PLANT SCIENCE TODAY
ISSN 2348-1900 (online)
Vol x(x): xx–xx
https://doi.org/10.14719/pst.6957

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RESEARCH ARTICLE

Exploring genetic diversity in banana germplasm utilizing multivariate analysis for morphological and yield attributes

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ARTICLE HISTORY
Received: 29 December 2024
Accepted: 02 March 2025
Available online
Version 1.0 : 28 April 2025

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

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Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc
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CITE THIS ARTICLE
Jegan P, Saraswathy S, Muthuvel I, Rajangam J, Angappan K, Jayakanthan M, Soman P, Auxcilia J, Manimaran G. Exploring genetic diversity in banana germplasm utilizing multivariate analysis for morphological and yield attributes. Plant Science Today (Early Access). https://doi.org/10.14719/pst.6957

Abstract

Bananas have different ploidy levels, including diploid, triploid and tetraploid, while triploids are most widely used in breeding programs. Although diploid and tetraploid plants have the potential to improve yield and other agronomic traits, they remain underutilized in crop improvement. This study uses multivariate analysis to evaluate the morphological and yield characteristics of 20 banana germplasm accessions belonging to the genome group AA, AB, AAA, AAB, ABB and AAAB. The findings revealed that substantial genetic variation was observed among the accession. Red Banana exhibited the tallest pseudostem height in morphological traits, while Karpooravalli had the largest pseudostem girth. Yield attributes indicated that Grand Naine and Gros Micheal recorded the highest bunch weights, while Calcutta 4 had the lowest. Additionally, Nendran has distinctive yield characteristics like longest finger length (FL), girth and weight. Correlation analysis showed a positive relationship between morphological and yield parameters such as pseudostem height, girth and bunch weight. Regression analysis revealed that pseudostem girth, leaf length and number of hands per bunch significantly contributed to bunch weight with an R^2 value of 0.80. Hierarchical clustering divided the accessions into three groups based on morphology and yield characteristics. Nendran and Red Banana were in one cluster, showing their genetic similarity. The clustering pattern suggests that these accessions have similar agronomic traits that could be useful for targeted breeding strategies. Principal component analysis (PCA) revealed that the first principal components accounted for 81.7% of the total variance, with major contributors including pseudostem girth, finger weight (FW) and bunch weight. Thus, these findings highlight the morphological and yield variations within banana germplasm and identify promising cultivars and traits for targeted breeding programs to enhance productivity and fruit quality.

Keywords

agronomic traits; cluster analysis; crop improvement; phenotypic variation; principal component analysis

Introduction

Bananas and plantains (*Musa* spp.) are important tropical fruit commodities, comprising 14% of global fruit production and 8% of primary tropical fruit production in international markets (1). Bananas and plantains originate from

Southeast Asia and belong to the Musaceae family (2). They are important crops for food security through their high yield and carbohydrate content, which give more than cereals the effective daily caloric intake per hectare (3). India is considered one of the largest producers of bananas in the world and contributes about 26.45% to the overall global banana production. In India, Andhra Pradesh is the largest producer with an annual production of 6.12 million tonnes followed by Maharashtra (5.56 million tonnes), Tamil Nadu (4.48 million tonnes), Gujarat (3.97 million tonnes) and Uttar Pradesh (3.39 million tonnes) (4).

Over 600 *Musa* germplasm, including native and cultivated species, have been identified (5). Nowadays, developed cultivars are primarily derived from a bispecific origin, with contributions from *Musa acuminata* and *Musa balbisiana*. The primary center of origin of *M. acuminata* is a polymorphic species located in the Malayan region, while *M. balbisiana* is of Indian ancestry (6). Most commercial dessert genotypes in India are AAA and AAB genomic groups, while cooking-type genotypes are ABB genomic groups (7). Breeders must possess precise information regarding the ploidy of a variety to manipulate a multi-ploidy crop like bananas (8). Hybridizing a triploid banana with a diploid variety produces diploid, triploid, tetraploid, aneuploid and hyperploid progeny (9).

Even though multiple varieties of bananas with varying genomic compositions (AAA, AAB, ABB, AB and AA) are available, there are still considerable gaps in research on these materials as breeding resources. There is inadequate research regarding the accession's ploidy levels and genetic characterizations, limiting viable tactics for targeted hybridization (10). Furthermore, additional important resources, like Rose, Tongat and Matti, have yet to be validated for their agronomic and stress-tolerance characteristics. Performance variation among genomes arises from differing abiotic or biotic stress conditions, illustrated by varieties such as Ney Poovan (AB) and Karpooravalli (ABB) (11). The latent potential of wild germplasm, such as Calcutta 4, is currently neglected despite its capacity to introduce valuable traits like disease resistance and adaptability into breeding programs (12).

The physiological state and compositional alterations of harvested bananas differ among varieties and may be influenced by climate, farming methods and postharvest storage conditions (13).The agronomic characterization of banana genetic resources is extremely important in selecting progenitors for hybridization and further improving these hybrids (14). Banana breeding becomes difficult because domesticated bananas have poor fertility and a lack of understanding regarding the genetic determinism of agronomical traits (15).

The genetic improvement technique is the most sustainable method for achieving this goal. However, improving bananas is difficult because they are clonally propagated, whereas asexual reproduction delays cross-breeding. The primary cultivars are also sterile and rarely produce seeds, even with hand-pollination (16).

The crop's polyploidy hinders breeding resulting in poor seed set and lowered fertility (9). Further, the environmental effects on these available accessions accelerate the continuous loss of hybrid vigor and its performance. Therefore, the parental line is essential in hybrid improvement and germplasm evaluation is also highly important. Those restrictions are the primary focus of the banana breeding program, which aims to generate better hybrids with high and stable yields and quality to satisfy the customer's needs.

To help unravel genetic diversity and improve selection, statistical approaches like PCA, correlation analysis and regression modeling are essential for studying extensive information. PCA lowers the dimensionality of complicated datasets, emphasizing critical factors responsible for the greatest variance among accessions (17). For example, in assessing banana crop germplasm, PCA can substantially reduce dimensionality while maintaining significant variability in banana species, including morphological and yield attributes. It distinguishes some unique varieties and clusters like varieties by identifying principal components that account for the most variation among accessions (18). Additionally, PCA identifies the characteristics that have contributed the most variability, which could challenge targeted breeding programs and effective germplasm utilization. It will also provide a definitive understanding of the relationships between accessions, facilitating and influencing decision-making in the larger context of breeding and conservation programs (19).

The potential relationship between morphological and yield traits is separated using correlation analysis, while the regression model reveals the main factors influencing yield performance (19, 20). Together, these strategies allow the effective selection of potential accessions for breeding programs. With this background, the present study examines the screening of twenty banana germplasm accessions, including commercial and wild cultivars, for morphological and yield attributes. An extensive approach that includes PCA, Correlation and regression analysis is used to determine the most important yield-affecting factors and choose accessions for future breeding in banana improvement.

Materials and Methods

Experimental site

The study was conducted at the Horticultural College and Research Institute, Tamil Nadu Agricultural University (TNAU), Coimbatore, Tamil Nadu, India. The following 20 genotypes have been described in Table 1. These 20 banana germplasm accessions were evaluated in a randomized complete block design (RCBD) with 3 biological replications. The genotypes have been maintained at a spacing of 1.8 m x 1.8 m within an identical block in the field at the AICRP-Tropical Fruits program. The cultural practices and plant protection measures for bananas that TNAU recommended were implemented.

Morphological and yield traits

The observation was recorded from 20 banana germplasm accessions for morphological and yield traits viz., planting to shooting (days), pseudostem height (cm), pseudostem girth (cm), number of leaves (NL), leaf length (cm), leaf width (cm), bunch weight (kg), number of fingers per hand, number of hands per bunch, number of fingers per bunch, FL (cm), finger girth (FG) (cm) and FW (g).

Table 1. Description and source of banana germplasm accessions

Genotype	Genome	Origin	Cultivar description
Gros Michel	AAA	Jamaica	Commercial cultivar
Red Banana	AAA	India	Commercial cultivar.
YKM-5	AAA	Repbulic of Congo	Wild type dessert banana
Grand Naine	AAA	Israel	Commercial cultivar
Nattu Poovan	AAB	India	Commercial cultivar
Rasthali	AAB	India	Commercial cultivar
Padali Moongil	AAB	India	Commercial cultivar
Nendran	AAB	India	Commercial cultivar
Anaikomban	AA	India (Western Ghats)	Indigenous wild type
Ambalakadali	AA	India (Kerala)	Indigenous wild type
Pisang Lilin	AA	Indonesia	Cultivated variety at Indonesia
Rose	AA	Indonesia	Cultivated as a niche variety in Southeast Asia.
Tongat	AA	Southeast Asia (India)	Traditional and local cultivar
Matti	AA	India (Tamil Nadu)	Cultivated by farmer in a specific region.
Kunnan	AB	India (Kerala)	Traditional variety
Ney Poovan	AB	India	Commercial variety
Monthan	ABB	India	Commercial variety
Karpooravalli	ABB	India (Tamil Nadu)	Commercial variety
Calcutta 4	AA	India	Subspecies of *Musa acuminata burmannica*
FHIA 1	AAAB	Honduras	Tetraploid Hybrid variety developed form *Musa acuminata* x *Musa balbisiana*

Statistical analysis

ANOVA was computed following a standardized procedure (21). The mean, standard deviation and the total coefficient of variation determined the selection of superior performers. ANOVA was used to analyze the data and compare the means with Tukey's HSD significant difference test. Statistical analyses of the observed data have also been done using statistical R software (2.14.1) for PCA, Correlation and Regression analyses. Pearson correlation was conducted using the "corrplot" and "Rcolorbrewer" packages, while PCA was performed using "prcomp". Cluster analysis was conducted using "NbClust" and "factoextra". Among these characteristics were conducted using R Studio software (4.3.3) and "FactoMineR" utilities.

Results and Discussion

Morphological characteristics

Morphological analysis of 20 banana germplasm accessions revealed a noticeable variation across various parameters. The germplasm accessions were grouped based on their genomic classification into groups, such as AA, AB, AAA, AAB, ABB and AAAB. The duration from planting to shooting in Nendran is quite lengthy (405.00), markedly differing from other varieties, whereas the shortest duration was measured in Pisang lilin, at (178.20) days. The greatest pseudostem height and girth were found in Red banana (384.50) and Karpooravalli (83.80), while the minimum pseudostem height and girth were observed in Pisang lilin (129.00, 31.50), respectively. Monthan exhibits the maximum leaf count (23.00), while Rose has the lowest (9.80). The greatest leaf length (323.00) and leaf width (99.60) were recorded in Padali Moongil and Nendran, while the shortest leaf length (105.70) and leaf width (45.70) were noted in Calcutta 4 and Monthan. Genetic diversity in banana germplasm is illustrated by individual representatives of these variants (Table 2).

Genetic variation of morphological traits plays a crucial role in banana breeding programs, facilitating the selection of diverse accessions (22). The notable differences in growth parameters, such as the duration from planting to shooting, pseudostem height and girth, leaf count and leaf dimensions, underscore the potential for identifying superior genotypes tailored to particular agricultural needs (23). Tetraploid and triploid hybrids had more leaves than the other hybrids (24). For example, the difference between the duration from planting

Table 2. Mean performance of banana germplasm accessions for morphological attributes

Banana Accession	Genome	Planting to shooting	Plant height (cm)	Plant girth (cm)	No. of leaves	Leaf length (cm)	Leaf breadth (cm)
Gros Micheal	AAA	254.00 ± 10.82^{efgh}	295.00 ± 13.32^{cde}	81.40 ± 6.40^{ab}	12.50 ± 1.01^{defg}	265.00 ± 5.55^{b}	85.25 ± 6.71^{abcd}
Red Banana	AAA	396.33 ± 13.02^{ab}	384.50 ± 16.35^{a}	76.80 ± 6.03^{abc}	12.00 ± 1.16^{efg}	161.50 ± 8.49^{fgh}	78.20 ± 4.30^{bcdef}
YKM -5	AAA	268.00 ± 0.98^{def}	242.00 ± 9.36^{efg}	61.00 ± 1.56^{efgh}	12.00 ± 0.01^{efg}	221.00 ± 8.14^{cde}	63.50 ± 2.79^{fghi}
Grand Naine	AAA	230.00 ± 5.27^{fghi}	250.00 ± 16.17^{defg}	76.00 ± 2.07^{abcd}	15.50 ± 1.40^{bcd}	220.00 ± 13.78^{cde}	84.00 ± 3.10^{abcde}
Nattu Poovan	AAB	291.00 ± 1.21^{def}	279.00 ± 6.33^{cdef}	73.00 ± 2.43^{abcde}	14.00 ± 0.23^{bcdef}	234.00 ± 12.34^{bc}	89.00 ± 3.55^{abc}
Rasthali	AAB	308.00 ± 17.20^{cde}	231.00 ± 16.73^{fg}	62.70 ± 1.53^{defg}	16.50 ± 1.24^{b}	180.50 ± 9.31^{efg}	59.50 ± 6.20^{fghi}
Padali Moongil	AAB	370.00 ± 17.53^{abc}	234.50 ± 11.30^{fg}	47.58 ± 1.07^{hi}	10.50 ± 0.58^{g}	323.00 ± 5.88^{a}	99.60 ± 4.48^{ab}
Nendran	AAB	405.00 ± 13.60^{a}	313.33 ± 12.03^{bc}	65.00 ± 1.75^{cdefg}	10.00 ± 1.15^{g}	198.50 ± 8.41^{cdef}	94.00 ± 7.83^{a}
Anaikomban	AA	186.00 ± 14.03^{hi}	212.54 ± 10.90^{gh}	52.88 ± 2.05^{ghi}	15.00 ± 0.10^{bcde}	182.50 ± 9.51^{efg}	66.50 ± 5.86^{defg}
Ambalikadali	AA	258.60 ± 14.31^{efg}	216.00 ± 5.51^{gh}	$53.50 \pm 1.88_{ghi}$	14.00 ± 0.21^{bcdef}	188.90 ± 2.75^{defg}	57.22 ± 2.73^{ghi}
Pisang Lilin	AA	178.20 ± 12.31^{i}	129.00 ± 7.66^{i}	31.50 ± 1.75^{j}	10.00 ± 0.07^{g}	108.20 ± 6.04^{i}	46.50 ± 0.43^{hi}
Rose	AA	196.80 ± 12.06^{ghi}	140.20 ± 12.67^{i}	31.94 ± 0.35^{j}	9.80 ± 0.19^{g}	137.60 ± 5.58^{hi}	53.00 ± 0.36^{ghi}
Tongat	AA	244.33 ± 8.78^{efghi}	302.50 ± 5.69^{cd}	62.20 ± 2.35^{efg}	12.00 ± 0.14^{efg}	137.60 ± 5.58^{hi}	59.00 ± 1.11^{fghi}
Matti	AA	331.00 ± 14.00^{bcd}	257.00 ± 4.28^{defg}	57.00 ± 0.03^{fgh}	14.00 ± 0.14^{bcdef}	192.50 ± 6.95^{defg}	68.79 ± 0.86^{defg}
Kunnan	AB	276.00 ± 14.78^{def}	254.00 ± 2.25^{defg}	62.00 ± 1.19^{efg}	11.00 ± 0.19^{fg}	186.75 ± 0.10^{defg}	65.41 ± 0.85^{efgh}
Ney Poovan	AB	242.50 ± 16.12^{efghi}	290.40 ± 6.50^{cde}	71.30 ± 0.52^{abcde}	16.00 ± 0.35^{bc}	168.30 ± 8.28^{fgh}	64.20 ± 0.27^{fghi}
Monthan	ABB	245.17 ± 25.95^{efghi}	297.10 ± 14.42^{cd}	73.51 ± 1.36^{abcde}	23.00 ± 0.37^{a}	152.30 ± 5.64^{gh}	45.70 ± 0.00^{i}
Karpooravalli	ABB	327.50 ± 1.53^{cd}	365.91 ± 1.14^{ab}	83.80 ± 1.74^{a}	13.00 ± 0.04^{cdefg}	155.50 ± 6.72^{gh}	71.50 ± 0.74^{cdefg}
Calcutta 4	AA	187.00 ± 5.56^{hi}	168.70 ± 3.95^{hi}	42.50 ± 1.94^{ij}	11.00 ± 0.17^{fg}	105.70 ± 0.55^{i}	45.80 ± 0.72^{i}
FHIA 1	AAAB	284.00 ± 5.06^{def}	205.00 ± 5.65^{gh}	68.80 ± 3.04^{bcdef}	10.50 ± 0.17^{g}	170.00 ± 5.79^{fgh}	78.00 ± 1.99^{bcdef}

*****Values are the mean of 3 replicates ± standard errors and means sharing common letter(s) in each column do not differ significantly at $p < 0.05$.

to shooting in Nendran (405.00 days) and Pisang lilin (178.20 days) indicates that Nendran may be more appropriate for regions with longer growing seasons. At the same time, Pisang lilin may be advantageous in areas with shorter growing periods. Future studies should investigate the genetic basis of the identified phenotypic variants and their possible uses in breeding programs (22). The morphological data demonstrates the accuracy of the classification system and its effectiveness in germplasm management (25). Similar research indicates that banana cultivars belonging to distinct genomic groups exhibit morphological and horticultural variation, with a combination of similarities and differences even among those belonging to the same genomic group (26). The morphological characterization of unique banana clones Prata Gorutuba R1 and R2 revealed recognized characteristics such as pseudostem tapering and anthocyanin intensity, identifying this pair within the Prata group. The findings highlight behavior toward genetic improvement and commercial acceptability (27). Similar findings reported that morphology and horticultural characteristics of various banana cultivars, including Nendran, Pisang Lilin, Karpooravalli, Njalipoovan, Grand Naine and YangambiKM - 5, varied in terms of fruit length, pulp weight and peel weight. This level of variability highlights the complexities of banana breeding and the need for more genetic research, even within the same chromosomal group(26).

Yield attributes

The yield parameter emphasizes the significant differences among banana accessions. Individual differences in bunch weight, number of hands per finger, number of fingers per hand, number of fingers per bunch, length of finger, girth of finger and weight of fruit specify differences in each variety's strengths and possible application. Grand Naine (27.12) and Gros Michel (24.30) recorded the highest bunch weight, whereas Calcutta 4 (2.31) exhibited the least. Matti (13.00) had the highest hands per bunch, while Calcutta 4 (6.50) had the least. Anaikomban (18.50) and Calcutta 4 (18.50) have the highest number of fingers per hand, while Nattu Poovan (10.50), Padali Moongil (10.50), Kunnan (10.50) and Monthan (10.50) recorded the lowest, respectively. The largest number of fingers per bunch was recorded in Matti (264.5), while the least was observed in Padali moongil (42.5). Nendran has the largest FL (22.87), FG (14.21) and FW (171.34), while the smallest FL (6.80) recorded in Karpooravalli and the minimum FG (6.30) and FW (20.12) were observed in Calcutta 4 (Table 3).

Similar research conducted on 26 banana accessions also revealed significant differences in the fruit length, ranging from 6.87 cm to 18.67 cm. The accession shows the maximum fruit length; however, it was found to be highly polyploid, which is believed to be associated with larger cell nuclear size, resulting in larger tissue size of plants (28, 29). Under Kerala conditions, assessing certain exotic cultivars, such as Popoulu and Kluai namwa khom, demonstrated their superior performance regarding bunch weight, yield and other biometric traits when compared with local varieties. Kluai Namwa Khom is used for table purposes, while the cultivar popoulu is used for table and dessert. Both cultivars are highly resilient to high wind-prone areas (30). Finger length, finger width and FW positively correlate with bunch weight. Increased finger size may substantially influence the bunch weight (31). The weight of the bunch is a crucial economic attribute that must not be compromised in *Musa* breeding programs. Diploids are commonly utilized in *Musa* breeding projects to improve the resilience of native cultivars and augment their output. Simultaneously, the selection of bunch weight is crucial (32). The observed variability emphasizes the significance of maintaining a diverse germplasm collection for banana breeding programs (33). The success of banana breeding programs can be further improved by integrating molecular and cytogenetic characterization techniques, which can provide detailed genetic data and facilitate the selection of desirable characteristics (25).

Table 3. Mean performance of banana germplasm accessions for yield attributes

Banana Accession	Genome	Bunch Weight (Kg)	No. of. hands bunch^{-1}	No. of. fingers hand^{-1}	No. of. fingers bunch^{-1}	Finger length (cm)	Finger girth (cm)	Finger weight (g)
Gros Micheal	AAA	24.30 ± 2.51^{a}	7.80 ± 0.50^{e}	16.2 ± 0.06^{c}	134.6 ± 6.44^{d}	18.40 ± 1.18^{bc}	13.18 ± 0.65^{a}	148.68 ± 14.91^{abcd}
Red Banana	AAA	8.32 ± 0.56^{fg}	5.00 ± 0.47^{ij}	11.5 ± 0.12^{f}	54.5 ± 5.88^{fg}	12.60 ± 0.96^{ef}	12.20 ± 0.67^{abc}	143.23 ± 8.33^{bcde}
YKM -5	AAA	15.64 ± 1.16^{bc}	9.50 ± 0.52^{c}	18 ± 0.07^{b}	167.5 ± 10.75^{bc}	12.80 ± 0.60^{def}	11.40 ± 1.14^{abcd}	83.50 ± 1.54^{hij}
Grand Naine	AAA	27.12 ± 1.11^{a}	9.35 ± 0.47^{c}	16.31 ± 0.12^{c}	153.56 ± 10.45^{c}	17.82 ± 0.77^{bc}	11.02 ± 0.61^{abcd}	163.89 ± 4.66^{ab}
Nattu Poovan	AAB	12.00 ± 0.62^{cdef}	8.00 ± 0.53^{de}	10.5 ± 0.17^{f}	121.5 ± 7^{d}	18.50 ± 1.12^{bc}	13.20 ± 0.45^{a}	110.70 ± 5.79^{fg}
Rasthali	AAB	11.53 ± 0.79^{def}	7.30 ± 0.65^{ef}	14 ± 0.18^{e}	88 ± 1.13^{e}	12.43 ± 1.14^{ef}	11.93 ± 0.57^{abcd}	108.90 ± 1.36^{fgh}
Padali Moongil	AAB	2.80 ± 0.04^{i}	4.30 ± 0.09^{j}	10.5 ± 0.05^{f}	42.5 ± 4.85^{g}	11.10 ± 0.75^{fg}	8.40 ± 0.13^{cde}	96.50 ± 0.90^{ghi}
Nendran	AAB	12.50 ± 0.29^{cde}	5.70 ± 0.11^{hi}	10.67 ± 0.05^{f}	62.53 ± 1.04^{f}	22.87 ± 1.31^{a}	14.21 ± 0.56^{a}	171.34 ± 6.56^{a}
Anaikomban	AA	7.50 ± 0.04^{gh}	7.24 ± 0.11^{ef}	18.5 ± 0.33^{b}	124.6 ± 1.7^{d}	16.50 ± 0.32^{bcd}	11.60 ± 0.19^{abcd}	115.50 ± 6.91^{fg}
Ambalikadali	AA	9.60 ± 0.00^{defg}	6.25 ± 0.08^{gh}	16.4 ± 0.15^{c}	90.24 ± 1.88^{e}	17.50 ± 0.07^{bc}	11.30 ± 0.47^{abcd}	118.70 ± 0.19^{efg}
Pisang Lilin	AA	3.78 ± 0.10^{hi}	5.78 ± 0.01^{hi}	14.2 ± 0.37^{de}	68.44 ± 0.46^{f}	12.80 ± 0.29^{def}	8.80 ± 0.20^{bcde}	52.75 ± 6.10^{kl}
Rose	AA	3.96 ± 0.10^{hi}	9.56 ± 0.05^{c}	14.5 ± 0.11^{de}	126.5 ± 0.06^{d}	10.36 ± 0.17^{fgh}	8.62 ± 0.56^{bcde}	37.40 ± 0.51^{lm}
Tongat	AA	11.87 ± 0.26^{cdef}	5.88 ± 0.06^{hi}	16 ± 0.07^{c}	102 ± 0.52^{e}	16.54 ± 0.37^{bcd}	12.78 ± 1.11^{ab}	131.30 ± 0.34^{cdef}
Matti	AA	18.45 ± 0.12^{b}	13.00 ± 0.11^{a}	21.31 ± 0.38^{a}	264.5 ± 3.89^{a}	15.60 ± 0.23^{cde}	13.40 ± 0.59^{a}	36.70 ± 0.86^{lm}
Kunnan	AB	9.75 ± 0.25^{defg}	7.00 ± 0.09^{fg}	15.4 ± 0.32^{cd}	105 ± 1.98^{e}	18.10 ± 0.30^{bc}	12.00 ± 0.15^{abc}	48.45 ± 1.21^{kl}
Ney Poovan	AB	8.80 ± 0.11^{efg}	10.50 ± 0.09^{b}	14 ± 0.5^{e}	153.3 ± 0.17^{c}	12.31 ± 0.55^{ef}	8.25 ± 0.07^{cde}	60.63 ± 0.98^{jkl}
Monthan	ABB	10.42 ± 0.19^{defg}	6.30 ± 0.07^{gh}	10.5 ± 0.22^{f}	64.36 ± 0.03^{f}	19.04 ± 1.12^{abc}	13.10 ± 0.47^{a}	156.80 ± 0.90^{abc}
Karpooravalli	ABB	12.80 ± 0.15^{cd}	12.20 ± 0.09^{a}	16.67 ± 0.28^{c}	170.75 ± 1.24^{b}	6.80 ± 0.02^{h}	7.77 ± 0.82^{de}	70.38 ± 1.54^{ijk}
Calcutta 4	AA	$2.31 \pm 0.04^{i,}$	6.50 ± 0.06^{fgh}	18.5 ± 0.79^{b}	68 ± 0.53^{f}	7.70 ± 0.03^{gh}	6.30 ± 2.03^{e}	20.12 ± 0.24^{m}
FHIA 1	AAAB	18.34 ± 0.02^{b}	8.30 ± 0.07^{d}	$16.4 \pm 10.45c$	131.6 ± 0.34^{d}	19.60 ± 0.49^{ab}	13.70 ± 1.21^{a}	126.87 ± 2.05^{def}

*****Values are the mean of 3 replicates ± standard errors and means sharing common letter(s) in each column do not differ significantly at $p < 0.05$.

Correlation coefficients

Favourable relationships were depicted by coefficients of correlation for significant banana attributes, with high positive correlations between plant height and plant girth (0.85), leaf length and plant height (0.71) and FL and FW (0.87). Thus, this result indicated that higher plants have better yield-related characteristics. Plant height (0.61) and FG (0.57) positively correlated substantially with bunch weight. Certain variables showed moderate correlations, including the number of hands per group the number of fingers per hand (0.60) and plant girth and leaf length (0.66). Leaf width and the NL were found to have negative correlations (-0.26). These data have been confirmed by scatter plot analysis, which revealed distinct upward patterns for highly correlated pairs. Concurrently, the histograms of the larger diagonal forms exhibited heterogeneity in individual characteristics (Fig.1). These data illustrate the substantial difference between morphological and yield-related attributes. The occurrence of substantial and positive values suggested a genetic relationship between bunch weight and FL (34). Similar findings indicate that relationships between bunch weight and other attributes, including the NL, number of suckers, pseudostem height and pseudostem girth exhibit substantial variability during the flowering stage (27). By comparable research, the average bunch weight was significantly and positively correlated with the number of fingers per bunch, confirming that yield is linked to certain morphological characteristics. This study observed a strong correlation between vegetative traits and yield-related characteristics in bananas, suggesting that precise morphological attributes might serve as indirect selection criteria for yield enhancement (33).

Regression analysis

The regression analysis shows that individual and collective variables impact bananas' bunch weight (BW), with an R^2 value of 0.8. This value indicated that the model explains over 80% of the variances in the dependent variable. The F static observed was 39.203, which indicates the model's statistical significance, similar to this model. In this model, the following attributes are listed as positively influencing bunch weight: plant girth (0.263) (PG), leaf length (0.014), number of hands per bunch (1.699) (NHOB), FL (0.031), FG (0.234) and FW (0.052) . However, the NL (- 0.342) and plant to stalk (PTS) (-0.007) are among the negative contributing factors (Fig.2). A negative intercept (-13.513) does not necessarily indicate a negative bunch weight, as it merely aligns with the regression model more effectively when all characteristics are taken into account. In practice, the predicted bunch weight (BW) will be positive as the combined effect of these attribute values increases. A larger positive coefficient number of hands per bunch (1.699) indicates that the predictor variable significantly impacts the dependent variable.

In contrast, a smaller positive coefficient, such as hands per bunch (0.014), suggests that the variable has almost no impact on the dependent variable. This regression model effectively identified the traits that were dominant in determining the weight of the bunch by utilizing various coefficients to illustrate the relative importance of each predictor. This information can potentially improve banana yield, a valuable asset for targeted improvement.

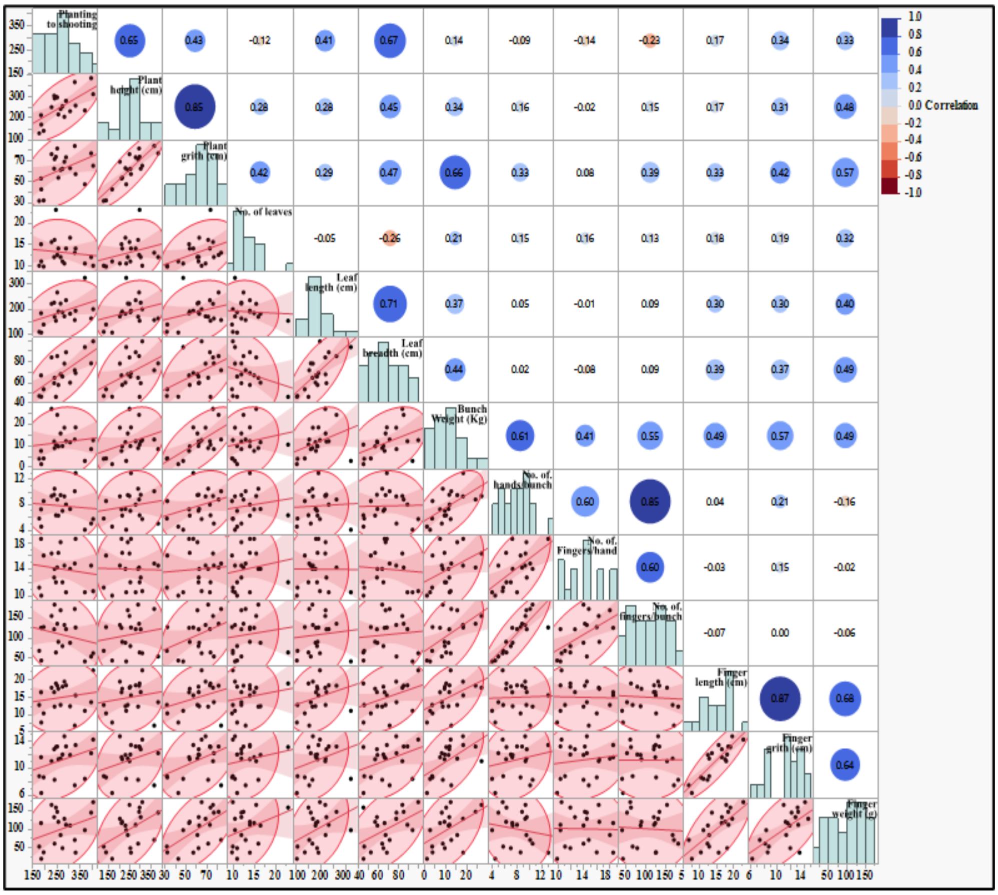

Fig.1. Correlation matrix was constructed in R utilizing the Performance Analytics package, demonstrating the relationship between morphological and yield characteristics of banana germplasm accessions. Positive correlations are depicted in blue, negative correlations in red and the distribution of various variables is illustrated using histograms.

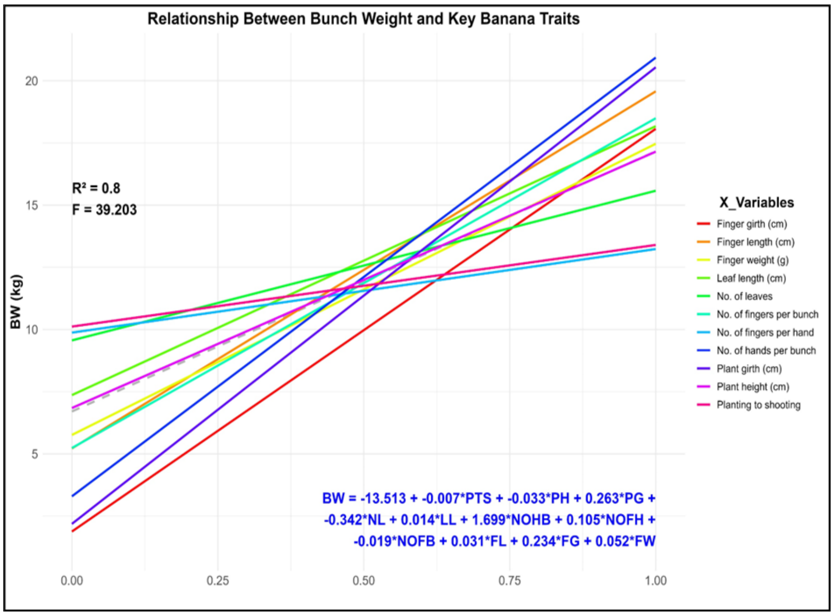

Fig.2. Multiple linear regression examined the relationship between bunch weight (BW) and morphological/yield variables of 20 banana germplasm accessions (R^2 = 0.8, F = 39.203). Notable characteristics include plant height, finger girth and the number of hands per bunch. The study and visualization were produced using R Software with ggplot2.

Similar findings underscore the importance of multiple linear regression models for estimating banana growth and fruit yield, while only a few studies have examined fiber yield. Robust predictions will be conducted effectively using advanced models such as artificial neural networks and SIMBA (35). To determine the BayesB model's superior performance for fruit content and bunch features, the current study compared 6 genomic prediction models for 15 attributes in a multi-ploidy banana population. The regression-based genomic prediction models combine additive genetic effects and show high predictive values (0.47- 0.75) for possible use in improving selection efficiency in banana breeding (27). According to multiple linear regression equations, they can estimate the crop yield and establish relationships between yield and other influencing characteristics (36).

Hierarchical clustering

The hierarchical clustering of banana varieties revealed clusters 3 different clusters. Clusters similarly exhibit varying colors, such as Red Banana and Nendran classified as cluster 1, whereas Rose, Pisang Lilin and Calcutta 4 fall under cluster 3. This applies to the hierarchical clustering algorithm, which elucidates how varieties are joined based on distance thresholds and similarity levels. Cluster 1, which contained 3 elements, merges into a lower height, which signifies a high degree of internal similarity, thereby establishing a unique group. Rather, Nendran and the red banana, which are closely related, are bound in a larger cluster containing a greater number of extremely dissimilar varieties, resulting in their shared cluster 3. To indicate where the sub-clusters are, the software colours differ by contrasting them in their primary clusters, with each color representing one of the high-level classifications (Fig.3). The elbow plot shows that the maximum number of clusters is three because, at that point in the plot, there is a considerable drop-off in the within-cluster sum of squares. Any further increases would give decreasing returns, as seen by the "elbow" produced at k = 3 (Fig.4). It identifies several genetic diversities by amplified fragment length polymorphism (AFLP) analysis on different banana cultivars in

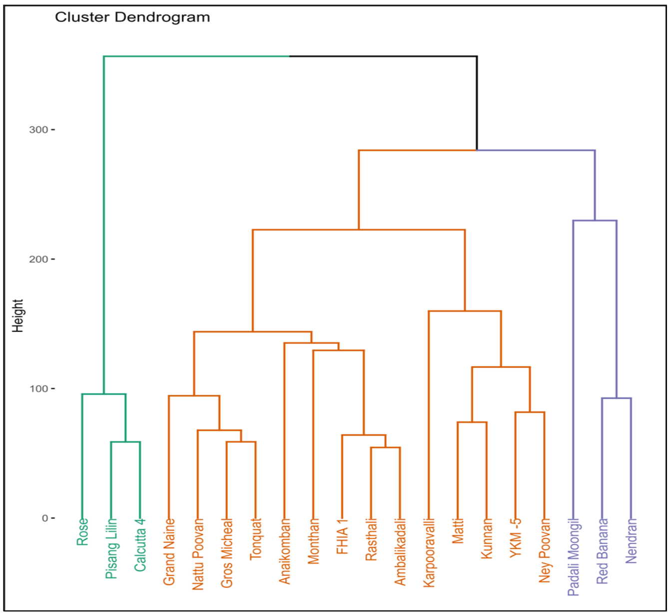

Fig.3. Hierarchical clustering of 20 banana germplasm accessions was performed using the Euclidean distance and linkage method. The dendrogram visualizes genetic relationships, grouping accessions into clusters at various levels. The analysis and plot were generated using R software and the ggdendro package.

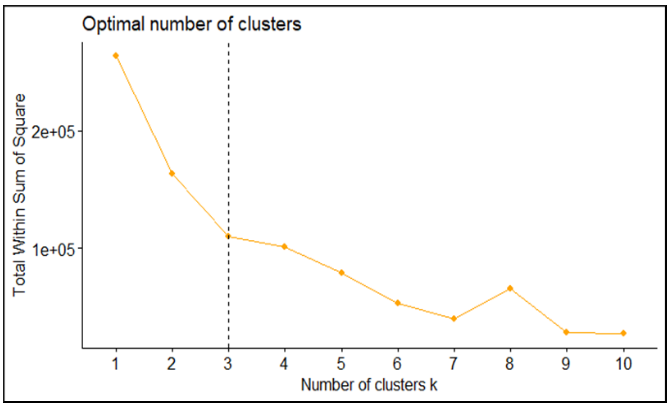

Fig.4. Elbow method was utilized to determine the optimal number of clusters for 20 banana germplasm accessions. The elbow point at k = 3 was determined to be optimal and the total within-cluster sum of squares (WSS) was computed using the k-means clustering algorithm for k = 1 to 10. The ggplot2 utilization and R software were employed to produce the analysis and plot.

Oman. Seven cultivars were identified with 82 different markers. Hierarchical clustering has been applied to classify into distinct groups. This grouping difference morphologically reinforces genetic relationships more than morphological analysis, constructing the common dendrogram (37). K-clustering aims to forecast the best crop types for certain environmental conditions and to understand crops according to their environmental conditions (38).

Multivariate analysis

The first 4 PCs had eigenvalues greater than 1, contributing cumulatively 81.7% of the total variation, with the first PC contributing a maximum of 37.1%, followed by PC2 with 21.6%, PC3 with 12.4% and PC4 with 10.6%. PC1 was strongly influenced by bunch weight, FW and plant girth, but PC2 was influenced by the number of fingers per hand and the number of hands per bunch (Table 4). Likewise, finger characters such as FG, FL and FW contributed the most to PC3 and plant traits such as NL, pseudostem girth and pseudostem height contributed more to PC4 (Fig.5).

The divergence is more influenced by the number of hands per bunch, the number of fingers per bunch and the bunch weight, while the NL is less significant. According to the trait contribution plot, the number of fingers per bunch, the number of hands per bunch and the number of fingers per hand were significantly correlated, as evidenced by the angle between their vectors being less than 90 degrees (39). Similarly, bunch weight had a positive correlation with hands and finger traits. The biplot analysis confirmed that the studied lines were different. The Calcutta 4, Rose, Pisang Lilin and Padali Moongil genotypes differed greatly from the other genotypes. The genotypes such as YKM-5, Matti, Ney Poovan and Karpooravalli were clustered together and clustered near the number of fingers per hand, number of hands per bunch and number of fingers per bunch, suggesting they are phenotypically similar and highly associated with these traits. Similarly, bunch weight is highly associated with Grand Naine and finger characters were associated with Nattu Poovan, Red Banana and Monthan.

Table 4. Principal components analysis and Eigenvalues for morphological and yield attributes of banana germplasm accessions

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13
PTS	0.25	0.3	- 0.35	-0.14	-0.41	-0.33	-0.18	0.21	0.23	-0.3	0.03	0.46	0.01
PH	0.32	0.07	-0.20	-0.49	-0.18	0.01	0.03	-0.35	-0.34	0.17	-0.4	-0.19	0.33
PG	0.38	-0.06	-0.06	-0.39	0.02	0.26	0.13	0.09	-0.08	0.33	0.43	0.14	-0.53
NL	0.12	-0.15	0.44	-0.49	0.33	- 0.29	- 0.36	0.15	0.39	0	- 0.01	-0.1	0.15
LL	0.26	0.14	-0.27	0.27	0.62	-0.25	-0.39	-0.11	-0.37	0.04	0.04	0.13	-0.07
LB	0.32	0.21	-0.36	0.23	0.12	0.05	0.13	0.03	0.58	0.2	-0.01	-0.5	0.04
BW	0.36	-0.24	0.04	0.16	0.05	0.2	0.15	0.72	-0.21	0.02	-0.19	0.08	0.33
NOHB	0.16	-0.50	- 0.14	0.08	- 0.19	0.14	- 0.4	- 0.03	0.01	-0.35	- 0.29	-0.27	-0.44
NOFH	0.09	-0.44	- 0.01	0.15	- 0.15	- 0.73	0.34	- 0.05	-0.03	0.3	-0.03	- 0.01	-0.12
NOFB	0.15	- 0.51	-0.2	0.03	0.15	0.21	0.1	- 0.41	0.26	- 0.17	0.26	0.35	0.39
FL	0.3	0.13	0.43	0.32	- 0.12	0.17	-0.12	- 0.26	0.21	0.34	-0.4	0.39	-0.12
FG	0.34	0.06	0.34	0.25	-0.37	- 0.06	-0.24	- 0.12	- 0.19	- 0.07	0.54	-0.31	0.24
FW	0.34	0.19	0.28	- 0.03	0.22	- 0.08	0.52	- 0.14	- 0.04	- 0.61	-0.1	- 0.05	- 0.19
Standard deviation	2.2	1.67	1.27	1.18	0.84	0.76	0.65	0.49	0.43	0.34	0.27	0.2	0.09
Proportion of variance	0.37	0.22	0.12	0.11	0.05	0.05	0.03	0.02	0.01	0.01	0.01	0	0
Cumulative proportion	0.37	0.59	0.71	0.82	0.87	0.92	0.95	0.97	0.98	0.99	1	1	1

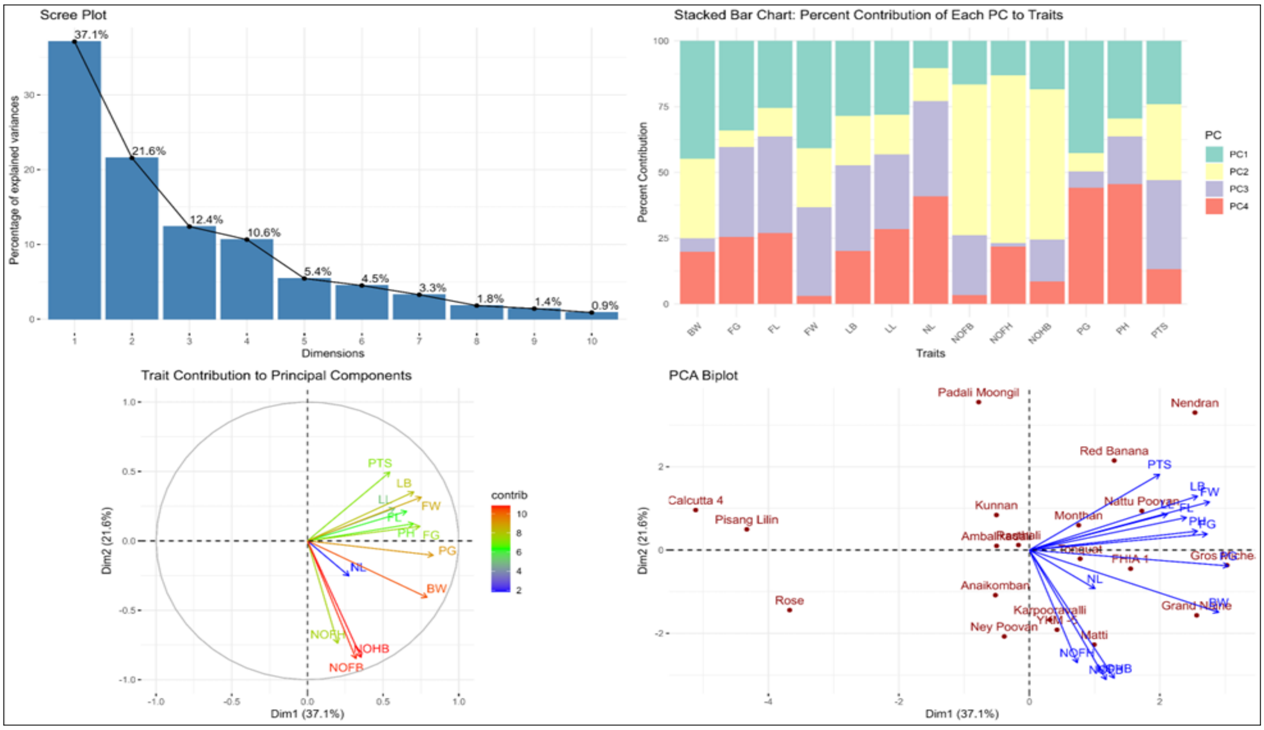

Fig.5. Multivariate analysis was performed in R using the factoextra and ggplot2 packages to visualize PCA results. The plots depict the contribution and relationships of morphological and yield traits across 20 banana germplasm accessions. *PH: Pseudostem height, PG: Pseudostem girth, NOL: Number of leaves, LL: Leaf length, LW: Leaf width, BY: Bunch Yield, NOFB: Number of fingers per bunch, NOFH: Number of fingers per hand, NOFB: Number of fingers per bunch, FL: Finger length, FG: Finger girth, FW: Finger weight.

Dichotomous branching in *Musa* (AAB genome) exhibits random, unstable phenotypic variations characterized by significant variation in morphological parameters. Multivariate analysis demonstrated substantial ($p \leq 0.05$) differences among cultivars, with essential yield-related components. Such as number of fingers per hand, number of fingers per bunch and no. of. hands per bunch and weight have been responsible for 73.035% of the total variability. These traits are potential selection criteria for improving plantain cultivars (40). Accordingly, similar results have been reported, where morpho agronomic analysis of somaclonal variations of the banana cultivar 'FHIA-18' showed as much as 79.23% variability in qualitative characteristics and 97.59% in quantitative traits of the 3 PCA components. The hybrid 'FHIA-25' exhibited unique characteristics compared to other genotypes in qualitative and quantitative analyses (41). PCA's potential to differentiate genotypes based on critical morphological and yield variables is a powerful tool for germplasm characterization, selection and breeding programs (42).

This study highlighted the significance of bunch weight, finger weight, plant girth and other yield-related characteristics as key variables for banana improvement. The different phenotypic divergence and associated grouping patterns revealed by PCA and biplot analyses give good insights into selecting parent genotypes in breeding. Such findings assist in improving the production, quality and adaptability of banana cultivars.

Conclusion

This study analyzed the genetic diversity across 6 banana genomic groups using morphological and yield data from 20 banana accessions. Significant variations in traits such as pseudostem height, girth and bunch weight were observed. Among the genotypes, Grand Naine, Nendran and Red Banana exhibited the highest yield traits, with bunch weight predominantly influenced by the total number of hands. Principal component analysis and clustering analysis observed important attributes that strongly influence banana production, including pseudostem girth, bunch weight and finger length. Based on these findings, Nendran, Grand Naine, Red Banana, Matti and Karpooravalli are recommended for breeding programs to enhance banana yield and genetic improvement.

Acknowledgements

The authors would like to extend their sincere gratitude to the Department of Fruit Science and All India Coordinated Rice Improvement Project - Tropical Fruits for sparing the accession of banana germplasm for successfully implementing the banana breeding program.

Authors' contributions

SS contributed to conceptualizing and supervising the research design and experimental planning. JP carried out the experiment, data collection, analysis and manuscript writing. MI and AJ contributed by imposing the experiment and RJ, AK, JM, SP and MG helped with statistical analysis.

Compliance with ethical standards

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

Ethical issues: None

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