

Morphological Diversity of Eight Bird's Eye Chili (*Capsicum* spp.) Accessions Evaluated on Peatland in Palangka Raya, Indonesia

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Keyword:

Capsicum spp, Morphological
rharacterization, Principal component
analysis, UPGMA clustering, Peatland.

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ABSTRACT

Bird's eye chili (*Capsicum* spp.) is an important horticultural crop in Palangka Raya, Central Kalimantan, but the morphological profiles of farmer-grown accessions remain insufficiently documented. This study characterized qualitative morphological variation in eight accessions and explored their patterns of similarity. The accessions comprised three commercial cultivars (Rawita F1, Tiger, and Tiung) and five local accessions (P1–P5). Thirty-six qualitative UPOV descriptors were recorded, with 21 representative traits presented in the tables. The coded data were examined using principal component analysis (PCA) and hierarchical cluster analysis. The first two principal components explained 60.54% of the variation in the coded dataset, with PC1 and PC2 accounting for 36.11% and 24.43%, respectively. Traits associated with accession separation included fruit shape, anthocyanin-related characteristics, leaf variegation, and leaf-surface features. At the 60% similarity level, the UPGMA dendrogram based on Gower similarity separated the accessions into three clusters: P5 formed a single-accession cluster, P1 grouped with P4, and Tiung, Tiger, P2, P3, and Rawita F1 formed the third cluster. P3 and Rawita F1 showed the closest morphological association within the third cluster. These findings document phenotypic differences among the evaluated accessions but do not establish genetic relationships or demonstrate adaptation to peatland. Further research should include replicated plants per accession, quantitative agronomic traits, and molecular markers.

INTRODUCTION

Bird's eye chili (*Capsicum* spp.) is an economically important horticultural crop in Indonesia and is widely used in household consumption and food products. Chili fruits contain bioactive compounds, including vitamins, flavonoids, phenolic compounds, carotenoids, and capsaicinoids, that contribute to their nutritional and functional properties (Khanema et al., 2024; Mohammadi, 2025). These characteristics support the crop's importance for agricultural livelihoods and food systems, including in Central Kalimantan.

The availability of diverse plant genetic resources provides a foundation for developing improved cultivars (Verma et al., 2024). Morphological characterization helps researchers document phenotypic variation among accessions and identify distinctive traits for further evaluation (Khatun et al., 2022). Standardized descriptors developed by the International Union for the Protection of New Varieties of Plants (UPOV, 2020) also facilitate consistent observations and comparisons among plant materials. However, morphological characteristics reflect both genetic differences and environmental influences. Researchers should therefore distinguish observed phenotypic variation from confirmed

genetic diversity and avoid interpreting morphological traits alone as evidence of environmental adaptation.

Multivariate statistical methods can summarize complex morphological datasets and reveal patterns of variation among accessions. Principal component analysis (PCA) reduces the dimensionality of a dataset while retaining information about variation, whereas hierarchical cluster analysis groups accessions according to a selected similarity or distance measure (Jolliffe & Cadima, 2016; Naveen et al., 2024). Researchers must select and apply these methods according to the nature of the observed variables. In particular, conventional PCA requires careful consideration when researchers encode qualitative descriptors numerically, because arbitrary codes for nominal categories may introduce relationships that do not reflect the underlying characteristics. The coding procedure and its implications for component interpretation should therefore be stated explicitly.

Palangka Raya, Central Kalimantan, contains peatland areas used for agricultural production, including chili cultivation. Peat soils can present agricultural constraints, including high acidity and limited nutrient availability (Jaya et al., 2022). Farmers cultivate bird's eye chili in this region, but information describing the qualitative morphological variation of farmer-grown accessions remains limited within the scope of the literature reviewed for this study. Documenting these accessions can establish a local phenotypic baseline and identify distinctive morphological characteristics for subsequent investigation. Nevertheless, morphological characterization alone cannot determine whether a trait provides an adaptive advantage under peatland conditions. Such a conclusion would require comparative environmental assessments, replicated evaluations, and relevant agronomic measurements.

This study aimed to characterize qualitative morphological variation among eight bird's eye chili (*Capsicum* spp.) accessions collected from farmer-grown populations in Palangka Raya using UPOV descriptors. It also explored patterns of accession differentiation through PCA and hierarchical cluster analysis. By documenting the observed morphological characteristics and examining their multivariate patterns, this study provides an initial description of the evaluated accessions. The findings are intended to support further characterization and selection research, rather than to establish genetic relationships or demonstrate adaptation to peatland environments..

MATERIALS AND METHODS

Study Area

The study was conducted from April to June 2026 at the Experimental Farm of the Department of Agrotechnology, Faculty of Agriculture, Universitas Palangka Raya, Central Kalimantan, Indonesia. The experimental field is located on peatland with high organic matter content and acidic soil conditions.

Materials and Data Sources

Eight bird's eye chili (*Capsicum* spp.) accessions commonly cultivated by farmers in Palangka Raya were included: three commercial cultivars (Rawita F1, Tiger, and Tiung) and five farmer-grown accessions of unknown varietal identity (P1–P5). The accessions were sourced from eight farmers in major chili-growing areas of Palangka Raya. For each accession, one plant representing the predominant phenotype in the farmer population was selected at the generative stage and established at the experimental farm for morphological observation under uniform conditions. Consequently, each accession was represented by a single plant. The design therefore describes the selected plants and does not estimate the range of variation within each accession or farmer population.

Research Design

This descriptive study compared qualitative morphological traits among the eight selected accessions. The analysis was intended to document phenotypic differences and explore patterns of similarity among accessions; it was not designed to test treatment effects, estimate within-accession variability, or assess adaptation to different environments.

Data Collection and Analysis

Morphological observations covered plant architecture, stem characteristics, leaf morphology, floral traits, and fruit characteristics using the UPOV guideline for *Capsicum* spp. (International Union for the Protection of New Varieties of Plants, 2020). The study recorded 36 qualitative descriptors, of which 21 representative traits are presented in Tables 1–3. Character states were converted to numerical codes for multivariate analysis. Because the descriptors include categorical states, the coding scheme is important for interpreting the resulting multivariate patterns.

PCA was used to explore patterns in the numerically coded descriptor matrix, and the first two components were plotted to visualize relationships between accessions and traits. Given the qualitative nature of the descriptors and the small number of accessions, the PCA results were interpreted as exploratory. Hierarchical clustering was based on the Gower similarity coefficient and the UPGMA method, as reported in the dendrogram and cluster results. All analyses were conducted using PAST software.

RESULTS AND DISCUSSION

Qualitative characters

Morphological characterization revealed variations in several qualitative traits among the eight chili accessions evaluated. Although 36 qualitative descriptors were recorded according to the UPOV guideline for *Capsicum* spp., only 21 representative traits are presented in this study to summarize the observed phenotypic diversity. These traits are vegetative and reproductive characteristics and serve as important descriptors for distinguishing chili accessions. The distribution of qualitative traits among accessions is shown in Tables 1–3.

Table 1. Plant habit, stem anthocyanin intensity at nodes, stem hairiness at nodes, leaf shape, leaf green colour intensity, leaf-margin undulation, and leaf blistering

Acc	Plant: Habit	Stem: Intensity of Anthocyanin of nodes	Stem: Hairiness of Nodes	Leaf: Shape	Leaf: Intensity of Green Color	Leaf: Undulation of Margin	Leaf: Blistering
Rawita F1	Upright	Medium	Weak	Ovate	Strong	Very Weak	Very Weak
Tiung	Semi upright	Very Weak	Strong	Ovate	Very Strong	Strong	Strong
Tiger	Upright	Very Weak	Very Weak	Ovate	Medium	Strong	Strong
P1	Upright	Strong	Very Weak	Ovate	Very Strong	Very Weak	Very Weak
P2	Upright	Very Weak	Strong	Ovate	Strong	Strong	Strong
P3	Upright	Very Weak	Weak	Ovate	Medium	Medium	Strong
P4	Semi upright	Weak	Strong	Ovate	Strong	Strong	Medium
P5	Semi upright	Weak	Weak	Ovate	Medium	Medium	Very Weak

Table 2. Leaf glossiness, flower peduncle attitude, flower colour, anthocyanin in the anther and filament, immature fruit colour, and fruit attitude

Acc	Leaf: Glossiness	Flower: Attitude of Peduncle	Flower Color	Anthocyanin in anther	Anthocyanin in Filament	Immature fruit Color	Fruit: Attitude
Rawita F1	Weak	Semi Drooping	White	Absent	Present	Yellowish green	Erect
Tiung	Medium	Erect	White	Absent	Absent	Whitish yellow	Erect
Tiger	Very Weak	Drooping	White	Absent	Absent	Yellowish green	Horizontal
P1	Medium	Drooping	White	Present	Absent	Green	Drooping
P2	Medium	Erect	White	Present	Present	Yellowish green	Drooping
P3	Weak	Erect	White	Present	Present	Yellowish green	Erect
P4	Very Weak	Drooping	White	Present	Present	Green	Drooping
P5	Weak	Semi Drooping	White	Present	Present	Green	Drooping

Table 3. Fruit shape, pericarp sinuosity at the basal part, fruit apex shape, fruit surface texture, mature fruit colour, capsaicin in the placenta, and fruit glossiness

Acc	Fruit: Shape	Fruit: Sinuation of Pericarp at basal part	Fruit: Shape of Apex	Fruit: Texture of Surface	Mature Fruit Color	Fruit: Capsaicin in Placenta	Fruit: Glossiness
Rawita F1	Trapezoidal	Weak	Moderately depressed	Slightly wrinkled	Red	Present	Medium
Tiung	Triangular	Medium	Moderately acute	smooth	Red	Present	Medium
Tiger	Triangular	Very Weak	Moderately acute	smooth	Red	Present	Medium
P1	Triangular	Medium	Very acute	Slightly wrinkled	Red	Present	Medium
P2	Rectangular	Medium	Very depressed	Slightly wrinkled	Red	Present	Medium
P3	Rectangular	Weak	Moderately acute	smooth	Red	Present	Medium
P4	Triangular	Strong	Very acute	Slightly wrinkled	Red	Present	Medium
P5	Triangular	Medium	Rounded	smooth	Red	Present	Medium

Principal Component Analysis

Principal component analysis (PCA) was used to summarize variation in the coded morphological dataset (Singh et al., 2020b; Hair et al., 2019). Seven components were obtained, with PC1 explaining 36.11% of the variation and PC2 explaining 24.43%. Together, the first two components accounted for 60.54% of the total variation, while the first three accounted for 74.62% (Table 4). Similar applications of multivariate analysis have demonstrated its usefulness in characterizing morphological diversity among chili accessions and cultivars (Amalia et al., 2023; Sahid et al., 2022). Nevertheless, the interpretation of PCA depends on the measurement scale and coding of the original variables. When nominal categories receive numerical codes, conventional PCA may imply numerical relationships that do not reflect the underlying categorical structure; categorical PCA provides an alternative for analyzing categorical variables (Linting et al., 2007). In addition, component structures may vary with the characteristics and size of the dataset, making validation important when interpreting PCA results (Jolliffe & Cadima, 2016; Costa et al., 2014). Given that this study included only eight accessions and used coded qualitative descriptors, the component patterns should be interpreted as exploratory and conditional on the coding scheme. Although the first two components summarize a substantial proportion of the variation represented in this dataset, the explained variance alone does not establish genetic relationships among accessions. The findings should therefore be interpreted as evidence of morphological differentiation, consistent with previous studies of chili diversity based on morphological characteristics (Ramadhanti & Waluyo, 2021).

Table 4. Eigenvalues and percentage of variance explained by principal components

Principal Component	Initial Eigenvalue		
	Eigenvalue	% Variance	Cumulative (%)
PC1	55.6085	36.1090	36.1090
PC2	37.6249	24.4320	60.5410
PC3	21.6758	14.0750	74.6160
PC4	17.2130	11.1770	85.7930
PC5	11.7503	7.6300	93.4230
PC6	5.21744	3.3879	96.8109
PC7	4.91019	3.1884	100.00

The loading values in Table 5 indicate that PC1 was most strongly associated with anthocyanin in the anther, capsaicin in the placenta, anthocyanin on the filament, fruit shape, shortened internodes, and leaf blistering. PC2 was most strongly associated with leaf variegation and anthocyanin on the filament, followed by leaf blistering and leaf-margin undulation. These patterns suggest that fruit morphology, pigmentation, and leaf characteristics contributed to the separation of accessions within the coded morphological dataset. Similar studies have demonstrated the usefulness of multivariate analysis for characterizing morphological diversity among chili genotypes and cultivars (Amalia et al., 2023; Sahid et al., 2022). However, the interpretation of individual loadings requires caution because PCA results depend on the measurement scale and coding of the original variables (Jolliffe & Cadima, 2016; Linting et al., 2007). When qualitative descriptors represent nominal categories, arbitrary numerical coding may affect the relationships among variables and the resulting component structure. Therefore, the loading patterns in this study should be interpreted as exploratory indicators of morphological variation rather than definitive evidence of genetic relationships among accessions.

Table 5. Major loading values of PC1 and PC2

Character	PC1	PC2
Anthocyanin in anther	-0.410	-0.024
Capsaicin in placenta	0.384	-0.187
Anthocyanin on filament	-0.377	0.368
Fruit shape	0.343	0.229
Leaf variegation	-0.181	0.462
Anthocyanin of leaf surface	-0.278	-0.284
Leaf blistering	0.271	0.279
Undulation of margin	0.135	0.274
Shortened internodes	0.291	-0.252

The PCA biplot (Figure 1) provides an exploratory representation of the relationships between accessions and coded morphological traits. Tiger and Tiung lie on the positive side of PC1, whereas P2 is separated along the positive side of PC2 and is associated with leaf variegation and anthocyanin on the filament. P5 lies on the negative side of PC1 and is associated with anthocyanin-related traits, while P1 lies in the negative region of PC2. Rawita F1, P3, and P4 appear relatively close to the origin, suggesting that the first two principal components provide limited separation among these accessions. Similar multivariate approaches have been used to characterize morphological variation among chili genotypes and cultivars (Amalia et al., 2023; Sahid et al., 2022). Nevertheless, PCA biplots represent patterns in the variables included in the analysis, and their interpretation depends on the coding and scaling of those variables (Jolliffe & Cadima, 2016). Therefore, the observed positions should be interpreted as patterns of phenotypic similarity in the recorded morphological traits, rather than direct evidence of genetic relatedness or adaptation to peatland conditions. Assessing genetic relationships would require additional evidence, such as molecular markers, while claims about peatland adaptation would require replicated evaluations of agronomic performance under relevant environmental conditions.

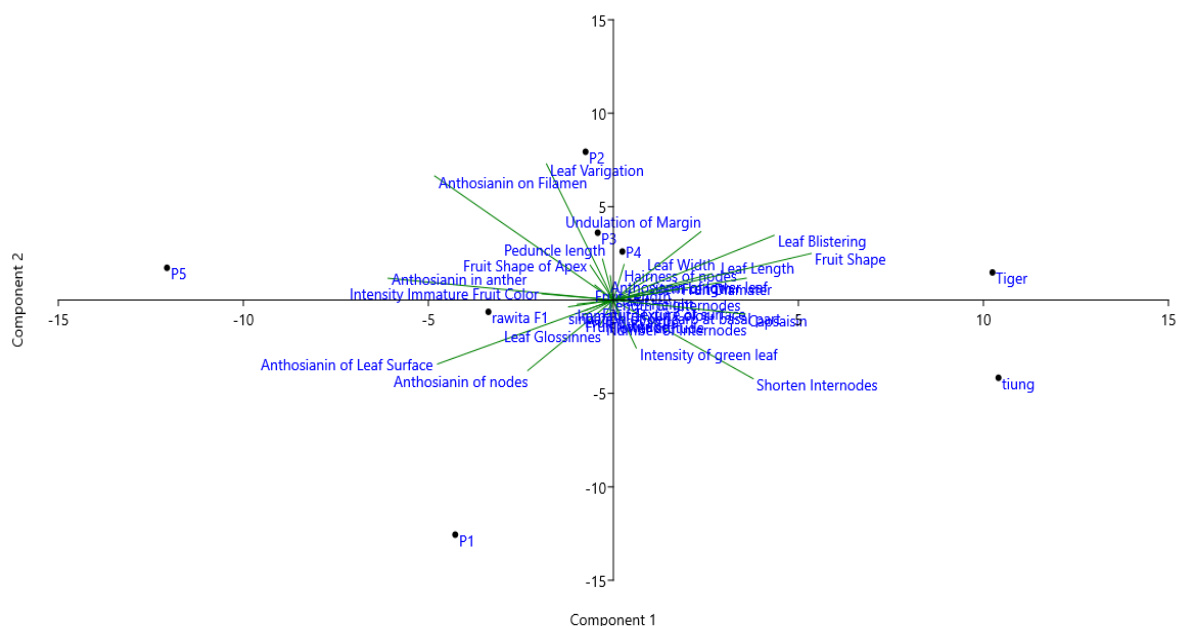


Figure 1. PCA biplot of eight bird's eye chili (*Capsicum* spp.) accessions based on coded qualitative morphological traits. Vectors indicate the direction and relative contribution of traits to the first two components.

Cluster Analysis

Hierarchical cluster analysis grouped the accessions according to their morphological similarity. The dendrogram was interpreted using the Gower similarity coefficient and the unweighted pair-group method with arithmetic mean (UPGMA) (Figure 2). Gower's coefficient provides a general measure of similarity that can accommodate different types of variables, including categorical descriptors, when the data are appropriately coded and consistently handled (Gower, 1971). Similar multivariate approaches have been applied to characterize diversity and classify chili genotypes cultivated on peatlands in Indonesia (Deviona et al., 2023). Cluster analysis has also been used to examine variation among plant accessions, although the interpretation of resulting groups depends on the data and analytical methods employed (Shrestha et al., 2022). In the present study, the clusters should therefore be interpreted as groups of accessions with similar recorded morphological characteristics rather than as definitive evidence of genetic relatedness. The validity of the grouping also depends on the consistency of the descriptor coding and the correct implementation of the selected similarity measure and clustering algorithm..

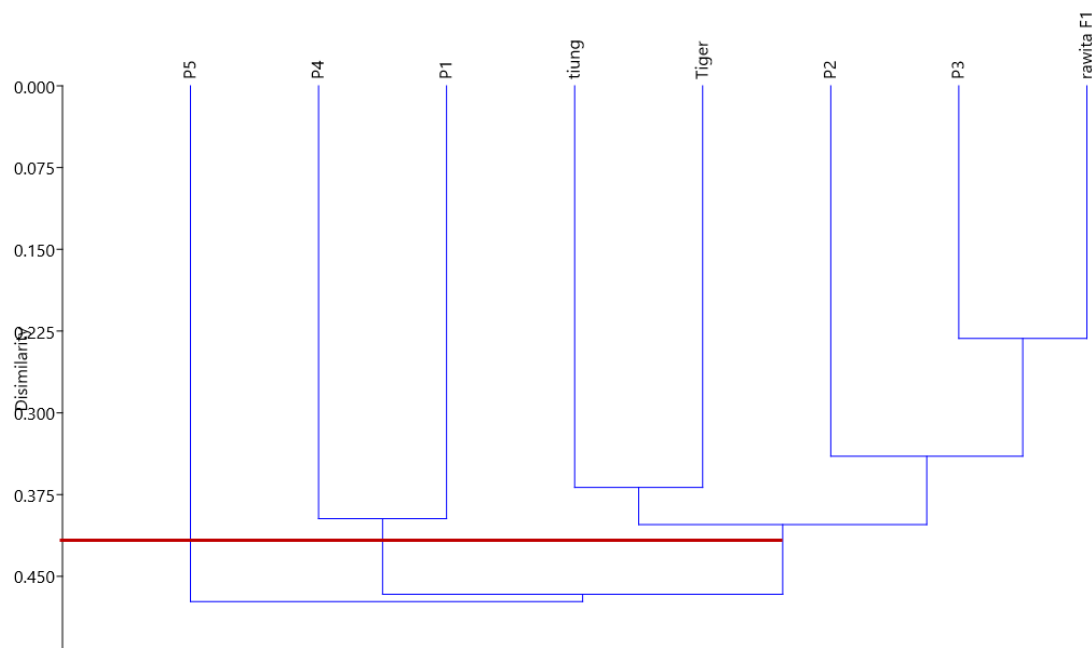


Figure 2. UPGMA dendrogram of eight bird's eye chili (*Capsicum* spp.) accessions based on Gower similarity.

At the 60% similarity level, the UPGMA dendrogram separated the eight accessions into three clusters. Cluster I contained P5; Cluster II contained P4 and P1; and Cluster III comprised Tiung, Tiger, P2, P3, and Rawita F1. Within Cluster III, P3 and Rawita F1 showed the closest morphological association. The separation of P5 into a single-member cluster indicates that it had a distinct morphological profile relative to the other accessions at the selected cut level, whereas P1 grouped with P4 despite exhibiting differences from several other accessions. Similarity-based clustering has been used to characterize variation among chili genotypes cultivated on peatlands in Indonesia (Deviona et al., 2023). However, cluster membership depends on the selected similarity measure, the coding of morphological descriptors, and the dendrogram cut level (Gower, 1971). Therefore, these results demonstrate differences in the observed morphological profiles rather than confirmed genetic divergence, because molecular markers were not included in this study. Further assessment using molecular markers and replicated morphological observations would help determine whether the observed patterns correspond to broader genetic differentiation among the accessions.

CONCLUSION

This study documented qualitative morphological variation among eight bird's eye chili (*Capsicum* spp.) accessions associated with farmer cultivation in Palangka Raya. The first two PCA components accounted for 60.54% of the variation in the coded dataset. Fruit shape, anthocyanin-related traits, leaf variegation, and leaf-surface characteristics contributed to the observed separation. At the 60% similarity level, UPGMA clustering based on Gower similarity placed P5 in a separate cluster, grouped P1 with P4, and placed Tiung, Tiger, P2, P3, and Rawita F1 in a third cluster. These results describe phenotypic differences among the accessions under the conditions evaluated; they do not establish genetic relationships or demonstrate adaptation to peatland. The use of one representative plant per accession limits the ability to characterize within-accession variation. Future studies should include replicated plants per accession, quantitative agronomic traits, repeated evaluation across environments, and molecular markers to assess genetic relationships and potential breeding value.

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