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Phenotype variability of *Pometia pinnata* from Riau, Indonesia based on qualitative characters

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Abstract. *Zulfahmi, Rosmaina. 2024. Phenotype variability of* Pometia pinnata *from Riau, Indonesia based on qualitative characters. Biodiversitas 25: 3953-3964. Matoa* (*Pometia pinnata* J.R.Forst. & G.Forst.) is an important underutilized fruit tree in Riau Province, Indonesia. Information on the genetic diversity of *P. pinnata* is poorly reported. This study aimed to estimate the phenotype variability of *P. pinnata* in Riau Province, Indonesia based on qualitative characters. Twenty-seven qualitative characters were used to study the phenotype variability of 24 *P. pinnata* genotypes. The diversity for each character was calculated using the Shannon-Weaver Index and cluster analysis among genotypes was constructed by an Unweighted Pair Group Method with Arithmetic Average (UPGMA). The results showed a high variability in almost all the characters observed. The estimated value of the Shannon-Weaver Index of *P. pinnata* ranged from 0.00-0.980. Eighteen characters exhibited a high diversity level (0.67-0.98), two characters demonstrated an intermediate level (0.41-0.66), and the remaining had low diversity (0.00-0.25). A dendrogram grouped 24 *P. pinnata* into four main clusters, i.e. black-skinned *P. pinnata* and green-skinned *P. pinnata*, yellow-skinned *P. pinnata*, red-skinned *P. pinnata*, and red-skinned *P. pinnata*. In general, *P. pinnata* was grouped based on the color of the ripe fruit skin, which indicated that fruit color characters play an important role in *P. pinnata* diversity. The ripe skin color can be used as the specific character to differentiate among *P. pinnata* genotypes easily. This information can be utilized for *P. pinnata* improvement and breeding in the future.

Keywords: Genetic diversity, morphological characters, *Pometia pinnata*, Shannon-Weaver Index, underutilized fruit tree

INTRODUCTION

Matoa (*Pometia pinnata* J.R.Forst. & G.Frost) is a member of the family Sapindaceae and is widespread in Sri Lanka to China (Yunnan) and South Pacific (POWO 2024). Currently, *P. pinnata* has been cultivated in several regions of Indonesia as a fruit tree, such as Riau, Bengkulu, North Sumatra, Aceh, Central Java, and East Java. Besides a fruit tree, *P. pinnata* has potential as a medicine plant, because of its ability as an anti-bacterial and anti-aging (Restuinjaya et al. 2019; Munirah et al. 2020; Setyaningsih et al. 2020; Adrian et al. 2021; Fatimah et al. 2021).

The *P. pinnata* is an important underutilized fruit tree in Riau Province, Indonesia. This species is managed traditionally and has not been fully commercialized. In the last decade, *P. pinnata* started to be domesticated by the community. The development of the *P. pinnata* plant as a fruit tree in Riau Province is promising. Based on our field survey in the traditional market, the selling price of *P. pinnata* fruit is around Rp. 20,000-30,000/kg, higher than rambutan fruit, so farmers are more interested in cultivating *P. pinnata* intensively. The color and taste of *P. pinnata* fruit in nature vary greatly. The exocarp color of *P. pinnata* fruit varies, i.e. green, yellow, red, and black, as well as the taste of *P. pinnata* fruit also varies among trees, it often has a mixture of flavors from several fruits such as durian, rambutan, lychee, longan, grapes, and other fruits.

Knowledge of the genetic background of plants is valuable in plant conservation and improvement activities (Kumar et al. 2024). The magnitude of the genetic variability greatly affects the success of plant improvement, the higher the diversity obtained the greater the chance of success in hybridization and improve the quality of the desired trait. The genetic diversity of plants can be determined based on morphological characteristics and molecular properties. Both methods have their advantages and weaknesses that complement each other. The diversity study of the *P. pinnata* has been done by Yuniastuti et al. (2023a) using chromosome analysis, as well as Yuniastuti et al. (2023b) and Zulfahmi et al. (2023) using the RAPD markers. Meanwhile, the diversity study of *P. pinnata* based on morphology character was restricted (Tehuayo et al. 2023), so it was important to perform.

Morphological characterization is the initial step in describing and identifying germplasm. Understanding morphological characters facilitates the pre-breeding process of identifying and selecting desirable characters (Singh et al. 2014). Morphological variability is actual data, which farmers and breeders can directly observe during the selection and hybridization process. Many characters are genetically related to economically and agronomically important traits, so selection can be carried out directly and reduce selection costs (Chesnokov et al. 2020; Zigene et al. 2022). In this study, the qualitative character was chosen to be investigated because qualitative characters are more influenced by genetic factors and less

influenced by the environment so the characters are considered more stable (Rosmaina et al. 2021), easier, simple, and no need high technology equipment (Khalid et al. 2016; Tesfa et al. 2024). Therefore, this study aimed to investigate the phenotype diversity of *P. pinnata* in Riau Province, Indonesia based on the qualitative character.

MATERIALS AND METHODS

Plant materials

Observations were made on 24 *P. pinnata* landraces (local genotype) cultivated by farmers in Riau Province, Indonesia from October to December 2021. The samples were collected from two locations, the first location is the Palas Village, Rumbai Sub-district, Pekanbaru City (MBlack-01-MBlack-05, MYellow-01-MYellow-09, MRed-01-MRed-07) and the second place is the Airtiris Village, Kampar Sub-district, Kampar District (MGreen-01-MGreen-03) (Figure 1). The *P. pinnata* plants observed are 7 years old and have produced fruit several times. Naturally, *P. pinnata* plants begin to produce fruit at the age of three years. Source and habitat of plant materials used in the study are shown in Table 1.

Table 1. Plant materials used in the study and their habitat

Genotypes	Source	Coordinate		Climate conditions		Altitude (m asl.)
		Latitude (N)	Longitude (E)	TA (ºC)	HA (%)	
MGreen-01	Airtiris Village, Kampar District	0°21'32.33"	101°5'44.52"	26.73	82.79	38.00
MGreen-02	Airtiris Village, Kampar District	0°21'32.76"	101°5'44.41"			33.50
MGreen-03	Airtiris Village, Kampar District	0°21'32.72"	101°5'44.36"			35.00
MBlack-01	Palas Village, Pekanbaru City	0°36'08.4"	101°22'51.3"	26.91	80.25	28.20
MBlack-02	Palas Village, Pekanbaru City	0°36'08.1"	101°22'51.1"			29.20
MBlack-03	Palas Village, Pekanbaru City	0°36'08.1"	101°22'51.2"			29.40
MBlack-04	Palas Village, Pekanbaru City	0°35'37.9"	101°21'59.6"			17.40
MBlack-05	Palas Village, Pekanbaru City	0°35'38.4"	101°21'59.9"			18.40
MYellow-01	Palas Village, Pekanbaru City	0°36'09.4"	101°22'50.7"			28.00
MYellow-02	Palas Village, Pekanbaru City	0°36'08.7"	101°22'50.3"			36.30
MYellow-03	Palas Village, Pekanbaru City	0°36'08.5"	101°22'50.2"			37.00
MYellow-04	Palas Village, Pekanbaru City	0°36'08.3"	101°22'50.5"			37.00
MYellow-05	Palas Village, Pekanbaru City	0°36'08.2"	101°22'50.8"			33.90
MYellow-06	Palas Village, Pekanbaru City	0°36'07.8"	101°22'51.1"			32.30
MYellow-07	Palas Village, Pekanbaru City	0°35'38.3"	101°21'59.9"			18.40
MYellow-08	Palas Village, Pekanbaru City	0°35'38.2"	101°21'59.9"			18.40
MYellow-09	Palas Village, Pekanbaru City	0°35'38.7"	101°22'00.5"			18.10
MRed-01	Palas Village, Pekanbaru City	0°36'09.3"	101°22'51.3"			26.80
MRed-02	Palas Village, Pekanbaru City	0°36'08.7"	101°22'51.2"			27.20
MRed-03	Palas Village, Pekanbaru City	0°35'35.0"	101°23'35.1"			28.40
MRed-04	Palas Village, Pekanbaru City	0°35'34.8"	101°22'35.1"			31.30
MRed-05	Palas Village, Pekanbaru City	0°35'38.6"	101°22'00.5"			31.30
MRed-06	Palas Village, Pekanbaru City	0°35'38.5"	101°22'00.2"			18.50
MRed-07	Palas Village, Pekanbaru City	0°35'38.7"	101°22'00.9"			14.50

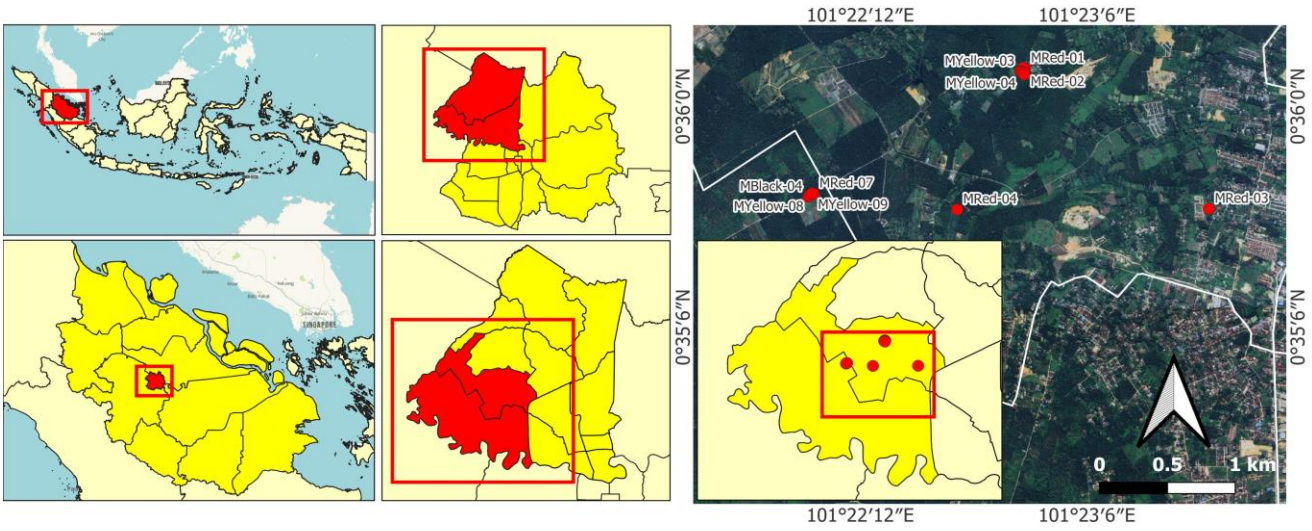

Figure 1. Location of *Pometia pinnata* observed in Pekanbaru City and Kampar District, Riau, Indonesia

Table 2. Qualitative characters observed in the study

Morphological character	Character state
Root pattern	without buttress (1); moderate buttress (2); buttress board (3)
Trunk surface	smooth (1); rough (2); very rough (3)
Tree growth habit	erect (1); semi-erect (2); spreading (3); drooping (4)
Branching pattern	upright (1); horizontal (2); irregular (3)
Branching density	sparse (1); medium (2); dense (3)
Crown shape	oblong (1); broadly pyramidal (2); semicircular (3); spherical (4)
Leaflet shape	ovate (1); obovate (2); elliptic (3); lanceolate (4); oblong (5)
Leaflet apex shape	slightly acute (1); apiculate (2); acute (3); cuspidate (4); obtuse (5); caudate (6); sub-acuminate (7); acuminate (8)
Leaflet base shape	cuneate (1); oblique (2); rounded (3); acute (4); equilateral (5); attenuate (6)
Leaf margin	undulate (1); entire (2); serrate (3); crenate (4)
Young leaf color	light green (1); yellow-green (2); green (3); pinkish green (4); reddish brown (5)
Mature leaf color	light green (1); green (2); dark green (3)
Position of inflorescence	terminal (1); axillary (2); both terminal and axillary (3)
Shape of inflorescence	pyramidal (1); conical (2); obtriangular (3)
The abundance of flowers in the inflorescence	sparse (1); moderate (2); profuse (3)
Fruit cluster density	sparse (1); medium (2); dense (3)
Fruit-bearing habit	regular (1); alternate years (2); irregular (3)
Type of flower in the inflorescence	hermaphrodite flowers functioning as female (1); hermaphrodite flowers functioning as male (2); hermaphrodite flowers functioning as female and male (3); male flowers (4).
Sepal color	greenish (1); yellowish green (2); green-white (3)
Petal color	whitish (1); yellowish (1); cream (3); white-purple (4)
Stigma color	greenish (1); yellow (2); orange (3)
Anther color	yellowish (1); cream (2); pink (3); maroon (4)
Young fruit rind color	light green (1); dark green (2)
Ripe fruit rind color	green (1); reddish green (2); green-yellow (3); yellow (4); pink (5); red maroon (6); red (7); black (8)
Aril color	white (1); light cream (2); cream (3); pale yellow (4); yellow (5); golden yellow (6); deep golden yellow (7)
Seed coat color	brown (1); dark brown (2); maroon (3); blackish-brown (4)
Shape of seed	rounded (1); obovoid (2); obovoid elongated (3); cylindrical (4)

Procedures

Morphological characterization was carried out on 27 qualitative characters (stems, leaves, inflorescences, flowers, fruit, and seeds) following the descriptor for Sapindaceae guidelines published by the International Plant Genetic Resources Institute (IPGRI 2003) (Table 2).

Data analysis

The phenotype frequency distribution of the characters was measured for all samples. The phenotype diversity index for each qualitative character was determined using the Shannon-Weaver diversity index with the formula described by Shannon and Weaver (1949) as follows: $H' = [-\sum pi*LnPi]/Ln(n)$, where H' = Shannon-Weaver diversity index, Pi = Frequency of each phenotypic class i^{th} of a given character, n = Number of phenotypic classes of each character. The value of H' was ranged from 0 to 1. The Diversity Index (H') reaches its minimum value, which is 0 for monomorphic characters, and the value of this index increases with the degree of polymorphism. It reaches a maximum value of 1 when all the phenotypic classes present in equal frequencies. The Shannon-Weaver diversity index was classified as low (0.00-0.33), intermediate (0.34-0.66), and high (0.67-1.00) (Shannon and Weaver 1949).

A dendrogram based on Jaccard's similarity coefficient was created using Unweighted Pair-Group Method with Arithmetic Averages (UPGMA) with the Sequential, Hierarchical, Agglomerative, and Nested Clustering (SAHN) module of the NTSYSpc software version 2.00 (Rohlf 1998) to display the phenotypic relationships expressed by similarity coefficients.

RESULTS AND DISCUSSION

Phenotype frequency of qualitative character

Qualitative traits have an important role in genetic inheritance, so understanding the inheritance system of qualitative characters is pivotal in developing desired new varieties. The distribution frequency of the 27 qualitative characters of the *P. pinnata* is displayed in Table 3. The distribution frequency of the qualitative characters of the *P. pinnata* plant varies, ranging from 4.17% to 100%. Six characters i.e. erect growth habit, medium branching density, the terminal position of inflorescence, regular fruit-bearing habit, yellowish green sepal color, and cream petal color have a phenotype frequency value of 100%, which means that these characters are dominant, stable, and expressed consistently in all *P. pinnata* genotypes. These characters are generally controlled by genetics and only slightly influenced by the environment (Keerthi et al. 2014; Benlloch et al. 2015; Hughes et al. 2020; Kellogg 2022). Stable characters are very important for breeders because the stability and consistency of expression of a character can be used as the main marker of a plant (Vernetti and Junior 2017). All *P. pinnata* genotypes observed have medium branching density. The character of branching density will determine plant structure, root system

architecture, light interception, branching system, and plant population density (Pagès 2019; Li et al. 2022).

Evaluation of root patterns in *P. pinnata* genotypes found two patterns, namely moderate buttress (37%) and without buttress (62.50%), while buttress board was not found in the genotypes investigated. Root patterns in plants are influenced by genetic factors and several environmental factors, such as groundwater and soil nutrient content (Rellán-Álvarez et al. 2016; Kaiser et al. 2023; Zhang et al. 2023). Buttress roots usually appear in less fertile soil conditions, so plants modify the roots to maintain the stability of plant growth, besides buttress roots also usually appear in less stable soil systems to maintain and strengthen the plant, roots will be modified to form buttress roots so that plants can stand stronger (Alencar et al. 2023).

Evaluation of the trunk surface revealed that this character had a polymorphic distribution in *P. pinnata* genotypes. Rough trunk surface exhibited the highest proportion in *P. pinnata* genotypes (95.83%), whereas smooth trunk surface had the lowest distribution across genotypes. Our result was in line with Kumar and Pandey (2023), who found rough trunk surface as the dominant character in the *Litchi chinensis* Sonn. The branching pattern in *P. pinnata* plants showed three patterns, namely erect (20.83%), horizontal (20.83%), and irregular (58.33%). The irregular branching pattern is the predominant phenotype in the *P. pinnata* investigated. Furthermore, 58.33% of *P. pinnata* genotypes had broadly pyramided shape of crown. Crown shape in plants is greatly influenced by the environment (latitude, light), species, and stage of plant development (Martin-Ducup et al. 2018).

Evaluation of the leaflet shape character revealed that elliptic shape was the commonly distributed class in *P. pinnata* genotypes, followed by obovate. The predominant apex and base leaflet shapes in *P. pinnata* are acuminate (70.83%) and equilateral (62.50%), respectively. The leaf margin of *P. pinnata* consists of undulate (70.83%), entire (25.00%), and serrated (4.17%). Leaf margin frequency significantly varies in various plant species and is strongly influenced by genetic factors (Feng et al. 2022) and climate conditions, especially temperature and rainfall (Zhang et al. 2019). Leaflet margin functions as a defense mechanism in plants (Hughes and Lev-Yadun 2015) so leaf margins are vital in plant identification (Kolivand et al. 2018).

Most of the evaluated *P. pinnata* genotypes possessed reddish brown young leaves color (75.00%), followed by young leaves color of pinkish green (25.00%). Zhao et al. (2020) explained that plant leaf color was controlled by genes associated with chloroplast development or chlorophyll metabolism. The red coloration of leaves can result from the delayed development of chloroplasts, the delayed synthesis of chlorophyll, or the active synthesis of anthocyanin (Chen et al. 2021). The red coloration of young leaves revealed high concentrations of tannins and anthocyanins, which are useful as a plant defense against attacking insect herbivores (Gong et al. 2020).

Evaluation of inflorescence shape revealed that this character had a polymorphic distribution in *P. pinnata* genotypes. Pyramidal inflorescence shape was exhibited with the highest proportion in genotypes (75.00%). On the other hand, conical shape of inflorescence had the lowest distribution across genotypes. The *P. pinnata* has a high abundance of flowers which 70.83% of panicles have a profuse abundance of flowers in the inflorescence, but have a medium fruit cluster density (66.67%), indicates that the percentage of fruit set may be low. The shape inflorescence architecture is determined by position and activity meristem that formed during reproductive development (Benlloch et al. 2015). On the other hand, inflorescence architecture also genetically regulated, which *TERMINAL FLOWER1 (TFL1, LEAFY (LFY)),* and *APETALA1* (*AP1*) genes involved in inflorescence architecture of *Jatropha curcas* L. (Chen et al. 2019).

The stigma color of *P. pinnata* varies and is dominated by orange (62.50%) then followed by greenish (29.17%), and the rest are yellow (8.33%). The anther color of flowers is maroon and yellowish, 91.76% and 8.33%, respectively. According to Li et al. (2021), stigma color is determined by chlorophyll and carotenoids contents, different compositions and different concentrations of chlorophyll and carotenoids result in a variety of colors, e.g. red, orange, yellow, green, light green, and white. Lv et al. (2022) reported that chlorophyll and carotenoid content in the green stigmas was higher compared to the yellow stigmas.

The color of young *P. pinnata* fruit was varied, e.g. light green (62.50%) and dark green (37.50%). The difference in the color of young fruit is influenced by the content and composition of anthocyanins and chlorophyll (Kayesh et al. 2013). Wang et al. (2020) found that chlorophyll a, chlorophyll b, and carotenoid content in the fruit skin of cucumbers with in dark green skin were higher than light green skin. Most fruit skin color in fruit early development exhibits green color, and the predominant colorations of yellow, orange, and red show in the post-stage due to chlorophyll metabolism (Xie et al. 2019).

There are four types of flowers in the inflorescence (Figure 2). The *P. pinnata* genotypes possessed hermaphrodite flower functions as male, hermaphrodite flower functions as male and female, hermaphrodite flower functions as female, male flower was 33.33%, 29.17%, 25.00%, and 12.50%, respectively (Table 3). Our results contrast the report of Arumugam et al. (2021), who found no diversity in *P. pinnata* flowers. The *P. pinnata* is a monoecious plant with bisexual flowers (hermaphrodite) where the male organs (pistils) and female organs (stamens) are in the same flower. Male flowers with imperfect ovaries are found in the same flower (Arumugam et al. 2021; Mong and Razili 2022), wherein one flower stalk (peduncle) there are 2-3 male flowers and 1-2 female flowers (Arumugam et al. 2021). Female flowers may appear bisexual, but the anthers are small and sterile. Male flowers usually mature first and outnumber female flowers. Male flowers do not have pistils, only have pollen, while female flowers have pollen but do not function (Thomson and Thaman 2006). Generally, the Sapindaceae family is a monoecious plant with hermaphrodite flowers (Windarsih and Efendi 2019). The development stages and types of flowers in *P. pinnata* are unique and require further study of the flower phenology of *P. pinnata* to reveal the diversity and uniqueness of the flower pollination system in *P. pinnata* until it is answered how the high diversity in fruit color can occur.

Table 3. Number of phenotype, and frequency of phenotype *Pometia pinnata* based on qualitative traits

Character	Phenotype	No. of class	No. of genotype	Frequency of phenotype (%)	H'
Root pattern	Moderate buttress	2	9	37.50	0.95
	Without buttress		15	62.50	
	Buttress board		0	0.00	
Trunk surface	Smooth	2	1	4.17	0.25
	Rough		23	95.83	
	Very rough		0	0.00	
Tree growth habit	Erect	1	24	100.00	0
	Semi-erect		0	0.00	
	Spreading		0	0.00	
	Drooping		0	0.00	
Branching pattern	Upright	3	5	20.83	0.88
	Horizontal		5	20.83	
	Irregular		14	58.33	
Branching density	Sparse	1	0	0.00	0
	Medium		24	100.00	
	Dense		0	0.00	
Crown shape	Oblong	2	0	0.00	0.98
	Broadly pyramide		14	58.33	
	Semicircular		10	41.67	
	Spherical		0	0.00	
Leaflet shape	Ovate	2	0	0.00	0.87
	Obovate		7	29.17	
	Elliptic		17	70.83	
	Lanceolate		0	0.00	
	Oblong		0	0.00	
Leaf apex shape	Slightly acute	3	0	0.00	0.73
	Apiculate		0	0.00	
	Acute		3	12.50	
	Cuspidate		0	0.00	
	Obtuse		0	0.00	
	Caudate		0	0.00	
	Sub-acuminate		4	20.00	
	Acuminate		17	70.83	
Leaf base shape	Cuneate	3	0	0.00	0.82
	Oblique		0	0.00	
	Rounded		6	25.00	
	Acute		3	12.50	
	Equilateral		15	62.50	
	Attenuate		0	0.00	
Leaf margin	Undulate	3	17	70.83	0.66
	Entire		6	25.00	
	Serrate		1	4.17	
	Crenate		0	0.00	
Young leaf color	Light green	2	0	0.00	0.81
	Yellow-green		0	0.00	
	Green		0	0.00	
	Pinkish green		6	25.00	
	Reddish brown		18	75.00	
Mature leaf color	Light green	2	0	0.00	0.95
	Green		15	62.50	
	Dark green		9	37.50	
Position of inflorescence	Terminal	1	24	100.00	0
	Axillary		0	0.00	
	Both terminal and axillary		0	0.00	
Shape of inflorescence	Pyramidal	2	18	75.00	0.81
	Conical		6	25.00	
	Obtriangular		0	0.00	
Abundance of flowers in the inflorescence	Sparse	3	2	8.33	0.71
	Medium		5	20.83	
	Profuse		17	70.83	
Fruit cluster density	Sparse	2	0	0.00	0.92
	Medium		16	66.67	
	Dense		8	33.33	

Fruit-bearing habit	Regular	1	24	100.00	0
	Alternate years		0	0.00	
	Irregular		0	0.00	
Type of flower in the inflorescence	Hermaphrodite flower function as female	4	6	25.00	0.96
	Hermaprhodite flower function as male		8	33.33	
	Hermaphrodite flower function as female and male		7	29.17	
	Male flower		3	12.50	
Sepal color	Greenish	1	0	0.00	0
	Yellowish green		24	100.00	
	Green-white		0	0.00	
Petal color	Whitish	1	0	0.00	0
	Yellowish		0	0.00	
	Cream		24	100.00	
	White-purple		0	0.00	
Stigma color	Greenish	3	7	29.17	0.78
	Yellow		2	8.33	
	Orange		15	62.50	
Anther color	Yellowish	2	2	8.33	0.41
	Cream		0	0.00	
	Pink		0	0.00	
	Maroon		22	91.67	
Young fruit rind color	Light green	2	15	62.50	0.95
	Dark green		9	37.50	
Ripe fruit rind color	Green	3	3	12.50	0.95
	Reddish green		0	0.00	
	Green-yellow		0	0.00	
	Yellow		9	37.50	
	Pink		0	0.00	
	Red-maroon		7	29.17	
	Red		0	0.00	
	Black		5	20.83	
Aril color	White	3	0	0.00	0.96
	Light cream		9	37.50	
	Cream		0	0.00	
	Pale yellow		10	41.67	
	Yellow		0	0.00	
	Golden yellow		5	20.83	
	Deep golden yellow		0	0.00	
Seed coat color	Brown	3	3	12.50	0.85
	Dark brown		14	58.33	
	Maroon		7	29.17	
	Blackish-brown		0	0.00	
Shape of seed	Rounded	3	2	8.33	0.81
	Obovoid		14	58.33	
	Obovoid elongated		8	33.33	
	Cylindrical		0	0.00	

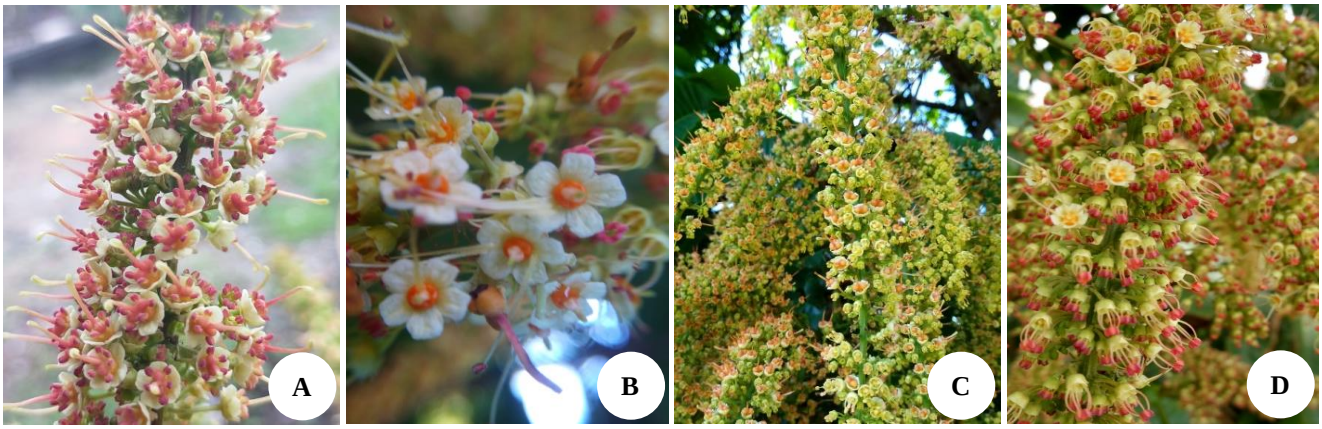

Figure 2. The type of inflorescence of *Pometia pinnata*: A. and B. Hermaphrodite function as male and female; C. Hermaphrodite function as female; D. Hermaphrodite function as male

Figure 3. Diversity in ripe fruit skin color in *Pometia pinnata*: A. Green; B. Yellow; C. and D. Red; and E. Black

The results showed at least four colors of ripe fruit rind, namely green (12.50%), red (29.17%), yellow (37.50%), and black (20.83%) (Figure 3). The frequency of color in the fruit is greatly influenced by the levels of anthocyanins and carotenoids contained in the fruit (Li et al. 2018; Ranganath 2022). The diversity of ripe fruit rind color has been reported by several researchers, such as Arumugam et al. (2021), Mong and Razili (2022), Yuniastuti et al. (2023a,b) and Zulfahmi et al. (2023). Fruit color plays an important role in the spreading and diversification of plant groups on a large scale, the more diverse the color of the fruit of a species, the greater its distribution and diversification, this is also related to the altitude of the plant growth (Lu et al. 2019: Karagiannis et al. 2020; Liu et al. 2023). Fruit color is an economic parameter and plays an important role in indicating diversity between genotypes so that in the selection of elite parents in plant breeding programs. Pigments are responsible for the formation of fruit color, i.e. carotenoids (xanthophylls, carotene) give yellow, red, and orange colors, while anthocyanins give red, blue, and purple colors (Ranganath 2022).

High variation in ripe skin color has also been reported in mango (Jena et al. 2021). This indicates that the fruit skin color character is heterozygous. Itle et al. (2022) reported that fruit color is influenced by many factors (environment, modifier genes, epistatic interactions, etc.) that need to be studied further. The large heritability of fruit color indicates the opportunity to obtain new variants through hybridization (Itle et al. 2022). Li et al. (2018) reported that the inheritance of fruit color traits is controlled by many genes (polygenetic), the inheritance of yellow fruit color is controlled by recessive alleles, and black color is controlled by two main genes that interact with each other, purple color is controlled by two co-dominant genes. Most studies of fruit color focus on chlorophyll, lycopene, and carotene content because the frequency of color that appears is a manifestation of the content of these pigments. The distribution and inheritance of fruit color in plants are controlled by more than one pair of genes. It is suspected that two pairs of main genes give additive and dominant effects, but the influence of the main genes is very large (Li et al. 2018; Itle et al. 2022; Wang et al. 2023a).

There were three variations of aril color in *P. pinnata* genotypes. The dominant aril color was pale yellow (41.67%), followed by light cream (37.50%), and golden yellow (20.83%). The discovery of different aril colors provides a good subject for fruit color formation study in the future. The observed color distinctions are closely related to the presence of specific pigments. Flavonoid biosynthesis is known to be involved in the production of various pigments (Wang et al. 2023b). Yan et al. (2024) explained that flavonoids and carotenoids contributed to Maire yew arils' observed color aril variations. The predominant seed coat color and seed shapes were dark brown (58.33%) and obovoid (58.33%), respectively. Seed coat color was determined by genetic factors and environmental conditions. Mau et al. (2023) stated that seed coat color in mungbean was controlled by one co-dominant gene. Cao et al. (2020) found that variations in seed coat color in *Suaeda aralocaspica* (Bunge) Freitag & Schütze are associated with environmental conditions, e.g. daylight, temperature, annual precipitation, and monthly distribution. Seed shape is a pivotal character in plant classification and identification (Cervantes et al. 2016). Seed shape is influenced by maternal effects. The maternal parent contributes genetic material to the seed, including cytoplasmic factors and genes located on the sex chromosomes (Marcel et al. 2024), whereas Cervantes et al. (2016) stated that other factors that determine the final shape of the seed are climatic, for example, wind, rainfall, or humidity, and intrinsic characteristics.

Phenotype diversity index

Polymorphic characters have more than one phenotype for each character, while characters that only consist of one phenotype are called monomorphic characters. Of the 27 qualitative characters observed, 21 characters were polymorphic and 6 phenotypes were monomorphic. The polymorphism level of character will determine the magnitude of variability in genotypes. The value of the Shannon-Weaver Index (H') for each qualitative character is presented in Table 3. The Shannon-Weaver Diversity Index (H') ranged from 0.00 to 0.98. The characters having the lowest diversity index (0) are observed in the character of growth habit, branching density, the terminal position of inflorescence, fruit-bearing habit, sepal color, and petal color. These characters are uniform for all genotypes. Low phenotype diversity was related to low allele frequency in a population. Low variants are often not detected in visual observations but have an important role in determining diversity and indicating the presence of specific characters that are limited to plants (Fournier et al. 2019). This can occur due to mutations or genetic deviations (Kostyn et al. 2023). The results were in line with the report of Kumar et al. (2024) on the diversity of *Dimocarpus longan* Lour.,

who reported that the species has a low diversity index in the branching pattern character.

The highest Shannon-Weaver Index (H') was observed in crown shape (0.980), aril color (0.964), the type of flower in the inflorescence (0.961), young fruit rind color (0.954), root pattern (0.954), mature leaf color (0.954), followed mature fruit rind color (0.948). All leaf characters (leaflet shape, leaf apex shape, leaf base shape, young leaf color, and mature leaf color) also have a high diversity index, which means that these characters are important characters that can be used for *P. pinnata* identification. Several other studies reported that leaves are important characters in plant identification (Lal et al. 2023; Qiying et al. 2023; Kumar et al. 2024).

Out of 21 polymorphic characters, 18 characters exhibited a high diversity (H' = 0.67-1.00) and three characters displayed intermediate diversity levels (H' = 0.34-0.66) (Table 3). The result implies that there is diversity among characters regarding qualitative characters tested in this study. The diversity in morphological qualitative characters observed among genotypes could be due to genetic factors interacting with the local climatic conditions. On the overall mean, the qualitative characters had intermediate variability with a value of 0.632 diversity index. The Shannon-Weaver (H') index value in this study was lower than the Shannon-Weaver Index value of *D. longan* (Kumar et al. 2024), *Mangifera indica* L. (Zhang et al. 2020), *Theobroma cacao* L. (Toramo et al. 2019), and *Euscaphis japonica* (Thunb.) Kanitz (Sun et al. 2019). However, our result was higher than the Shannon-Weaver Index value of robusta coffee (Martono et al. 2022), *M. indica* (Calimpang et al. 2024).

Particular character to distinguish among *P. pinnata* genotypes

The specific characters for each group of *P. pinnata* genotypes are shown in Table 4. Yellow *P. pinnata* genotypes can be identified specifically with semicircular crown shape, dark green mature leaf color, the moderate and sparse abundance of flowers in the inflorescence, dark green young fruit rind color, and dark brown seed coat color. The characters that can differentiate red *P. pinnata* from other *P. pinnata* are moderate buttress root patterns, upright branching patterns, rounded and obliqua leaflet base shapes, serrate leaf margin, pinkish green young leaf color, greenish stigma color, and yellowish anther color. An obovate leaflet shape, apiculate leaflet apex shape, and golden yellow aril color can be used to distinguish black *P. pinnata* from others. The *P. pinnata* can be identified using a slightly acute leaflet apex shape, cuneate leaflet base shape, yellow stigma color, brown seed coat color, and rounded seed shape.

This study showed that qualitative characters were a valuable tool for genotype identification. Our results were in line with Zulfahmi et al. (2023), who found specific bands to distinguish among *P. pinnata* genotypes (green *P. pinnata*, yellow *P. pinnata*, red *P. pinnata*, and black *P. pinnata*) in Riau Province based on RAPD markers. Another study showed that the green *P. pinnata*, yellow *P. pinnata*, and red *P. pinnata* found in Central Java, Indonesia, have the same karyotype formula so the *P. pinnata* genotypes are not distinguishable (Yuniastuti et al. 2023b). However, based on *Mat*K gene sequencing obtained that green *P. pinnata* have a base pair (bp) length of 905 bp, whereas other *P. pinnata* genotypes (yellow *P. pinnata*, red *P. pinnata*, purple *P. pinnata*, and brown *P. pinnata*) have a length of more than 1000 bp (Sholiha et al. 2024). Information on the particular characters of each *P. pinnata* genotype can be used by breeders and farmers. The breeder can use this information as a basis to select the parents for the genetic improvement of *P. pinnata*, and cultivar protection. Meanwhile, for farmers, this information could be used to differentiate the *P. pinnata* genotypes that have been cultivated.

Cluster analysis

Twenty four of *P. pinnata* genotypes were clustered into four main clusters at a similarity level of 70% (Figure 4), the first cluster consisted of black-skinned *P. pinnata* and green-skinned *P. pinnata*. The second and third clusters consisted of yellow-skinned *P. pinnata* and red-skinned *P. pinnata*, respectively, while the fourth cluster only consisted of red-skinned *P. pinnata*. The similarity of qualitative characters in this study plays an important role in the clustering of *P. pinnata*. Grouping various plant genotypes using similar qualitative characters has been widely reported for various plant species including *M. indica* (Neguse et al. 2019), robusta coffee (Martono et al. 2022), *D. longan* (Kumar et al. 2024) and Asteraceae family including *Ageratum conyzoides* L., *A. houstonianum* Mill., *Tithonia diversifolia* (Hemsl.) A.Gray, *Sonchus arvensis* L., *Erechtites valerianifolia* (Kunth) Cuatrec. ex Belcher, *Eupatorium odoratum* L., and *Tagetes erecta* L. (Nahdloh et al. 2022).

Green-skinned *P. pinnata* and black-skinned *P. pinnata* are clustered within one cluster (Table 4). The ten qualitative characters are shared between green *P. pinnata* and black *P. pinnata*, viz. root pattern, crown shape, leaflet shape, young leaf color, mature leaf color, abundance of flower in the inflorescence, fruit cluster density, type of flower in the inflorescence, stigma color, anther color, and young fruit rind color. The similarity of these characters causes a closely relationship between green-skinned *P. pinnata* and black-skinned *P. pinnata* with a similarity coefficient value of 84%, which means that the difference between the both *P. pinnata* based on their qualitative characters is only 16% (Figure 4).

In the second and third clusters, two genotypes *P. pinnata* of yellow-skinned *P. pinnata* with one sample of red-skinned *P. pinnata* are clustered in one cluster with a similarity percentage of 74%. Surprisingly, individuals having red-skinned *P. pinnata* are found to be clustered into yellow-skinned *P. pinnata*, this means that the characters in red *P. pinnata* are shared into yellow-skinned *P. pinnata*. There are nine similar characters between red-skinned *P. pinnata* and yellow-skinned *P. pinnata* as presented in Table 4. The similarities in these characters are root pattern, leaflet shape, leaflet apex shape, leaflet base shape, leaflet margin, shape of inflorescence, abundance of flower in the inflorescence, fruit cluster density, and anther color. The fourth cluster only consists

of red-skinned *P. pinnata*. Red-skinned *P. pinnata* have more than one phenotype in several qualitative characteristics observed including root pattern, branching pattern, leaflet base shape, leaf margin, shape of inflorescence, type of flower in the inflorescence, and anther color.

Table 4. Specific character to differentiate among *Pometia pinnata* genotypes

Qualitative characters	Kind of *P. pinnata* based on the rind color			
	Green	Black	Yellow	Red
Root pattern	Without buttress	Without buttress	Without buttress	Moderate buttress Without buttress
Branching pattern	Horizontal	Irregular	Irregular	Upright Horizontal
Crown shape	Broadly pyramide	Broadly pyramide	Semicircular	Broadly pyramide
Leaflet shape	Elliptic	Elliptic Obovate	Elliptic	Elliptic
Leaflet apex shape	Slightly acute	Apiculate	Acute	Acute
Leaflet base shape	Cuneate	Equilateral	Equilateral	Rounded Oblique Equilateral
Leaf margin	Entire	Undulate	Undulate	Entire Undulate Serrate
Young leaf color	Reddish brown	Reddish brown	Reddish brown	Pinkish green
Mature leaf color	Green	Green	Dark green	Green
Shape of inflorescence	Pyramidal	Conical	Pyramidal	Pyramidal Conical
The abundance of flower in the inflorescence	Profuse	Profuse	Profuse Moderate Sparse	Profuse
Fruit cluster density	Dense	Dense	Medium	Medium
Stigma color	Yellow Orange	Orange	Orange	Greenish
Anther color	Maroon	Maroon	Maroon	Yellowish Maroon
Young fruit rind color	Light green	Light green	Dark green	Light green
Aril color	Pale yellow	Golden yellow	Light cream	Pale yellow
Seed coat color	Brown	Maroon	Dark brown	Maroon
Shape of seed	Rounded Obovoid elongated	Obovoid	Obovoid	Obovoid elongated

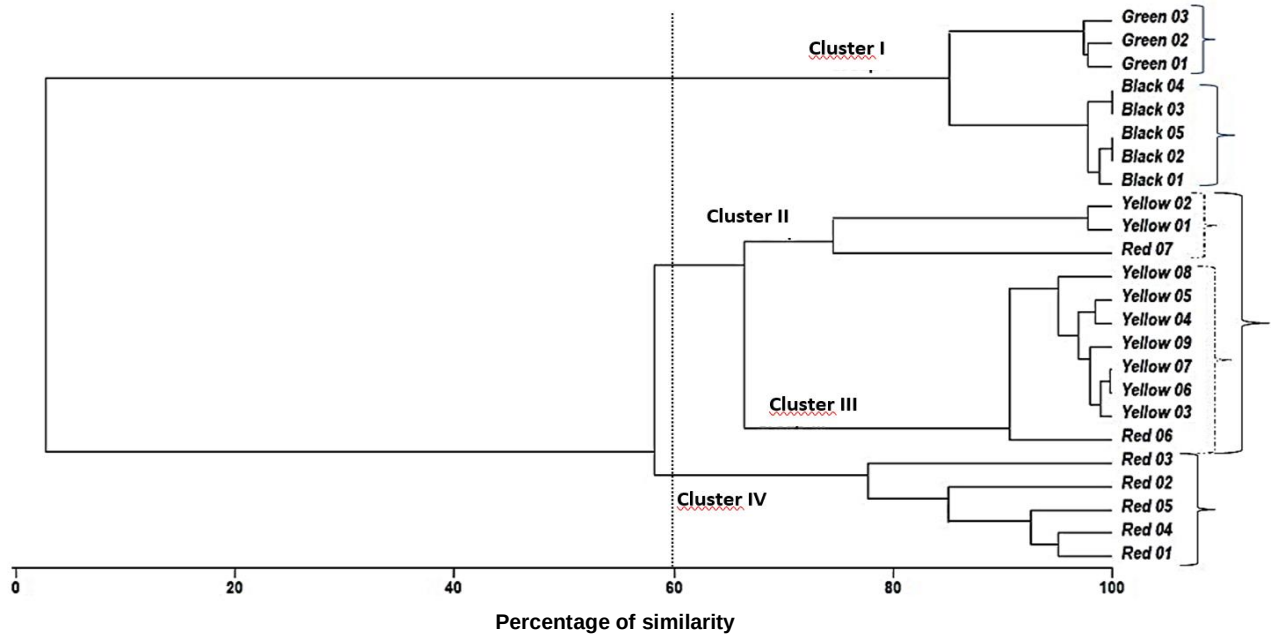

Figure 4. A Dendogram among *Pometia pinnata* genotypes generated by UPGMA cluster analysis based on 27 qualitative characters

Our results are in contrast to Sholiha et al. (2024) that clustered yellow, green, and red *P. pinnata* into one cluster, while brown and purple *P. pinnata* were clustered into other clusters based on *Mat*K gene analysis. Information on the clustering of plant genotypes into different clusters can be used as a basic consideration to formulate a breeding strategy, particularly in identifying parental lines for variety development through selection and hybridization (Rosmaina et al. 2016; Neguse et al. 2019). Therefore, the resulting cluster of *P. pinnata* genotypes with prominent characters can be used in *P. pinnata* improvement programs in the future.

In conclusion, a high variability in almost all the characters was observed in this study. The estimated value of the Shannon-Weaver Index of *P. pinnata* ranged from 0.00 to 0.980. Eighteen characters exhibited a high diversity level of 0.67-0.98, two characters demonstrated an intermediate level of 0.41-0.66, and the remaining characters had low diversity of 0.00-0.25. A dendrogram grouped 24 *P. pinnata* genotypes into four main clusters, i.e. black-skinned and green-skinned, yellow-skinned, red-skinned, and red-skinned. In general, was grouped based on the color of the ripe fruit skin, which indicated that fruit color characters play an important role in *P. pinnata* diversity. The ripe skin color can be used as the specific character to differentiate among *P. pinnata* genotypes easily.

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