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RESEARCH ARTICLE

Understanding the variation in morphology and rhizome yield of Indian ginger (*Zingiber officinale* Rosc.) through distinctness, uniformity and stability (DUS) descriptors: A natural marker to enhance crop productivity

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Abstract

Ginger (*Zingiber officinale*) is a widely consumed and economically significant plant known for its medicinal and culinary properties. Understanding the diversity within ginger germplasm is vital for its successful use in breeding programs and conservation efforts. Morphological characterization plays a key role in identifying distinct varieties, ensuring uniform traits, protecting breeders' rights and conserving genetic diversity, all of which support commercial production and drive innovation in breeding. The present investigation was carried out at the Hybrid Rice Evaluation Centre, Gudalur, Nilgiris, with 32 genotypes to study the variability for identifying the best performing ginger genotypes. Genotypes were examined for 2 qualitative and 8 quantitative traits using Distinctness, Uniformity and Stability (DUS) parameters. Out of the traits assessed, plant height, number of leaves on the main stem and dry recovery were monomorphic, with no variation within the population. However, 4 characters, normal growth habit, shoot diameter, leaf length and leaf width, exhibited 2 distinct variations within the genotypes, indicating dimorphism. Additionally, 3 traits such as the number of tillers per clump, rhizome thickness and rhizome shapes showed multiple variations among the studied genotypes, illustrating polymorphism within the population. Principal component analysis was conducted on 7 principal components with eigenvalues of more than one accounted for 98.28 % of the total variability. Among these traits, leaf length, rhizome thickness and number of tillers demonstrated the highest variation, while the remaining traits showed lower variability. Based on PCA and cluster analysis, the genotypes Nadia, Manipur Local, Aswathy, Nagaland Local, Bhaise, ACC 578, Himachal Local, Rio De Janeiro, IISR Vajra, Humnabad Local, Hassan Local, Thalavadi Local and Chikkamagalore Local 2 were identified as the most diverse genotypes.

Keywords

cluster analysis; DUS descriptors; Indian ginger; morphological traits; principal component analysis

Introduction

Ginger, scientifically known as *Zingiber officinale* Rosc. is a native spice plant that holds a significant place in both culinary and medicinal traditions across the globe. It has been grown for thousands of years and has been essential in many cultures because of its distinct taste, flavor and potent medicinal properties. This rhizomatous spice plant is a member of the Zingiberaceae family and is distinguished by its knobby, underground rhizomes, which are the ginger of commerce. From infusing flavor and complexity into food preparations to providing relief from digestive problems and inflammation, ginger has captured the fascination and interest of researchers, healthcare professionals and consumers alike.

The Zingiberaceae family, found across tropical regions worldwide, stands as the largest family within the Zingiberales order, encompassing 53 genera and comprising over 1200 species (1). Ginger is one of the commercial spice crops in this family. It is a herbaceous perennial plant that typically grows as an annual, reaching heights of 0.50 to 0.75 m. The stem is surrounded by the sheathing bases of its leaves. The plant has aerial shoots, known as pseudostem, which bear leaves along with an underground stem called a rhizome (2). Botanically, the inflorescence and fruit of ginger are known as the spike and capsule respectively (3). India is the world's largest producer, exporter and consumer of ginger, accounting for 45.31 % of total global production, followed by China, Nigeria, Nepal, Thailand and Bangladesh. In India, Madhya Pradesh stands first in production contributing to 31.18 % of the total nation's production, followed by Karnataka, Assam, Maharashtra and West Bengal. Currently, the average productivity of ginger in India is 12.2 MT/ha (4). Different ginger cultivars are cultivated across different regions of India, typically having names that reflect the specific locales where they are cultivated. Poor flowering and seed set, along with limited genetic variability, pose substantial obstacles in the crop improvement of ginger through hybridization. However, the primary factor responsible for the diversity in this clonally propagated crop is the geographical spread, which has led to genetic differentiation into locally adapted populations evolved through the process of mutation (5). Morphological characterization involves the systematic study of the physical and structural features of ginger plants, including plant height, rhizome size, shape and color as well as leaf and flower characteristics. This information can aid in the identification and selection of superior genotypes with desirable traits for breeding programs and to adapt to changing climates, contributing to sustainable agriculture and food security (6).

Ginger genotypes are assessed based on certain qualitative and quantitative parameters known as Distinctness, Uniformity and Stability (DUS), established by the Protection of Plant Varieties and Farmer's Rights Act of India (7). These guidelines rely on morphological traits that remain consistent regardless of environmental influences, making genotype identification easier. Understanding variability structure can aid in developing conservation strategies for future breeding attempts as well as in characterizing different genotypes (8). Therefore, the study focused on the evaluation of ginger genotypes collected across India for various morphological and rhizome characteristics to identify the best performing genotype through DUS descriptors and multivariate analysis.

Materials and Methods

The field experiment was carried out at the Hybrid Rice Evaluation Centre (TNAU), Gudalur, Nilgiris district, during the years 2022 to 2024. The site has an altitude of 1300 m. above mean sea level with a latitude of 9° 40' 41.74 N" towards the north and a longitude of 77° 14' 58.24 E" towards the east. The climate is tropical and moderately humid, with temperatures ranging between 18-28 ˚C and relative humidity around 70 %. The area receives approximately 289.5 mm of annual precipitation. The experimental plot soil is sandy loam and well drained.

A total of 32 ginger genotypes were collected from various regions of India, including released varieties, promising genotypes and local cultivars (Table S1). The experimental design employed was a Randomized Block Design (RBD), with each genotype replicated 3 times. Healthy seed rhizomes weighing 25-30 g were selected and treated with 0.3 % mancozeb for 30 min. to avoid soil-borne diseases and planted on a raised bed sizes of 3 m x 1 m at a spacing of 30 cm x 25 cm between rows and in between plants respectively. The rhizomes were planted at a depth of 5-7 cm and the intercultural operations followed the standard package of practices recommended by Tamil Nadu Agricultural University.

Data collection and statistical analysis

For each plot, 5 plants were randomly selected and tagged to assess 10 DUS traits, including growth habit, plant height, number of tillers per clump, shoot diameter, number of leaves on the main shoot, leaf length, leaf width, rhizome thickness, rhizome shape and dry recovery. Morphological characteristics were recorded at the end of the growth phase (150 days after planting), while rhizome traits were recorded after harvest. Statistical analysis was performed using R software version 4.3.1.

Results and Discussion

Grouping of genotypes based on DUS descriptors

Morphological traits facilitate the easy and quick identification of genotypes and serve primarily as a natural marker since they are expressed genetically through 1 or 2 genes. Among the 10 DUS characters studied traits such as growth habit, number of tillers per clump, shoot diameter, leaf length, leaf width, rhizome thickness and rhizome shape exhibited maximum degree of variation within the population. Plant height, number of leaves on the main stem and dry recovery were monomorphic with no variation within the population. Four characters i.e., growth habit, shoot diameter, leaf length and leaf width were dimorphic and 3 characters were polymorphic including number of tillers, rhizome thickness and rhizome shape. These findings suggest that certain characteristics show a narrow range of variance within the population, indicating potential genetic diversity or environmental influences on those traits, whereas others exhibited limited variation within the population. The classification of genotypes according to the DUS guidelines is outlined in Table 1 and depicted in Fig. 1.

Table 1. Grouping of 32 ginger genotypes as per the DUS guidelines.

Characteristic	Status	Note	No. of genotypes	Genotypes
Growth habit	Erect	1	16	Aswathy, Nadia, Suravi, Suruchi, Maran, Gorubathane, ACC 247, ACC578, ACC 581, GCP 49, IISR 1GB, Chikkamagalore Local-1, Chikkamagalore Local-2, Manipur Local, Thadimaran, Nagaland Local
	Semi erect	3	16	Sourabh, Athira, IISR Rejthatha, IISR Mahima, IISR Varada, Rio De Janeiro, Himachal, Bhaise, Chikkamagalore Local-3, Hassan Local, Humnabad Local, Gudalur Local, IISR Vajra, Palakkad Local Thalavadi Local, HD Kote Local
	Spreading	5	0	Nill
Plant height (cm)	Short (<100)	3	32	IISR Rejatha, IISR Mahima, IISR Varada, Aswathy, Nadia, Suravi, Suruchi, Maran, Gorubathane, ACC 247, ACC578, ACC 581, GCP 49, IISR 1GB, Chikkamagalore Local-1, Chikkamagalore Local-2, Manipur Local, Thadimaran, Nagaland Local, Rio De Janeiro, Himachal, Bhaise, Chikkamagalore Local-3, Hassan Local, Humnabad Local, Gudalur Local, IISR Vajra, Palakkad Local Thalavadi Local, HD Kote Local, Sourabh, Athira
	Medium (100-120)	5	0	Nil
	Tall (>120)	7	0	Nil
Number of tillers	Few (<10)	3	16	IISR Rejatha, GCP 49, Chikkamagalore Local-1, Maran, Thadimaran, IISR 1 GB, IISR Vajra, ACC 581, Gudalur Local, ACC 578, Athira, Bhaise, Rio De Janeiro, Suravi, Himachal, Gorubathane
	Medium (10-15)	5	14	IISR Varada, IISR Mahima, Nagaland Local, Manipur Local, Sourabh, Aswathy, ACC 247, Hassan Local, HD Kote Local, Humnabad Local, Suruchi, Palakkad Local, Chikkamagalore Local -3, Thalavadi Local
	Many (>15)	7	02	Nadia, Chikkamagalore Local-2
Shoot diameter (cm)	Narrow (<3)	3	28	IISR Mahima, IISR Varada, IISR Rejatha, Nagaland Local, Sourabh, ACC 247, Hassan Local, Humnabad Local, Suruchi, Palakkad Local, Chikkamagalore Local-3, Thalavadi Local, GCP 49, Chikkamagalore Local-1, Maran, Thadimaran, IISR 1 GB, IISR Vajra, ACC 581, Gudalur Local, ACC 578, Athira, Rio De Janeiro, Suravi, Himachal, Gorubathane, Chikkamagalore Local -2, HD Kote Local
	Medium (3-5)	5	04	Aswathy, Nadia, Bhaise, Manipur Local
	Broad (>5)	7	0	Nil
Number of leaves on the main shoot	Few (<25)	3	32	Sourabh, ACC 247, Hassan Local, Humnabad Local, Suruchi, Palakkad Local, Chikkamagalore Local-3, Thalavadi Local, GCP 49, Chikkamagalore Local-1, Maran, Thadimaran, IISR 1 GB, IISR Vajra, ACC 581, Gudalur Local, ACC 578, Athira, Rio De Janeiro, Suravi, Himachal, Gorubathane, Chikkamagalore Local-2, HD Kote Local, IISR Mahima, IISR Varada, IISR Rejatha, Aswathy, Nadia, Bhaise, Manipur Local, Nagaland Local
	Medium (25-35)	5	0	Nil
	Many (>35)	7	0	Nil
Leaf length (cm)	Short (<25)	3	14	IISR Varada, IISR Vajra, Nagaland Local, GCP 49, Sourabh, Aswathy, ACC 581, HD Kote Local, Chikkamagalore Local-2, Humnabad Local, Rio De Janeiro, Chikkamagalore Local-3, Thalavadi Local, Gorubathane
	Medium (25-30)	5	18	IISR Mahima, IISR Rejatha, Manipur Local, Chikkamagalore Local-1, Maran, ACC 247, Bhaise, Nadia, Suruchi, Suravi, Palakkad Local, Himachal, Thadimaran, IISR 1 GB, Gudalur Local, ACC 578, Hassan Local, Athira
	Long (>30)	7	0	Nil
Leaf width (cm)	Narrow (<2.5)	3	07	IISR Varada, GCP 49, Thadimaran, ACC 578, Hassan Local, Himachal, Thalavadi Local
	Medium (2.5-3.5)	5	25	IISR Mahima, IISR Rejatha, Manipur Local, Chikkamagalore Local-1, Maran, ACC 247, Bhaise, Nadia, Suruchi, Suravi, Palakkad Local, IISR 1 GB, Gudalur Local, Athira, Chikkamagalore Local-2, Chikkamagalore Local-3, ACC 581, Nadia, Nagaland Local, Gorubathan, HD Kote Local, Rio De Janeiro, Aswathy, Humnabad Local, Sourabh
	Broad (>3.5)	7	0	Nil
Rhizome thickness (cm)	Thin (<2)	3	04	Nagaland Local, IISR vajra, Humnabad Local, Chikkamagalore Local-1
	Medium (2-3)	5	20	IISR Varada, Rio De Janeiro, Athira, Nadia, Aswathy, ACC 581, Manipur Local, Sourabh, ACC 247, Thadimaran, Chikkamagalore Local-3, Gorubathane, GCP 49, Gudalur Local, HD Kote Local, Hassan Local, Maran, Thalavadi Local, Chikkamagalore Local-2, Suruchi
	Bold (>3)	7	08	Bhaise, ACC 578, Himachal, IISR Rejatha, IISR Mahima, Suravi, Palakkad Local, IISR 1 GB
Rhizome shape	Straight	1	11	IISR Vajra, IISR Mahima, Aswathy, ACC 581, Maran, Chikkamagalore Local-1, Nagaland, GCP 49, Palakkad Local, Humnabad Local, HD Kote Local
	Curved	3	13	Sourabh, Suruchi, Suravi, Rio De Janeiro, Nadia, Himachal, Gorubathane, Manipur Local, Gudalur Local, Chikkamagalore Local -1, Chikkamagalore Local -3, IISR 1 GB, Thalavadi Local
	Zigzagged	5	08	IISR Varada, IISR Rejatha, Athira, Bhaise, ACC 578, ACC 247, Hassan Local, Thadimaran

Dry recovery (%)	Low (<10)	3	0	Nil
	Medium (16-18)	5	0	Nil
	High (>18)	7	32	Sourabh, ACC 247, Hassan Local, Humnabad Local, Suruchi, Palakkad Local, Chikkamagalore Local-3, Thalavadi Local, GCP 49, Chikkamagalore Local-1, Maran, Thadimaran, IISR 1 GB, IISR Vajra, ACC 581, Gudalur Local, ACC 578, Athira, Rio De Janeiro, Suravi, Himachal, Gorubathane, Chikkamagalore Local-2, HD Kote Local, IISR Mahima, IISR Varada, IISR Rejatha, Aswathy, Nadia, Bhaise, Manipur Local, Nagaland Local

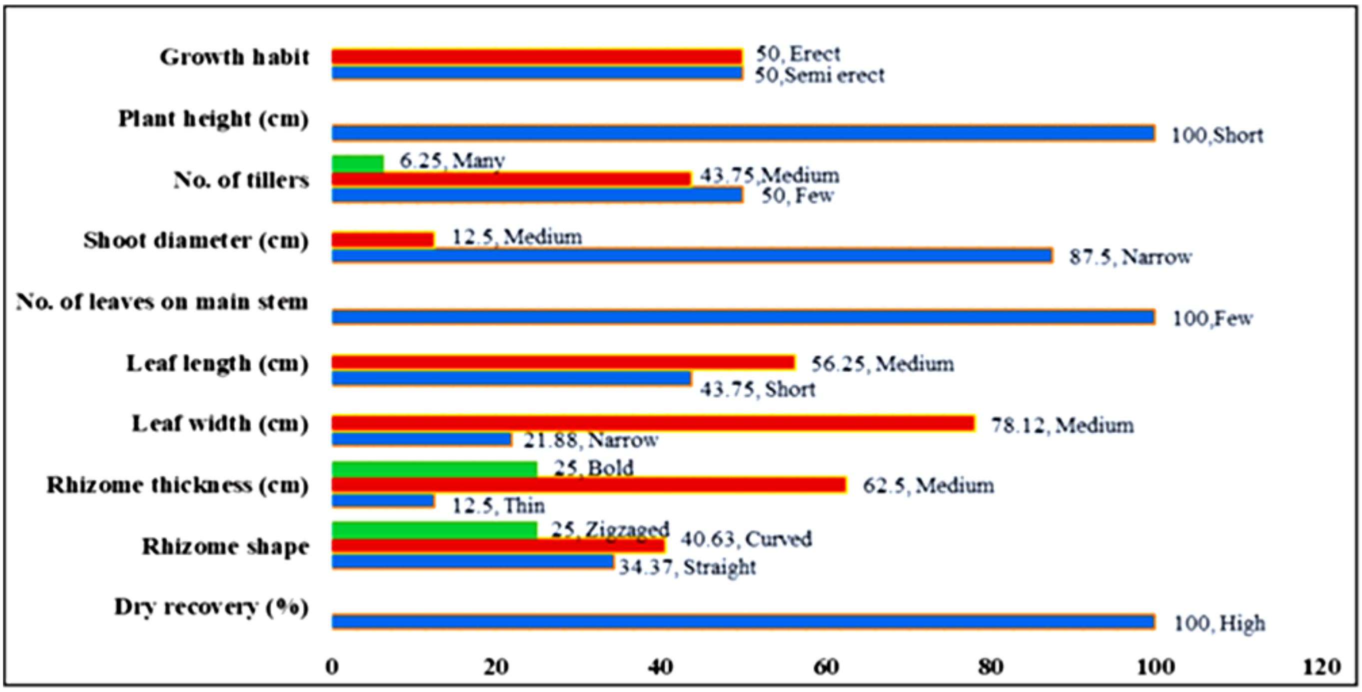

Fig. 1. Grouping of 32 ginger genotypes through DUS guidelines.

Plant characters

The growth habit of the 32 ginger genotypes were classified as erect and semi-erect. It was found that there was an equal distribution of genotypes i.e., 16 genotypes (50 %) in each category. Plant height was monomorphic, with all genotypes classified as short (<100 cm). The number of tillers exhibited polymorphism, with genotypes grouped as follows: 16 genotypes (50 %) with few (<10) tillers, 14 genotypes (43.75 %) with medium (10-15) tillers and 2 genotypes (6.25 %), specifically Nadia and Chikkamagalore Local-3, with many (>15) tillers. Twenty-eight genotypes (87.5 %) exhibited narrow (<3) shoot diameter while 4 genotypes (12.5%) exhibited medium shoot diameter (3-5). These finding are aligned with previous studies (8, 9), who also reported considerable variability with the majority of the genotypes being erect or semi-erect, short and having a narrow shoot diameter.

Leaf characters

According to the DUS guidelines, this study examined the leaf characteristics of 32 ginger genotypes, focusing on the number of leaves on the main stem, leaf length and leaf width. It was noted that among these traits, the number of leaves on the main stem (few; <25) was monomorphism. Fourteen genotypes (43.75 %) showed short (<25) leaf length, while 18 genotypes (56.25 %) exhibited medium (25-30) leaf length. Seven genotypes (21.88 %) showed narrow (<2.5) leaf width, while 25 genotypes (78.12 %) fell into the medium (2.5-3.5) category. These findings are aligned with previous study (10), who also reported similar results for the number, length and narrowness of leaves in ginger varieties.

Rhizome characters

The economic importance of the rhizome in ginger cultivation is substantial, as it plays a vital role in distinguishing various genotypes, thereby impacting overall yield. Moreover, there is a positive correlation between rhizome thickness and yield, highlighting the importance of this trait in enhancing productivity. Rhizome thickness exhibited polymorphism and among the 32 genotypes, 4 (12.50 %) were thin (<2) with slender rhizomes, while 20 genotypes (62.50 %) fell into the medium with thickness ranging from 2 to 3 cm and 8 genotypes (25 %) exhibited bold rhizomes, measuring over 3 cm in thickness (Fig. 2). Polymorphism was evident in rhizome shape among the examined genotypes (Fig. 3). Approximately 34.37 % of the genotypes (11) exhibited straight rhizomes, while 40.63 % (13 genotypes) displayed curved shapes. Additionally, zigzagged rhizome shapes were observed in 25.00 % of the genotypes (08). Dry recovery is another important trait that influences the total rhizome yield on a dry weight basis. A higher dry recovery typically correlates with the increased rhizome yield. None of the 32 genotypes exhibited low or medium dry recovery; instead, all genotypes were categorized as high, with dry recovery rates exceeding 18 %. The findings regarding rhizome traits in the current study followed the previous research by (8, 10-15). In all these studies, a consistent observation was made regarding the presence of all 3 types of rhizome shapes. Additionally, the rhizomes tended to be predominantly of medium and bold sizes, with high levels of dry recovery.

Bold **Medium** **Thin**

Fig. 2. Variation in the thickness of the rhizomes.

Curved **Straight** **Zigzagged**

Fig. 3. Variation in the shape of the rhizomes.

Principal component analysis (PCA)

Principal Component Analysis (PCA) is a powerful multivariate statistical technique used to identify the primary sources of variation within datasets. In this study, PCA was applied to examine the diversity among 32 ginger genotypes collected from various regions across India. The 10 ten characteristics (Plant height, number of leaves on main stem and dry recovery) were excluded due to uniformity across all genotypes. The PCA revealed that 7 principal components (PCs) accounted for 98.28 % of the total variability observed in the ginger samples. Notably, the first 3 PCs, each with eigenvalues exceeding one, collectively explained 63.485% of the total variance. Specifically, PC1 contributed 27.88 %, PC2 accounted for 19.09 %, and PC3 represented 16.51 % of the total variability (Table 2). The results suggest opportunities for selecting and developing improved ginger varieties based on the most influential traits associated with the primary principal components (16).

Further scree plot shows the % of explained variance for different dimensions or components. The plot displays a steep initial decline followed by a more gradual

Table 2. Eigenvalues, variance and cumulative variability of ginger genotypes.

Principal component	Eigenvalue	% variance	Cumulative variance
1	1.952	27.88	27.88
2	1.336	19.09	46.97
3	1.156	16.51	63.48
4	0.946	13.51	76.99
5	0.652	9.32	86.31
6	0.558	7.96	94.28
7	0.40	5.71	98.28

decrease. The first dimension explains the highest percentage of variance at 27.9 %, with subsequent dimensions explaining progressively less: 19.1 %, 16.5 %, 13.5 % and so on (Fig. 4). This pattern suggests that the first few dimensions capture a substantial portion of the total variance in the data, while later dimensions contribute relatively little additional explanatory power. Therefore, selection of PC1, PC2 and PC3 will result in maximum variability among 32 ginger genotypes.

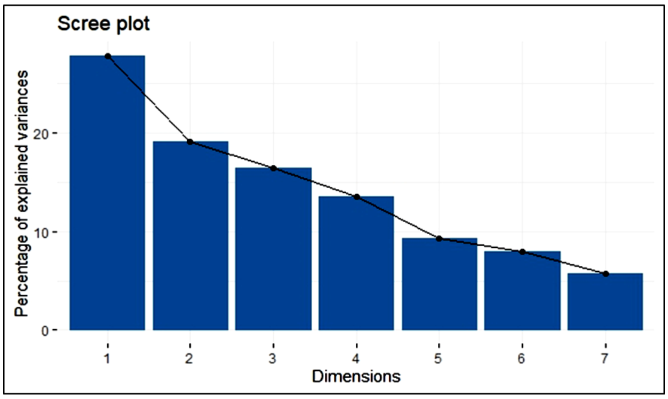

Fig. 4. Scree plot based on percentage of variance explained.

The analysis reveals the key variables influencing each PCs and is presented in Table 3 and Fig 5. PC1 is primarily shaped by leaf length (26.26 %), rhizome thickness (26.09 %), and rhizome shape (21.19 %). PC2 is heavily influenced by shoot diameter (44.51 %) and growth habit (22.99 %). PC3 is mostly defined by the number of tillers (34.68 %) and rhizome shape (22.76 %). This breakdown highlights the most significant morphological traits contributing to variation in the dataset. Understanding these influential variables helps in differentiating between samples or populations in the study and provides insight into the most important characteristics for classification or further analysis (17).

Table 3. Percent contribution of variables on PCs.

Variables	PC1	PC2	PC3
Growth habit	2.47	22.99	11.50
Number of tillers	6.83	12.26	34.68
Shoot diameter	2.12	44.51	2.31
Leaf length	26.26	7.11	13.35
Leaf width	15.01	3.47	14.19
Rhizome thickness	26.09	8.34	1.18
Rhizome shape	21.19	1.28	22.76

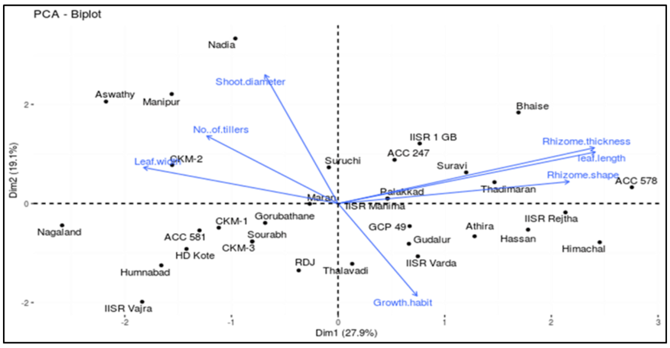

Fig. 5. Genotypes biplot illustrating the relationship between PC1 and PC2.

Cluster analysis

The hierarchical cluster analysis of the 32 ginger genotypes, based on seven key morphological traits, produced a dendrogram that revealing complex relationships among the samples (Fig. 6). The analysis identified 2 primary clusters, I and II, each representing a distinct group of genotypes with significant differences. These main clusters further divide into subclusters, highlighting more nuanced similarities and differences among the genotypes. Cluster I encompasses 17 genotypes and is subdivided into 2 groups: A and B. Group A consists of 6 genotypes (Acc578, Himachal, Thadimaran, Hassan Local, IISR Varada and Thalavadi Local). Group B includes 11 genotypes (IISR 1 GB, IISR Mahima, Palakkad Local, GCP-49, Maran, Gudalur Local, Acc 247, Suruchi, Athira, IISR Rejatha and Suravi), characterized by more upright growth patterns, few to medium tillers and potentially medium-sized rhizomes.

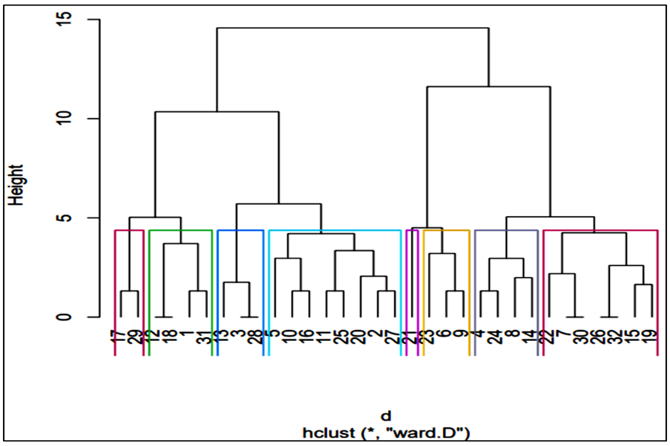

Fig. 6. Agglomerative Hierarchical Clustering pattern of 32 ginger genotypes.

Cluster II comprises 15 genotypes and is also divided into 2 subclusters: C and D. Subcluster C contains four genotypes (Bhaise, Nadia, Manipur Local and Aswathy), while subcluster D includes 11 genotypes (Nagaland Local, Humnabad Local, Chikkamagalore Local-1, ISSR Vajra, Chikkamagalore Local-2, Sourabh, Chikkamagalore Local-3, Rio De Janeiro, Gorubathane, Acc 578 and HD Kote Local). The genotypes in Cluster II generally display semi-erect growth habits, medium shoot diameters and leaf widths and medium to large rhizomes. This clustering suggests that genotypes within the same group likely share similar performance characteristics. This information can be valuable for breeding programs, as genotypes within a cluster could potentially be used interchangeably (18).

Conclusion

The ginger genotypes underwent classification according to the DUS (Distinctness, Uniformity and Stability) guidelines, considering both quantitative and qualitative traits. The grouping of genotypes unveiled a narrow difference in morphological characters. This suggests a limited variation in morphological traits among the genotypes. However, when considering rhizome characteristics, the grouping provided insights into the available variation among the genotypes. This information is valuable for selecting genotypes with desirable rhizome traits for future breeding programs. Additionally, it aids in the protection of plant varieties by identifying distinct genotypes adaptable to changing climates, contributing to sustainable agriculture and food security.

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Authors' contributions

BAV conducted the experiment, recorded observations and analysed the data. KV guided the research by formulating the data and approved the final manuscript. MM reviewed, edited, summarized and revised the manuscript. NS, VP and SPT assisted. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None.

AI Declaration

We acknowledge using the AI tool Grammarly for grammar checking in the manuscript. After using this tool/service, the author(s) reviewed and edited the content as needed and take(s) full responsibility for the content of the publication.

Supplementary data

Table 1. List of ginger germplasm utilized in the study.

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