Nitrate |
| 6. Plant spread E- W | 13. No. of inflorescence per plant | 20. Protein | 27. Total Phenol |
| 7. Plant spread N-S | 14. Fresh weight of plant | 21. Calcium | 28. Foliage yield per plant |

Table 5: Per cent contribution of the different characters to the total divergence in bathua genotypes

Sl. NO	Character	No. of first rank	Per cent contribution
1	Plant Height (cm)	0	0.00
2	Plant spread E-W(cm)	0	0.00
3	Plant spread N-S(cm)	0	0.00
4	Number of leaves per plant	0	0.00
5	Number of branches per plant	0	0.00
6	Leaf area(cm)	0	0.00
7	Stem girth (cm)	0	0.00
8	Days to first flowering	0	0.00
9	Days to 50% flowering	4	1.45
10	Number of inflorescence per plant	0	0.00
11	Inflorescence length (cm)	3	1.09
12	Inflorescence fresh weight(g)	5	1.81
13	Inflorescence dry weight (g)	0	0.00
14	Fresh weight of plant (g)	0	0.00
15	Dry weight of plant (g)	0	0.00
16	Foliage yield per plant (g)	0	0.00
17	Foliage yield per plot(kg)	0	0.00
18	Foliage yield per hectare (tonnes)	3	1.09
19	Vitamin- A(mg)	0	0.00
20	Vitamin –C(mg)	9	3.26
21	Protein (mg)	3	1.09
22	Calcium(mg)	2	0.72
23	Magnesium (mg)	103	37.32
24	Iron (mg)	32	11.59
25	Zinc(mg)	99	35.87
26	Oxalates (mg)	1	0.36
27	Nitrates (mg)	5	1.81
28	Total Phenols (mg)	7	2.54

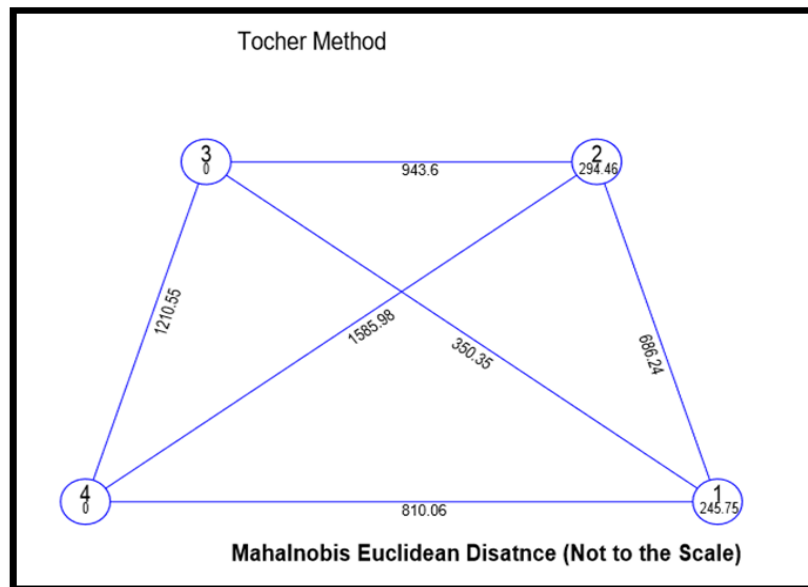


Fig 1: Diagrammatic representation of different intra and inter cluster distance of bathua genotypes

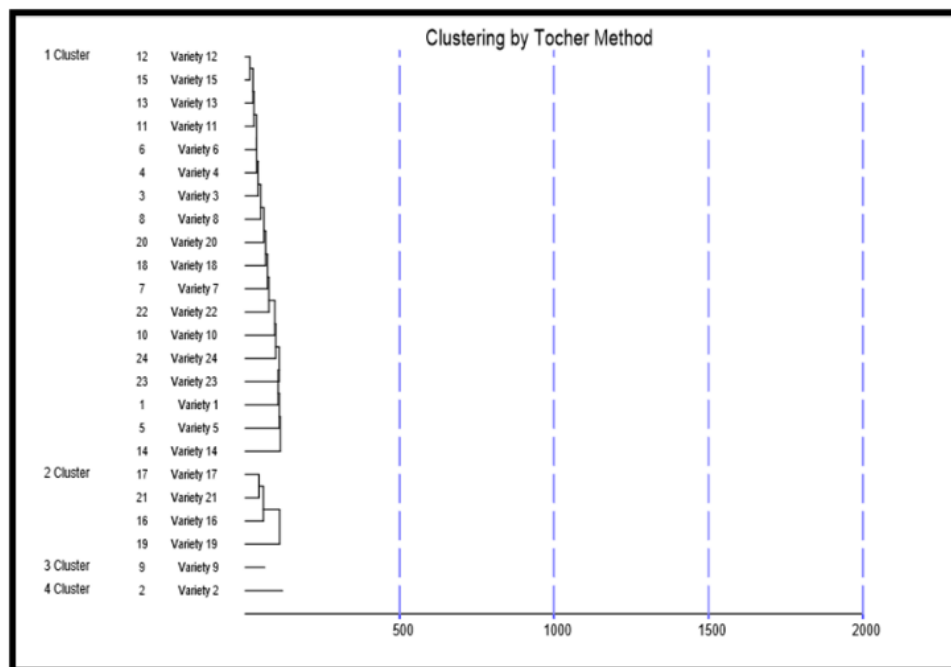


Fig 2: Cluster analysis dendrogram of the 24 genotypes of bathua

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