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Cluster analysis to explore morphological variation of banana (*Musa* spp.): A case study in Jember and Lumajang, East Java, Indonesia

Abstract. Banana (*Musa* spp.) is an important horticultural plant with a high diversity in Indonesia; yet, knowledge on the morphological characteristics of indigenous bananas in East Java remains inadequate. This research aims to identify the variation and classify banana cultivars in East Java based on morphological characters. The exploration was conducted using the accidental sampling method. The observations include 15 qualitative and 9 quantitative characters. The statistical methods used in this study include descriptive analysis to evaluate the data, correlation analysis to identify relationships between quantitative characters, and cluster analysis to group banana cultivars based on similarity. In the cluster analysis, Euclidean distance was used as a measure of proximity between banana cultivars, and the average linkage method was applied for grouping. The boxplot assisted in studying important characters of each group. The exploration resulted in 15 banana cultivars with varying morphology. The cluster analysis shows banana cultivars can be divided into four major groups. The first group includes six banana cultivars distinguished by many hands per bunch and a short petiole length. The second group comprises seven banana cultivars with medium leaf length and stem diameter, with Morosebo and Musang being the outliers. The third and fourth groups have only one banana cultivar, Musang, and Agung, respectively. The Musang banana has distinct physical characters, most notably a large stem diameter, whilst the Agung banana has a longer fruit length and wider fruit circumference than others. The coefficient of variation (CV) is moderate, with the fruit length, fruit circumference, fruit stem diameter, and stem diameter all having a CV greater than 47%. Thus, they show promise for further improvement. The banana distinct group based on morphological diversity identified in this study provides valuable information for developing targeted conservation strategies and serves as a base for selecting potential parent cultivars in banana breeding programs.

Keywords: Banana · East Java · Morphology · Variation.

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Introduction

Musaceae, also known as the family of banana, is a group of monocotyledons comprising plants of considerable commercial significance and decorative plants (Jenny et al., 2024). *Musaceae* plants are recognized for their huge, lush foliage and distinct, tropical appearance, making them attractive landscaping choices in warmer areas (Parameswaran & Mamiyil, 2018). Banana is one of the most important plants in the *Musa* genus since it contributes to food security and is a popular fruit worldwide (Rouard et al., 2022). Banana is a staple food crop in many tropical locations. In Africa and South America, banana is grown in huge quantities for both domestic use and export. Overall, the Musaceae family plays an important role in the global agriculture and horticulture industries.

Banana consists of wild and cultivated bananas (Ahmad et al., 2020). Wild *Musaceae* species are diploid, having basic chromosome numbers x = 9, 10, and 11. Cultivated banana is derived from hybridization between different wild banana species and subspecies, *Musa acuminata* and *Musa balbisiana* , leading to genomic groups such as AA, BB, AAB, and ABB (Ahmad et al., 2020; Maseko et al., 2024; Nyine et al., 2017). Cultivated banana, which produces edible fruit, is typically parthenocarpic, sterile, triploid (2n = 3x = 33), and propagated primarily vegetatively. Although certain cultivars are diploid or tetraploid, most cultivars differ in chromosome count due to their distinct wild ancestors (Droc et al., 2022). This unique genomic foundation reflects the evolutionary processes behind the development of cultivated banana.

Building upon this genetic basis, edible banana fruit cultivars are a manufactured genetic complex based on two wild diploid species originating from South-East Asia, *Musa acuminata* (AA) and *Musa balbisiana* (BB) (Maseko et al., 2024). *M. acuminata*, has been proposed to have originated in Malaysia or Indonesia (Nasution, 1991), whereas *M. balbisiana* is found in Myanmar, Sri Lanka, India, Malaya, Papua New Guinea, the Philippines, Thailand, and Indonesia. In Indonesia, *M. balbisiana* is widely distributed in Java and Sulawesi (Sunandar, 2017). According to Sunandar & Kurniasih (2019), Indonesia is a banana distribution center with various cultivars, morphologies, and nutritional content. Banana contains varying levels of vitamins, minerals, and carbohydrates. According to Sahmsiah et al. (2024), many properties of each banana cultivar are influenced by genetic and environmental variables, as well as their interaction.

Due to its extraordinary genetic and morphological diversity, Indonesia plays a vital role in global banana production. In 2022, Indonesia's banana production reached 9.6 million tons, with East Java being the top-producing province at 2.6 million tons. Notably, Jember and Lumajang Regencies contributed considerably to this output (BPS, 2023). Given the substantial banana production in Indonesia, particularly in East Java, the need to preserve and enhance this diversity becomes crucial. To preserve this diversity, characterization based on morphological traits can be used, as this method is relatively simple and quick, allowing it to be applied directly to plant populations and the data to be used as a plant description (Kurnianingsih et al., 2018; Sadiyah et al., 2020; Sari et al., 2024). In addition to benefiting biodiversity conservation efforts, the characterization results can serve as a foundation for applied research in various banana-related disciplines, promoting food security and the sustainability of local genetic resources with high economic potential (Maryani et al., 2020).

The diversity of bananas is important because it has the potential to make significant contributions to conservation strategies, enhance the utilization of banana genetic resources, and improve the sustainability of plant production (De Langhe et al., 2018). Currently, efforts are being made to increase the diversity and availability of genetic resources for genetic conservation, including characterization (Droc et al., 2022). Meanwhile, characterization studies can provide valuable information about banana cultivar kinship. This information is useful in breeding efforts because it aids in the development of new cultivars as well as the identification of closely related substitute cultivars when problems arise during cultivation (Hapsari & Lestari, 2016; Weber et al., 2017). The characterization of banana using morphology has been extensively studied by some researchers (Aquino et al., 2017; Sivirihauma et al., 2017; Adheka et al., 2018; Baysal & Ercisli, 2022; Malikongwa et al., 2022; Soares et al., 2023). Banana research in Indonesia has also

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been conducted (Sumardi & Wulandari, 2010; Lesta et al., 2018; Dewi & Damanhuri, 2019; Maryani et al., 2020; Weihan et al., 2020; Sari et al., 2023; Widyayanti et al., 2024). Although previous studies have explored banana diversity, they often focused on broader regions or limited populations, providing insufficient data on local cultivars in major production areas. In East Java, morphology-based characterization remains limited. This study focuses on characterizing bananas in Jember and Lumajang regencies, addressing gaps in regional morphological research and providing valuable insights into their genetic relationships and breeding potential. Specifically, it aims to explore the superior qualities of local banana plants and deepen understanding of their kinship to support breeding programs. To achieve this, cluster analysis was utilized as a multivariate approach to comprehensively examine morphological traits and relationships.

Materials and Methods

Banana exploration. The banana exploration was carried out in East Java province, i.e., the Jember and Lumajang regencies. The exploration used the accidental sampling method (Eichhorn, 2022), based on information from residents. Banana plants as samples were found in residents' yards and fields. Each cultivar of banana is represented by one individual plant. A total of 24 morphological characters were observed, including 15 qualitative and nine quantitative characters. The morphological characters were based on the banana plant descriptor issued by the International Plant Genetic Resources Institute (IPGRI).

Data analysis. The qualitative character data was analyzed using descriptive analysis, which calculated the proportion of frequency of each morphology category. The quantitative character data was evaluated using descriptive, correlation analysis, and clustering methods. The attribute characters are described using descriptive statistics, including minimum, maximum, mean, and coefficient of variation (CV). The relationship between characters would be displayed by corrplot (R software) using Pearson correlation analysis. Cluster analysis (Rodriguez et al., 2019) was used for banana grouping based on quantitative characters. It used the average linkage method and Euclidean distance with the help of PBSTAT 2.2.1 software (Suwarno et al., 2025). Data transformation was carried out first by dividing the original data of each variable by its standard deviation. This transformation had been suggested as a preliminary step before distance calculation to eliminate the scale effect on classification results (DeCastellarnau, 2018). The boxplot helped to study important characters of each group as a result of cluster analysis.

Results and Discussion

This study found 12 banana cultivars from six districts of Jember, namely Ambulu, Balung, Wuluhan, Silo, Kaliwates, and Sumbersari. Meanwhile, three banana cultivars were found in the district of Lumajang, namely Senduro and Pasrujambe (Figure 1). Thus, the exploration obtained 15 different banana cultivars (Table 1). Several banana cultivars obtained were similar to those explored in the study by Hermanto, et al. (2013) in the Ambon, Seram, Flores, Sumba, and Bali areas, namely Candi, Tanduk, Raja, Susu, and Nangka banana.

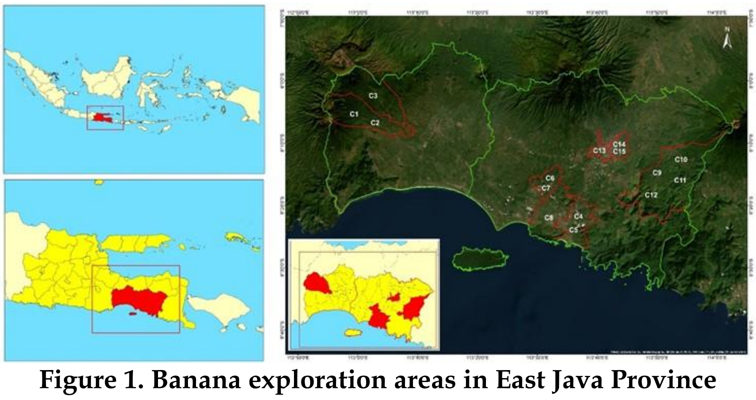


Figure 1. Banana exploration areas in East Java Province

Table 1. Results of banana plant exploration in East Java Province

Number of cultivars	Banana cultivars	Village	District	Regency
C1	Agung	Pasrujambe	Pasrujambe	Lumajang
C2	Cavendish	Pasrujambe	Pasrujambe	Lumajang
C3	Musang	Sari Kemuning	Senduro	Lumajang
C4	Candi	Andongsari	Ambulu	Jember
C5	Janten	Sabrang	Ambulu	Jember
C6	Susu	Balung Lor	Balung	Jember
C7	Raja Nangka	Balung Lor	Balung	Jember
C8	Nangka	Glundengan	Wuluhan	Jember
C9	Sisir/Jari Buaya	Garahan	Silo	Jember
C10	Embug	Sempolan	Silo	Jember
C11	Seribu	Sempolan	Silo	Jember
C12	Rayapan	Sempolan	Silo	Jember
C13	Kepok Makassar	Gebang	Kaliwates	Jember
C14	Awak	Tegal Gede	Sumbersari	Jember
C15	Morosebo	Tegal Gede	Sumbersari	Jember

Identification of qualitative characters of banana. Table 2 showed that the pseudostem color was green-red by 40%, yellowish green by 33.33%, and none of them were dark green or blue. The difference in pseudostem color was due to the metabolic process that produced a color pigment, and each cultivar of banana had a different pigment gene (Dewi & Damanhuri, 2019). The content of anthocyanin pigment was the cause of the variety in pseudostem colors. The anthocyanin pigment content had different biosynthesis pathways between the two ancestors, namely *M. acuminata* and *M. balbisiana*. Bracts, male bud shape, and mature fruit color allow the differentiation between ploidies and banana subgroups (Beaton et al., 2023). Most bananas have red, purple, or violet bracts, however, a few are acyanic (green or yellow). The color of the bracts varies according to the composition of the anthocyanins present, which is unique to each species and subspecies. As a result, taxonomic tools such as anthocyanin were utilized to differentiate taxa. Different species' bracts have been found to contain all six prevalent anthocyanidins (Pazmiño et al., 2001).

Table 2 also shows that the largest percentage of the petiole shape character was a category of wide with erect margins, accounting for 40.0%. Then, the categories of open with margins spreading, straight with erect margins, and margins curved inward were 26.67%, 20%, and 13.33%, respectively. According to Dewi & Damanhuri (2019), *M. acuminata*-derived banana had a petiole growth type with upright sides, while *M. balbisiana* was an inward-curved type. Meanwhile, more than half of the banana varieties had slightly hairy banana bunch stalks. The length of fruit stalks had three categories (long, medium, and short) observed by measuring from the base of the stem to the tip (IPGRI, 1996). In this study, all the bananas explored in the long category were more than 21 cm. The arrangement of ovules had two categories, namely 2 and 4 rows, each with almost the same proportion, nearly 50%.

Table 2. Frequency of 15 qualitative characters in each cultivar of banana

Character	Category	Frequency (%)	Banana cultivars
Pseudostem color	1. Green-yellow	33.33	Candi, Susu, Nangka, Awak, Embug
	2. Medium green	6.67	Sisir/Jari Buaya
	3. Green	6.67	Kepok Makassar
	4. Dark green	0	-
	5. Green-red	40	Raja Nangka, Agung, Cavendish, Seribu, Rayapan, Morosebo
	6. Red	6.67	Musang
	7. Red-purple	6.67	Janten
	8. Blue	0	-
	9. Other	0	-

Character	Category	Frequency (%)	Banana cultivars
Petiole canal	1. open with margins spreading	26.67	Raja Nangka, Cavendish, Nangka, Sisir/Jari Buaya
	2. Wide with erect margins	40	Candi, Susu, Agung, Musang, Morosebo, Janten
	3. Straight with erect margins	20	Seribu, Kepok Makassar, Embug
	4. Margins curved inward	13.33	Rayapan, Awak
	5. Margins overlapping	0	-
Peduncle hairness	1. Hairless	40	Candi, Susu, Agung, Kepok Makassar, Awak, Janten
	2. Slightly hairy	53.33	Raja Nangka, Musang, Nangka, Sisir/Jari Buaya, Seribu, Rayapan, Morosebo, Embug
	3. Very hairy, short hairs (similar to velvet touch)	6.67	Cavendish
	4. Very hairy, long hairs (>2mm)	0	-
Fruit pedicle length	1. Long (≥ 21 cm)	100	Candi, Susu, Raja Nangka, Agung, Cavendish, Musang, Nangka, Seribu, Rayapan, Kepok Makassar, Awak, Morosebo, Sisir/Jari Buaya, Janten, Embug
	2. Intermediate (11 to 20 cm)	0	-
	3. Short (≤ 10 cm)	0	-
Arrangement ovules	1. Two-rowed	53.33	Raja Nangka, Agung, Cavendish, Nangka, Seribu, Rayapan, Morosebo, Sisir/Jari Buaya
	2. Four-rowed (more or less)	46.67	Candi, Susu, Musang, Kepok Makassar, Awak, Janten, Embug
Male bract shape	1. $x/y < 0.28$ (lanceolate)	6.67	Agung
	2. $0.28 < x/y < 0.30$	0	-
	3. $x/y > 0.30$ (ovate)	93.33	Candi, Susu, Raja Nangka, Cavendish, Musang, Nangka, Seribu, Rayapan, Morosebo, Sisir/Jari Buaya, Kepok Makassar, Awak, Janten, Embug
Bract behavior before falling	1. Revolute (rolling)	46.67	Susu, Raja Nangka, Musang, Nangka, Kepok Makassar, Awak, Morosebo
	2. Not revolute (not rolling)	53.33	Candi, Agung, Cavendish, Seribu, Rayapan, Sisir, Janten, Embug
Bract base shape	1. Large shoulder	26.67	Musang, Kepok Makassar, Janten, Embug
	2. Medium	26.67	Candi, Susu, Cavendish, Awak
	3. Small shoulder	46.67	Raja Nangka, Agung, Nangka, Seribu, Rayapan, Morosebo, Sisir/Jari Buaya
Bract apex shape	1. Pointed	26.67	Raja Nangka, Agung, Rayapan, Morosebo
	2. Slightly pointed	33.33	Candi, Cavendish, Nangka, Seribu, Sisir/Jari Buaya
	3. Intermediate	26.67	Susu, Musang, Kepok Makassar, Awak
	4. Obtuse	6.67	Janten
	5. Obtuse and split	6.67	Embug
Color of the bract external face	1. Yellow	0	-
	2. Green	0	-
	3. Red	20	Sisir/Jari Buaya, Janten, Embug
	4. Red-purple	53.33	Susu, Raja Nangka, Agung, Nangka, Seribu, Rayapan, Kepok Makassar, Awak
	5. Purple-brown	0	-
	6. Purple	13.33	Candi, Cavendish
	7. Blue	0	-
	8. Pink-purple	6.67	Morosebo
	9. Orange-red	6.67	Musang
Fading of color on bract base	1. Colour discontinuing towards the base	26.67	Agung, Morosebo, Janten, Embug
	2. Colour homogenous	73.33	Candi, Susu, Raja Nangka, Cavendish, Musang, Nangka, Seribu, Rayapan, Kepok Makassar, Awak, Sisir/Jari Buaya
Bract scars	1. Very prominent	86.67	Candi, Raja Nangka, Agung, Cavendish, Musang, Nangka, Seribu, Rayapan, Kepok Makassar, Awak, Morosebo, Sisir/Jari Buaya, Janten
	2. Not prominent	13.33	Susu, Embug

Character	Category	Frequency (%)	Banana cultivars
Free tepal of male flower	1. Simple folding under apex	40	Candi, Susu, Raja Nangka, Kepok Makassar, Awak, Sisir/Jari Buaya
	2. More or less smooth	33.33	Cavendish, Nangka, Seribu, Rayapan, Morosebo
	3. Several folding under apex (corrugated)	26.67	Agung, Musang, Janten, Embug
Male flower color	1. White	0	-
	2. Cream	46.67	Susu, Raja Nangka, Cavendish, Nangka, Seribu, Rayapan, Embug
	3. Yellow	33.33	Candi, Musang, Kepok Makassar, Awak, Morosebo
	4. Pink/pink-purple	13.33	Agung, Janten
Stigma color	1. Cream	66.67	Sisir/Jari Buaya, Susu, Agung, Janten, Nangka, Kepok Makassar, Awak, Morosebo, Sisir/Jari Buaya, Candi, Embug
	2. Yellow	0	-
	3. Pink/pink-purple	6.67	Cavendish
	4. Bright yellow	13.33	Seribu, Rayapan
	5. Orange	13.33	Raja Nangka, Musang

Table 3. Minimum, maximum, mean, and coefficient of variation (CV) of the quantitative character of banana

Character	Min	Banana Cultivar	Max	Banana Cultivar	Mean	CV (%)
Fruit length (FL, cm)	6.17	Morosebo	30.00	Agung	12.30	48.85
Fruit circumference (FC, cm)	1.23	Janten	16.60	Agung	8.24	55.33
Peduncle diameter (PLD, cm)	1.23	Janten	7.33	Cavendish	4.34	49.92
Petiole length (PL, cm)	7.50	Morosebo	64.50	Awak	39.56	44.86
Leaf blade length (LL, cm)	76.00	Candi	338.33	Sisir	214.44	33.72
Leaf blade width (LW, cm)	35.00	Rayapan	79.67	Kepok Makassar	62.72	22.2
Pseudostem diameter (PSD, cm)	11.33	Morosebo	77.33	Musang	24.08	70.57
Number of hands per bunch (NC)	2.00	Agung	12.00	Cavendish	7.07	34.02
Pseudostem height (PSH, cm)	109.00	Morosebo	489.00	Kepok Makassar	288.67	40.91

Qualitative characters were only controlled by one or two genes (simple genes) with small environmental influences (Ritonga et al., 2022). For example, the yellow color character in banana is controlled by one gene, namely the ZmPsy1 gene (Paul et al., 2017). The 15 banana cultivars explored in this study show variation in qualitative morphological character (Figure 2). The uniqueness of this morphology could be influenced by different environments and banana genome ancestors such as *M. acuminata* and *M. balbisiana*, and it could be expressed as a unique category (Herwitarahman & Sobir, 2014).

Identification of quantitative characters in banana. Morphological characters can be classified into qualitative and quantitative characters (Serpico, 2020). Quantitative traits, especially leaves, flowers, and stems, are characters of plants that vary and often undergo changes. This can be influenced by the environment and genes that affect physiological processes (Sari et al., 2023). The descriptive analysis of quantitative morphological characters in this study is presented in Table 3.

Table 3 shows that the fruit length ranges from 6.17-30.00 cm, which is not significantly different from the research by Lesta et al. (2018) on 22 banana germplasm from Bangka, where the fruit length ranges from 11.06-32.22 cm. The width and length of the leaves in this study were, respectively, within the intervals of 35.00-79.67 cm and 76.00-338.33 cm. Both variables of the leaves are also not different from the banana from Bangka, where the width and length of the leaves range from 35.03-71.35 and 135-272 cm. However, the range of leaf length from this study is almost twice the range of leaf length of banana from Bangka. Meanwhile, the height of the banana stems from Bangka ranges between 245-645 cm, relatively taller compared to the banana trees in this study.

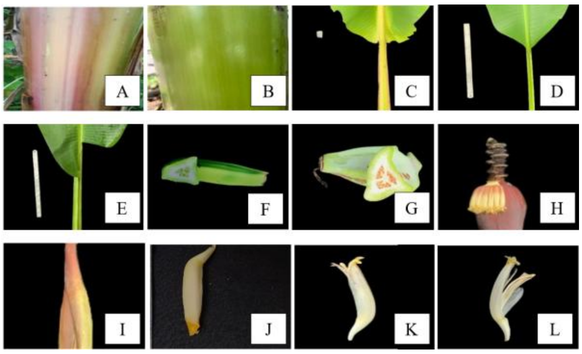


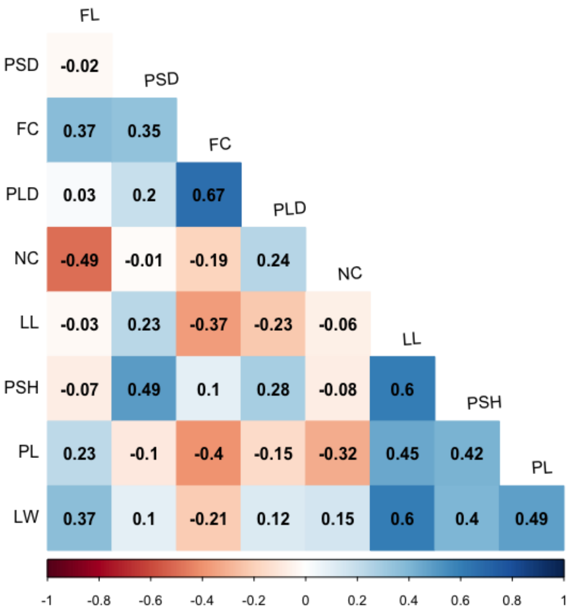
Figure 2. The Qualitative Characters of Explored Banana. Pseudostem Color: Reddish Green (A), Green (B); Petiole Canal: Open with Margins Spreading (C), Wide with Margins Spreading (D), Margins Curved Inward (E); Arrangement of Ovules: Two-Rowed (F), Four-Rowed (More or Less) (G); Male Bract Shape: Ovate (H), Lanceolate (Ii; Free Tepal of Male Flower: More or Less Smooth (J), Simple Folding Under Apex (K), Corrugated (L)

Quantitative traits in banana plants have a certain level of variation. The relative variation of each quantitative character can be measured using the coefficient of variation (CV). The CV provides important information about how consistent or variable the data obtained from various genotypes is, which is crucial in decision-making for selecting superior varieties (Gangappa et al., 2022). The CV value can help in identifying traits with high variability that have the potential for development in plant breeding programs. The smaller the CV of a character, the lower the level of variation of that character, or the more homogenous it is. Conversely, the higher the CV value, the greater the variability (Weihan et al., 2020).

The CV in this study ranges from 22.2% (leaf width) to 70.57% (pseudostem diameter). Meanwhile, for fruit characters, both fruit circumference and fruit length have relatively high CVs compared to other characters, except for stem diameter and fruit peduncle diameter. Compared with the study by Weihan et al. (2020) in 6 sub-districts in the mainland area of Tanjung Jabung Timur Regency, Jambi Province, Indonesia, which produced a CV ranging from 13.05% (fruit length) to 30.02% (number of hands), this study found a higher value of CV.

Variation is essential for plant breeding programs, as it allows breeders to select specific traits and create new varieties with desired characters. By understanding the genetic and environmental factors that influence phenotype variation, breeders can make informed decisions about which plants to cross and which traits to select for future generations. Additionally, studying phenotype variation can help researchers better understand the underlying genetic mechanisms that control important traits in plants, leading to more targeted and efficient breeding strategies (Mackill & Khush, 2018; Upadhyaya et al., 2019).

The quantitative characters of plants are affected by numerous genes as well as environmental factors. The environment has a significant impact on how plants grow. Different planting timings and environmental factors like sunlight, temperatures, and soil properties (humidity, pH, texture) might contribute to variations in quantitative characters (Kurnianingsih et al., 2018).



	FL	PSD	FC	PLD	NC	LL	PSH	PL
PSD	-0.02							
FC	0.37	0.35						
PLD	0.03	0.2	0.67					
NC	-0.49	-0.01	-0.19	0.24				
LL	-0.03	0.23	-0.37	-0.23	-0.06			
PSH	-0.07	0.49	0.1	0.28	-0.08	0.6		
PL	0.23	-0.1	-0.4	-0.15	-0.32	0.45	0.42	
LW	0.37	0.1	-0.21	0.12	0.15	0.6	0.4	0.49

Figure 3. Correlation of quantitative character in banana

Plant breeding programs often use correlation analysis for indirect selection. If vegetative traits, which can be observed earlier, are strongly correlated with main traits to be improved (e.g., production characteristics like fruit number and size), indirect selection can accelerate the selection process. In this study, most correlations between variables were not statistically significant (Figure 3). There was a significant correlation between the fruit circumference and the peduncle diameter (r=0.67, p-value < 0.05), the length and width of the blade of leaves (r=0.6, p-value < 0.05), as well as the leaf blade length and the pseudostem height (r=0.6, p-value=0.05). Based on the correlation analysis, indirect selection was not recommended in the banana breeding process, especially the cultivars included in this study.

The clustering of banana cultivars by quantitative characters. The explored bananas were grouped based on quantitative characters presented in the circlized dendrogram in Figure 4. Based on the dendrogram, 15 cultivars of banana were grouped into four main groups. Group 1 consisted of six banana cultivars, Group 2 had seven banana cultivars, and Groups 3 and 4 consisted of only one banana cultivar. The distance between groups used a value of cophenetic distance close to 4.3. The boxplots for each group on each quantitative character are created to find out the main character of each group (Figure 5).

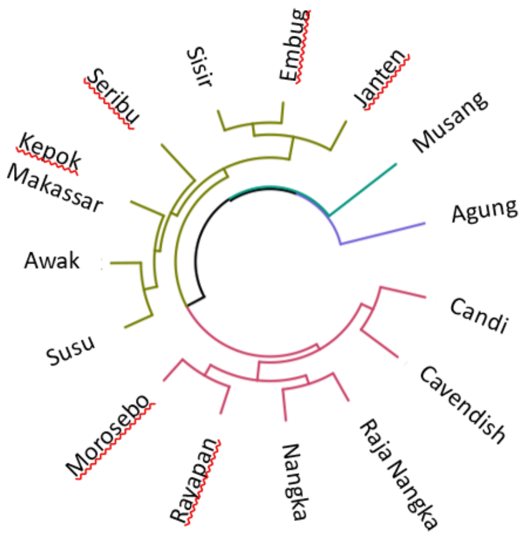


Figure 4. Circlized dendrogram of cluster analysis of 15 banana cultivars based on nine quantitative characters using euclidean distance from transformed data and the average linkage method

Group 1 consisted of Banana Candi, Cavendish, Raja Nangka, Nangka, Rayapan, and Morosebo. The closest distance in Group 1 included Morosebo and Rayapan, with a cophenetic distance of 1.73. All cultivars of banana in Group 1 had the same ovule arrangement, which is two rows, except for the Candi banana. The main character of Group 1 was a high value of the number of hands per bunch and a low value of petiole length. The variance of the leaf blade width was high, indicated by the box size on the boxplot being relatively long. It could be interpreted that Group 1 had a leaf width size that varied in value.

Group 2 consisted of Susu, Awak, Kepok Makasar, Seribu, Sisir, Embug, and Janten banana. The stigma color of all bananas in Group 2 was cream, except the stigma color of the Seribu banana was bright yellow. Group 2 was also characterized by high values of leaf blade length and petiole length relative to the others, as well as moderate pseudostem diameters.

Groups 3 and 4 consisted of only one cultivar of banana, namely Musang and Agung banana, respectively. The prominent character in Group 3 was the pseudostem diameter, which was larger than the others, and the peel color when ripe was red. Meanwhile, the Agung banana (Group 4) had a much higher length and circumference of fruit than other bananas, as well as the lowest number of hands per bunch, which was only two hands per bunch.

Cluster analysis is grouping cultivars based on their similarities. The more character differences, the lower the similarity value, indicating a greater distance in the kinship relationship between the compared cultivars. The closer the position of two cultivars in the dendrogram, the greater their similarity. Banana cultivars with a low similarity coefficient are well-suited to be used as parents in crosses. The smaller the genetic similarity between the parents used, the greater the chance of obtaining hybrids with relatively high genetic variation, which will produce individuals with higher heterozygosity (Rao & Hodgkin, 2002).

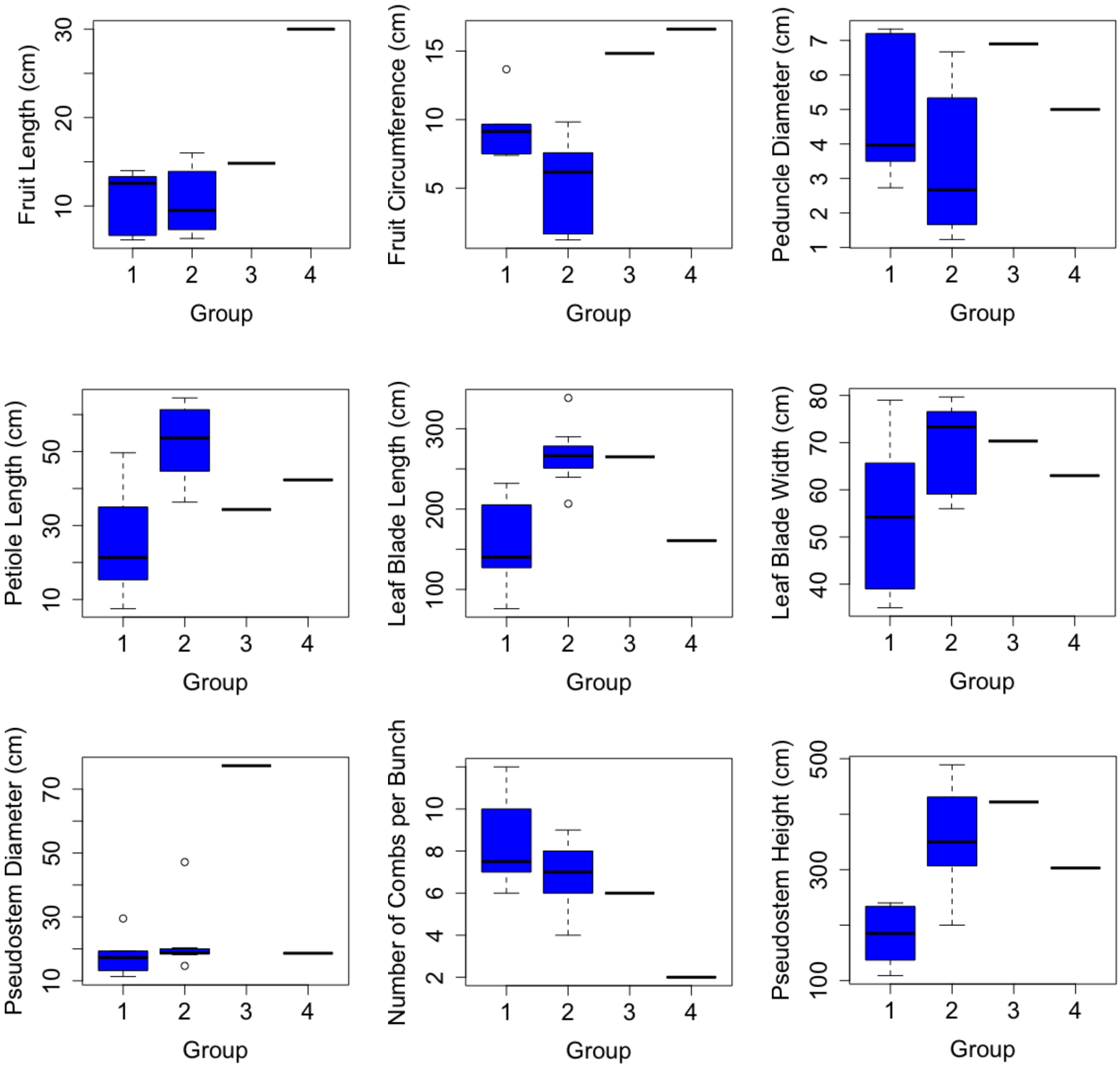


Figure 5. Boxplot per group for each quantitative character

The research of Widyayanti et al. (2024) on banana germplasms from Yogyakarta produced four groups, which consisted of 3-12 cultivars per group. The main characters of each group were the appearance of the upper surface of the leaves, the presence of male flowers, and the existence of hermaphrodite flowers, which had a more dominant visualization color than the others. Meanwhile, research on 22 banana germplasms in Bangka by Lesta et al. (2018) showed that the variability of banana in Bangka was relatively wide. High variability indicated the diversity of germplasm and the high effectiveness of selection. If the genetic variability was narrow, the selection could not be carried out because the observed population was uniform (Salgotra & Chauhan, 2023).

Banana populations with narrow variation have to broaden. Broadening the crop's genetic base while maintaining quality characteristics and enhancing production performance is critical. Furthermore, the huge genetic group will be useful for future genomic selection research in the crop, as well as for profiling conservation methods (Arvanitoyannis et al., 2008).

Germplasm that has large variations is a source of genes for the traits of high yield, resistance to pests or diseases, early maturity, and other good traits. Plants in the same group, if used as parents for crosses, will produce offspring with low genetic variation, while crosses between groups will produce high genetic variation. To determine the role of genotype and environment can be calculated through the phenotype diversity in a generation (Sari et al., 2023). However, genetic limitations such as sterility and parthenocarpy in bananas make traditional breeding difficult and time-consuming. Therefore, modern molecular breeding technology become an inevitable requirement for genetic improvement of bananas and breeding of new varieties (Miao et al., 2025).

Conclusion

Based on the observations of banana varieties from the exploration in Jember and Lumajang regencies, it can be concluded that these bananas have moderate genetic variability, making the selection of germplasm quite effective in supporting the local banana breeding program. Selection should be conducted directly because the correlation analysis results show low to moderate values; thus, indirect selection is not recommended. In general, the banana resulting from the exploration can be grouped into four groups, each with distinct prominent characters. This research is expected to provide insights that can be used in plant breeding programs, conservation of germplasm, and management of local genetic resources with high economic potential.

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