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Genetic variability, heritability and genetic divergence among vegetable amaranth (*Amaranthus tricolor* L.) genotypes

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Abstract

Vegetable amaranth (*Amaranthus tricolor* L.) is a fast-growing, nutritionally rich leafy vegetable crop that remains largely underutilized despite its outstanding potential as a food security crop. The present study was conducted at the Horticulture Research Centre, Murthal, Sonapat (Haryana), during the kharif season of 2024 to assess genetic variability, heritability, genetic advance, and genetic divergence among 30 germplasm lines of vegetable amaranth. The experiment was laid out in a Randomized Block Design with three replications. Observations were recorded on six key traits: fresh leaf weight (FLW), dry leaf weight (DLW), fresh shoot weight per plant (FSW/Plant), dry shoot weight per plant (DSW/Plant), number of leaves per plant (NOL/Plant), and chlorophyll content. Wide and significant variation was observed among the genotypes for all traits studied. Moderate to high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values were recorded across traits, with dry leaf weight showing the highest GCV (37.71%) and PCV (42.17%). Heritability estimates were high to very high (68.54–92.18%), and genetic advance as percentage of mean ranged from 14.35% (NOL/Plant) to 69.46% (DLW), suggesting that additive gene action predominantly controls most of the studied traits. Cluster analysis using Mahalanobis D² statistics grouped the 30 genotypes into four distinct clusters, with maximum inter-cluster distance recorded between Cluster II and Cluster IV (361.42). Genotypes EC-386966, VRAM-330, Pusa Kiran, and Arka Arunima emerged as consistently superior performers and are recommended for use as parents in future breeding programmes.

Keywords: Vegetable amaranth, genetic variability, heritability, genetic advance, cluster analysis

1. Introduction

Amaranth (*Amaranthus* sp.) is an ancient crop with enormous nutritional and agricultural value, belonging to the family Amaranthaceae and order Caryophyllales. It is grown mainly in tropical and subtropical parts of the world and is often referred to as an "orphan crop" - a plant largely overlooked by modern science despite its rich genetic diversity and ability to grow in difficult conditions. Historical records show that amaranth has been cultivated for more than 8,000 years, with its roots in the pre-Columbian civilizations of Central and South America, where it was one of the most important food crops ^[1]. Over the centuries, it has spread across the globe because it can thrive at temperatures of 20-40 °C, at elevations between 500 and 2,500 metres above sea level, and with rainfall between 800 and 1,500 mm ^[2].

Amaranth is classified as a pseudocereal and is valued for its edible leaves, tender stems, and grains, all of which contribute significantly to human nutrition ^[3]. The crop is well known as a good source of dietary fibre, vitamins and their precursors such as ascorbic acid, riboflavin and carotenoids, and important minerals including calcium, iron, magnesium, potassium, copper, zinc and manganese ^[4]. It is especially noteworthy for its high iron and β -carotene content. In addition, amaranth has a well-balanced amino acid profile, making it nutritionally superior to many common leafy vegetables ^[5]. Its tender stems and leaves are also rich in moisture (85.70%), protein (4.0 g), carbohydrates (6.30 g), calcium (397.0 mg), iron (25.5 mg), phosphorus (83.0 mg), vitamin A (9,200 IU) and vitamin C (99 mg) per 100 g fresh weight ^[7].

Being a C4 plant, vegetable amaranth has very high production potential, growing rapidly and producing large amounts of biomass in a short time, making it an excellent crop for rotation with

other vegetables [8]. Its tough nature, combined with natural resistance to heat, drought, diseases and pests, has led to its rediscovery as a promising crop for food security in recent decades [9,10]. These qualities make amaranth particularly relevant in the context of climate change and the growing need for nutritionally rich, stress-tolerant food crops, especially in densely populated and undernourished regions of the world [11,12].

Despite its immense potential, detailed evaluation studies for yield and quality traits remain scarce under Indian conditions. A thorough understanding of the extent and nature of genetic variability among available germplasm accessions is essential before starting any meaningful crop improvement programme. Estimates of heritability and genetic advance - studied alongside variability measures - help the breeder understand how much of the variation is genetic versus environmental, and guide the choice of the most effective selection strategies [14]. Cluster analysis using Mahalanobis D² statistics is one of the most reliable multivariate approaches for measuring genetic divergence among genotypes and identifying genetically diverse parents for hybridization programmes [15]. With this in mind, the present investigation was undertaken to evaluate 30 amaranth genotypes for important foliage yield and quality traits, estimate genetic variability parameters, and assess genetic divergence - with the ultimate aim of identifying superior genotypes and promising parent combinations for future breeding work under Haryana conditions.

2. Materials and Methods

2.1 Location and Climate of the Experimental Site

This investigation was carried out at the Research Farm of the Horticulture Research Centre, Murthal, Sonipat (Haryana), during the kharif season (June-July) of 2024. The experimental site has a semi-arid, subtropical climate with hot summers and cool, dry winters. Summer temperatures often reach 42-45 °C in May and June, while winter temperatures typically hover around 7-8 °C. The soil at the site is predominantly sandy loam, non-saline and slightly to moderately alkaline in nature.

2.2 Experimental Material

The experimental material consisted of 30 genotypes of vegetable amaranth (*Amaranthus tricolor* L.). During the present experiment, three released varieties Arka Arunima, Pusa Kiran, and Pusa Lal Chaulai were used as standard checks.

2.3 Experimental Design and Layout

The experiment was set up in a Randomized Block Design (RBD) with three replications, giving a total of 90 experimental plots. Each plot measured 3 m × 3 m. The crop was raised following standard agronomic practices recommended for vegetable amaranth cultivation. A row-to-row spacing of 50 cm and a plant-to-plant spacing of 20 cm were maintained. Five cuttings were taken during the crop's growth period to record observations on the various growth and yield parameters.

3. Results

3.1 Mean Performance of Genotypes for Various Traits

The mean performance of all 30 genotypes was evaluated for six important traits: fresh leaf weight (FLW), dry leaf weight (DLW), fresh shoot weight per plant (FSW/Plant), dry shoot weight per plant (DSW/Plant), number of leaves per plant (NOL/Plant), and chlorophyll content. Analysis of variance revealed highly significant differences among genotypes for all six traits studied (Table 1), confirming the presence of meaningful genetic variation within the experimental material.

Fresh Leaf Weight (FLW): FLW ranged from a minimum of 0.62 g (IC-582922) to a maximum of 2.30 g (VRAM-330), with an overall mean of 1.23 g. VRAM-330, EC-386966, and Sel-4-1-A recorded notably higher fresh leaf weight, well above the population mean. Among the check varieties, Pusa Kiran (1.48 g) and Arka Arunima (1.34 g) performed comparatively well, while Pusa Lal Chaulai (0.99 g) recorded a value below the population mean.

Dry Leaf Weight (DLW): DLW showed the widest relative variation among all six traits, ranging from 0.02 g (IC-551483) to 0.64 g (EC-386966), with a population mean of 0.28 g. EC-386966 and VRAM-330 stood out as the top performers, recording values more than twice the population mean.

Fresh Shoot Weight per Plant (FSW/Plant): FSW/Plant ranged from 51.24 g (IC-582925) to 77.21 g (Pusa Kiran), with a population mean of 66.47 g. Pusa Kiran recorded the highest FSW/Plant, closely followed by EC-386966 (76.20 g) and VRAM-368 (76.13 g). Several IC accessions recorded FSW/Plant values well below the population mean.

Dry Shoot Weight per Plant (DSW/Plant): DSW/Plant ranged from 10.99 g (IC-551486) to 16.94 g (Pusa Kiran), with a population mean of 13.89 g. Pusa Kiran again topped the list, followed by Arka Arunima (16.52 g) and VRAM-368 (16.10 g).

Number of Leaves per Plant (NOL/Plant): NOL/Plant ranged from 52.54 (IC-551483) to 81.49 (EC-386966), with a population mean of 69.97 leaves per plant. EC-386966 produced the highest number of leaves per plant, followed by VRAM-21 (77.04) and IC-582928 (77.03).

Chlorophyll Content: Chlorophyll content ranged from 8.53 SPAD units (IC-551506) to 17.22 SPAD units (VRAM-C-2), with a population mean of 13.48. VRAM-C-2 stood out as the clear top performer, followed by EC-386966 (17.11) and VRAM-327 (16.08).

The coefficient of variation (CV) values ranged from 7.58% (FLW) to 9.64% (DSW/Plant), indicating acceptable experimental precision. Overall, EC-386966, Pusa Kiran, and VRAM-330 emerged as consistently outstanding performers across all six traits. The mean performance of all 30 genotypes is presented in Table 2.

Table 1: Analysis of Variance (ANOVA) of Morphological Traits

Source	d.f.	FLW	DLW	FSW/Plant	DSW/Plant	NOL/Plant	Chlorophyll
Replication	2	0.31	0.02	1205.75	1.43	154.23	0.97
Treatment	29	0.47**	1.36**	144.50**	8.91**	118.22**	16.82**
Error	58	0.06	0.21	3.97	0.31	15.77	0.55

** Significant at 1% level of probability. FLW = Fresh Leaf Weight; DLW = Dry Leaf Weight; FSW/Plant = Fresh Shoot Weight per Plant; DSW/Plant = Dry Shoot Weight per Plant; NOL/Plant = Number of Leaves per Plant.

Table 2: Mean Performance of 30 Genotypes for Morphological Traits (Mean $\pm$ SE)

Sr. No.	Genotype	FLW (g)	DLW (g)	FSW/Plant (g)	DSW/Plant (g)	NOL/Plant	Chlorophyll
1	IC-551468	1.38 $\pm$ 0.17	0.49 $\pm$ 0.06	66.03 $\pm$ 2.01	13.02 $\pm$ 0.68	59.89 $\pm$ 1.81	9.81 $\pm$ 0.81
2	IC-551483	0.97 $\pm$ 0.06	0.22 $\pm$ 0.02	55.59 $\pm$ 1.17	11.40 $\pm$ 0.33	52.54 $\pm$ 0.29	13.87 $\pm$ 0.70
3	IC-551486	0.93 $\pm$ 0.09	0.24 $\pm$ 0.02	55.09 $\pm$ 2.39	10.99 $\pm$ 0.31	66.84 $\pm$ 1.28	13.70 $\pm$ 0.68
4	IC-551492	0.87 $\pm$ 0.06	0.25 $\pm$ 0.03	56.89 $\pm$ 2.23	11.26 $\pm$ 0.27	76.89 $\pm$ 4.84	9.51 $\pm$ 0.53
5	IC-551494	1.07 $\pm$ 0.09	0.23 $\pm$ 0.06	62.73 $\pm$ 2.64	12.28 $\pm$ 0.20	70.82 $\pm$ 1.08	9.55 $\pm$ 0.52
6	IC-551506	0.69 $\pm$ 0.12	0.20 $\pm$ 0.02	55.67 $\pm$ 2.46	11.30 $\pm$ 0.45	64.53 $\pm$ 2.43	8.53 $\pm$ 0.60
7	IC-582922	0.62 $\pm$ 0.12	0.20 $\pm$ 0.03	62.11 $\pm$ 2.11	12.12 $\pm$ 0.27	66.03 $\pm$ 0.32	11.41 $\pm$ 0.47
8	IC-582925	1.12 $\pm$ 0.12	0.28 $\pm$ 0.03	51.24 $\pm$ 2.28	11.29 $\pm$ 0.48	71.09 $\pm$ 2.37	9.87 $\pm$ 0.55
9	IC-582928	1.01 $\pm$ 0.06	0.22 $\pm$ 0.03	69.26 $\pm$ 2.80	13.86 $\pm$ 0.10	77.03 $\pm$ 3.76	11.17 $\pm$ 0.22
10	EC-386966	2.04 $\pm$ 0.17	0.64 $\pm$ 0.03	76.20 $\pm$ 4.13	15.29 $\pm$ 0.73	81.49 $\pm$ 2.04	17.11 $\pm$ 0.19
11	VS-18	1.43 $\pm$ 0.17	0.36 $\pm$ 0.02	67.63 $\pm$ 2.89	14.92 $\pm$ 0.32	74.12 $\pm$ 1.54	11.61 $\pm$ 0.53
12	VS-21	0.96 $\pm$ 0.15	0.26 $\pm$ 0.01	74.25 $\pm$ 2.25	15.51 $\pm$ 0.19	70.57 $\pm$ 2.07	13.04 $\pm$ 0.28
13	VS-79	1.35 $\pm$ 0.06	0.29 $\pm$ 0.01	63.52 $\pm$ 3.06	12.32 $\pm$ 0.16	75.01 $\pm$ 2.49	15.05 $\pm$ 0.24
14	VRAM-7	0.77 $\pm$ 0.06	0.20 $\pm$ 0.02	69.73 $\pm$ 3.78	15.30 $\pm$ 0.27	65.85 $\pm$ 1.86	14.13 $\pm$ 0.26
15	VRAM-17	0.90 $\pm$ 0.12	0.28 $\pm$ 0.02	65.71 $\pm$ 5.74	14.68 $\pm$ 0.23	73.79 $\pm$ 1.29	15.45 $\pm$ 0.88
16	VRAM-21	1.19 $\pm$ 0.03	0.28 $\pm$ 0.05	66.28 $\pm$ 2.56	14.63 $\pm$ 0.18	77.04 $\pm$ 2.48	14.88 $\pm$ 0.25
17	VRAM-150	0.84 $\pm$ 0.06	0.19 $\pm$ 0.02	63.61 $\pm$ 2.24	12.73 $\pm$ 0.22	68.00 $\pm$ 2.73	14.75 $\pm$ 0.28
18	VRAM-303	1.29 $\pm$ 0.12	0.36 $\pm$ 0.03	61.40 $\pm$ 2.85	12.67 $\pm$ 0.17	64.37 $\pm$ 3.56	13.80 $\pm$ 0.21
19	VRAM-327	1.17 $\pm$ 0.06	0.30 $\pm$ 0.03	69.72 $\pm$ 3.04	14.82 $\pm$ 0.13	67.06 $\pm$ 3.78	16.08 $\pm$ 0.22
20	VRAM-330	2.30 $\pm$ 0.23	0.64 $\pm$ 0.02	68.73 $\pm$ 2.80	13.69 $\pm$ 0.24	69.65 $\pm$ 0.57	15.30 $\pm$ 0.31
21	VRAM-357	1.73 $\pm$ 0.17	0.40 $\pm$ 0.02	71.33 $\pm$ 3.41	14.96 $\pm$ 0.19	64.65 $\pm$ 1.38	13.20 $\pm$ 0.42
22	VRAM-368	1.08 $\pm$ 0.05	0.39 $\pm$ 0.02	76.13 $\pm$ 3.00	16.10 $\pm$ 0.15	72.79 $\pm$ 2.22	16.42 $\pm$ 0.27
23	VRAM-C-2	1.14 $\pm$ 0.11	0.24 $\pm$ 0.02	72.40 $\pm$ 3.31	15.64 $\pm$ 0.22	57.82 $\pm$ 1.86	17.22 $\pm$ 0.28
24	VRAM-C-6	1.37 $\pm$ 0.06	0.31 $\pm$ 0.06	70.37 $\pm$ 2.05	15.80 $\pm$ 0.33	65.03 $\pm$ 2.68	14.30 $\pm$ 0.25
25	KPIDRB-21-131	1.06 $\pm$ 0.06	0.26 $\pm$ 0.02	69.98 $\pm$ 2.91	13.43 $\pm$ 0.39	70.26 $\pm$ 2.03	14.29 $\pm$ 0.21
26	KPIDRB-21-150	1.10 $\pm$ 0.29	0.22 $\pm$ 0.06	62.26 $\pm$ 2.39	13.64 $\pm$ 0.31	73.83 $\pm$ 2.87	13.76 $\pm$ 0.23
27	Sel-4-1-A	2.03 $\pm$ 0.22	0.56 $\pm$ 0.03	59.72 $\pm$ 3.16	13.91 $\pm$ 0.57	71.06 $\pm$ 4.07	12.65 $\pm$ 0.34
28	Arka Arunima	1.34 $\pm$ 0.09	0.26 $\pm$ 0.02	75.77 $\pm$ 0.78	16.52 $\pm$ 0.21	70.06 $\pm$ 0.19	14.85 $\pm$ 0.24
29	Pusa Kiran	1.48 $\pm$ 0.12	0.38 $\pm$ 0.06	77.21 $\pm$ 1.96	16.94 $\pm$ 0.04	75.84 $\pm$ 3.19	13.99 $\pm$ 0.33
30	Pusa Lal Chaulai (Check)	0.99 $\pm$ 0.41	0.40 $\pm$ 0.06	67.06 $\pm$ 2.17	14.65 $\pm$ 0.26	75.56 $\pm$ 1.80	15.97 $\pm$ 0.08
	C.D.	0.40	0.09	3.26	0.91	6.50	1.21
	SE(m)	0.14	0.05	1.15	0.32	2.29	0.42
	C.V. (%)	10.64	9.88	10.01	11.99	12.70	5.49

FLW = Fresh Leaf Weight; DLW = Dry Leaf Weight; FSW/Plant = Fresh Shoot Weight per Plant; DSW/Plant = Dry Shoot Weight per Plant; NOL/Plant = Number of Leaves per Plant; C.D. = Critical Difference; SE(m) = Standard Error of Mean; C.V. = Coefficient of Variation.

3.2 Variability Parameters, Heritability, and Genetic Advance

The estimates of variability parameters, heritability and genetic advance for all six traits are presented in Table 3. The genotypic coefficient of variation (GCV) values ranged from 8.41% (NOL/Plant) to 37.70% (DLW). Correspondingly, phenotypic coefficient of variation (PCV) values ranged from 10.16% (NOL/Plant) to 42.17% (DLW). Shoot weight traits and number of leaves per plant recorded comparatively lower GCV and PCV values, though sufficient variation still exists for selection purposes. Chlorophyll content recorded moderate GCV (17.23%) and PCV (18.09%) values.

Heritability in the broad sense was highest for fresh shoot weight per plant (92.17%), followed by chlorophyll content (90.78%), dry shoot weight per plant (90.37%), and dry leaf weight

(79.95%). Even the lowest heritability estimate recorded for NOL/Plant (68.54%), remains in the moderate-to-high range and is broadly favorable for selection.

Genetic advance as percentage of mean (GA%) ranged from 14.352% (NOL/Plant) to 69.45% (DLW). The combination of high heritability with high genetic advance as percentage of mean, as observed for dry leaf weight ($h^2 = 79.95\%$, $GA\% = 69.45\%$) and fresh leaf weight ($h^2 = 68.84\%$, $GA\% = 52.45\%$), clearly indicates the predominance of additive gene action governing these traits^{17,18}. Chlorophyll content also recorded a high heritability (90.78%) with a moderately high genetic advance (33.83%). Number of leaves per plant showed the lowest heritability (68.54%) and the lowest genetic advance as percentage of mean (14.35%) among all traits.

Table 3: Mean, Range, GCV, PCV, Heritability, Genetic Advance, and GA as Percentage of Mean

Trait	Mean	Range		GCV (%)	PCV (%)	Heritability (%)	Genetic Advance	GA as% of Mean
		Min.	Max.					
FLW (g)	1.23	0.62	2.30	30.68	36.98	68.84	0.63	52.45
DLW (g)	0.28	0.02	0.64	37.70	42.17	79.95	0.22	69.45
FSW/Plant (g)	66.4	51.24	77.23	10.35	10.78	92.17	13.53	20.47
DSW/Plant (g)	13.8	10.99	16.97	12.22	12.86	90.37	3.31	23.94
NOL/Plant	69.9	52.53	81.49	8.41	10.16	68.54	9.99	14.35
Chlorophyll	13.48	8.53	17.22	17.24	18.09	90.78	4.57	33.83

GCV = Genotypic Coefficient of Variation; PCV = Phenotypic Coefficient of Variation; GA = Genetic Advance

3.3 Cluster Analysis and Genetic Divergence

Cluster analysis based on Mahalanobis D² statistics was performed to quantify genetic divergence among the 30 amaranth genotypes and group them into homogeneous clusters based on their overall similarity across all six morphological traits. The results are presented in Tables 4, 5, and 6. The 30 genotypes were grouped into four distinct clusters showing considerable variation in cluster size, inter-cluster and intra-cluster distances, and cluster mean values. Cluster IV was the largest group, comprising 11 genotypes. Cluster I was the second largest with 9 genotypes, followed by Cluster II with 7 genotypes. Cluster III was the smallest, containing only 3 genotypes - Sel-4-1-A, VRAM-330, and EC-386966. The intra-cluster distances ranged from 201.07 (Cluster III) to

314.44 (Cluster II). The maximum inter-cluster distance was observed between Cluster II and Cluster IV (D² = 361.42), indicating that these two clusters are the most genetically divergent. The second largest inter-cluster distance was between Cluster III and Cluster IV (D² = 339.41), followed by Cluster II and Cluster III (D² = 326.40). The minimum inter-cluster distance was observed between Cluster I and Cluster III (D² = 183.06). Cluster II recorded the highest mean values for most yield and quality traits: FLW (1.32 g), DLW (0.32 g), FSW/Plant (73.27 g), DSW/Plant (15.82 g), and chlorophyll content (15.15). Cluster III, despite having only three genotypes, recorded the highest cluster means for FLW (2.12 g) and DLW (0.61 g). Cluster I recorded the lowest mean values for most traits, indicating that genotypes in this cluster are generally modest performers.

Table 4: Cluster Classification of 30 Genotypes based on Mahalanobis D² Statistics

Cluster	Genotypes Included	No. of Genotypes
Cluster I	IC-551494, IC-551468, IC-551484, IC-551492, IC-551486, IC-551506, IC-582922, IC-582925, VRAM-303	9
Cluster II	Arka Arunima, Pusa Kiran, VRAM-C-2, VRAM-C-6, VRAM-327, VRAM-368, VRAM-357	7
Cluster III	Sel-4-1-A, VRAM-330, EC-386966	3
Cluster IV	IC-582928, Pusa Lal Chaulai, VRAM-21, VRAM-7, VS-79, VS-21, VS-18, VRAM-17, VRAM-150, KPIDRB-21-131, KPIDRB-21-150	11

Table 5: Estimates of Inter and Intra-Cluster Distances for different Clusters of 30 Genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	223.57 (intra)	—	—	—
Cluster II	241.34	314.44 (intra)	—	—
Cluster III	183.06	326.40	201.07 (intra)	—
Cluster IV	272.11	361.42	339.41	301.67 (intra)

Diagonal values represent intra-cluster distances; off-diagonal values represent inter-cluster distances.

Table 6: Cluster Means for Morphological Traits

Cluster	FLW (g)	DLW (g)	FSW/Plant (g)	DSW/Plant (g)	NOL/Plant	Chlorophyll
Cluster I	0.99	0.27	58.52	11.81	65.88	11.11
Cluster II	1.32	0.32	73.27	15.82	67.60	15.15
Cluster III	2.12	0.61	68.21	14.29	74.07	15.01
Cluster IV	1.05	0.26	67.21	14.15	72.82	14.01

FLW = Fresh Leaf Weight; DLW = Dry Leaf Weight; FSW/Plant = Fresh Shoot Weight per Plant; DSW/Plant = Dry Shoot Weight per Plant; NOL/Plant = Number of Leaves per Plant.

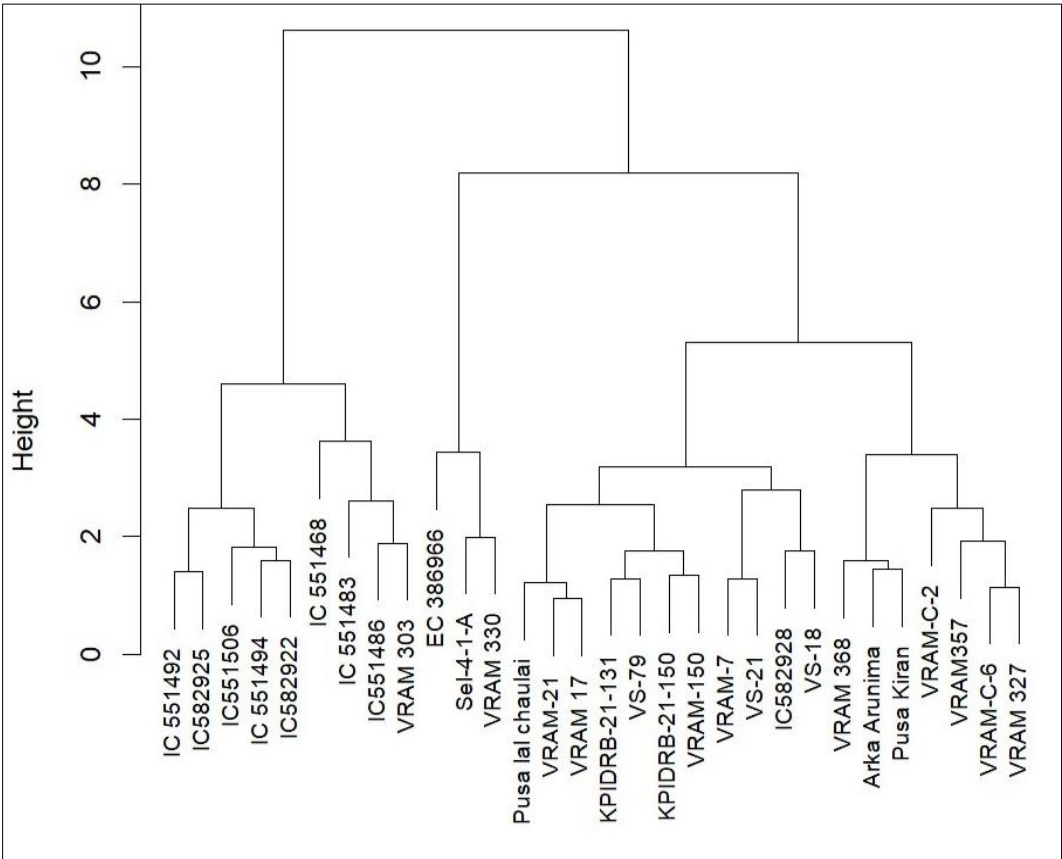


Fig 1: Dendrogram showing clustering pattern among 30 genotypes of vegetable amaranth for morphological traits

4. Discussion

4.1 Mean Performance of Genotypes for Yield and Quality Traits

The present study revealed substantial and statistically significant variation among the 30 evaluated amaranth genotypes for all six yield and quality traits, confirming the existence of rich and exploitable genetic diversity within the experimental germplasm. The considerable variation observed for fresh leaf weight and dry leaf weight is in close agreement with earlier findings of Shukla *et al.* [12] and Dhangra *et al.* [14], who also documented significant genotypic differences for leaf weight traits in vegetable amaranth germplasm. The genotypes EC-386966 and VRAM-330, which recorded the highest values for both FLW and DLW, are particularly noteworthy as they combine high fresh biomass production with high dry matter accumulation per leaf - making them potentially superior both in terms of fresh market yield and nutritional quality [5, 17].

Fresh shoot weight per plant and dry shoot weight per plant are among the most economically critical yield-contributing traits in vegetable amaranth. The superior performance of improved check varieties Pusa Kiran and Arka Arunima, along with advanced lines such as VRAM-368 and EC-386966, for these traits is consistent with the findings of Maurya and Arya⁶ and Mandal *et al.* [13], who reported that improved varieties and selected advanced lines tend to produce significantly higher shoot biomass compared to unimproved accessions. The consistently poor performance of several IC accessions (IC-551483, IC-551486, IC-551506) for both shoot weight traits suggests that these accessions have inherently lower vegetative vigour under the experimental conditions.

The number of leaves per plant showed wide genotypic differences, with EC-386966 producing the highest number of leaves and IC-551483 the lowest. This is in conformance with earlier reports of Ozimede *et al.* [3] and Mobina *et al.* [19], who noted significant variation for leaf number among amaranth accessions evaluated under different agro-climatic conditions. The fact that EC-386966 simultaneously recorded the highest number of leaves per plant as well as one of the highest values for FLW, DLW, and chlorophyll content makes it a uniquely superior genotype.

Chlorophyll content showed considerable variation among genotypes, in line with findings of Prakash and Pal [11] and Shukla *et al.* [12]. The standout performance of VRAM-C-2 for chlorophyll content, together with its high shoot weight values, makes it a particularly attractive genotype for programmes aiming to develop nutritionally superior and visually appealing varieties of vegetable amaranth.

4.2 Variability Parameters, Heritability, and Genetic Advance

The moderate to high GCV and PCV values recorded for most traits confirmed the existence of considerable variability at both genotypic and phenotypic levels. The narrow gap between GCV and PCV across traits is a particularly important finding, indicating that environmental influence on trait expression was relatively minimal and that the observed phenotypic differences among genotypes reliably reflect their true genetic differences. Similar trends have been consistently reported by Dhangra *et al.* [14] and Shukla *et al.* [12].

The very high heritability estimates recorded across all traits are encouraging and indicate that the genotypic contribution to total phenotypic variation was high throughout. High heritability values for yield and quality traits in vegetable amaranth have been consistently reported in earlier studies by Mandal *et al.* [13] and

Ozimede *et al.* [3].

The combination of high heritability with high genetic advance as percentage of mean - as observed for dry leaf weight and fresh leaf weight - provides the most conclusive evidence for the predominance of additive gene action governing these traits, and is the most favourable condition for achieving rapid genetic progress through direct selection [18]. For fresh shoot weight and dry shoot weight per plant, the very high heritability values but moderate genetic advance as percentage of mean suggest that some degree of non-additive gene effects may also be contributing. Similar observations have been reported by Rana *et al.* [8] and Dhangra *et al.* [14]. The number of leaves per plant, with the lowest heritability and lowest genetic advance, suggests that this trait may be influenced by both genetic and environmental factors, as also observed by Mobina *et al.* [19].

4.3 Cluster Analysis and Genetic Divergence

The cluster analysis using Mahalanobis D² statistics successfully grouped the 30 amaranth genotypes into four distinct clusters, clearly reflecting the presence of considerable genetic divergence within the evaluated germplasm. The distribution of genotypes into clusters of unequal size is a common and expected outcome in genetic divergence studies, as also reported by Mandal *et al.* [13] and Dhangra *et al.* [14] in vegetable amaranth.

The formation of the very small Cluster III, comprising only three genotypes (EC-386966, VRAM-330, and Sel-4-1-A), is particularly significant from a breeding standpoint. Genotypes that form small isolated clusters are generally considered to carry unique and rare allelic combinations not commonly found in the broader germplasm pool and are therefore of high value as parents in hybridization programmes [15, 16]. The additional fact that EC-386966 and VRAM-330 also ranked among the very top performers for leaf weight traits further reinforces their exceptional value as parent materials.

The maximum inter-cluster distance was observed between Cluster II and Cluster IV, indicating that genotypes from these two clusters are the most genetically divergent. According to the foundational principles outlined by Mahalanobis [15], crosses between genotypes from the most divergent clusters are expected to generate the widest range of variability in segregating generations and provide the greatest opportunities for recovering superior transgressive segregants. Based on this principle, crosses involving genotypes from Cluster II (Pusa Kiran, VRAM-368, Arka Arunima, VRAM-C-2) with genotypes from Cluster IV (VRAM-21, VS-21, Pusa Lal Chaulai) are strongly recommended. These recommendations are consistent with the findings of Rana *et al.* [8] and Ozimede *et al.* [3].

An interesting observation from the cluster analysis was that genotypes from geographically and genetically diverse backgrounds were sometimes grouped together within the same cluster, reinforcing the finding of McGrath and Quiros¹⁶ that genetic diversity does not always align with geographical origin. This underscores the importance of phenotypic and molecular characterization-based germplasm evaluation for accurate identification of genetically diverse accessions.

5. Conclusion

The present investigation clearly demonstrated that a wide range of genetic diversity exists among the 30 vegetable amaranth (*Amaranthus tricolor* L.) genotypes evaluated under Haryana conditions. All six traits studied showed highly significant variation, confirming the availability of ample genetic material for effective selection and plant breeding work. High heritability estimates combined with moderate to high genetic advance as

percentage of mean - especially for dry leaf weight, fresh leaf weight, and chlorophyll content - indicate that these traits are predominantly controlled by additive genes, making simple selection methods such as mass selection or progeny selection effective strategies for improvement. The number of leaves per plant, with moderate heritability and lower genetic advance, may require complementary breeding approaches such as heterosis breeding or recurrent selection.

Cluster analysis using Mahalanobis D^2 statistics successfully grouped the 30 genotypes into four distinct clusters, revealing meaningful genetic divergence among the germplasm. The maximum inter-cluster distance between Cluster II and Cluster IV suggests that crosses between superior genotypes from these two clusters are likely to produce the greatest range of variability and the most productive segregants for selection. Genotypes from Cluster III - EC-386966 and VRAM-330 - which performed consistently well across multiple traits, are strong candidates as parents for hybridization with superior genotypes from Cluster II. Overall, the study recommends EC-386966, VRAM-330, Pusa Kiran, Arka Arunima, and VRAM-368 as the most promising genotypes for direct selection as well as for use in future hybridization programmes aimed at developing high-yielding, nutritionally superior varieties of vegetable amaranth suited to the agro-climatic conditions of Haryana and similar environments.

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