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Morphological diversity and cluster relationships of indigenous *Musa* spp. based on biosystematic in North Maluku, Indonesia

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Abstract. *Suparman S, Tamalene MN, Bahtiar B, Ilmi ZL. 2025. Morphological diversity and cluster relationships of indigenous* Musa *spp. based on biosystematic in North Maluku, Indonesia. Biodiversitas 26: 4220-4228.* The banana (*Musa* spp.) is a culturally and economically vital crop in North Maluku, yet its local morphological diversity remains underdocumented. This study examined 40 indigenous banana cultivars from five islands (Morotai, Halmahera, Ternate, Tidore, Bacan) using 52 standardized morphological descriptors. Genomic groups were inferred morphologically (AA/AAA, AAB, ABB, AB). Phenetic relationships were analyzed via Principal Component Analysis (PCA) and UPGMA clustering using Euclidean and Ward's methods. Four distinct clusters were identified, i.e., group A (penganten), group B (tanduk), group C (takoapi), and group D (mas); the clusters were independent of genomic classification. Genome group distribution included AA/AAA (52.5%), AAB (32.5%), ABB (12.5%), and AB (2.5%). Key traits differentiating clusters included petiole canal morphology, bract coloration, and fruit shape. Most cultivars (75%) were distributed below 100 masl, showcasing their ecological adaptability. A few (e.g., Sarango, Goroho Putih) were found at elevations >150 m, indicating ecological adaptability. The incongruence between morphological clusters and genomic groups suggests the influence of somaclonal variation, ecological adaptation, and cultural selection. These findings provide a crucial baseline for in situ conservation and targeted breeding of regionally adapted banana germplasm in eastern Indonesia. Conservation efforts are especially critical for cultivars possessing rare genome types, given their vulnerability and genetic significance.

Keywords: In situ conservation, local banana germplasm, morphological diversity, phenetic analysis, UPGMA clustering

INTRODUCTION

Banana (*Musa* spp.), a member of the Musaceae family (Zingiberales), ranks among the world's most economically important tropical fruits (Sardos et al. 2018; Singh et al. 2020). As the most consumed tropical fruit globally (FAO 2022), bananas play a central role in food security and trade, with exports reaching 20.5 million tons in 2021 (International Trade Centre 2021). Despite producing about 8.7 million tons, Indonesia exports only around 7,000 tons annually (BPS 2022), emphasizing the crop's domestic importance. This paradox highlights Indonesia's reliance on bananas as a staple food rather than an export commodity.

In Indonesia, bananas are cultivated in diverse agroecosystems, from home gardens to commercial plantations. Their versatility—from fresh fruit and cooking ingredients to processed products and animal feed—illustrates their multifunctional value. Beyond economics, bananas also embody cultural traditions. In North Maluku, Indonesia, cultivars such as the endemic Mulut Bebek (AA genome) are integral to local diets and rituals (Iskandar et al. 2018; Poerba et al. 2018). This underscores how banana diversity is interwoven with cultural identity and traditional practices.

Globally, more than 1,000 cultivars have been documented (Li and Ge 2017), with over 200 reported in Indonesia (Probojati et al. 2019). These figures confirm the exceptional richness of *Musa* diversity in the Indo-Malayan region. However, detailed morphometric and genomic studies remain uneven, particularly in Eastern Indonesia. Prior works in North Maluku have been fragmented, focusing on specific uses or traits, such as small-scale morphological surveys (Hendaru et al. 2017), food product innovation (Lumba et al. 2017), or animal feed utilization (Ishak et al. 2019). Such studies, while useful, do not provide a comprehensive understanding of regional banana diversity.

The Maluku Islands are biogeographically unique as part of Wallacea, an area of high endemism and complex evolutionary histories. Geographic isolation, ecological gradients, and farmer-driven selection may have generated distinctive banana lineages. In many cases, smallholder farmers preserve local landraces due to cultural preferences and ecological suitability, fostering the survival of rare cultivars. Without systematic documentation, however, these genetic resources risk erosion from agricultural modernization and land-use change. This makes North Maluku an urgent priority for banana diversity research and conservation.

Morphological characterization provides a practical approach to assess diversity, especially where molecular analyses are limited. Standardized descriptors (IPGRI-INIBAP/CIRAD 1966) allow for genome inference and cultivar classification (Simmonds and Shepherd 1955). Though less precise than molecular markers, morphometric analysis remains indispensable for field-level identification, germplasm evaluation, and rapid diversity assessment.

Recent works in Java and elsewhere show that morphology-based clustering continues to support conservation and breeding efforts (Hapsari et al. 2022; Slameto 2023). Integrating morphometric descriptors with phenetic analysis, therefore remains a valuable tool to reveal cultivar relationships and ecological adaptations.

In North Maluku, bananas are distributed across islands such as Halmahera, Morotai, Tidore, Ternate, and Bacan. These islands form a mosaic of ecological conditions where bananas thrive in coastal yards, upland fields, and moorlands. Yet no integrated morphometric and cluster analysis has been performed in the province. The absence of such data restricts conservation planning and reduces the potential for breeding programs to utilize local germplasm in developing cultivars resilient to climate change, pests, and diseases. Given the rapid pace of agricultural transformation, documenting these resources is both scientifically and practically significant.

To address this gap, the present study provides the first comprehensive morphometric and phenetic analysis of 40 local *Musa* cultivars from five islands in North Maluku. By employing 52 standardized morphological descriptors combined with Principal Component Analysis (PCA) and UPGMA clustering, this research aims to (i) document the extent of morphological diversity, (ii) evaluate the concordance between morphological clusters and genome groups, and (iii) establish a baseline for conservation and breeding of regionally adapted banana germplasm. This integrated approach offers essential insights into the biosystematics of bananas in North Maluku, contributing both to scientific understanding and to strategies for the sustainable management of local cultivars.

MATERIALS AND METHODS

Study area

This study was conducted in North Maluku Province and encompassed five major islands—Morotai, Halmahera, Tidore, Ternate, and Bacan. These islands were selected as they represent the full spectrum of North Maluku's ecological zones and geographic gradients, ranging from the northernmost to the southernmost parts of the region, providing a diverse habitat for local banana (*Musa* spp.) cultivation. Figure 1 presents a map of the sampling sites across the study area.

Sampling period and procedure

Fieldwork was carried out from March to November 2024 using an exploratory sampling technique. Farmers, or the elder and knowledgeable about local banana plants and agricultural extension workers, were consulted to locate and access banana cultivars. Each identified local cultivar was regarded as a separate Operational Taxonomic Unit (OTU) in the analysis and was represented by 5 to 10 individuals to record morphometric traits and calculate average values.

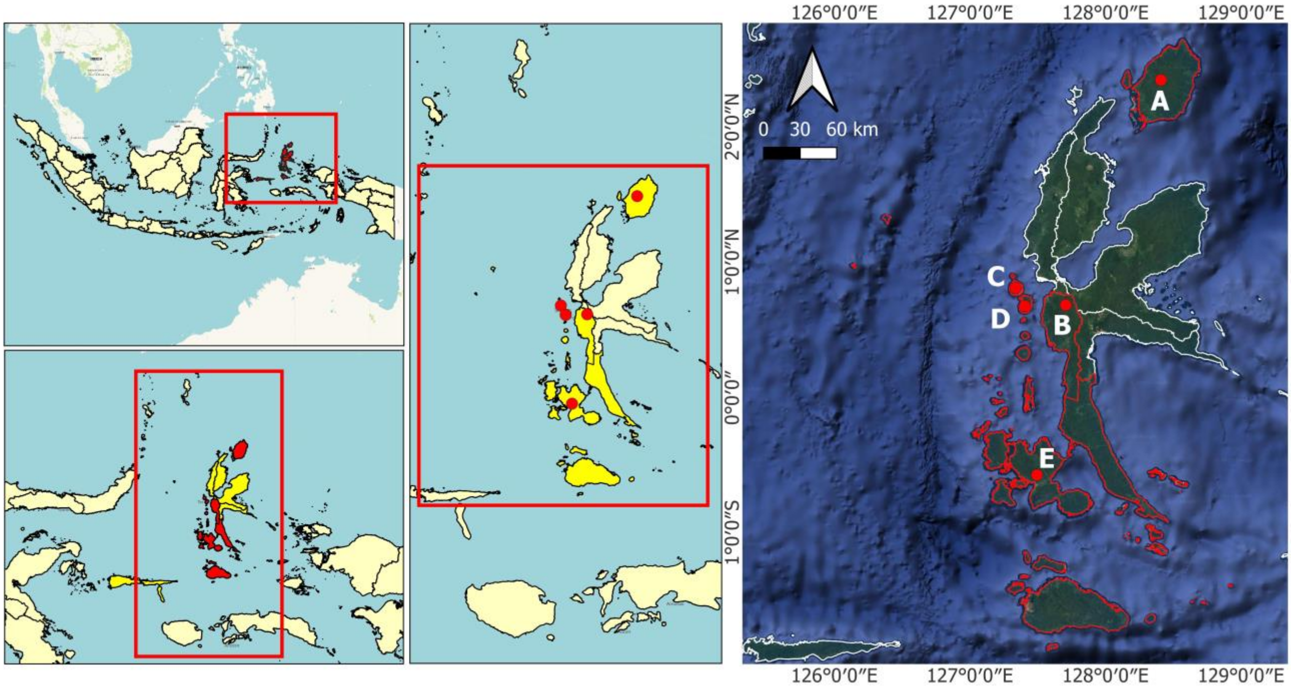

Figure 1. Map of the study area in North Maluku Province, Indonesia, showing the five major islands where banana cultivars were sampled: A. Morotai, B. Halmahera, C. Ternate, D. Tidore, E. Bacan

Morphological characterization and genomic group classification

A total of approximately 52 morphometric characters were recorded for each cultivar, encompassing both quantitative and qualitative traits. Character states were documented and modified using the standard banana descriptor guidelines developed by IPGRI-INIBAP/CIRAD (1966). The standard morphometric was also confirmed by Premjet et al. (2022) and Hapsari et al. (2022).

The genomic composition of each banana cultivar was determined based on morphological descriptors that were conducted using Simmonds and Shepherd's genome-based nomenclature system (Simmonds and Shepherd 1955). Six genomic groups were identified: AA, AAA, AAB, ABB, AB, and BBB, based on a combination of diagnostic on 15 morphological traits (Slameto 2023). This non-molecular approach, while indicative, allows preliminary genome assignment for local cultivars.

Trait scoring and multivariate analysis

Quantitative and qualitative traits were converted into ordinal numerical values using a predefined scoring rubric. The 52 characters in detail with their character states and the scoring for every character are in the appendix. The compiled data matrix (cultivars × characters) served as the basis for multivariate analysis.

Two statistical techniques were applied, ie. Principal Component Analysis (PCA) — to identify key traits contributing to variation among cultivars. Cluster analysis using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) — based on Euclidean distance and Ward's linkage, both executed using PAST 4.1 software. The resulting dendrogram and PCA biplots were used to interpret phenetic relationships and assess the stability of cultivar groupings.

RESULTS AND DISCUSSION

Morpho-geographical and genomic passport data of *Musa* sp. cultivars

A total of 40 local banana (*Musa* spp.) cultivars were successfully documented across five major islands in North Maluku Province—Morotai, Halmahera, Ternate, Tidore, and Bacan—through intensive field surveys conducted from March to November 2024. These cultivars were identified through direct observation and interviews with local farmers. Each cultivar was classified based on habitat type (yard or moorland), banana type (dessert or cooking), distribution range within the province, and precise geolocation coordinates. The data provide a comprehensive morphogeographic snapshot of the region's banana diversity and serve as the foundation for subsequent phenetic analyses. Table 1 provides a complete list of the recorded cultivars, including their local names, habitat preferences, island-level distribution, and precise sampling coordinates (latitude and longitude). The presence of cultivars across multiple islands and ecological zones indicates a high level of morphogeographic diversity in the regional banana germplasm.

To elucidate the genomic structure of the documented cultivars, each cultivar was classified into one of four primary genome groups based on the morphological descriptor: AA/AAA, AAB, ABB, and AB. As shown in Figure 2, the AA/AAA group dominates the local banana population, comprising 52.5% (21 cultivars) of the total cultivars. These are typically diploid dessert bananas, many of which—such as Mas, Jarum, and Mulu Bebek—are widely cultivated in yard-based agroecosystems for fresh consumption. The AAB group accounts for 32.5% (13 cultivars), representing a mixture of dessert and cooking types, frequently found in both yard and moor habitats. Cultivars such as Atote, Woku, and Penganten fall under this group and are known for their agronomic adaptability across upland zones. The ABB group is less frequent, making up 12.5% (5 cultivars), and includes mostly cooking bananas such as Bandung and Sepatu. A single rare cultivar, Wai, was morphologically categorized under the AB group (2.5%), indicating limited hybrid characteristics.

Elevation is a key ecological factor influencing the distribution and adaptation of banana cultivars. To explore the altitudinal preferences of local *Musa* cultivars in North Maluku, each sampling site was geo-referenced and its elevation above sea level (masl) recorded using GPS tools. Figure 3 illustrates the vertical distribution of the 40 documented banana cultivars, ranging from 24 m to 162 masl, highlighting the presence of both lowland-and upland-adapted genotypes. Most cultivars (approximately 75%) were collected from low-elevation zones (<100 m), which correspond to coastal and yard-based agroecosystems, especially in Halmahera and Ternate. In contrast, a subset of cultivars—including Sarango, Raja Kecil, and Goroho Putih—were found at elevations exceeding 150 m, suggesting adaptation to upland ecological niches. This elevational distribution may reflect both natural selection pressures and local planting traditions based on landform and accessibility.

Multivariate delineation of morphological diversity among *Musa* sp. cultivars

To elucidate the phenotypic structure and morphological differentiation among 40 local *Musa* cultivars, a combined multivariate approach was employed, integrating Principal Component Analysis (PCA) and hierarchical cluster analysis (UPGMA). The analysis was based on 50 standardized morphological descriptors encompassing both quantitative and qualitative traits.

The PCA revealed that the first four Principal Components (PCs) accounted for a cumulative 80.21% of the total morphological variance (Table 2), providing a statistically robust basis for dimensional reduction and cultivar classification. PC1 and PC2, contributing 30.69% and 25.75% of the variance, are particularly effective in capturing the major gradients of phenotypic variation, providing clear and distinct results. The subsequent components, PC3 (13.59%) and PC4 (11.18%), contribute to finer-scale differentiation, while components beyond PC4 explain progressively marginal variance (<8%), consistent with the Kaiser-Guttman criterion and scree plot inflection.

Table 1. Local banana (*Musa* spp.) cultivars documented in North Maluku, Indonesia, including type, habitat, geographic distribution, and GPS coordinates

Cultivar's name	Type of banana	Habitat	Distribution in North Maluku	Sampling site
Ambon Galela	Desert	Yard	Hiri, Halmahera, Ternate, Tidore	0°46'21.8"N 127°18'10.7"E
Atote	Cooking	Yard	South Halmahera	0°21'21.8"N 127°25'53.0"E
Bandung	Cooking	Yard	Ternate, Tidore	0°38'24.3"N 127°26'00.7"E
Batu	Cooking	Moor	Halmahera	1°48'23.2"N 127°55'47.3"E
Dawaka	Cooking	Moor	Halmahera, Ternate, Tidore	0°41'51.3"N 127°22'35.4"E
Gaba	Cooking	Moor	Halmahera, Ternate, Tidore	0°50'32.3"N 127°22'18.1"E
Goba	Cooking	Yard	Tidore.	0°41'49.3"N 127°22'34.2"E
Goroho Ternate	Cooking	Moor	Halmahera, Ternate, Tidore	0°44'55.6"N 127°24'48.0"E
Goroho Manado	Cooking	Yard	Halmahera, Ternate, Tidore	0°51'32.6"N 127°20'39.9"E
Goroho Putih	Cooking	Moor	Halmahera, Ternate, Tidore	0°48'10.8"N 127°22'28.0"E
Irian	Cooking	Yard	Ternate	0°49'38.9"N 127°22'36.8"E
Jailolo	Cooking	Yard	Halmahera, Ternate, Tidore	0°37'49.9"N 127°22'50.3"E
Jarum	Desert	Yard	Halmahera, Ternate, Tidore Morotai	0°49'28.8"N 127°23'07.0"E
Kanaya	Desert	Moor	Ternate	0°50'01.2"N 127°22'32.7"E
Koi Manado	Cooking	Yard	North Halmahera	1°46'03.2"N 127°58'16.4"E
Mas	Desert	Yard	Hiri, Halmahera, Ternate, Tidore	0°41'35.9"N 127°27'11.0"E
Mas Biasa	Desert	Yard	Hiri, Halmahera, Ternate, Tidore	0°49'30.2"N 127°22'37.1"E
Mas Jarum	Dessert	Moor	Halmahera, Ternate, Tidore	0°45'35.5"N 127°19'02.1"E
Minyak	Cooking	Yard	Halmahera, Ternate, Tidore	0°49'10.8"N 127°23'22.2"E
Mulu Bebek	Cooking	Moor	Hiri, Halmahera, Morotai, Ternate, Tidore	1°03'16.7"N 127°25'42.6"E
Mulut Bebek Putih	Cooking	Yard	Hiri, Halmahera, Ternate, Tidore	0°49'29.9"N 127°22'40.8"E
Panta Kapal	Desert	Moor	Halmahera	0°46'41.3"N 127°38'31.4"E
Penganten	Cooking	Moor	Halmahera, Ternate	0°45'37.0"N 127°22'01.3"E
Perusahaan	Desert	Moor	Halmahera, Ternate	0°50'57.1"N 127°21'29.5"E
Pinang	Desert	Moor	North Halmahera	1°46'02.9"N 127°58'15.7"E
Raja	Desert	Moor	Halmahera, Ternate, Tidore	0°41'09.5"N 127°27'17.0"E
Raja Kecil	Desert	Yard	Halmahera, Ternate, Tidore	0°42'03.7"N 127°33'38.9"E
Sarango	Desert	Yard	North Halmahera	1°46'01.0"N 127°58'09.3"E
Sepatu	Cooking	Moor	Hiri, Halmahera, Morotai, Ternate, Tidore	0°37'59.4"N 127°22'46.8"E
Sepatu Putih	Cooking	Yard	Halmahera, Morotai, Ternate, Tidore	2°02'42.5"N 128°21'07.2"E
Seribu	Desert	Yard	Halmahera, Ternate, Tidore	0°43'38.6"N 127°23'21.6"E
Sun	Desert	Moor	Halmahera, Ternate	0°49'36.7"N 127°23'10.9"E
Susu	Desert	Yard	Halmahera, Ternate, Tidore	0°21'20.2"N 127°25'53.2"E
Sutra	Desert	Moor	West Halmahera	1°24'50.7"N 127°30'29.9"E
Takoapi	Cooking	Moor	Halmahera, Ternate, Tidore	0°40'04.9"N 127°21'56.4"E
Tanduk	Cooking	Moor	Halmahera, Ternate, Tidore	0°45'53.1"N 127°21'25.8"E
Tanduk Halmahera	Cooking	Moor	Halmahera, Ternate	0°44'04.4"N 127°34'11.7"E
Tembaga	Desert	Yard	Halmahera, Ternate, Tidore	0°41'52.9"N 127°22'33.3"E
Wai	Cooking	Yard	South Halmahera	0°21'24.6"N 127°25'50.3"E
Woku	Cooking	Yard	Halmahera, Ternate, Tidore	0°45'35.5"N 127°19'02.1"E

Table 2. Eigenvalues and variance explained by the first ten Principal Components (PCs) in the morphological dataset of banana cultivars

PC	Eigenvalue	Variance (%)
1	3.79	30.69
2	3.18	25.75
3	1.68	13.59
4	1.38	11.18
5	0.96	7.81
6	0.58	4.67
7	0.33	2.69
8	0.21	1.62
9	0.18	1.43
10	0.07	0.56

The PCA biplot (Figure 4) delineated four phenotypically distinct clusters (Groups A-D), reflecting divergent morphological syndromes among the cultivars. Group A (yellow ellipse) comprised morphologically unique genotypes such as Mulu Bebek Putih, Woku, Koi Manado, and Penganten, exhibiting extreme scores on the negative axes of PC1 and PC2. This group was primarily distinguished by bract pigmentation and other floral traits. Group B (black ellipse) encompassed predominantly cooking-type cultivars (e.g., Sepatu, Dawaka, Bandung), unified by leaf architectural traits, notably the incurved and overlapping margins of the petiole canal. Group C (red ellipse) included Ambon Galela, Takoapi, Minyak, and others, which exhibited moderate divergence along PC2 and PC3, largely associated with intermediate pseudostem morphology. Group D (blue ellipse) represented the largest and most continuous cluster, incorporating both dessert and cooking bananas (e.g., Mas, Goroho, Pantakapal), sharing overlapping genomic constitutions (predominantly AA/AAA and AAB genomes).

Table 3 revealed the loading analysis, which identified the ten most discriminative morphological traits, with petiole canal structure (PC1 = 0.5731), fruit shape in transversal view (PC2 = 0.5963; PC3 = −0.6168), and bract pigmentation (PC2-PC3) showing the highest absolute loadings. Notably, pseudostem height loaded strongly and negatively on PC4 (−0.5903), indicating its contribution to higher-order variation. These features were critical in structuring the cultivar space in the principal component domain.

Complementing the ordination analysis, a hierarchical clustering procedure was conducted using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) based on Euclidean distance matrices (Figure 5). The resulting dendrogram revealed hierarchical relationships consistent with the PCA-defined clusters, further supporting the presence of structured morphological differentiation across the dataset. While several clusters were congruent with genomic classifications (e.g., AA/AAA, AAB), the overall phenetic pattern indicated that morphological similarity does not always align strictly with genome constitution. This decoupling may reflect the influence of local selection pressures, microenvironmental adaptation, and potential somaclonal variation, underscoring the dynamic nature of banana domestication and diversification in the region. The integration of PCA and UPGMA thus provides a robust and multidimensional framework for elucidating phenetic relationships among *Musa* cultivars and offers valuable implications for their classification, conservation, and utilization in breeding programs, thereby intriguing the scientific community with the ever-evolving nature of banana domestication and diversification.

Table 3. Loadings of key morphological traits on the first four PCs

Important characters	PC 1	PC 2	PC 3	PC 4
Genome	0.3651	-0.2571	-0.0413	-0.2880
High of pseudostem	0.3225	-0.1601	-0.0376	-0.5903
Petiole canal leaf	0.5731	-0.3146	0.1795	0.3675
Colour leaf upper	0.1982	-0.1296	0.0988	0.3364
Shape leaf base	-0.2270	-0.1062	0.1715	0.4633
Colour bract outer	0.2428	0.3671	0.6111	-0.1204
Colour bract inner	0.2012	0.5103	0.3567	0.0363
Fruit length	0.2425	-0.1283	-0.0683	0.1945
Fruit circumference	0.2719	-0.1184	-0.1994	0.1408
Fruit shape in transversal view	0.3335	0.5963	-0.6168	0.1796

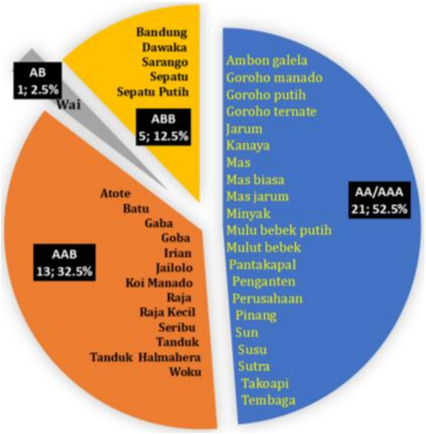

Figure 2. Distribution of banana genome groups (AA/AAA, AAB, ABB, AB) based on morphological classification of 40 cultivars from North Maluku, Indonesia

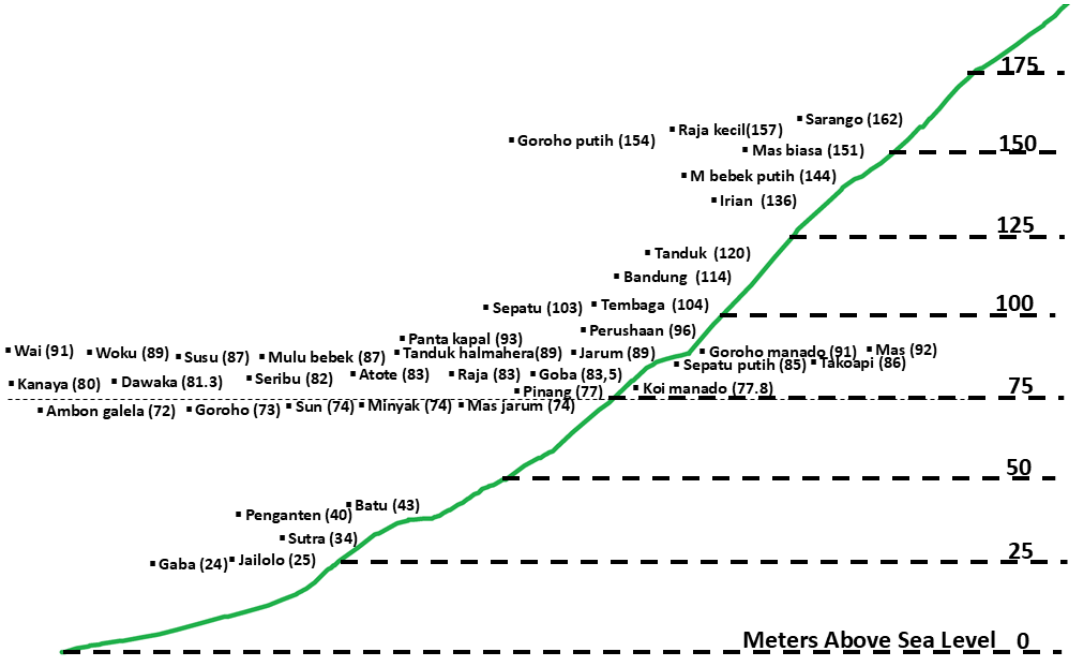

Figure 3. Altitudinal distribution of 40 banana cultivars (*Musa* spp.) collected across North Maluku Province. Elevation measured in meters above sea level (masl)

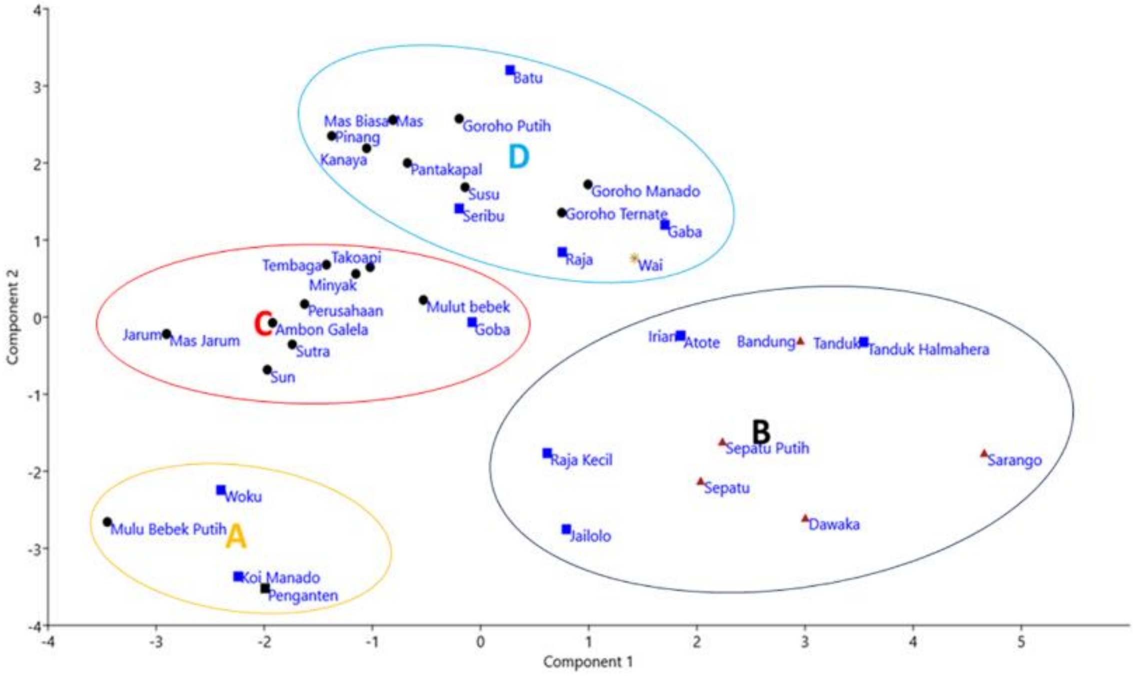

Figure 4. Principal Component Analysis (PCA) of 40 banana cultivars (*Musa* spp.) based on 50 morphological traits. Four major morphotype clusters (A-D) were identified

Discussion

Morpho-geographical diversity and genomic structure

The documentation of 40 *Musa* cultivars across five major islands in North Maluku highlights remarkable morpho-geographical diversity within a relatively compact island system. This variation is evident in cultivar nomenclature, morphological differentiation, and ecological adaptability across altitudinal gradients (24-162 masl). The spatial heterogeneity of cultivars such as Mas, Goroho, and Mulu Bebek suggests multiple domestication trajectories and regionally embedded selection processes, as similarly reported in East Java (Hapsari et al. 2018) and East Kalimantan (Sunaryo et al. 2020). The coexistence of these cultivars across yard and moorland agroecosystems further reflects cultural adaptability and polyfunctional use, in accordance with Meitha et al. (2020).

Genome profiling based on morphological traits revealed a predominance of AA/AAA (52.5%) and AAB (32.5%) genomic groups, in line with broader South-east Asian patterns (Rouard et al. 2018). These genome types have long been selected for fresh consumption, ease of vegetative propagation, and favorable agronomic traits. The underrepresentation of AB hybrids (2.5%) may indicate historical isolation or limited introgression from *Musa balbisiana*, as discussed by Mertens et al. (2021). These results support the hypothesis proposed by Christelová et al. (2017) that the Maluku region functions as a micro-refugium for ancestral and locally adapted *Musa* germplasm within the wider "Indonesian triangle" of banana diffusion.

Ecological adaptation and phenotypic plasticity

Altitudinal distribution analysis (Figure 3) revealed that most cultivars occupy zones below 100 m, typically associated with coastal agricultural systems. Nonetheless, accessions such as Sarango, Raja Kecil, and Goroho Putih were found above 150 m, indicating significant ecological amplitude. This lack of a strict correlation between genome group and elevation, also observed by Wahyudi et al. (2020), points to the limited role of topography in constraining morphological diversity. The widespread occurrence of A-genome cultivars across various elevations echoes findings from Poerba et al. (2019) and Hapsari et al. (2022), further supporting the notion that both environmental gradients and cultural selection influence cultivar distribution. Such ecological plasticity reflects local adaptation mechanisms, with implications for breeding programs targeting variable agroecological conditions.

Morphotype structuring and genotype-phenotype decoupling

Multivariate analyses (PCA and UPGMA) revealed four phenotypically distinct cultivar clusters (Groups A-D), explaining over 80% of total morphological variance. Group A (Mulu Bebek Putih, Woku) exhibited distinct upland morphotypes, possibly influenced by moisture availability and wind exposure, similar to patterns in *Musa balbisiana* (Mertens et al. 2021). Group B (Sepatu, Bandung, Tanduk Halmahera) included mid-elevation cooking bananas with semi-erect leaf posture and robust pseudostems. Group C represented transitional morphotypes with mixed genome affiliations. Group D, the largest group, included both dessert and cooking types (Mas, Goroho, Pantakapal), reflecting phenotypic plasticity and likely hybrid convergence.

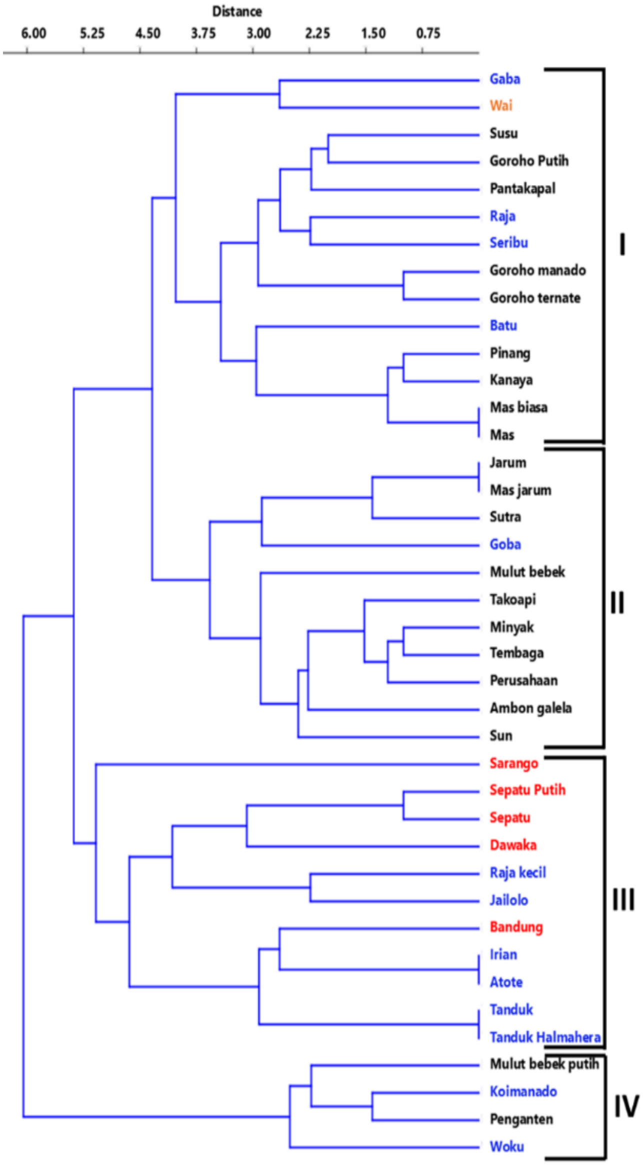

Figure 5. UPGMA dendrogram showing phenetic relationships among 40 *Musa* cultivars based on Euclidean distance using standardized morphometric data. The colors in the cultivar names indicate the respective genomes. AA/AAA: Black, AAB: Blue, ABB: Red, AB: Orange

Trait loadings from the first four principal components (Table 3) identified key morphological contributors that shaped this clustering pattern. Notably, petiole canal leaf structure had a high loading on PC1 (0.5731), fruit shape in transversal view showed contrasting loadings on PC2 (0.5963) and PC3 (-0.6168), while pseudostem height strongly influenced PC4 (-0.5903). These traits played central roles in cultivar separation within the PCA space and correspond to visual groupings observed in the biplot. Their influence supports the robustness of morphological clustering as a reflection of underlying phenotypic architecture.

A notable finding is the discrepancy between phenotypic clustering and genomic classification, revealing a genotype-phenotype decoupling. This aligns with previous reports on the influence of somaclonal variation (Sardos et al. 2022), epigenetic modulation (Rouard et al. 2018), and repeated hybridization events during domestication (Perrier et al. 2019). For example, Sarango (AAB) grouped with ABB-like cultivars such as Sepatu Putih, indicating morphological convergence driven by environmental adaptation or farmer preference (Meitha et al. 2020).

The UPGMA dendrogram further confirmed the phenetic groupings. Cultivars like Goroho Manado, Goroho Ternate, and Gaba clustered closely, likely reflecting frequent co-cultivation and shared morphological traits. Early-diverging accessions such as Penganten and Mulu Bebek Putih formed basal clades, consistent with the divergence observed in molecular studies (Dwivany et al. 2020). The reliability of this phenetic structure is further supported by similar hierarchical patterns found in molecular marker studies (Suparman et al. 2023).

Conservation and breeding implications

The morphological and genomic diversity documented in this study carries important implications for conservation planning and genetic improvement strategies. In situ conservation is urgently needed for rare and morphologically distinct landraces, such as Wai (AB) and Mulu Bebek Putih (AAB), to prevent erosion through landscape transformation or varietal homogenization. A core collection framework, as proposed by Sardos et al. (2022), can leverage PCA-UPGMA groupings to select representative accessions for germplasm repositories and ex situ conservation. Cultivars from Groups A and D, which show either upland adaptability or broad morphological plasticity, are excellent candidates for breeding climate-resilient cultivars in response to environmental stressors.

Although morphological classification provides an essential foundation, its resolution remains limited. Therefore, the integration of molecular markers (e.g., ISSR, SCoT, ITS, RAPD) is recommended to validate clonal identity and lineage structure (Wahyudi et al. 2020; Fajri et al. 2024). Longitudinal studies are also needed to monitor the impact of land-use changes, climatic variability, and cultivar turnover on genetic integrity (Akech et al. 2024; Chase et al. 2025).

In conclusion, this study demonstrates that the morphological and genomic diversity of *Musa* cultivars in North Maluku reflects complex domestication histories, ecological adaptations, and ongoing cultural selection. The integration of PCA and UPGMA analyses revealed four phenotypically distinct groups, each representing a unique set of traits and characteristics. These groups with clear yet non-parallel alignment to genomic classifications provide a comprehensive understanding of the diversity within the *Musa* cultivars. This genotype-phenotype decoupling highlights the dynamic processes shaping banana diversity in insular South-East Asia.

From an applied perspective, the results have three direct implications. Core collection design should prioritize cultivars that represent the extremes of morphological variation, such as Mulu Bebek Putih from Group A and Goroho or Mas from Group D, as representative accessions for Genebanks and breeding initiatives. In terms of conservation zoning, upland sites where morphologically unique cultivars—such as Penganten and Sarango—were recorded should be designated as in situ conservation areas to safeguard rare landraces from loss due to landscape transformation or varietal homogenization. For breeding applications, high-altitude and phenotypically plastic cultivars with AA and AAB genomic backgrounds—such as Goroho Putih or Sarango—represent promising sources of tolerance to environmental stress, and can be targeted for hybridization or introgression to enhance resilience in future banana cultivars. This research underscores the strategic importance of North Maluku as a microcenter of banana diversity. Future integration with molecular genotyping and trait-based phenomics will be essential to validate lineage hypotheses and unlock the full potential of local landraces for food security and crop improvement, a promising prospect for the future.

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REFERENCES

Akech V, Bengtsson T, Ortiz R, Swennen R, Uwimana B, Ferreira CF, Amah D, Amorim EP, Blisset E, den Houwe IV, Arinaitwe IK, Nice L, Bwesigye P, Tanksley S, Uma S, Suthanthiram B, Saraswathi MS, Mduma H, Brown A. 2024. Genetic diversity and population structure in banana (*Musa* spp.) breeding germplasm. Plant Genome 17 (3): e20497. DOI: 10.1002/tpg2.20497.

BPS [Badan Pusat Statistik]. 2022. Produksi Tanaman Buah-buahan 2022. https://www.bps.go.id/indicator/55/62/1/produksi-tanaman-buah-buahan.html. [Indonesian]

Chase RR, Borrell JS, Rodenburg J, Roux N, Wendawek A, Büchi L. 2025. Farmer selection of drought-tolerant enset landraces reduces trait diversity in drier environments. Plants People Planet 2025: 1-15. DOI: 10.1002/ppp3.70032.

Christelová P, De Langhe E, Hřibová E, Čížková J, Sardos J, Hušáková M, Van den houwe I, Sutanto A, Kepler AK, Swennen R, Roux N, Doležel J. 2017. Molecular and cytological characterization of the global *Musa* germplasm collection provides insights into the treasure of banana diversity. Biodivers Conserv 26: 801-824. DOI: 10.1007/s10531-016-1273-9.

Dwivany FM, Stefani G, Sutanto A, Nugrahapraja H, Wikantika K, Hiariej A, Hidayat T, Rai IN, Sukriandi N. 2020. Genetic relationship between tongka langit bananas (*Musa troglodytarum* L.) from Galunggung and Maluku, Indonesia, based on ITS2. Hayati J Biosci 27 (3): 258-265. DOI: 10.4308/hjb.27.3.258.

Fajri H, Sunandar A, Qurbaniah M. 2024. Phylogenetic analysis of wild bananas (*Musa* spp.) in West Kalimantan, Indonesia, based on maturase K (*mat*K) genes. Biodiversitas 25 (8): 2612-2618. DOI: 10.13057/biodiv/d250833.

FAO [Food and Agriculture Organization of the United Nations]. 2022. Food Outlook - Biannual Report on Global Food Markets (June 2022). FAO, Rome.

Hapsari L, Azrianingsih R, Arumingtyas EL. 2018. Genetic variability and relationship of banana cultivars (*Musa* L.) from East Java, Indonesia based on the Internal Transcribed Spacer Region nrDNA sequences. J Trop Biol Conserv 15: 101-120. DOI: 10.51200/jtbc.v15i0.1482.

Hapsari L, Damaiyani J, Yulistyarini T, Auliya I, Gusmiati LH, Zaro RM. M. 2022. Characterization, potential and conservation of Pisang Kates (*Musa* cv. ABB), a unique local banana cultivar from Pasuruan, East Java, Indonesia. Biodiversitas 23 (7): 3521-3532. DOI: 10.13057/biodiv/d230727.

Hendaru IH, Hidayat Y, Ramdhani M. 2017. Morphological character of seven accessions of banana from North Maluku. Bul Plasma Nutfah 23 (1): 13-22. [Indonesian]

International Trade Centre. 2021. Trade Map - Banana exports by country (HS 0803). https://www.trademap.org/

IPGRI-INIBAP/CIRAD. 1966. Descriptors for Banana (*Musa* spp.). https://www.bioversityinternational.org/e-library/publications/detail/descriptors-for-banana-musa-spp/.

Ishak H, Nursjafani N, Lestari S. 2019. Utilization of banana skin (*Musa pariciae*) silage for increasing the productivity of pea goats (*Capra hircus*): Case study in Golo Village, Sahu District, West Halmahera Regency. Agrikan: J Agribisnis Perikanan 12 (2): 279-283. DOI: 10.29239/j.agrikan.12.2.279-283. [Indonesian]

Iskandar J, Kusmoro J, Mubarokah M, Partasasmita R. 2018. Ethnobotany of banana plants (*Musa* x *paradisiaca*) of Palintang Hamlet, Cipanjalu Village, Bandung, West Java, Indonesia. Biodiversitas 19 (6): 2059-2072. DOI: 10.13057/biodiv/d190611.

Li L-F, Ge X-J. 2017. Origin and domestication of cultivated banana. Ecol Genet Genom 2: 1-2. DOI: 10.1016/j.egg.2016.10.001.

Lumba R, Djarkasi GSS, Molenaar R. 2017. Modification of the Halmahera indigenous "Mulu Bebe" plantain (*Musa acuminata*) flour as a source of prebiotics food. Jurnal Teknologi Pertanian 8 (1): 1-16. [Indonesian]

Meitha K, Fatmawati I, Dwivany FM, Sutanto A, Pratama SN, Nugrahapraja H, Wikantika K. 2020. Phylogenetic analysis of 23 accessions of Indonesian banana cultivars based on Internal Transcribed Spacer 2 (ITS2) region. Indonesian J Biotechnol 25 (1): 1-11. DOI: 10.22146/ijbiotech.49506.

Mertens A, Bawin Y, Abeele SV, Kallow S, Vu DT, Le LT, Vu TD, Swennen R, Vandelook F, Panis B, Janssens SB. 2021. Genetic diversity and structure of *Musa balbisiana* populations in Vietnam and its implications for the conservation of banana crop wild relatives. PLoS One 16 (6): e0253255. DOI: 10.1371/journal.pone.0253255.

Perrier X, Jenny C, Bakry F, Karamura D, Kitavi M, Dubois C, Hervouet C, Philippson G, De Langhe E. 2019. East African diploid and triploid bananas: A genetic complex transported from South-East Asia. Ann Bot 123 (1): 19-36. DOI: 10.1093/aob/mcy156.

Poerba YS, Martanti D, Ahmad F, Herlina, Handayani T, Witjaksono. 2018. Deskripsi Pisang: Koleksi Pusat Penelitian Biologi Lembaga Ilmu Pengetahuan Indonesia (LIPI). LIPI Press, Jakarta. [Indonesian]

Poerba YS, Martanti D, Ahmad F. 2019. Genetic variation of Wild *Musa acuminata* Colla from Indonesia. Biotropia 26 (2): 115-126. DOI: 10.11598/btb.2019.26.2.896.

Premjet D, Boonsrangsom T, Sujipuli K, Rattanasut K, Kongbungkerd A, Premjet S. 2022. Morphological and molecular characterizations of *Musa* (ABB) 'Mali-Ong' in Thailand. Biology 11 (10): 1429. DOI: 10.3390/biology11101429.

Probojati RT, Wahyudi D, Hapsari L. 2019. Clustering analysis and genome inference of *Pisang Raja* local cultivars (*Musa* spp.) from Java Island by Random Amplified Polymorphic DNA (RAPD) marker. J Trop Biodivers Biotechnol 4: 42-53. DOI: 10.22146/jtbb.44047.

Rouard M, Droc G, Martin G, Sardos J, Hueber Y, Guignon V, Cenci A, Geigle B, Hibbins MS, Yahiaoui N, Baurens F-C, Berry V, Hahn MW, D'Hont A, Roux N. 2018. Three new genome assemblies support a rapid radiation in *Musa acuminata* (wild banana). Genome Biol Evol 10 (12): 3129-3140. DOI: 10.1093/gbe/evy227.

Sardos J, Breton C, Perrier X, Van den Houwe I, Carpentier S, Paofa J, Rouard M, Roux N. 2022. Hybridization, missing wild ancestors and the domestication of cultivated diploid bananas. Front Plant Sci 13: 969220. DOI: 10.3389/fpls.2022.969220.

Sardos J, Christelová P, Čížková J, Paofa J, Sachter-Smith GL, Janssens SB, Rauka G, Ruas M, Daniells JW, Doležel J, Roux N. 2018. Collection of new diversity of wild and cultivated bananas (*Musa* spp.) in the autonomous region of Bougainville, Papua New Guinea. Genet Resour Crop Evol 65: 2267-2286. DOI: 10.1007/s10722-018-0690-x.

Simmonds NW, Shepherd K. 1955. The taxonomy and origins of the cultivated bananas. J Linn Soc London Trans 55 (359): 302-312. DOI: 10.1111/j.1095-8339.1955.tb00015.x.

Singh LJ, Dwivedi MD, Kasana S, Naik MC, Ekka GA, Pandey AK. 2020. Molecular systematics of the genus *Musa* L. (Zingiberales: Musaceae) in Andaman and Nicobar Islands. Biologia 75: 1825-1843. DOI: 10.2478/s11756-020-00552-5.

Slameto S. 2023. Genetic diversity and molecular analysis using RAPD markers of banana cultivars in the five regions of East Java, Indonesia. Biodiversitas 24: 5035-5043. DOI: 10.13057/biodiv/d240947.

Sunaryo W, Wahida, Idris SD, Pratama AN, Ratanasut K, Nurhasanah. 2020. Genetic relationships among cultivated and wild bananas from East Kalimantan, Indonesia based on ISSR markers. Biodiversitas 21 (2): 824-832. DOI: 10.13057/biodiv/d210250.

Suparman S, Pornpongrungrueng P, Chantaranothai P. 2023. Molecular studies of coralberry (*Ardisia crenata* Sims; Primulaceae) from Thailand based on SCoT markers. Biodiversitas 24 (6): 3183-3189. DOI: 10.13057/biodiv/d240611.

Wahyudi D, Rifliyah K, Uslan. 2020. Genome evaluation of banana cultivars based on morphological character and Inter-Simple Sequence Repeat (ISSR) molecular marker. Biodiversitas 21 (7): 2982-2990. DOI: 10.13057/biodiv/d210715.