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Morphological characterization of papaya accessions in Jember through multivariate analysis

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Abstract

This study aimed to select the most informative morphological descriptors in characterizing and distinguishing papaya accessions in Jember. The multivariate analysis was used to i) determine the closeness between the papaya accessions collected based on morphology descriptors and ii) define a list of sufficient minimum descriptors to distinguish papaya accessions in Jember. Five quantitative and fifteen qualitative descriptors were used in evaluating 23 accessions. The data collected through quantitative descriptors were analyzed by the means of PCA-biplot analysis and qualitative descriptors were analyzed using entropy level. Statistical analysis was carried out by R studio software using two packages, i.e. biotools and factoextra packages. Based on the research results, the first two principal components of the PCA-biplot representation of 23 accessions were able to evaluate 67.18% of the total variability. The accessions located in KAL-SUK, GUM-PUR 1, and GUM-PUR 2 had similarities in tree diameter and width of mature leaf characters, while KAL-PLA, MUM-SUM 1, LED-SLA, MUM-LEN 1, SUM-RO 2, and SUM-JAM accessions shared similarities in the length of mature leaf, petiole, and peduncle. The minimum descriptors that could be used to characterize papaya plant accessions in Jember were two quantitative descriptors (tree diameter and length of mature leaf) and three qualitative descriptors (general shape of mature leaf teeth, height to first fruit, and stem color). The combination of quantitative-qualitative descriptors allowed the simple and rapid characterization of papaya accession. In addition, it could reduce costs and labor without losing information in the characterization of papaya plants.

INTRODUCTION

Papaya (Carica papaya L.) is a herbaceous fruit plant from the family of Caricaceae. Papaya is classified as a non-seasonal plant and could bear fruit at any time. Papaya fruit is widely popular due to its sweet taste and nutrients and vitamins content (Febjislami et al., 2018). Papaya has the potential to be developed as a fresh fruit as well as an industrial raw material. Papaya fruit is currently widely processed into various kinds of food products with high economic value. Based on data from the Agriculture Office of Jember in Komarayanti (2017), papaya in Jember is local fruit. Local fruit plants are fruit plants grown in Indonesia and planted by Indonesian people. By region, East Java was the largest papaya producer in Indonesia, reaching 268,375 tons in 2020. Meanwhile, Jember is the largest supplier of papaya in East Java, which could be seen based on the number of papaya production among areas. Jember regency in 2021 informed that papaya production was 2,155,682 kw (2019) and 950,565 kw (2020) spread across several regions in Jember (BPS, 2021). These data showed that papaya is the important commodity in Jember.

The Callina variety is widely traded in Jember, indicating that most farmers grow this variety which

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is influenced by consumer preferences. The Callina papaya plants are selected with a higher selling price in mind and inclined to be stable. The papaya harvest is distributed directly to big cities such as Jakarta. The yield of papaya plants could reach approximately 20 tons per year (Ariefianto and Ulum, 2019). If farmers have grown the same variety, the concern leads to the genetic erosion which can occur and the possible loss of many papaya genotypes. Thus, exploration and efforts to maintain the germplasm diversity of papaya are needed, especially in Jember since germplasm diversity is a fundamental asset in the plant breeding process. The types of papaya obtained from the exploration need to be characterized, one of which is morphologically. Morphological characterization is needed as the first step in determining the potential of species and highly recommended before using other characteristics. In addition, such characterization is valuable since plant breeders and germplasm collectors recorded the morphological information during routine germplasm assessment (Sadiyah et al., 2020).

Collecting, characterizing, and conserving are necessary activities to support the genetic basis of genetic breeding programs. It could be assisted by morphologic, agronomic, and botanic descriptors, which could be either quantitative or qualitative (da Silva et al., 2019). The more the descriptors measured, and the more the accessions observed, and it would result in difficult interpretation. Therefore, multivariate analysis that makes it easier for simultaneous interpretation between descriptors and accessions is needed. In addition, when the number of descriptors is huge, it is conceivable that a few of them were excessive and did not have numerous contribute to recognizing the accession under analysis. It was probably due to correlated descriptors (da Silva et al., 2019). Descriptor selection techniques had been used in Maranta arundinaceus (Hariyono et al., 2022), Physalis species (Sadiyah et al., 2020), Capsicum spp. (Sudré et al., 2010), and Cassava (Silva et al., 2017). In any case, in spite of the demonstrated significance of papaya, constrained inquiry about it has been found within the writing on the discriminative control of descriptors, or the satisfactory number of descriptors that could distinguish varieties. Some studies have been conducted to characterize papaya (Nishimwe et al., 2019; Fatria et al., 2019; Magdalita et al., 2021). However, most of these studies characterized papaya based on the desired character, using only part of the descriptors currently available for papaya, and in the different locations. In this manner, it is required that Jember consider to supply data that could guide further investigation, both within the field of hereditary assets and the change of this plant species, utilizing multivariate investigation.

Multivariate analysis is a useful method for determining the closeness between the papaya accessions collected based on morphological descriptors and identifying more informative descriptors for characterization in genetic improvement programs. The use of multivariate analysis has been applied efficiently, as it discarded redundant descriptors and did not contribute much (da Silva et al, 2019). The use of multivariate analysis to discard redundant characters

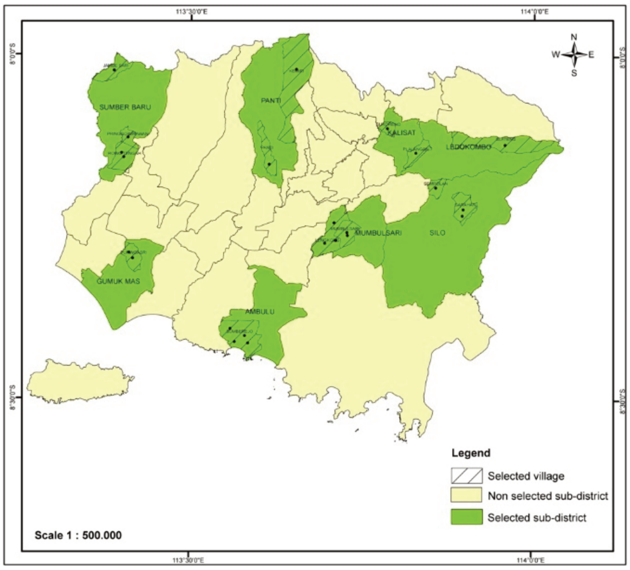

Figure 1. The study location of papaya accessions in Jember

Table 1. List of the papaya accessions origins that evaluated along with code accession, sub-district, village and geographical coordinates

No	Code accession	Sub-districts	Village	Geographical coordinates	
				Latitude	Longitude
1	KAL-PLA	Kalisat	Plalangan	8°8’22.664” S	113°49’12.169” E
2	SIL-SEM	Silo	Sempolan	8°11’25.872” S	113°51’33.077” E
3	SIL-GAR 1	Silo	Garahan	8°13’25.216” S	113°54’2.232” E
4	SIL-GAR 2	Silo	Garahan	8°13’43.421” S	113°54’15.566” E
5	LED-SLA	Ledokombo	Slateng	8°7’49.872” S	113°54’11.311” E
6	MUM-LEN 1	Mumbulsari	Lengkong	8°15’0.893” S	113°43’16.745” E
7	MUM-LEN 2	Mumbulsari	Lengkong	8°15’1.084” S	113°43’15.683” E
8	MUM-SUM 1	Mumbulsari	Sumber tengah	8°15’43.837” S	113°43’26.029” E
9	MUM-SUM 2	Mumbulsari	Sumber tengah	8°15’44.442” S	113°43’27.361” E
10	MUM-LEN 3	Mumbulsari	Lengkong	8°14’54.082” S	113°42’36.328” E
11	PAN-KEM	Panti	Kemiri	8°7’22.213” S	113°38’6.778” E
12	PAN-DAR	Panti	Darungan	8°10’11.683” S	113°37’33.024” E
13	AM-SUM 1	Ambulu	Sumberejo	8°23’20.879” S	113°35’11.911” E
14	AM-SUM 2	Ambulu	Sumberejo	8°23’21.113” S	113°35’14.334” E
15	AM-SUM 3	Ambulu	Sumberejo	8°23’35.887” S	113°35’49.585” E
16	AM-SUM 4	Ambulu	Sumberejo	8°23’10.781” S	113°35’13.427” E
17	KAL-SUK	Kalisat	Sukoreno	8°06’14.793” S	113°47’42.891” E
18	GUM-PUR 1	Gumukmas	Purwoasri	8°16’42.852” S	113°24’39.294” E
19	GUM-PUR 2	Gumukmas	Purwoasri	8°16’41.995” S	113°25’0.376” E
20	SUM-RI	Sumberbaru	Pringgowirawan	8°6’53.082” S	113°24’31.651” E
21	SUM-RO 1	Sumberbaru	Rowo tengah	8°8’30.944” S	113°25’8.278” E
22	SUM-RO 2	Sumberbaru	Rowo tengah	8°9’3.852” S	113°24’18.403” E
23	SUM-JAM	Sumberbaru	Jambesari	8°16’42.852” S	113°24’39.294” E

towards descriptor selection had been applied by Afonso et al. (2014) and de Oliveira et al. (2018). This study aimed to select the most informative morphological descriptors in characterizing and distinguishing papaya accessions in Jember.

MATERIALS AND METHODS

Data collection

Data collection was carried out stepwise in a chronological manner from July to November 2022. The exploration sites were selected primarily using graticule methods (Hijmans et al., 2012) as used in the study of Physalis angulata (Sadiyah et al., 2021) and Pinus taiwanensis (Gao et al., 2015). The graticule method applied perpendicular grids or geographical lines to divide the study area. Jember was divided into four regions, and then two sub-districts were selected for each region. The selected sub-districts were determined based on the secondary information of Jember Regency Publication in 2021 figures about papaya distribution. The selected sub-districts were Sumberbaru, Panti, Ambulu, Gumukmas, Kalisat, Ledokombo, Mumbulsari and Silo (Figure 1). Papaya accession was taken from each selected sub-district by convenience sampling of eight districts, 23 accessions were used as the sample for analysis (Table 1). The circle in Figure 1 indicated sampling location for accession inventory. Observation of morphological characters was carried out by directly observing predetermined plant parts based on distinguishing characters. Five quantitative and fifteen qualitative descriptors were used. Table 2 shows the Papaya Descriptors issued by IBPGR (1988). Length and width of mature leaf, and length of petiole were measured in the same five leaves from each accession.

Data analysis

Statistical analysis was carried out by R studio software using two packages, i.e. biotools and factoextra packages. The quantitative descriptor data was analyzed using descriptive and PCA-biplot analysis. The descriptive analysis was conducted to describe the data attributes, including minimum, maximum, mean and standard deviation. The coefficient of variation was used for observing data variation or data distributions from its means. The relative contribution

Table 2. Quantitative and qualitative descriptor for the characterization of papaya accessions in Jember

Quantitative descriptor	Measurement
Length of Mature Leaf Petiole (LMLP)	It was calculated the mean of the middle leaves of 5 randomly picked leaves (cm)
Length of Mature Leaf (LML)	It was measured from the base of the middle leaflet midrib to tip (average of same 5 leaves) (cm)
Width of Mature Leaf (WML)	It was measured at maximum breadth (average of same 5 leaves) (cm)
Length of Peduncle (LP)	It measured peduncle length (cm)
Qualitative descriptor	**Classes**
Tree Habit (THT)	(1) single stem; (2) multiple stems
Stem Colour (SC)	(1) greenish or light grey; (2) greyish brown; (3) green and shades of red-purple (pink); (4) red-purple (pink); (5) other
Stem Pigmentation (SP)	(1) only or mostly basal; (2) only or mostly lower; (3) only or mostly median; (4) only or mostly upper; (5) indiscriminate
Colour of Mature Leaf Petiole (CMLP)	(1) pale green; (2) normal green; (3) dark green; (4) green and shades of red-purple; (5) red-purple; (6) other
Type of tree hermaphroditism (TTH)	(1) staminate flowers and a few hermaphrodite; (2) a few staminate flowers and many hermaphrodite flowers; (3) a few staminate flowers, many hermaphrodite flowers and a few pistillate flowers; (4) hermaphrodite flowers only; (5) hermaphrodite flowers and a few pistillate flowers; (6) a few hermaphrodite flowers and many pistillate flowers
Colour of inflorescence stalk (CIS)	(1) greenish; (2) purplish/pinkish; (3) dark red-purple/pink; (4) other
Colour of hermaphrodite flower (CHF)	(1) white; (2) cream; (3) yellow; (4) orange; (5) greenish; (6) dark green; (7) yellow/green and red-purple shades; (8) pinkish; (9) pink; (10) other
Tree Height (TH)	(1) short (<1 m); (2) intermediate; (3) tall (>2m)
Height to First Fruit (HFF)	(1) < 1m; (2) intermediate; (3) > 1.5m
General Shape of Mature Leaf Teeth (GSMLT)	(1) straight; (2) convex; (3) concave; (4) other
General Shape of Petiole Sinus (GSPS)	(1) open; (2) slightly open; (3) slightly closed; (4) strongly closed; (5) other
Density of Inflorescences on Trunk (DIT)	(1) few inflorescences; (2) intermediate; (3) many inflorescences
Inflorescences Density (ID)	(1) few flowers; (2) intermediate; (3) many flowers
Skin Colour of Immature Fruits (SCIF)	(1) yellow; (2) light green; (3) green; (4) other
Stalk End Fruit Shape (SEFS)	(1) depressed; (2) flattened; (3) inflated; (4) pointed

Remarks: descriptor of papaya (IBPGR, 1988).

of each quantitative descriptor was estimated by the Singh method (da Silva et al., 2019). This method was used to determine the relative importance of the descriptors (de Oliveira et al., 2012). PCA-biplot analysis as the multivariate method was useful for studying the similarities of accession. The quantitative descriptors were reduced using Principal Component Analysis (PCA). From numerous observed variables, it was reduced to several main components (principal component) that were smaller in dimension and independent. Principal components (PC) as new variables were constructed as linear combinations or a mixture of the initial variables (Jolliffe and Cadima, 2016). The relationship between accessions would be displayed by mapping the scores from the PC1 and PC2 values in the biplot. It provided a graphical representation of the X matrix data in a plot by overlapping vectors in two-dimensional space that represented row vectors of the X matrix (object descriptions) with vectors that represent columns X matrix (variable description) (Dewi and Nonik, 2015). The qualitative descriptors were analyzed using descriptive analysis and entropy level. The percentage of frequency of each of the classes was used in the descriptive analysis of the qualitative descriptors. The Shannon index was used to calculate the descriptor's entropy level (Marcon et al., 2014).

$$H' = -\sum_{i=1}^{S} p_i \ln p_i$$

p_i is the proportion (n/N) of accession number of one particular class to a descriptor (n) divided by the total number of accessions found (N), S is the number of classes in a descriptor.

RESULTS AND DISCUSSION

Descriptive statistics of quantitative descriptors are presented in Table 3. The coefficient of variation (CV) showed variability in relation to the mean of the population. The CV ranged between 17.57% to 70.32%, the lowest CV was length of mature leaf, and the highest CV was tree diameter. The tree diameter had the highest variability (CV >40%). The CV in this study (70.32%) had a higher CV than papaya in the study of Sunyoto et al. (2015) (5.36%). The CV of the length of mature leaf in this study was categorized as low because Zulfahmi et al. (2020) stated that the CV < 20% showed less variation. This CV was not significantly different from the result of Emede et al. (2017), who reported that the lowest CV was showed by leaf length (13.52%). According to da Silva et al. (2019), the significant genetic diversity of the analyzed material was reflected in the descriptors' high coefficient of variation. Thus, the descriptors which had high CV was suggested to be explored in breeding programs.

The relative contribution of each quantitative descriptor in genetic divergence is presented in Table 4. The length of peduncle expressed the largest (23.28%) genetic divergence among accessions. The tree diameter, length of mature leaf petiole, length of mature leaf, the width of mature leaf and length of peduncle contributed by 20.12%, 18.36%, 18.45%, 19.77% and 23.29%, respectively. It was in line with research by de Oliveira et al. (2012) who evaluated the genetic divergence between 27 genotypes of papaya belonging to the papaya breeding program at Embrapa Cassava and Fruits Brazil using 30 quantitative descriptors. They reported a similar result from the one found in this work, length of peduncle that was

Table 3. Descriptive statistics for the quantitative descriptor of papaya accessions in Jember

Descriptor	Min	Max	Mean	Std. Dev	CV (%)
TD	8	60	15.43	10.85	70.32
LMLP	49	117	82.98	16.55	19.94
LML	27.6	50	38.64	6.79	17.57
WML	12	50	20.65	7.9	38.26
LP	2.8	11	4.85	1.52	31.34

Remarks: Tree Diameter (TD) in cm; Length of Mature Leaf Petiole (LMLP) in cm; Length of Mature Leaf (LML) in cm; Width of Mature Leaf (WML) in cm; Length of Peduncle (LP) in cm. Coefficient of variation (CV).

Table 4. The relative contribution of quantitative descriptor to the divergence between 23 papaya accessions as Singh Method

Quantitative descriptor	S.j.	Relative contribution S.j. (%)
TD	572.418	20.121
LMLP	522.454	18.365
LML	524.873	18.450
WML	562.636	19.778
LP	662.452	23.286

Remarks: Tree Diameter (TD) in cm; Length of Mature Leaf Petiole (LMLP) in cm; Length of Mature Leaf (LML) in cm; Width of Mature Leaf (WML) in cm; Length of Peduncle (LP) in cm. Singh's statistics (S.j).

Table 5. Variance (eigenvalue), percentage variance and cumulative variance of principal component

Principal Component	Variance (eigenvalue)	Percentage variance (%)	Cumulative variance (%)
1	2.120	42.409	42.409
2	1.238	24.767	67.176
3	0.795	15.891	83.067
4	0.642	12.84	95.907
5	0.205	4.093	100

the most contributed to the genetic difference.

According to Sadiyah et al. (2020), PCA analysis could use to determine the relative importance of variables. The eigenvalue, percentage variance, and cumulative variance from the results by PCA are presented in Table 5. The eigenvalues were ordered from largest to smallest. The appropriate number of components was determined by eigenvalues greater than 1 (Rencher, 2002). 42.41% of the sample's overall variance was explained by the first principal component. The first two main components collectively accounted for 67.18% of the sample's total variance. Therefore, the sample variation could be summarized by two principal components and a reduction of 23 papaya accessions from 5 characters to 23 accessions on 2 main components. The first two principal components in this study (67.18%) had total variation higher than the result in the study of de Oliveira et al. (2012) (52.09%), but lower than Emede et al. (2017) (85.18%).

Table 6 represents the correlation between descriptor and principal components (eigenvector), while the value in parentheses is the t-value which tests the significant contribution of the variable to those selected PCs. The quantitative descriptors were significant if the t-value in parentheses was higher than 2.079 ($t_{0.025;21}$). The greater the coefficient of a variable on the principal component, the greater the relationship of the influence of that variable on the corresponding

Table 6. The value of eigenvector for 5 quantitative characters of 23 accessions papaya in Jember

Quantitative descriptor	PC1	PC2
TD	0.294 (1.409)	0.785 (5.807*)
LMLP	0.594 (3.384*)	-0.505 (-2.681)
LML	0.924 (11.073*)	-0.033 (-0.151)
WML	0.768 (5.495*)	0.411 (2.066)
LP	0.488 (2.562*)	-0.444 (-2.271)

Remarks: Tree Diameter (TD) in cm; Length of Mature Leaf Petiole (LMLP) in cm; Length of Mature Leaf (LML) in cm; Width of Mature Leaf (WML) in cm; Length of Peduncle (LP) in cm. *significant at 5% of t-test in parentheses.

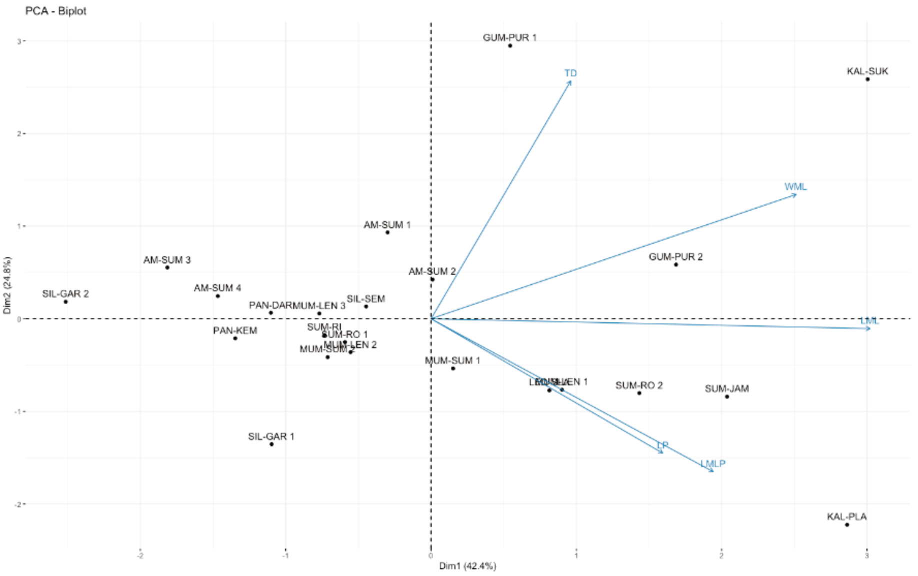

Figure 2. PCA-Biplot analysis of the 5 quantitative characters of 23 accessions papaya in Jember

Remarks: KAL-PLA: Kalisat-Plalangan; SIL-SEM: Silo-Sempolan; SIL-GAR 1: Silo-Gragahan 1; SIL-GAR 2: Silo-Gragahan 2; LED-SLA: Ledokombo-Slateng; MUM-LEN 1: Mumbulsari-Lengkong 1; MUM-LEN 2: Mumbulsari-Lengkong 2; MUM-LEN 3: Mumbulsari-Lengkong 3; MUM-SUM 1: Mumbulsari-Sumber tengah 1; MUM-SUM 2: Mumbulsari-Sumber tengah 2; PAN-KEM: Panti-Kemiri; PAN-DAR: Panti-Darungan; AM-SUM 1: Ambulu-Sumberejo 1; AM-SUM 2: Ambulu-Sumberejo 2; AM-SUM 3: Ambulu-Sumberejo 3; AM-SUM 4: Ambulu-Sumberejo 4; KAL-SUK: Kalisat-Sukoreno; GUM-PUR 1: Gumukmas-Purwoasri 1; GUM-PUR 2: Gumukmas-Purwoasri 2; SUM-RI: Sumberbaru-Pringgowirawan; SUM-RO 1: Sumberbaru-Rowo tengah 1; SUM-RO 2: Sumberbaru-Rowo tengah 2; SUM-JAM: Sumberbaru-Jambesari principal component. The first principal component was significantly and positively correlated to the length of mature leaf petiole, the length of mature leaf, the width of mature leaf and the length of peduncle. The second principal component was significantly and positively correlated to the tree diameter. The largest coefficient in PC1 was the length of mature leaf, while in PC2 was the tree diameter. Therefore, 3 out of 5 quantitative descriptors of papaya might be eliminated. According to Karuniawan et al. (2017), an eigenvalue of 1 and an eigenvector value exceeding the value of 0.7 indicated that the genetic influence of accessions had a great contribution to the variety of descriptors. The application of PCA was useful for evaluating the contribution of each of the descriptors explored against the total variation between the accessions studied and allowed the removal of less informative descriptors, due to the correlation with the remaining variables or due to their invariants (da Silva et al., 2019).

PCA-biplot investigation could be used as a choice instrument for variety improvement (Hariyono et al., 2022). The graphic of PCA-biplot representation of the dispersion of the 23 accessions by the first two principal components (67.18% of the total variability). It revealed a divergence between the different accessions materialized by the dispersion of points representative of the accession studied (Figure 2). The biplot consisted of four quadrants. The accessions that had the same characteristics would be described as points with adjacent positions in one quadrant. The first quadrant consisted of seven accessions, namely SIL-GAR 2, AM-SUM 1, PAN-DUR, AM-SUM 3, AM-SUM 4, MUM-LEN 3, and SIL-SEM. The AM-SUM 1 accession, AM-SUM 3 accession, and AM-SUM 4 accession belonged to the same group. These accessions came from the same sub-district and village, while AM-SUM 2 accession had a separate position. The second quadrant group comprised three accessions, namely KAL-SUK, GUM-PUR 1, and GUM-PUR 2. The third quadrant had SIL-GAR 1, MUM-SUM 2, MUM-LEN 2, PAN-KEM, SUM-RI, and SUM-RO 1 accessions. The

Table 7. Descriptive statistics for the qualitative descriptor of papaya accession in Jember

Qualitative descriptor	Classes	Frequency (%)	Shanon index
Tree habit (THT)	(1) single stem	82.6	0.462
	(2) multiple stem	17.4	
Stem Color (SC)	(1) greenish or light grey	43.5	0.702
	(2) greyish brown	52.2	
	(3) green and shakes of red-purple (pink)	4.3	
	(4) red-purple (pink)	0	
	(5) other	0	
Stem Pigmentation (SP)	(1) only or mostly basal	21.7	0.611
	(2) only or mostly lower	65.2	
	(3) only or mostly median	4.3	
	(4) only or mostly upper	0	
	(5) indiscriminate	8.7	
Color of Mature Leaf Petiole (CMLP)	(1) pale green	56.5	0.627
	(2) normal green	17.4	
	(3) dark green	4.3	
	(4) green and shades of red-purple	8.7	
	(5) red-purple	8.7	
	(6) other	4.3	
Type of tree hermaphroditism (TTH)	(1) staminate flowers and a few hermaphrodite	13	0.597
	(2) a few staminate flowers and many hermaphodite flowers	21.7	
	(3) a few staminate flowers, many hermaphodite flowers and a few pistillate flowers	0	
	(4) hermaphrodite flowers only	60.9	

Table 7. Descriptive statistics for the qualitative descriptor of papaya accession in Jember

Qualitative descriptor	Classes	Frequency (%)	Shanon index
	(5) hermaphrodite flowers and a few pistillate flowers	0	
	(6) a few hermaphrodite flowers and many pistillate flowers	4.3	
Color of inflorescence stalk (CIS)	(1) greenish	100	0.000
	(2) purplish/pinkish	0	
	(3) dark red-purple/pink	0	
	(4) other	0	
Color of hermaphrodite flower (CHF)	(1) white	73.9	0.555
	(2) cream	21.7	
	(3) yellow	0	
	(4) orange	0	
	(5) greenish	0	
	(6) dark green	0	
	(7) yellow/green and red-purple shades	0	
	(8) pinkish	0	
	(9) pink	0	
	(10) other	4.3	
Tree Height (TH)	(1) short (<1 m)	0	0.462
	(2) intermediate	17.4	
	(3) tall (>2m)	82.6	
Height to First Fruit (HFF)	(1) < 1 m	26.1	0.713
	(2) intermediate	43.5	
	(3) > 1.5 m	30.4	
General Shape of Mature Leaf Teeth (GSMLT)	(1) straight	39.1	0.718
	(2) convex	26.1	
	(3) concave	34.8	
	(4) other	0	
General Shape of Petiole Sinus (GSPS)	(1) open	8.7	0.425
	(2) slightly open	8.7	
	(3) slightly closed	26.1	
	(4) strongly closed	56.5	
	(5) other	0	
Density of Inflorescences on Trunk (DIT)	(1) few inflorescences	52.2	0.692
	(2) intermediate	47.8	
	(3) many inflorescences	0	
Inflorescences Density (ID)	(1) few flowers	52.2	0.692
	(2) intermediate	47.8	
	(3) many flowers	0	
Skin Color of Immature Fruits (SCIF)	(1) yellow	0	0.179
	(2) light green	4.3	
	(3) green	95.7	
	(4) other	0	
Stalk End Fruit Shape (SEFS)	(1) depressed	56.5	0.690
	(2) flattened	39.1	
	(3) inflated	4.3	
	(4) pointed	0	

fourth quadrant contained KAL-PLA, MUM-SUM 1, LED-SLA, MUM-LEN 1, SUM-RO 2, and SUM-JAM. The variance of quantitative descriptors was shown from the length of variable vectors. The length of mature leaf descriptor had a long vector line from the point of origin since this descriptor contributed to high diversity and the most dominant in quantitative descriptors. KAL-SUK, GUM-PUR 1, and GUM-PUR 2 accessions located in the second quadrant had similarities in tree diameter and width of mature leaf descriptors, while accessions located in the third quadrant had dissimilarity in those descriptors. The accessions located in the fourth quadrant had similarities in the length of mature leaf petiole, length of mature leaf, and length of peduncle descriptors.

The descriptive statistics of qualitative descriptors in each of the classes is presented in Table 7. Zhang et al. (2021) reported that the Shannon diversity index on all qualitative descriptors of papaya cultivars collected from Fujian Province, China reached over 0.8, meaning high genetic diversity. The differences in level diversity were caused not only by genotypes but also by the large geographical scale. Based on the what comes about to the calculation of the diversity index, value of the Shannon index ranged from 0 (color of inflorescence stalk) to 0.718 (general shape of mature leaf teeth). The Shannon index of all qualitative descriptors in this study did not reach 0.8, indicating moderate genetic diversity of papaya accessions collected. The color of inflorescence stalk character was discarded which presented an entropy level equal to zero. The accessions were concentrated in the greenish class with a 100% frequency. It indicated monomorphic for each class under evaluation. The general shape of mature leaf teeth (0.718), height to first fruit (0.713) and stem color (0.702) were the three highest entropy indexes, indicating genetic variability to these descriptors in the accession studied. Nevertheless, from this study, three qualitative and two quantitative descriptors of leaves and stem descriptors could be used to identify papaya in Jember District. Zulfahmi et al. (2020) stated that the morphological traits of leaves in tree species could provide rich information about the evolution of genetics and phenotypic diversity.

CONCLUSIONS

The results of the papaya plant inventory from eight districts in Jember obtained 23 papaya accessions. KAL-SUK, GUM-PUR 1, and GUM-PUR 2 accessions had similarities in tree diameter and width of mature leaf characters, while accessions from SIL-GAR 1, MUM-SUM 2, MUM-LEN 2, PAN-KEM, SUM-RI, and SUM-RO 1 had dissimilarity in those descriptors. The accessions located in the KAL-PLA, MUM-SUM 1, LED-SLA, MUM-LEN 1, SUM-RO 2, and SUM-JAM had similarities in the length of the length mature leaf, petiole, and peduncle. The minimum descriptors to characterize papaya accessions in Jember contained two quantitative descriptors (tree diameter and length of mature leaf) and three qualitative descriptors (general shape of mature leaf teeth, height to first fruit and stem color). The combination of quantitative-qualitative descriptors allowed the simple and rapid characterization of papaya accession. In addition, the use of such characters could reduce costs and labor without losing information in the characterization of papaya plants.

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