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ASSESSMENT OF GROUNDNUT GENETIC DIVERSITY THROUGH DUS DESCRIPTOR

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Abstract

This study evaluated 33 groundnut (*Arachis hypogaea* L.) genotypes based on Distinctness, Uniformity, and Stability (DUS) guidelines using morphological traits. Significant variations were observed in key agronomic characteristics. Plant height ranged from 10.01 cm to 36.02 cm, with ICGV-5268 being the tallest. Plant width varied between 15.00 cm and 41.20 cm. Leaflet traits showed diversity, with Khenkhon having the longest leaflet (49.70 mm) and ICGV-93389 the widest (28.33 mm). Pod and seed dimensions also varied, with ICGV-1352 had the longest pods (36.70 mm) and ICGV-4514 the longest seed size (13.33 mm). Pod yield per plant ranged from 14.33 g to 48.86 g, with ISD-1314 exhibiting the highest yield potential. Qualitative traits indicated differences in growth habit, branching pattern, pigmentation, and leaflet morphology. Most germplasm displayed an erect growth habit (57.58%), while 30.30% were decumbent-3 type. Leaflet shape and margin characteristics further differentiated the genotypes. Cluster analysis grouped the genotypes into two main clusters, revealing genetic diversity. ICGV-5268, ISD-1314 and ICGV-4514 emerged as promising candidates for breeding due to their superior plant vigor, seed size, and yield potential. These findings highlight their importance as valuable genetic resources for groundnut improvement and breeding strategies.

Keywords: Groundnut (*Arachis hypogaea* L.), Germplasm, DUS descriptor, Characterization, Frequency distribution.

Introduction

Groundnut (*Arachis hypogaea* L.), a vital oilseed and cash crop, plays a significant role in global agriculture, serving as an important source of edible oil, protein, and essential nutrients. Major groundnut production is concentrated in various regions worldwide, with leading producers in Asia including China, India, Indonesia, Myanmar, and Vietnam; in Africa, key contributors are Nigeria, Sudan, the Democratic Republic of Congo, Chad, Mozambique, Zimbabwe, Burkina Faso, Uganda, and Mali; the United States is the primary producer in North America; while in Latin America and the Caribbean, Argentina, Brazil, and Mexico are the main producers (Motagi *et al.*, 2022). Among over 100 groundnut-producing countries, China is the world's largest producer and conservator of groundnut germplasm. In Bangladesh, groundnut production covered approximately 40,000 hectors, with a total yield of 75,000 metric tons. Groundnut accounted for just 7.18% of the total land

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under all oil crops and contributed approximately 6.41% of total oilseed production in 2022-2023 (BBS, 2023). The demand for groundnut in Bangladesh is increasing rapidly; however, only a small portion is utilized for oil production, while the majority is used as an ingredient in various industrially processed foods (Jahan *et al.*, 2022).

Most of the popular varieties and local cultivars in Bangladesh have not been characterized according to the DUS (Distinctness, Uniformity, and Stability) descriptor guidelines, making it challenging at times to distinguish between released varieties and local germplasm. As the demand for groundnut continues to rise, breeding programs face the challenge of developing high-yielding, disease-resistant, and climate-resilient varieties to meet the needs of both farmers and consumers. In this context, characterized groundnut germplasm serves as a key genetic resource, providing diverse genetic material for breeding efforts. Morphological data is vital for managing ex-situ genetic resources, helping classify germplasm and identify traits like early maturity, disease resistance, and improved pods of groundnuts.

Several studies have been conducted following DUS guidelines, such as those by Karthikeyan *et al.* (2023) and Yadav *et al.* (2010). Therefore, characterizing the quantitative and qualitative traits of groundnut germplasm provides breeders with valuable information for improving agronomic traits, including high yield, stress tolerance, and enhanced nutritional quality in newly developed varieties. This study explores the variation in quantitative and qualitative traits of collected germplasms role in addressing the evolving challenges faced by the agricultural sector.

Materials and Methods

In this study, 33 groundnut genotypes were used as plant materials, including one BINA variety (Binachinabadam-4) and one BARI variety (BARI Chinabadam9) two varieties were collected from the Plant Breeding Division, BINA, Mymensingh, while rest of the genotypes were collected from the Oilseed Research Centre (ORC), BARI, Joydebpur, Gazipur (Table 1). A total of 25 observations were recorded, comprising 16 qualitative and 9 quantitative traits, of groundnuts following the Descriptors for Groundnut established by the International Plant Genetic Resources Institute (IPGRI), 2000. The experiment was conducted under Department of Agronomy, Bangladesh Agricultural University, Mymensingh, Bangladesh, located at latitude 24.72º N and longitude 90.43º E. The evaluation was carried out during the Kharif season of 2022-2023. The experiment followed a randomized block design (RBD) with three replications as described by Sravanti *et al.* (2024) and Karthikeyan *et al.* (2023). Each plot consisted of four rows, with a row length of three meters, maintaining a plant spacing of 30cm × 10cm. The recommended fertilization and agronomic practices were followed for proper crop management. Morphological traits were recorded using DUS descriptors (IPGRI, 2000).

To conduct the DUS test, nine quantitative traits (height of the main stem, plant width/spread, leaflet length, leaflet width, pod length, pod width, seed length, seed weight and pod yield per plant) and 16 qualitative traits (growth habit, branching pattern, stem pigmentation, stem surface, peg pigmentation, leaf color, leaflet shape, leaflet surface, leaflet margin, leaflet tip, number of seeds per pod, pod beak, pod constriction, pod reticulation, seed color, and primary seed color) were assessed. For genotypes grouping based on trait similarity, genotypes were clustered using the R (Studio) statistical program, and a dendrogram was generated to visualize the relationships among the genotypes.

Table 1. List of 33 groundnut genotypes used in diversity study

Sl. No.	Name	Collector's Number	Sl. No.	Name	Collector's Number
1	7112-4-4-1	FI-29	18	ICGV-1901	FI-45
2	7112-2-1-2	FI-30	19	ICGV-5261	FI-46
3	ICGV-94322	FI-31	20	PK-1	FI-47
4	9112-2-1-1	FI-32	21	Beijing-2	FI-48
5	ICGV-1352	FI-33	22	ISD-4414	FI-49
6	Khenkhon	F-02	23	Vietnam	FI-50
7	ICGV-93389	FI-34	24	Mahosha	FI-51
8	7112-4-3-1	FI-35	25	ICGV-347	FI-52
9	9112-2-1-2	FI-36	26	ICGV-87055	FI-53
10	ICGV-94062	FI-37	27	ICGV-5268	FI-54
11	Binachinabadam-4	FI-38	28	ICGV-93199	FI-55
12	SM-6	FI-39	29	BARI Chinabadam-9	FI-56
13	7112-4-1-2	FI-40	30	ISD-1314	FI-57
14	ICGV-4514	FI-41	31	ICGV-94366	FI-58
15	ICGV-211	FI-42	32	ICGV-88388	FI-59
16	9112-5-2-2	FI-43	33	Boro Elachibadam	H-03
17	China Badam-1	FI-44			

Results and Discussion

The quantitative variations of nine descriptors in groundnut are presented in Table 2 and Figure 1. The height of the main stem ranged from 10.01 cm to 36.02 cm, with an average of 23.96 cm. The tallest plant was recorded in ICGV-5268 (36.02 cm), while the shortest (10.01 cm) was observed in 7112-2-1-2. The coefficient of variation (CV%) and standard deviation (SD) for plant height were 28.18% and 6.75, respectively. Plant width varied between 15.00 cm and 41.20 cm, with an average of 25.33 cm. The widest plant (41.20 cm) was observed in ICGV-5268, whereas the narrowest (15.00 cm) was found in ICGV-1901. The highest CV% (30.47%) was recorded for plant width.

Leaflet length and width ranged from 25.33 mm to 49.70 mm and 17.33 mm to 28.33 mm, with mean values of 39.64 mm and 23.03 mm, respectively. The longest leaflet was observed in Khenkhon (49.70 mm), while ICGV-52 had the shortest (25.33 mm). The widest leaflet was found in ICGV-93389 (28.33 mm), whereas ISD-4414 had the narrowest (17.33 mm). Pod length and width varied from 18.34 mm (ICGV-1901) to 36.70 mm (ICGV-1352), with a mean of 27.23 mm, and 6.33 mm (ICGV-1901) to 15.33 mm (7112-4-4-1), with a mean of 11.31 mm, respectively. Seed length ranged from 5.67 mm to 13.33 mm, while seed width ranged from 4.00 mm to 10.67 mm. The longest seed was found in ICGV-4514 (13.33 mm), whereas ICGV-1901 had the shortest seed (5.67 mm), with an average of 10.25 mm. The widest seed was recorded in ICGV-93199 (10.67 mm), while ICGV-1901 had the narrowest (4.00 mm), with an average of 2.52 mm. The pod yield per plant ranged from 14.33 g (7112-4-3-1) to 48.86 g (ISD-1314), with an average of 32.86g plant^{-1}.

These results indicate the presence of genetic variability among the studied genotypes, which is consistent with findings from previous studies by Yami and Abtew (2025), Daudi *et al*. (2021), and Gulluoglu *et al*. (2016). The observed quantitative variations in groundnut traits provide a strong basis for breeding programs aimed at enhancing yield with desired plant architecture. The significant variability in plant height, width, and leaflet dimensions offers opportunities for selecting genotypes suited for agro-ecology. Differences in pod and seed size influence consumer preference and processing efficiency, making them crucial targets for genetic improvement.

Table 2. Quantitative variation of different descriptors in groundnut

Sl. No.	Name of descriptor	Range	Mean	SD	CV (%)
1.	Height of main stem (cm)	10.01-36.02	23.96	6.75	28.18
2.	Plant width or spread (cm)	15.00-41.20	25.33	7.71	30.47
3.	Leaflet length (mm)	25.33-49.70	39.36	6.12	15.56
4.	Leaflet width (mm)	17.33-28.33	23.03	3.26	14.17
5.	Pod length (mm)	18.34-36.70	27.23	5.50	20.20
6.	Pod width (mm)	6.33-15.33	11.31	2.35	20.74
7.	Seed length (mm)	5.67-13.33	10.25	2.03	19.77
8.	Seed width (mm)	4.00-10.67	7.57	1.55	20.53
9.	Pod yield plant^{-1} (g)	14.33-48.86	32.86	9.23	28.09

The qualitative variations in groundnut traits are presented in Table 3, highlighting significant diversity among 33 genotypes. These traits play a crucial role in agronomic performance, adaptability, and breeding strategies for improving groundnut varieties. The plant growth habit varied considerably, with 57.58% (19 genotype) exhibiting an erect growth form, while the rest displayed different decumbent and procumbent types. Among the leaf spreading types, 30.30% (10 genotypes) were classified as Decumbent-3, while 6.06% (2 genotypes) belonged to Procumbent-2. Decumbent-1 and Decumbent-2 exhibited as 3.03% (1 genotype) for each other. The predominance of erect types (57.58%) advantageous for mechanical harvesting, uniform plant stand, and efficient space utilization in intensive cropping systems (Nigam, 2014). Conversely, decumbent and procumbent types offer benefits such as improved drought tolerance and enhanced ground coverage, reducing soil moisture loss (Songsri *et al*., 2013).

Branching patterns also showed variation, with 78.79% (26 genotypes) exhibiting an alternate branching pattern, a common feature in cultivated groundnut that supports balanced canopy development and uniform pod distribution (Upadhyaya *et al*., 2012). Two germplasm displayed irregular branching with flowers on the main stem, while five had irregular branching without flowers. Irregular branching often leads to lower pod-setting efficiency due to uneven nutrient distribution (Krapovickas and Gregory, 2007).

Pigmentation traits are important markers for genetic differentiation and stress tolerance (Bhad *et al.,* 2016). Stem pigmentation was absent in 22 genotypes (66.67%), indicating that non-pigmented stems are more prevalent in the studied collection. The complete absence of peg pigmentation in all genotypes (100%) suggests a genetic fixation of this trait, which may have implications for pod attachment and soil interaction during pegging (Sharma and Bhatnagar-Mathur, 2013).

Leaf morphology showed notable variation among the germplasm, which could influence photosynthetic efficiency, drought tolerance, and adaptability to different environments. Leaf color varied significantly, with 39.39% exhibiting light green leaves, 24.24% showing yellow leaves, and 36.36% having orange-yellow leaves. Leaf color differences are often linked to chlorophyll content and plant vigor, with darker green leaves generally indicating higher photosynthetic potential and better nitrogen utilization (Songsri *et al*., 2013). Leaflet shape also showed diversity, with three genotypes having elliptic leaflets, 15 classifieds as oblong-elliptic, 11 as wide elliptic while showed 2 genotypes each for narrow elliptic and ovate. These variations may impact light interception, transpiration rate, and overall plant productivity. Furthermore, 72.73% of the genotypes exhibited hairy leaflet margins, while 27.27% had entire margins. Hairy leaf margins genotypes often associated with increased resistance to insect pests and reduced water loss, making them a desirable trait for breeding programs aimed at improving drought resilience and pest tolerance (Sharma and Bhatnagar-Mathur, 2013).

Groundnut genotypes exhibited diverse leaf surface traits, influencing transpiration, pest resistance, and adaptability. Most had hairs on surfaces (63.64%), aiding pest deterrence and water regulation (Upadhyaya *et al*., 2005). Additionally, 15.15% were nearly glabrous, while 12.12% had woolly surfaces, enhancing drought tolerance (Janila *et al*., 2016). Bristles in 12.12% suggest genetic variations linked to stress resistance (Pandey *et al*., 2012). Leaflet tip variations was observed acute in 18 genotypes, mucronate in 11 genotype and and obtuse in 4 genotypes highlight genetic diversity, supporting breeding programs (Sravanti *et al*., 2024; Karthikeyan *et al*., 2023).

Substantial qualitative variability was observed in pod morphology including pod beak type, pod constriction, and seed number per pod. Despite these variations, seed coat color remained commonly uniform across all the genotypes, suggesting genetic stability for this trait. All the genotypes produced one to two-seeded pods are primarily controlled by genetics with limited environmental influence (Nigam, 2014). Pod beak characteristics varied, with 21 genotypes exhibiting a moderate beak, eight having a slight beak, one displaying a prominent beak, and three lacking a beak entirely. These differences are crucial for breeding programs, as pod beak traits affect pod morphology, harvesting efficiency, and seed extraction (Krapovickas and Gregory, 2007).

Pod constriction varied among the genotypes, with 12 showing no constriction, 10 moderates, eight slight, and three deep constrictions. Even though deep constriction complicates shelling, it strengthens pods against pests and stress (Sujay *et al*., 2018). These variations are useful for breeding improved varieties. Similarity in seed coat color was observed in all the genotypes, confirming genetic control (Khedikar *et al*., 2010). Pod reticulation, crucial for shell strength and seed protection, varied, with moderate types balancing strength and processing efficiency. Selecting optimal reticulation patterns can enhance post-harvest quality and storage potential.

Table 3. The qualitative descriptors for individual groundnut genotypes

Sl. No.	Qualitative character	State of character	No. of genotypes	Frequency distribution (%)
1.	Growth habit	Procumbent-2	2	6.06
		Decumbent-1	1	3.03
		Decumbent-2	1	3.03
		Decumbent-3	10	30.30
		Erect	19	57.58
2.	Branching Pattern	Alternate	26	78.79
		Irregular with flower on main stem	2	6.06
		Irregular without flower on main stem	5	15.15
3.	Stem pigmentation	0 Absent	22	66.67
		+ Present	11	33.33
4.	Stem surface	Sub glabrous	1	3.03
		Moderately hairy	26	78.79
		Very hairy	5	15.15
		Woolly	1	3.03
5.	Peg pigmentation	Absent (0)	33	100.00
		Present(+)	0	0.00
6.	Leaf color	Light green	13	39.39
		Yellow	8	24.24
		Orange yellow	12	36.36
7.	Leaflet shape	Elliptic	3	9.09
		Oblong-elliptic	15	45.45
		Narrow-elliptic	2	6.06
		Wide-elliptic	11	33.33
		Ovate	2	6.06

Table 3. Continued

Sl. No.	Qualitative character	State of character	No. of genotypes	Frequency distribution (%)
8.	Leaflet surface	Almost glabrous on both surface	1	3.03
		Almost glabrous bellow, hair above	4	12.12
		Hairs on both surface, without bristol	21	63.64
		Hairs on both surface, with bristol	3	9.09
		Woolly without bristol	3	9.09
		Woolly with bristol	1	3.03
9.	Leaflet margin	Entire	9	27.27
		Hairy	24	72.73
10.	Leaflet tip	Obtuse	4	12.12
		Acute	18	54.55
		Mucronate	11	33.33
11.	No. of seeds pod^{-1}	1-2 seed	33	100.00
12.	Pod beak	Absent	3	9.09
		Slight	8	24.24
		Moderate	21	66.67
		Prominent	1	3.03
13.	Pod constriction	None	12	36.36
		Slight	8	24.24
		Moderate	10	30.30
		Deep	3	9.09
14.	Pod reticulation	None	2	6.06
		Slight	11	33.33
		Moderate	12	36.36
		Prominent	6	18.18
		Very prominent	2	6.06
15.	Seed color	One color	33	100.00
16.	Primary seed color	White	1	3.03
		Off-white	2	6.06
		Rose	28	84.85
		Light red	2	6.06

In terms of primary seed color, most of the genotypes produced rose-colored seeds. The variation in primary seed color suggests that different genes regulate pigment production in seeds, resulting in a diverse range of colors such as black, brown, yellow, red, and white. These variations in seed formation and seed color align with the findings of Karthikeyan *et al.* (2023) and Anothai *et al.* (2008) in groundnut, Gupta *et al.* (2015) in soybean, and Yadav *et al.* (2010) in maize.

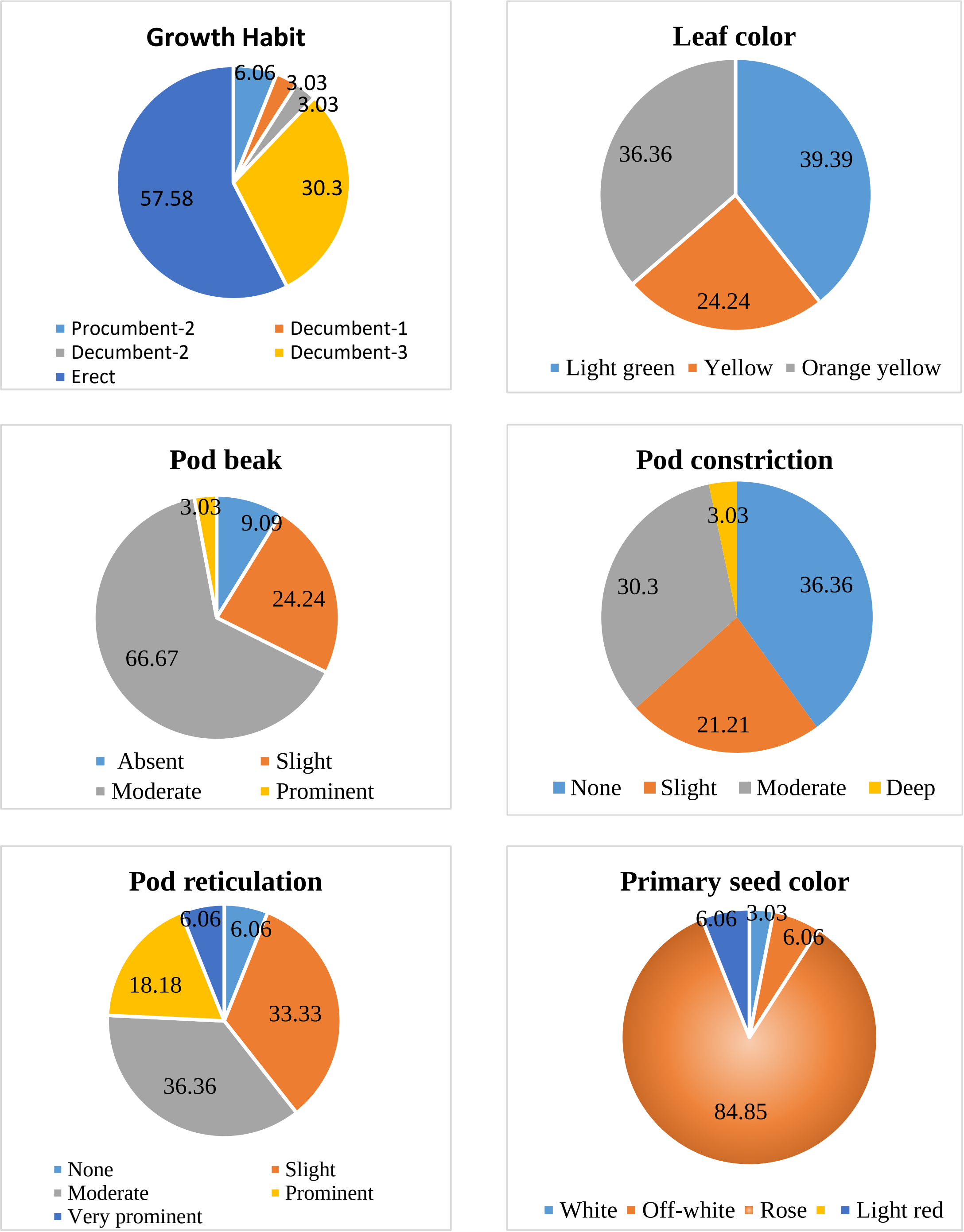

Fig. 1. Frequency distribution of 33 groundnut genotype for different qualitative traits.

The observed qualitative variations in groundnut genotypes provide valuable traits for breeding high-yielding, stress-tolerant, and market-preferred varieties. The predominance of erect growth supports mechanical harvesting, while decumbent types enhance drought resilience. Variability in leaf traits and pod morphology offers opportunities for improving photosynthetic efficiency, pest resistance, and processing quality. These findings guide selective groundnut breeding for better adaptability, productivity, and commercial viability.

Cluster analysis of groundnut germplasm using dendrogram

The dendrogram generated using R (Studio) statistical analysis provided a clear representation of the genetic relationships among the 33 groundnut selective groundnut breeding for better, grouping them into two major clusters: Main Cluster I and Main Cluster II (Fig. 2). The vertical axis of the dendrogram, which ranges from 0 to 12, signifies the dissimilarity between selective groundnut breeding for better, where higher values reflect greater genetic distance. This clustering pattern highlights the substantial genetic variability within the studied germplasm. Main Cluster I was further subdivided as Sub-cluster I and Sub-cluster II. Sub-cluster I contained only two genotypes, indicating a close genetic relationship between them, while Sub-cluster II showed more diversity, dividing into two sub-groups (Ia-1 and Ia-2), with two and four varieties, respectively. Similarly, Main Cluster II was divided into two sub-clusters. Sub-cluster I had two sub-groups (IIa-1 with two varieties and IIa-2 with five), while Sub-cluster II was split into two sub-groups, Ia-1 and Ia-2, containing six and 12 genotypes, respectively. These divisions demonstrate the complexity of the genetic structure and the presence of both closely related and might be genetically diverse genotypes.

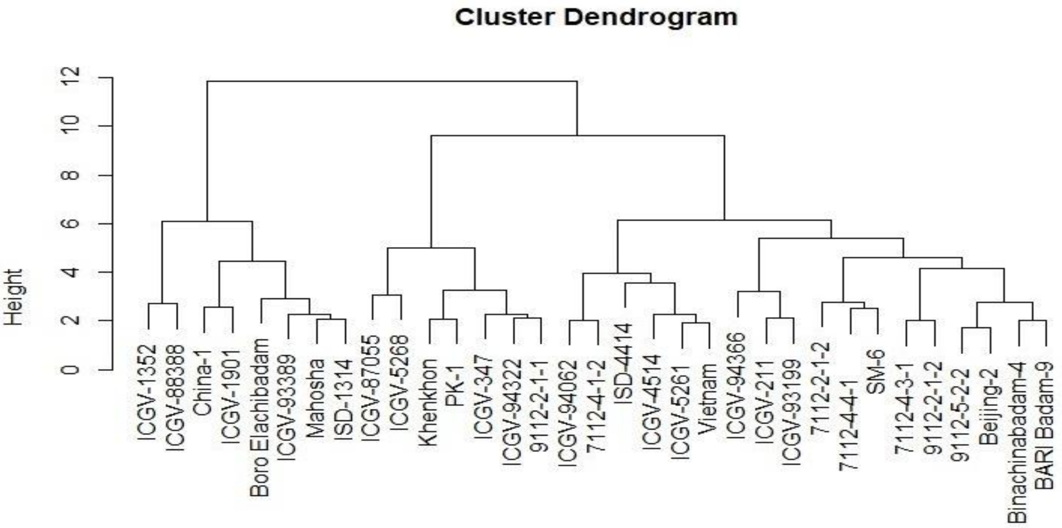

Fig. 2. Dendrogram of 33 varieties of groundnut based on 25 morphological traits.

The merging points or nodes in the dendrogram are crucial for understanding the genetic similarities among genotypes. For example, the genotypes ICGV-1352 and ICGV-88388 merged at a lower height, indicating that they are genetically closer compared to other genotypes. Such clustering is useful for identifying closely related genotypes, which could serve as parents for improving specific trait(s). These findings align with earlier studies that utilized dendrogram analysis to explore genetic diversity and relatedness in groundnut and other crops (Nigam., 2014; Upadhyaya *et al*., 2012). In conclusion, the dendrogram analysis reveals significant genetic variability within the 33 groundnut genotypes, highlighting opportunities for selecting diverse parental lines for breeding programs aimed at improving agronomic traits, stress resistance, and overall groundnut productivity.

Conclusion

This study reveals significant genetic variability among 33 groundnut genotypes, highlighting their potential for breeding programs. Variations in plant height, leaflet size, pod and seed characteristics, and pod yield suggest these germplasms can be used to develop improved varieties. The clustering of genotypes into two groups further confirms their genetic diversity. Notably, ICGV-5268, ISD-1314, and ICGV-4514 showed superiority in pod yield, vigor, and seed quality, making them promising as parents for groundnut improvement.

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