JJBS

Volume 19, Number 1,March 2026
ISSN 1995-6673
Pages 13 – 21
https://doi.org/10.54319/jjbs/190102

Jordan Journal of Biological Sciences

Morphological and molecular data reveal two distinct clades of *Xanthosoma undipes* (Araceae) on Mount Karang, Banten, Indonesia

Gut Windarsih[1,*] , Muhammad Rifqi Hariri[2], Ina Erlinawati[2], I Putu Gede P. Damayanto[2], Indira Riastiwi[3] , Surya Diantina[3], Andi Salamah[4]

[1] Program of Biology, Faculty of Science and Technology, Universitas Islam Negeri Sultan Maulana Hasanuddin Banten. Jl. Syech Nawawi Al Bantani, Serang, 42116, Banten, Indonesia; [2] Research Center for Biosystematics and Evolution, Herbarium Bogoriense, National Research and Innovation Agency, Indonesia. Jl. Raya Jakarta-Bogor, km 46, Cibinong, Bogor, 16911, West Java, Indonesia; [3] Research Center for Applied Botany, National Research and Innovation Agency, Indonesia. Jl. Raya Jakarta-Bogor, km 46, Cibinong, Bogor, 16911, West Java, Indonesia; [4] Department of Biology, Faculty of Mathematics and Natural Sciences, Universitas Indonesia. Jl. Margonda Raya, Pondok Cina, Beji, Depok, 16424, West Java, Indonesia

Received: January 21, 2025; Revised: May 27, 2025; Accepted: June 30, 2025

Abstract

Xanthosoma undipes, locally known in Indonesia as *talas beneng*, is a taro plant with edible corms. Two distinct morphological groups have been identified in three locations on Mount Karang, Banten, Indonesia. This study investigates the variation among *X. undipes* accessions from Mount Karang based on morphological traits and the chloroplast *psb*A-*trn*H intergenic spacer (IGS) marker. Accessions of *X. undipes* were collected from Mount Karang as herbarium specimens and DNA samples. Morphological data were gathered, scored, and analyzed using the UPGMA method. DNA was isolated using a modified CTAB method with 2% polyvinylpyrrolidone, leaf tissue was ground in CTAB buffer, incubated, extracted with chloroform:isoamyl alcohol (24:1), and DNA was precipitated with isopropanol, washed with 70% ethanol, and resuspended in TE. PCR amplification was performed using *psb*A-*trn*H IGS primers (forward: 5’-GTT ATG CAT GAA CGT AAT GCT C-3’ and reverse: 5’-CGC GCA TGG TGG ATT CAC ATT CAC AAT-3’). DNA sequencing was conducted by 1st Base. A phylogenetic tree was constructed using the Maximum Likelihood method with 1000 bootstrap replications, using *Alocasia macrorrhizos* as an outgroup because it belongs to the same family but a different genus, with sequences available in NCBI. Nucleotide variations were visualized using Multalin. Morphological analysis revealed two distinct clades of *X. undipes* accessions from Mount Karang. Clade I consists of accessions GW1, GW3, GW12, GW14, and GW22, while Clade II consists of GW6, GW18, GW19, GW20, and GW21. Morphological characters, including corms, cormels, leaf petiole junctions, leaf sheaths, peduncles, spathes, sterile flowers, and male flowers, distinguish *X. undipes* accessions into two clades. Molecular analysis using the chloroplast *psb*A-*trn*H IGS marker supported the clustering observed in the morphological data. A notable difference between the two clades was found at nucleotide base position 156, where clade I had a cytosine, while clade II had a thymine. In the end, morphological and molecular evidence revealed two distinct clades among *X. undipes* accessions from Mount Karang.

Keywords: dendrogram, phylogeny, *talas beneng*, taro, *psb*A-*trn*H IGS, *Xanthosoma undipes*

1. Introduction

Xanthosoma undipes (K.Koch & C.D.Bouché) K.Koch (Araceae), locally known as *talas beneng* in Indonesia, is a taro plant with the main tuber being an edible corm that serve as a source of carbohydrates. According to Windarsih *et al.* (2023), morphologically, *X. undipes* has corms that range from rounded to elongated in shape, which develop into a pseudostem that can grow up to 2 meters tall in height. The underground corms branch into lateral tubers (cormels). The leaf blades are sagittate, green, thin, soft, with undulate margins, acute tips, and a bowl-shaped surface. The inflorescence is erect, featuring spoon-shaped bracts with a tubular form at the lower part and a flattened shape at the upper part. The female and sterile flowers are enclosed within a spathe tube, while the male flowers become visible when the spathe opens. Milky-white, sticky exudates are present in nearly all parts of the plant.

Xanthosoma undipes has significant economic value, as various plant parts are utilized for multiple purposes, including food, raw materials for crafts, clothing, ornamental plants, and traditional medicine. It has been reported to possess anti-diabetic (Windarsih *et al*., 2023), anti-malarial (Frausin *et al*., 2015), and potential heart disease and cancer treatment properties (Nurtiana *et al*., 2022). Additionally, it is used in the production of cigarettes (Fitriyah and Wahyudi, 2022), and the tannin content in leaves suggests their potential as a raw material

---

[*] Corresponding author. e-mail: gut_windarsih@yahoo.com.

for biopesticides (Fatmawaty *et al*., 2019). *Xanthosoma undipes* grows in tropical humid areas and is native to tropical America (POWO, 2024) at elevations between 200 and 2700 m above sea level (Kerbs, 2015; Croat *et al*., 2017). During the era of the transatlantic slave trade, *Xanthosoma* was introduced to Africa, and by the 19th and early 20th centuries, it spread throughout Oceania and into Asia (Jansen and Premchand, 1996). In Indonesia, *X. undipes* has been found in Java, particularly on Mount Karang, Banten (Budiarto and Rahayuningsih, 2017; Fatmawaty *et al*., 2019; Hakiki *et al*., 2019; Yursak *et al*., 2021; Windarsih *et al*., 2023). Since *Xanthosoma* often escapes cultivation and becomes naturalized (Jansen and Premchand, 1996), it is unsurprising that *X. undipes* has also naturalized in mountainous areas.

Two distinct groups of *X. undipes* are found in Mount Karang based on morphological observation, one with a green leaf sheath and the other with a red sheath (Windarsih *et al*., 2023). Morphological data are commonly used for initial evaluations due to their simplicity and speed (Beyene *et al*., 2005). However, this method is vulnerable to environmental factors and subjective interpretation (Fendiyanto *et al.*, 2024). Therefore, molecular techniques, such as DNA sequencing, which is a powerful tool for species identification and evaluation, should be used to support morphological data (Kress *et al*., 2015). DNA-based analysis has been applied to various plants, including *Colocasia esculenta* (L.) Schott (Nunes *et al*., 2015), *Cynosurus cristatus* L., *Dactylis glomerata* L., and *Trisetum flavescens* (L.) P.Beauv. (Loera-Sánchez *et al*., 2020), as well as several plants that produce nectar (Balkanska *et al*., 2020).

The DNA loci commonly used as markers in plant variety analyses are *rbc*L (Talley and Kolondam, 2015), *mat*K (Ali *et al*., 2015), Internal Transcribed Spacer (ITS) (Chen *et al*., 2010) and the *psb*A-*trn*H intergenic spacer (IGS) (Kress *et al*., 2005). The *psb*A-*trn*H IGS locus is an intergenic spacer region in the plant chloroplast genome. It is the most variable barcode region within the Angiospermae group (Kress *et al*., 2005). Due to its tendency to accumulate mutations rapidly, the sequence of the *psb*A-*trn*H IGS locus is currently utilized for establishing lower taxonomic levels, such as genus, species, and subspecies (Kress and Erickson, 2007).

As mentioned earlier, several accessions of *X. undipes* from Mount Karang exhibit variations in morphological characteristics (Windarsih *et al.*, 2023). This morphological variation should be validated using *psb*A-*trn*H IGS molecular data. Therefore, a study was conducted to evaluate variation among *X. undipes* accessions from Mount Karang, using morphological characteristics and the *psb*A-*trn*H IGS marker. The integration of molecular analysis with morphological data presented in this study provides a critical foundation for a new formal classification of the Araceae. It also enhances our understanding of the evolutionary history of this ancient family (Cusimano *et al*., 2011), as *Xanthosoma* is considered as one of the least understood genera in the Araceae family (Croat and Ortiz, 2020).

2. Materials and Methods

2.1. Study area

Samples of *X. undipes* were collected from the Mount Karang area in Pandeglang Regency, Banten Province, Indonesia, between August and October 2023 at three locations: Pandeglang Village in Pandeglang District, Juhut Village in Karang Tanjung District, and Saninten Village in Kaduhejo District (Figure 1). The study sites were selected using purposive sampling.

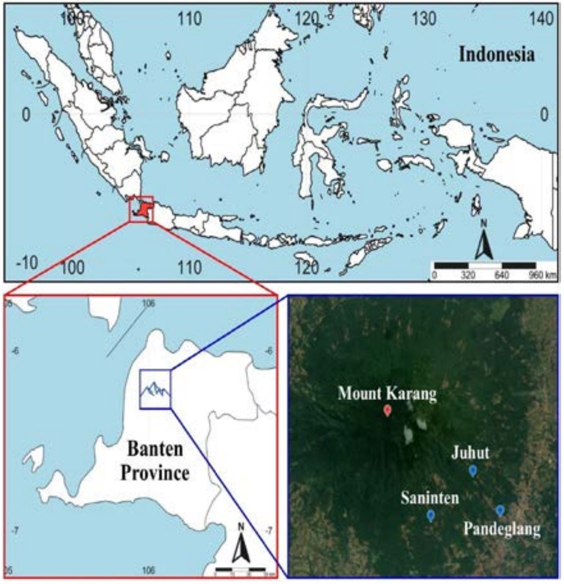

Figure 1. Map showing the sample collection sites in three villages (Pandeglang, Juhut, and Saninten) on Mount Karang, Banten Province, Indonesia.

2.2. Sampling methods

Samples of *X. undipes* were collected as herbarium specimens for morphological study using the method of taxonomic data collection from Rugayah *et al*. (2004). Herbarium specimens were processed using the method of Djarwaningsih *et al*. (2002) and stored at the Herbarium Bogoriense (BO), Herbarium Bandungense (FIPIA), and Herbarium Faculty of Science and Technology Universitas Islam Negeri Sultan Maulana Hasanuddin Banten. Young leaves were also collected for molecular analysis (Table 1), placed in tea bags, and dried using silica gel. Data of *X. undipes* habitat were recorded, including altitude, soil pH and temperature, relative humidity, and air temperature. Measurements were taken three times daily at 10:00, 12:00, and 14:00, respectively, and the average values were calculated.

Table 1. Accessions of *Xanthosoma undipes* from Mount Karang used for molecular analysis.

Accessions	Locations	Coordinates
GW1	Pandeglang Village	6°18'23.8"S 106°06'01.0"E
GW3	Pandeglang Village	6°18'23.2"S 106°06'01.6"E
GW6	Pandeglang Village	6°18'25.1"S 106°05'58.9"E
GW12	Juhut Village	6°17'40.8"S 106°05'27.6"E
GW14	Juhut Village	6°17'33.3"S 106°05'13.2"E
GW18	Saninten Village	6°18'14.5"S 106°03'59.4"E
GW19	Saninten Village	6°18'14.2"S 106°03'59.4"E
GW20	Saninten Village	6°18'15.2"S 106°03'58.2"E
GW21	Saninten Village	6°18'15.4"S 106°04'00.4"E
GW22	Saninten Village	6°18'30.1"S 106°04'05.8"E

2.3. Morphological observation

Herbarium specimens were observed, and morphological data were gathered following the method of Minantyorini and Hanarida (2002). The plant parts observed included corms, cormels, stems, leaves, and inflorescences (Table 2).

Table 2. Morphological characteristics used for scoring in the morphological analysis.

Morphological characters	Scoring
Stem habits	0 = erect; 1 = creeping
Color of corms cortex	0 = white; 1 = pink
Color of corms bud	0 = greenish-yellow; 1 = pink
Color of cormel cortex	0 = white; 1 = white-pink
Color of cormel apex	0 = white-cream/yellowish; 1 = pink
Color of abaxial leaf veins	0 = green; 1 = reddish-green
Color of abaxial leaf petiole junction	0 = green; 1 = pink
Color of leaf sheath margin	0 = yellow with brownish-red spots; 1 = purplish-red
Leaf sheath margin	0 = overlapping; 1 = curving inward
Color of leaf sheath base	0 = whitish; 1 = pink
Color of peduncles	0 = green; 1 = reddish-green
Color of leaf flag	0 = purplish; 1 = pink; 2 = green
Color of outer surface of spathe tube	0 = green; 1 = purplish-dark red
Color of inner surface of spathe tube	0 = light green; 1 = upper part is yellow, lower part is purplish-dark red
Color of outer surface of spathe blade	0 = yellow; 1 = pink
Color of inner surface of curved portion of spathe	0 = yellowish-green; 1 = yellow
Spadix apex	0 = capitate; 1 = rounded; 2 = obtuse
Color of sterile flower	0 = yellowish-cream; 1 = pink
Color of male flower	0 = cream; 1 = pink

2.4. Molecular analyses

DNA isolation was performed using the modified CTAB method (Doyle and Doyle, 1987) with 2% polyvinylpyrrolidone (PVP). PCR amplification was performed using the *psb*A-*trn*H IGS primers (forward: 5’-GTT ATG CAT GAA CGT AAT GCT C-3’ and reverse: 5’-CGC GCA TGG TGG ATT CAC ATT CAC AAT-3’). The PCR reaction was carried out in a 50 µL total volume, containing 25 µL MyTaq Master Mix (Bioline), 10 µL DNA 10 ng/µL, 5 µM of each primer, and 5 µL ddH_2O. The PCR conditions involved an initial denaturation step at 94°C for 5 minutes, followed by 35 cycles of denaturation at 94°C for 30 seconds, annealing at 54°C for 30 seconds, and extension at 72°C for 30 seconds. A final extension was performed at 72°C for 5 minutes. DNA sequencing was performed by 1st Base (https://base-asia.com) with assistance from PT Genetika Science Indonesia.

2.5. Data analyses

The scoring morphological data were analyzed using the Simple Matching (SM) index to assess the similarity among *X. undipes* accessions. Grouping was performed using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) in NTSYs software version 2.02 (Rohlf, 1997). The similarity data were visualized as a dendrogram in TREE format.

Forward and reverse sequences were edited using BioEdit software (Hall, 1999), and their chromatograms were validated to avoid nucleotide reading bias. The two sequences were assembled into a contig and matched against the National Center for Biotechnology Information (NCBI) database. Sequences of *Alocasia macrorrhizos* (L.) G.Don (JN406925.2 and MW940647.1) from NCBI were used as outgroups. All sequences were aligned using the ClustalW method. The phylogenetic tree was constructed using the Maximum Likelihood (ML) method with the Kimura-2-Parameter substitution model and 1000 bootstrap replications. The analysis was performed using MEGA 11 software (Tamura *et al*., 2021). A clade with an ML bootstrap value above 85 indicates strong support, while below 85 indicates low support (Cusimano *et al*., 2011). Nucleotide variations were visualized through multiple sequence alignment using hierarchical clustering on the Multalin web tool (http://multalin.toulouse.inra.fr/multalin) (Corpet, 1988).

3. Results

3.1. Habitat conditions

Habitat conditions varied among *X. undipes* accessions collected from the three locations in Mount Karang, with altitudes ranging from 444–604 m above sea level (a.s.l.), soil pH 6.5–7.0, soil temperature 24–28°C, relative humidity 46–73%, and air temperature 26.8–36.1°C (Table 3).

Table 3. Habitat conditions of *Xanthosoma undipes* collected from Mount Karang.

Accession number	Location (Village)	Altitude (m a.s.l.)	Soil pH	Soil temperature (^oC)	Relative humidity (%)	Air temperature (^oC)
GW1	Pandeglang	444	7.0	27	46	36.1
GW3	Pandeglang	461	6.5	25	58	34.4
GW6	Pandeglang	486	7.0	26	65	30.2
GW12	Juhut	567	7.0	26	73	28.5
GW14	Juhut	604	7.0	26	72	26.8
GW18	Saninten	585	7.0	25	59	29.0
GW19	Saninten	599	7.0	25	63	28.5
GW20	Saninten	590	7.0	28	65	28.1
GW21	Saninten	601	7.0	24	65	28.3
GW22	Saninten	541	7.0	27	56	30.5

3.2. Morphological observation

Xanthosoma undipes accessions from Mount Karang exhibited morphological variation (Table 4). UPGMA analysis revealed high morphological diversity, with similarity coefficients ranging from 0.14 to 1. The dendrogram grouped the *X. undipes* accessions from Mount Karang into two main clades with a similarity coefficient of 0.14, with Clade I including accessions GW1, GW3, GW12, GW14, and GW22, and Clade II comprising GW6, GW18, GW19, GW20, and GW21 (Figure 2). The highest similarity (similarity coefficient = 1) was observed among accessions GW1, GW3, and GW14 in Clade I. Similarly, in Clade II, the highest similarity (similarity coefficient = 1) is observed between GW6 and GW20, as well as between GW18 and GW21.

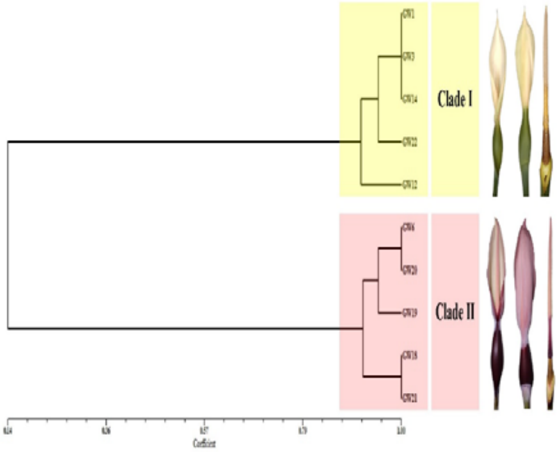

Figure 2. Dendrogram of *Xanthosoma undipes* accessions collected from Mount Karang based on morphological characters, analyzed using UPGMA.

Table 4. Morphological variation of *Xanthosoma undipes* accessions from Mount Karang.

Morphological characters	Accession numbers GW…)
Stem is erect	1, 3, 12, 14, 18, 19, 21, 22
Stem is creeping	6, 20
Corms cortex is white	1, 3, 12, 14, 22
Corms cortex is pink	6, 18, 19, 20, 21
Corms bud is greenish-yellow	1, 3, 12, 14, 22
Corms bud is pink	6, 18, 19, 20, 21
Cormel cortex is white	1, 3, 12, 14, 22
Cormel cortex is white-pink	6, 18, 19, 20, 21
Cormel apex is white-cream/yellowish	1, 3, 12, 14, 22
Cormel apex is pink	6, 18, 19, 20, 21
Abaxial leaf veins is green	1, 3, 6, 12, 14, 19, 20, 22
Abaxial leaf veins is reddish-green	18, 21
Abaxial leaf petiole junction is green	1, 3, 12, 14, 22
Abaxial leaf petiole junction is pink	6, 18, 19, 20, 21
Leaf sheath margin is yellow with brownish-red dots	1, 3, 12, 14, 22
Leaf sheath margin is purplish-red	6, 18, 19, 20, 21
Leaf sheath margin is overlapping	1, 3, 12, 14, 22
Leaf sheath margin is curving inward	6, 18, 19, 20, 21
Leaf sheath base is whitish	1, 3, 12, 14, 22
Leaf sheath base is pink	6, 18, 19, 20, 21
Peduncle is green	1, 3, 12, 14, 22
Peduncle is reddish-green	6, 18, 19, 20, 21
Leaf flag is purplish	1, 3, 12, 14
Leaf flag is pink	6, 18, 19, 20, 21
Leaf flag is green	22
Outer surface of spathe tube is green	1, 3, 12, 14, 22
Outer surface of spathe tube is purplish-dark red	6, 18, 19, 20, 21
Inner surface of spathe tube is light green	1, 3, 12, 14, 22
Inner surface of spathe tube in upper part is yellow, in lower part is purplish-dark red	6, 18, 19, 20, 21
Outer surface of spathe blade is yellow	1, 3, 12, 14, 22
Outer surface of spathe blade is pink	6, 18, 19, 20, 21
Inner surface of curved portion of spathe is yellowish-green	1, 3, 12, 14, 22
Inner surface of curved portion of spathe is yellow	6, 18, 19, 20, 21
Spadix apex is capitate	1, 3, 6, 14, 18, 19, 20, 21, 22
Spadix apex is rounded	12
Spadix apex is obtuse	12
Sterile flower is yellowish-cream	1, 3, 12, 14, 22
Sterile flower is pink	6, 18, 19, 20, 21
Male flower is cream	1, 3, 12, 14, 22
Male flower is pink	6, 18, 19, 20, 21

Morphological characters distinguish *X. undipes* accessions from Mount Karang into two clades, including features such as corm cortex, corm buds, cormel cortex, cormel tips, petiole junction on the underside of the leaf, leaf sheath edges, leaf sheath base, peduncles, outer and inner tube of the spathe, outer and inner spathe blade, sterile flowers, and male flowers (Table 5 and Figure 3).

Tabel 5. Morphological comparison of *Xanthosoma undipes* clades from Mount Karang.

Morphological characters	Clade I	Clade II
Corm cortex	White	Pink
Corm bud	Yellowish-green	Pink
Cormel cortex	White, tip white to cream or yellowish	White with pink hues, tip pink
Abaxial petiole junction	Green	Pink
Leaf sheath margin	Yellow with reddish-brown spots, overlapping	Reddish-purple, curving inward
Leaf sheath base	Whitish	Pink
Peduncle	Green	Greenish-red
Outer spathe tube	Green	Dark red to purplish
Inner spathe tube	Bright green	Yellow at top, dark red to purplish at base
Outer spathe blade	Yellow	Pink
Inner spathe groove	Yellowish-green	Yellow
Sterile flowers	Cream to yellowish	Pink
Male flowers	Cream	Pink

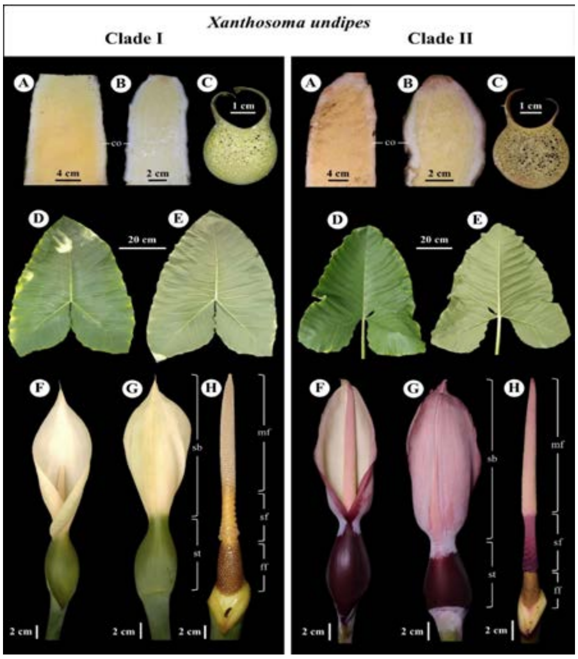

Figure 3. Representative morphological traits of two *Xanthosoma undipes* clades from Mount Karang. A. Corm showing cortex (co); B. Cormel showing cortex (co); C. Cross section of leaf sheath; D. Adaxial leaf; E. Abaxial leaf; F. The front part of inflorescence; G. The back part of inflorescence showing spathe blade (sb) and spathe tube (st); H. Inflorescence, spathe is removed, showing male flowers (mf), sterile flowers (sf), and female flower (ff). Photos: Gut Windarsih.

3.3. Molecular analyses

Based on the phylogenetic tree using the *psb*A-*trn*H IGS marker with Maximum Likelihood method and 1000 Bootstrap, *X. undipes* accessions were grouped into two main clades. Clade I, comprising accessions GW1, GW3, GW12, GW14, and GW22, and Clade II, consisting of GW6, GW18, GW19, GW20, and GW21, were strongly supported by bootstrap values of 100 (Figure 4). A bootstrap value of 100 means that every resampled dataset consistently grouped those accessions into the same clade.

Based on the alignment results and analysis of nucleotide variations (Figure 5), *X. undipes* accessions showed distinct sequence differences from the outgroup, *A. macrorrhizos*, at nucleotide base positions 124–128, 131–135, and 150. A notable difference between the two clades was found at nucleotide base position 156, where clade I had a cytosine (C), while clade II had a thymine (T) (Figure 5).

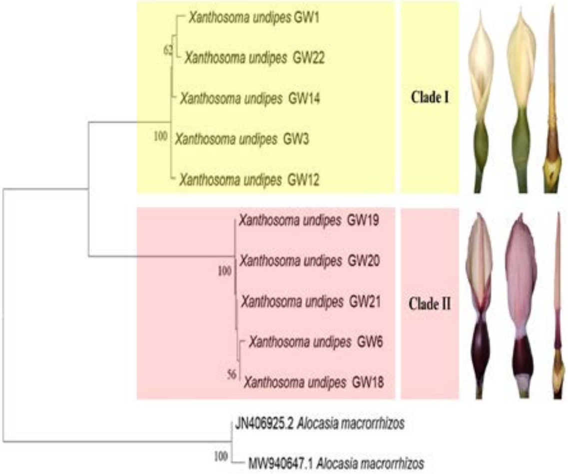

Figure 4. Phylogenetic tree of *Xanthosoma undipes* accessions collected from Mount Karang using the *psb*A-*trn*H IGS marker with Maximum Likelihood and 1000 Bootstrap. Bootstrap percentages are shown next to branches.

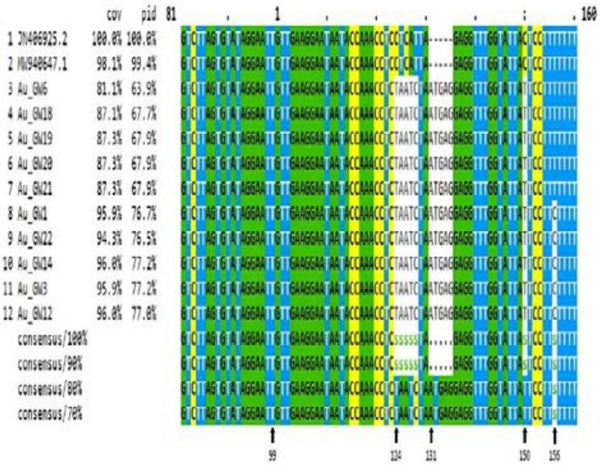

Figure 5. Nucleotide base variation based on the *psb*A-*trn*H IGS locus in *Xanthosoma undipes* accessions collected from Mount Karang.

4. Discussion

Xanthosoma undipes was first described in 1856, highlighting its morphological characteristics (Seemann and Seemann, 1856) and is native to tropical America (POWO, 2024). According to its protologue (Seemann and Seemann, 1856), *X. undipes* features a conspicuous stem, triangular leaves with pointed lobes at the base, and petioles with a wavy sheath. The spadix is slightly curved in the middle, narrower, and shorter than the spathe. Its antheridia, or male reproductive organs, are numerous and have a slightly flattened top (Seemann and Seemann, 1856). Croat *et al.* (2017) in a taxonomic revision of *Xanthosoma* in Central America, further described *X. undipes* as having a large stem, broad leaves with convex major veins, and 5–7 inflorescences per axil. The peduncles are pale green, the spathe blade is pale yellow-green to white outside and white inside, and the tube is usually green with reddish-purple tinges near the tip (sometimes purplish) outside and dark purple-violet inside, especially at the base. The sterile male flowers are white to yellowish cream, while the female flowers are bright orange (Croat *et al*., 2017).

In contrast, *X. undipes* from Indonesia, particularly Mount Karang, exhibit a green or greenish-red peduncle. The outer spathe tube varies from green to dark red or purplish, while the inner spathe tube is bright green or yellow at the top and transitions to dark red or purplish at the base. Additionally, the outer spathe blade is yellow or pink. These findings align with the observations of Windarsih *et al.* (2023) for *X. undipes* in Indonesia. The spathe coloration of *X. undipes* from Central America, as described by Croat *et al.* (2017), appears to exhibit a combination of morphological characteristics observed in the two distinct clades identified among *X. undipes* accessions on Mount Karang. On Mount Karang, *X. undipes* displays spathe colour variations that clearly differentiate the accessions into two clades: Clade I is characterized by a green outer spathe tube, a bright green inner spathe tube, and a yellow outer spathe blade, whereas Clade II exhibits a dark red to purplish outer spathe tube, an inner spathe tube that is yellow at the apex and transitions to dark red-purple at the base, and a pink outer spathe blade.

Beyond spathe coloration, other morphological features, including corm cortex and bud colour, cormel cortex and tip colour, petiole junction colour on the leaf underside, leaf sheath coloration, peduncle colour, and the coloration of both sterile and male flowers, further support the delineation of these two clades. This observation is corroborated by a morphological similarity analysis, which clustered the *X. undipes* accessions from Mount Karang into two primary clades with a similarity coefficient of 0.14 using the UPGMA method (Figure 2). A detailed morphological comparison of these clades is presented in Table 5 and Figure 3. Notably, the most prominent distinctions between the two clades are associated with colour variations in various plant structures.

As well established, the phenotypes or morphological characteristics of a plant are determined by its genes and their interactions (Campbell *et al*., 2002). Environmental factors can influence gene expression, potentially leading to different phenotypes. However, based on the habitat conditions of *X. undipes* collected from Mount Karang (Table 3), no specific habitat conditions were identified as being associated with the phenotype of two clades *X. undipes* on Mount Karang. Further research is needed on the influence of environmental factors on spathe colour variations in *X. undipes*. Nevertheless, it is undeniable that the environment can affect plant phenotypes (Fritz *et al*., 2018). A classic example of environmental factors affecting gene expression is seen in hydrangeas (*Hydrangea* sp.) (Campbell *et al*., 2002; Rahmati *et al*., 2022). In acidic soil (pH < 5.5), hydrangea flowers appear blue due to the availability of aluminium ions, which influence anthocyanin pigments. Conversely, limited aluminium ions result in pink flowers in neutral to alkaline soil (pH > 6.5).

Phylogenetically, molecular analysis using the ML method on *X. undipes* accessions collected from Mount Karang, which utilizing chloroplast DNA sequences from the *psb*A-*trn*H IGS region, revealed results consistent with the UPGMA analysis based on morphological characteristics. This ML analysis of DNA sequencing at the *psb*A-*trn*H IGS locus strongly differentiated (bootstrap = 100) the *X. undipes* accessions from Mount Karang into two distinct clades (Figure 4), with each clade comprising the same set of *X. undipes* accessions as identified in the morphological analysis. The ML clustering with a bootstrap value of 100 is considered strongly supported, according to Cusimano *et al.* (2011). Nucleotide base position 156 at the *psb*A-*trn*H IGS locus (Figure 5) serves as a distinguishing marker between the two clades.

A similar pattern was observed in a phylogenetic study of Araceae, where comparisons were made between morphological characteristics and molecular phylogenies. The clustering analyses based on qualitative morphological characteristics and Simple Sequence Repeat (SSR) markers effectively distinguished the purple *X. sagittifolium* (L.) Schott accessions from the green accessions (Wada *et al*., 2021). Meanwhile, the resulting ML phylogeny is well-resolved and strongly supported, with most of the 44 larger clades of Araceae also exhibiting synapomorphies in morphology (Cusimano *et al*., 2011). Synapomorphies are derived characteristics shared by two or more taxonomic groups (Assis and Rieppel, 2011). In this study, the inflorescence characters (‘spathe + spadix’ model) of *X. undipes* represent a synapomorphic trait that distinguishes the two clades. However, it is crucial to note that the ‘spathe + spadix’ model inflorescence is not exclusively a synapomorphy of Araceae, as plants in the order Acorales also produce a similar type of inflorescence (Tippery *et al*., 2021).

In this study, the accessions *X. undipes* GW18, GW19, GW20, GW21, and GW22, collected from Saninten Village, are known to be the source of planting material for the five other accessions cultivated in Pandeglang Village and Juhut Village. The phenomenon of farmer-to-farmer exchange of planting materials is also commonly observed with *X. sagittifolium* accessions in Ethiopia (Wada *et al*., 2021). The clustering phenomenon suggests that, in the past, clonal propagation of *X. undipes* likely occurred, involving the multiplication of genetically identical individuals through asexual reproduction. Additionally, *X. undipes* may have also reproduced sexually through seeds resulting from cross-pollination, similar to what has been observed in Araceae species, such as *Amorphophallus variabilis* Blume (Santosa *et al*., 2012), *A. konjac* K. Koch (Pan *et al*., 2015), and *Cyrtosperma merkusii* (Hassk.) Schott (Erlinawati *et al*., 2018).

Xanthosoma undipes has strong potential to support food security. Its tubers are a source of carbohydrates, while the leaves can be used as a tobacco substitute and herbal tea. However, the plant remains poorly known (Suhaendah *et al*., 2025). This study contributes to expanding current knowledge of *X. undipes.* On the other hand, traditional vegetative propagation methods often result in limited phenotypic diversity of *X. undipes* (Wardhani *et al*., 2025), thus the findings of this study can serve as baseline data for experimental research, such as propagation.

5. Conclusion

Morphological data reveal two distinct clades of *X. undipes* accessions on Mount Karang, Banten, Indonesia. Some distinguishing morphological characters differentiate the two clades of *X. undipes*, including corms, cormels, leaf petiole junctions, leaf sheaths, peduncles, spathes, sterile flowers, and male flowers. Molecular analysis using the *psb*A-*trn*H IGS marker supports the clustering observed in the morphological data. In the end, morphological and molecular evidence clearly confirmed the presence of two distinct clades among *X. undipes* accessions from Mount Karang.

Acknowledgments

We extend our gratitude to the Faculty of Science, UIN Sultan Maulana Hasanuddin Banten, for funding this research. We extend our sincere gratitude to the Director of Scientific Collection Management (Herbarium Bogoriense), National Research and Innovation Agency, Indonesia, Herbarium Bandungense (FIPIA), and Herbarium Faculty of Science and Technology UIN Sultan Maulana Hasanuddin Banten, for permitting us to deposit the specimens. We also express our sincere appreciation to Maman, Ddedi Muhadi, Azizah Fauziah Rahma, Deni Mulyana, Saiful Iman Maulana, and Fitri Novianti for their valuable assistance in characterizing the morphological features and collecting *Xanthosoma undipes* leaves for molecular analysis. We acknowledge the National Center for Biotechnology Information (NCBI) database for their valuable data. We sincerely thank the Directorate of Repositories, Multimedia, and Scientific Publishing, National Research and Innovation Agency, for the linguistic review (ID: LG20241734903718).

References

Ali MA, Gabor G and Al-Hemaid F. 2015. **Plant DNA Barcoding and Phylogenetics**. Lambert Academic Publishing, Germany. pp. 155-170.

Assis LCS and Rieppel O. 2011. Are monophyly and synapomorphy the same or different? Revisiting the role of morphology in phylogenetics. *Cladistics*., **27(1)**: 94–102. https://doi.org/10.1111/j.1096-0031.2010.00317.x

Balkanska R, Stefanova K, Stoikova-Grigorova R and Ignatova M. 2020. A preliminary assessment of *trn*H-*psb*A as DNA barcode for botanical identification of polyfloral honey samples and comparison with *rbcL* marker. *Bulg J Agric Sci*., **26(1)**: 238–242.

Beyene P, Botha A and Myburg AA. 2005. A comparative study of molecular and morphological methods of describing genetic relationships in traditional Ethiopian highland maize. *Afr J Biotechnol*., **4(7)**: 586–595. https://doi.org/10.5897/AJB2005.000-3107

Budiarto MS and Rahayuningsih Y. 2017. Economic value potency of talas beneng (*Xanthosoma undipes* K. Koch) based on nutrient content. *J Kebij Pembang Daer*., **1(1)**: 1–12. https://doi.org/10.56945/jkpd.v1i1.1

Campbell NA, Reece JB and Mitchell LG. 2002. **Biologi**, edisi kelima, jilid I. Erlangga, Jakarta.

Chen S, Yao H, Han J, Liu C, Song J, Shi L, Zhu Y, Ma X, Gao T, Pang X, Luo K, Li Y, Li X, Jia X, Lin Y and Leon C. 2010. Validation of the ITS2 region as a novel DNA barcode for identifying medicinal plant species. *PLoS One*., **5(1)**: e8613. https://doi.org/10.1371/journal.pone.0008613

Corpet F. 1988. Multiple sequence alignment with hierarchical clustering. *Nucleic Acids Res*., **16(22)**: 10881–10890. https://doi.org/10.1093/nar/16.22.10881

Croat TB and Ortiz OO. 2020. Distribution of Araceae and the diversity of life forms. *Acta Soc Bot Pol*., **89(3)**: 8939. https://doi.org/10.5586/asbp.8939

Croat TB, Delannay X and Ortiz OO. 2017. A revision of *Xanthosoma* (Araceae). Part 2: Central America. *Aroideana*., **40(2)**: 504–581.

Cusimano N, Bogner J, Mayo SJ, Boyce PC, Wong SY, Hesse M, Hetterscheid WLA, Keating RC and French JC. 2011. Relationships within the Araceae: Comparison of morphological patterns with molecular phylogenies. *Am J Bot*., **98(4)**: 654–668. https://doi.org/10.3732/ajb.1000158

Djarwaningsih T, Sunarti S and Kramadibrata K. 2002. **Panduan Pengolahan dan Pengelolaan Material Herbarium serta Pengendalian Hama Terpadu di Herbarium Bogoriens**e. Herbarium Bogoriense-Bidang Botani, Pusat Penelitian Biologi, Lembaga Ilmu Pengetahuan Indonesia, Bogor.

Doyle JJ and Doyle JL. 1987. A rapid DNA isolation from small amount of fresh leaf tissue. *Phytochem Bull*., **19**: 11−15.

Erlinawati I, Abinawanto, Salamah A and Rugayah. 2018. Genetic diversity analysis of daluga (*Cyrtosperma merkusii*) using sequence-related amplified polymorphism in Siau, Sangihe and Talaud Islands, North Sulawesi, Indonesia. *Biodiversitas*., **19(6)**: 2374–2380. https://doi.org/10.13057/biodiv/d190648

Fatmawaty AA, Hermita N, Hastuti D, Kartina AM and Hilal S. 2019. Phytochemical analysis of beneng taro (*Xanthosoma undipes* K. Koch) leaves: Cultivation as raw material for biopesticides for eco-friendly agriculture. *IOP Conf Ser: Earth Environ Sci*., **383:** 012006. https://doi.org/10.1088/1755-1315/383/1/012006

Fendiyanto MH, Supena EDJ, Sari IE, Pratami MP, Satrio RD and Nikmah IA. 2024. Biological diversity of seawater microalgae isolated from Ujung Genteng Sukabumi and their novel genomic DNA isolation technique. *Jordan J Biol Sci*., **17(3)**: 495–505. https://doi.org/10.54319/jjbs/170312

Fitriyah N and Wahyudi M. 2022. Efektivitas penambahan zat pengatur tumbuh pada stek mikro tanaman porang (*Amorphophallus muelleri* Blume) dan talas beneng (*Xanthosoma undipes* K. Koch). *Innofarm*., **24(2)**: 64–72.

Frausin G, Lima RBS, Hidalgo AF, Ming LC and Pohlit AM. 2015. Plants of the Araceae for malaria and related diseases: A review. *Rev Bras Plantas Med*., **17(4)**: 1–21. https://doi.org/10.1590/1983-084X/14_024

Fritz MA, Rosa S and Sicard A. 2018. Mechanisms underlying the environmentally induced plasticity of leaf morphology. *Front Genet*., **9**: 478. https://doi.org/10.3389/fgene.2018.00478

Hakiki DN, Rostianti T, Nasir and Nursuciyoni. 2019. Development of local food biodiversity of nata de taro from talas beneng (*Xanthosoma undipes* K. Koch). *IOP Conf Ser: Earth Environ Sci*., **309:** 012030. https://doi.org/10.1088/1755-1315/309/1/012030

Hall TA. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symp Ser*., **41**: 95–98.

Jansen PCM and Premchand V. 1996. *Xanthosoma* Schott. In: Flach, M., & Rumawas, F. (Editors). **Plant Resources of South-East Asia** No. 9: Plants yielding non-seed carbohydrates. PROSEA Foundation, Bogor, Indonesia. pp. 159–164.

Kerbs B. 2015. *Xanthosoma undipes* (Araceae) as a food source for black-chinned mountain-tanager (*Anisognathus notabilis*) and orange-bellied euphonia (*Euphonia xanthogaster*) in northwest Ecuador. *Ornitol Neotrop*., **26(1)**: 103–107. https://doi.org/10.58843/ornneo.v26i1.16

Kress WJ and Erickson DL. 2007. A Two-locus global DNA barcode for land plants: The coding *rbc*L gene complements the non-coding *trn*H–*psb*A spacer region. *PLoS One*., **2(6):** e508. https://doi.org/10.1371/journal.pone.0000508

Kress WJ, Garcia-lobredo C, Uriarte M and Erickson DL. 2015. DNA Barcodes for Ecology, Evolution, and Conversation. *Trends Ecol Evol*., **30(1)**: 25–35. https://doi.org/10.1016/j.tree.2014.10.008

Kress WJ, Wurdack KJ, Zimmer EA, Weigt LA and Janzen DH. 2005. Use of DNA barcodes to identify flowering plants. *Proc Natl Acad Sci U S A*., **102(23):** 8369–8374. https://doi.org/10.1073/pnas.0503123102

Loera-Sánchez M, Studer B and Kölliker R. 2024. DNA barcode *trn*H-*psb*A is a promising candidate for efficient identification of forage legumes and grasses. *BMC Res Notes*., **13(35)**: 1–6. https://doi.org/10.1186/s13104-020-4897-5

Minantyorini and Hanarida I. 2002. **Panduan Karakterisasi dan Evaluasi Plasma Nutfah Talas**. Departemen Pertanian Badan Penelitian dan Pengembangan Pertanian Komisi Nasional Plasma Nutfah, Bogor, Indonesian.

Nunes RSC, Aguila EMD, Paschoalin VMF and da Silva JT. 2015. DNA barcoding assessment of the genetic diversity of varieties of taro, *Colocasia esculenta* (L.) Schott in Brazil. **Breeding and Genetic Engineering**. iConcept Press Ltd., Queensland.

Nurtiana W, Rismaya R, Sulistyawati EYE, Fauziyyah A, Hakiki DN, Radiansyah MR and Rahmawan A. 2022. The effect of beneng taro (*Xanthosoma undipes* K.Koch) flour substitution on physical and sensory characteristics of muffins. ~~*Food Sci Tech J*~~ *Food ScienTech J*., **4(2)**: 129–144. https://doi.org/10.33512/fsj.v4i2.17413

Pan C, Gichira AW and Chen JM. 2015. Genetic variation in wild populations of the tuber crop *Amorphophallus konjac* (Araceae) in central China as revealed by AFLP markers. *Genet Mol Res*., **14(4)**: 18753–18763. https://doi.org/10.4238/2015.December.28.24

POWO [Plants of the World Online]. 2023. **Plants of the World Online**. Facilitated by the Royal Botanic Gardens, Kew. http://www.plantsoftheworldonline.org/. [2 December 2023].

Rahmati R, Hamid R, Ghorbanzadeh Z, Jacob F, Azadi P, Zeinalabedini M, Farsad LK, Kazemi M, Ebrahimi MA, Shahinnia F, Salekdeh GH, Ghaffari MR and Hajirezaei MR. 2022. Comparative transcriptome analysis unveils the molecular mechanism underlying sepal colour changes under acidic pH substratum in *Hydrangea macrophylla*. *Int J Mol Sci*., **23(23)**: 15428. https://doi.org/10.3390/ijms232315428

Rohlf FJ. 1997. **NTSYS-pc. Numerical taxonomy and multivariate analysis. Version 2.0**. Exeter Software, New York.

Rugayah, Retnowati A, Windadri FI and Hidayat A. 2004. Pengumpulan Data Taksonomi. In: Rugayah, Widjaja EA and Praptiwi (Eds.). **Pedoman Pengumpulan Data Keanekaragaman Flora**. Pusat Penelitian Biologi-LIPI, Bogor, Indonesia. pp. 5–42.

Santosa E, Sugiyama N, Kawabata S and Hikosaka S. 2012. Genetic variations of *Amorphophallus variabilis* Blume (Araceae) in Java using AFLP. *J Agron Indones*., **40(1)**: 62–68. https://doi.org/10.24831/jai.v40i1.14941

Seemann WEG and Seemann B. 1856. **Bonplandia**. Zeitschrift für die gesammte Botanik. C. Rümpler, Hannover.

Suhaendah E, Sudomo A, Suhartono S, Fauziyah E and Geraldine LA. 2025. Understory cultivation practices of *Xanthosoma undipes* K.Koch: Lessons learned from private forests in Sukabumi, West Java, Indonesia. *AIP Conf Proc*., **3172(1)**: 020012. https://doi.org/10.1063/5.0240941

Talley TE and Kolondam BJ. 2015. DNA barcoding of Sangihe Nutmeg (*Myristica fragrans*) using *mat*K gene. *Hayati J Biosci*., **22(1)**: 41–47. https://doi.org/10.4308/hjb.22.1.41

Tamura K, Stecher G and Kumar D. 2021. MEGA11: Molecular evolutionary genetics analysis version 11. *Mol Biol Evol*., **38(7)**: 3022–3027. https://doi.org/10.1093/molbev/msab120

Tippery NP, Les DH, Appenroth KJ, Sree KS, Crawford DJ and Bog M. 2021. Lemnaceae and Orontiaceae are phylogenetically and morphologically distinct from Araceae. *Plants*., **10(12)**: 2639. https://doi.org/10.3390/plants10122639

Wada E, Feyissa T, Tesfaye K, Asfaw Z and Potter D. 2021. Genetic diversity of Ethiopian cocoyam (*Xanthosoma sagittifolium* (L.) Schott) accessions as revealed by morphological traits and SSR markers. *PLoS One*., **16(1)**: e0245120. https://doi.org/10.1371/journal.pone.0245120

Wardhani KA, Dinarti D, Santosa E and Nurcholis W. 2025. Gamma ray irradiation effects on embryogenic calli growth in Indonesian taro. *Pertanika J Trop Agric Sci*., **48(3)**: 733–746. https://doi.org/10.47836/pjtas.48.3.05

Windarsih G, Rahma AF, Mulyana D, Hariri MR, Erlinawati I, Riastiwi I and Efendi M. 2023. Pragmatical utilization of beneng taro (*Xanthosoma undipes* K.Koch) based on local knowledge of the community of Mount Karang, Pandeglang, Indonesia. *Biodiversitas*., **24(12)**: 6415–6424. https://doi.org/10.13057/biodiv/d241202

Yursak Z, Hidayah I, Saryoko A, Kurniawati S, Ripasonah O and Susilawati PN. 2021. Morphological characterization and development potential of beneng variety (*Xanthosoma undipes* K. Koch) Pandeglang - Banten. *IOP Conf Ser: Earth Environ Sci*., **715**: 012022. https://doi.org/10.1088/1755-1315/715/1/012022