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Morphological and Molecular Identification of Porang Plants in Manggarai Regency, East Nusa Tenggara

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ABSTRACT: Porang (*Amorphophallus* sp.) is a high-value tropical commodity due to its glucomannan content, which is widely utilized in the food and pharmaceutical industries. Accurate species identification is essential to ensure genetic purity and support sustainable cultivation. This study combines morphological and molecular approaches to identify Porang plants from Desa Sita, East Manggarai Regency. Morphological characteristics were observed on the leaves, pseudostems, and corms. Molecular analysis was conducted through DNA amplification using the chloroplast matK gene marker, followed by DNA sequencing, BLAST analysis, and phylogenetic reconstruction using the Maximum Likelihood method with 1000 bootstrap replicates. Morphological observations revealed typical features of the genus *Amorphophallus*, including compound leaves, cylindrical pseudostems, and corm-type tubers. PCR amplification produced a single DNA band of approximately 800 bp, indicating successful target gene amplification. Homology analysis showed 90–100% sequence similarity with reference species. Phylogenetic analysis demonstrated that Porang 1 is closely related to *Amorphophallus bulbifer*, while Porang 2 clusters with to *Amorphophallus muelleri*. The integration of morphological identification and matK DNA barcoding proves effective in confirming taxonomic identity and genetic relationships of Porang plants. This approach has potential to support germplasm conservation and the development of Porang as a sustainable bioindustrial commodity in Indonesia.

KEYWORDS: porang, DNA barcode, matK, phylogenetics, molecular identification

I. INTRODUCTION

Porang *(Amorphophallus sp.)* is a tuber-producing plant with high economic value and significant potential to increase farmers' income. This plant is widely cultivated in Indonesia because it grows well under tropical climatic conditions (Ikayanti *et al*., 2021). Porang tubers contain the primary compound glucomannan (mannan), which has substantial economic value and is widely utilized in various industries, including food, cosmetics, adhesives, textiles, and paper (Sumarwoto, 2007). Therefore, optimal development of Porang cultivation could contribute to increasing non-oil export commodities and improving community welfare. Market demand for Porang continues to rise in various forms such as fresh tubers, dried chips, and flour. Indonesia has exported Porang products to several countries including Japan, Australia, Malaysia, Korea, the United Kingdom, and Italy. However, national Porang production remains limited because cultivation practices are not yet fully intensive, the cultivation area is still relatively small, and optimal cultivation guidelines are not yet widely available (Wijanarko, 2009). One of the regions that has recently begun developing Porang cultivation is East Manggarai Regency, East Nusa Tenggara Province, particularly in Lendo Hamlet, North Kota Komba District. This area is becoming known as a Porang production center that provides economic benefits for the local community. In 2024, farmers in the region were able to produce Porang valued at approximately IDR 9,000/kg, generating a total production value of around IDR 9 billion. Preliminary characterization indicated that local Porang from East Manggarai can reach a maximum tuber weight of 7.2 kg, with an average of approximately 4 kg per tuber, and exhibits relatively diverse morphological characteristics. Nevertheless, scientific identification of Porang species in East Manggarai Regency has not yet been conducted. Plant species identification can be performed through morphological and molecular approaches. Morphological identification relies on similarities in plant structure; however, these characteristics can be influenced by environmental conditions and plant growth stages (Sarjani *et al*., 2017). Therefore, molecular approaches are required to obtain more accurate species identification. In molecular analysis, DNA extraction is an essential initial step to obtain purified DNA that will subsequently be used for

amplification through the Polymerase Chain Reaction (PCR) method. PCR allows the amplification of specific DNA fragments from limited DNA quantities, enabling further analysis including DNA sequencing (Gabriyan & Avashia, 2013). This approach can be used to determine species identity and genetic relationships among plants. Based on these considerations, this study aimed to identify Porang plants in East Manggarai Regency using both morphological and molecular approaches in order to determine their characteristics and genetic relationships.

II. RESEARCH METHODS

A. MATERIALS

The materials used in this study included fresh leaf and tuber samples of Porang plants collected from East Manggarai Regency, 96% alcohol, distilled water, TAE buffer, ethanol, matK primers, Quick-DNA Plant/Seed Miniprep Kit (Geneaid), liquid nitrogen, PCR kit, agarose gel, and template DNA.

B. LOCATION

Field sampling was conducted using purposive sampling in Sita Village, Rana Mese District, East Manggarai Regency, East Nusa Tenggara Province (coordinates: −8.713983, 120.571619). The study was carried out from September 2025 to February 2026 at the Biotechnology Laboratory, Faculty of Agriculture, Udayana University, while DNA sequencing was performed at 1st BASE Malaysia.

C. MORPHOLOGICAL IDENTIFICATION

This study aimed to characterize the morphology of Porang plants originating from East Manggarai Regency. Observations were conducted directly in the field through visual observation and documentation of plant parts including the canopy, stem, leaves, and flowers. Morphological characterization followed the plant morphology guidelines proposed by Tjitrosoepomo (2001). The obtained morphological data were then compared with previously reported Porang morphological characteristics from studies conducted in Indonesia and other countries to obtain a preliminary species identification. The observed characteristics included stem morphology (type, shape, structure, surface, color, growth direction, branching pattern),leaf morphology (type, shape, margin, apex, base, venation, surface color, texture, thickness, area, and leaf arrangement) and tuber morphology (shape, color, and position).

D. MOLECULAR IDENTIFICATION

Leaf samples of Porang plants were collected from Sita Village, Rana Mese District, East Manggarai Regency, East Nusa Tenggara. The samples were washed with clean water to remove dirt and pesticide residues. Approximately 20 g of fresh leaves were stored at 4°C to maintain sample quality prior to molecular analysis. Total DNA extraction was performed using the Quick-DNA Plant/Seed Kit (Geneaid). Approximately 50–100 mg of leaf tissue was homogenized and mixed with extraction buffer and RNase A, followed by incubation at 60°C for 10 minutes. The mixture was then centrifuged and purified using a spin column, and the purified DNA was eluted using elution buffer. The extracted DNA was amplified using PCR with the matK gene primer, targeting a fragment of approximately 850 bp. The PCR reaction was performed in a total volume of 50 µL. PCR products were analyzed using gel electrophoresis to visualize amplified DNA bands. PCR products were analyzed using 1% agarose gel electrophoresis in TBE buffer. DNA samples were loaded into gel wells together with a 100 bp DNA marker and run at 90 V for approximately 30 minutes. The resulting DNA bands were visualized under UV illumination. Successful PCR products were sequenced bidirectionally using forward and reverse primers. The resulting sequences were analyzed using BLAST in the NCBI database to determine sequence similarity. Sequence alignment was performed using ClustalW in MEGA software. The obtained DNA sequences were compared with GenBank sequences with the highest similarity values. Phylogenetic trees were constructed using the Maximum Likelihood (ML) method in MEGA software, with 1000 bootstrap replicates to assess tree topology reliability.

III. RESULT

A. MORPHOLOGICAL IDENTIFICATION RESULTS

Morphological observations indicated that the leaves of Porang plants are arranged as compound leaves. Porang 1 exhibited a pinnatisect leaf type with lanceolate leaflets, entire margins, an acuminate apex, and a cuneate base. The venation was clearly pinnate, with a smooth and glossy surface, dark green coloration, moderate thickness, and a flexible, non-succulent texture. In contrast, Porang 2 showed a palmate leaf type with leaflets ranging from lanceolate to elliptic in shape. The leaf margins were entire to slightly undulate, with an acuminate apex and an attenuate base. The venation pattern was pinnate with a prominent midrib, while the leaf surface appeared smooth and reflective, with coloration ranging from light green to dark green. The leaf thickness was thin to moderate, and the texture was herbaceous.All paragraphs must be indented. All paragraphs must be

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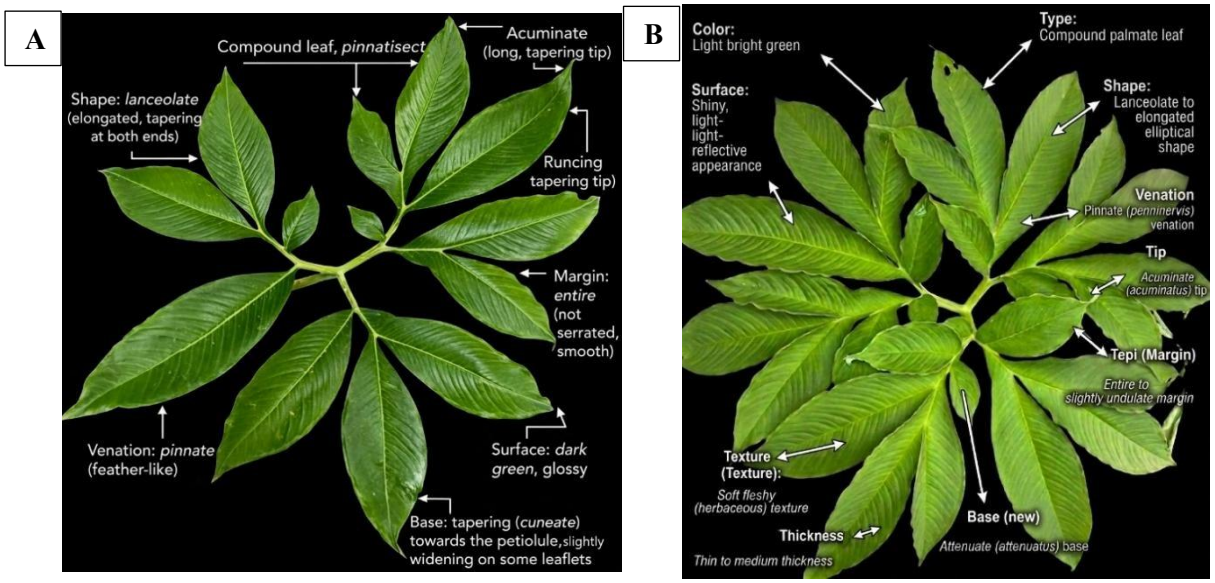


Figure 1. Leaf morphology of Porang Plant 1 (A) and Porang Plant 2 (B) from Sita Village

Morphological observations showed that the stems of both Porang individuals are cylindrical pseudostems *(terete)* formed from the modification of the petiole *(petiolus),* with a smooth *(glabrous)* surface and a herbaceous structure. Porang 1 had a stem height of approximately 20 cm with a diameter of about ±8 cm, whereas Porang 2 was considerably taller, reaching 148 cm, but with a smaller diameter of approximately ±5 cm. Stem growth was upright without true branching, although pseudo-branching appeared at the apex, forming a palmate pattern. The stem color was green with irregular mottled spots, which represents a typical morphological characteristic of the genus *Amorphophallus*.

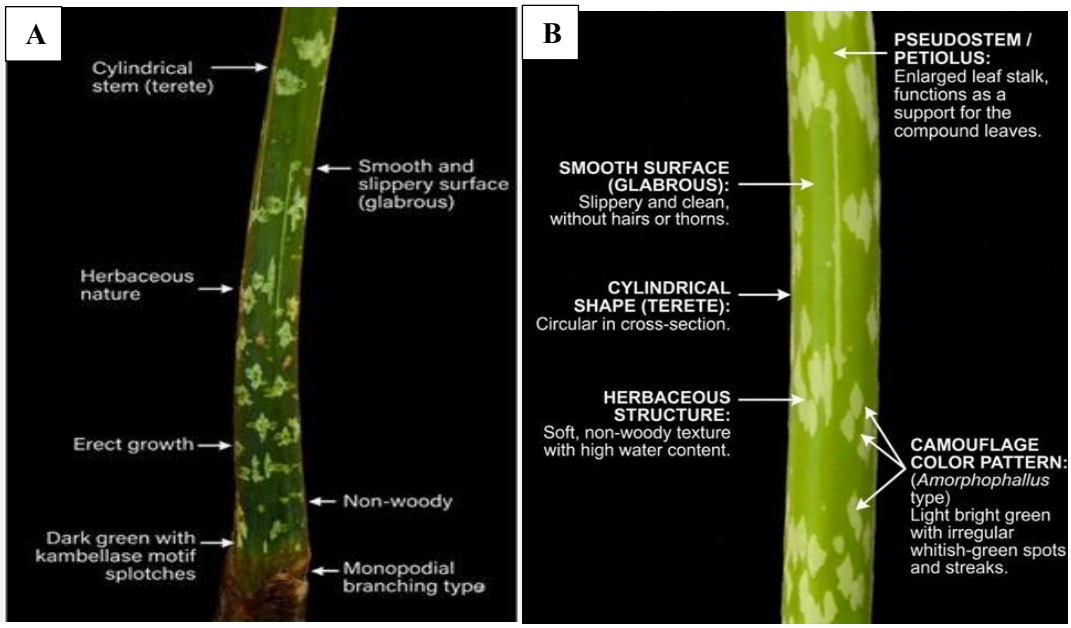


Figure 2. Stem morphology of Porang Plant 1 (A) and Porang Plant 2 (B) from Sita Village.

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Morphological observations indicated that the tubers of both Porang individuals are modified stem tubers (corms) with a round to flattened-round shape. Porang 1 had a tuber diameter of approximately 9.8 cm, whereas Porang 2 was larger, reaching 14.5 cm in diameter. The tuber surface was dark brown to blackish with a rough texture and small protrusions, and remnants of root tissues were also observed. The main bud eye was clearly visible in a depression located at the apical part of the tuber (Porang 1) or near the central region (Porang 2), indicating the location of the active meristem responsible for subsequent vegetative growth.

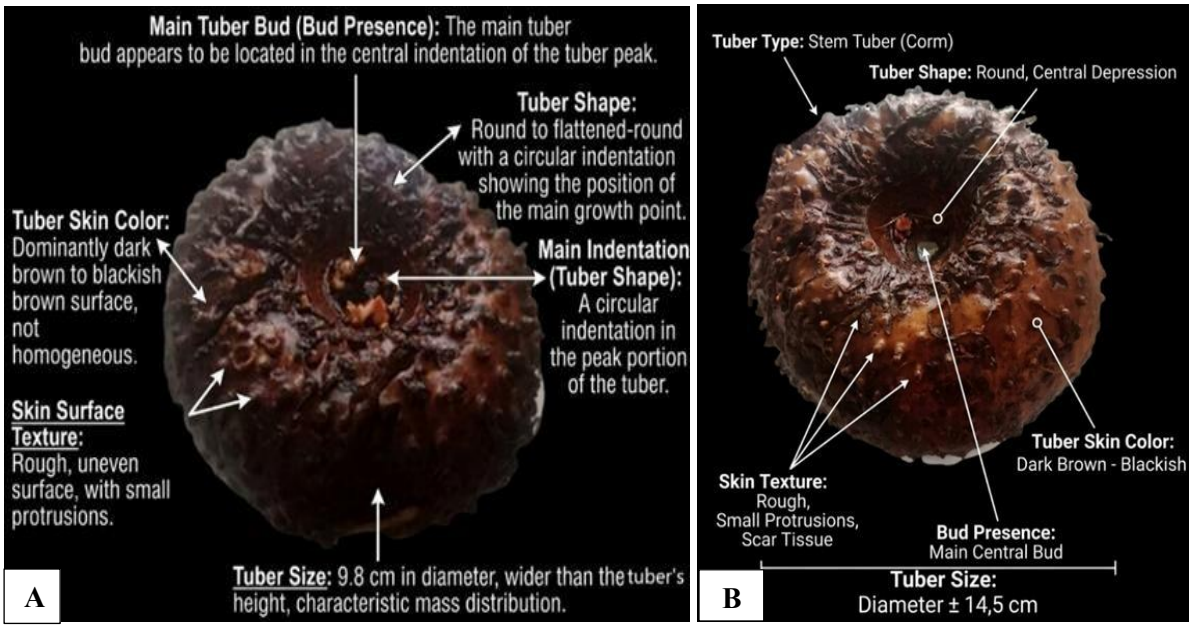


Figure 3. Morphology of the corm of Porang Plant 1 (A) and Porang Plant 2 (B) from Sita Village

B. MOLECULAR IDENTIFICATION

Molecular identification of the Porang plants, conducted using PCR techniques and genetic sequence analysis, revealed that both samples collected from Sita Village exhibit a very high sequence similarity with species within the genus *Amorphophallus*. The electrophoresis image in Figure 4 shows DNA bands corresponding to a length of approximately 800 bp, which represents the size of the targeted gene identified.

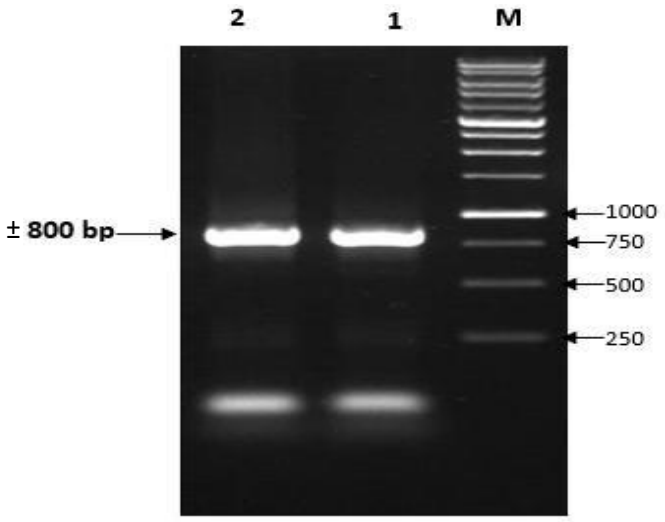


Figure 4. Visualization of Electrophoresis of Porang Plant Samples 1 and 2 from Sita Village under a UV Transilluminator.

As shown in Table 1, the two Porang plant samples (1 and 2) exhibit very high similarity with several *Amorphophallus* species, including *Amorphophallus muelleri*, *Amorphophallus hirtus*, and *Amorphophallus bulbifer*, with DNA sequence similarity ranging from 90–100% according to GenBank database records. This indicates that both samples share a high degree of genetic similarity with species of the genus *Amorphophallus*, suggesting that the Porang plants belong to the same genus as the species documented in these genetic databases.

Table 1. DNA Sequence Identity Matrix of Porang Plant Samples 1 and 2 from Sita Village.

NO	Sekuen	No Aksesi Genbank	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	Tanaman Porang 1 Desa Sita	Na	ID																
2	Tanaman porang 2 Desa Sita	Na	90%	ID															
3	*Amorphophallus muelleri*	AF387406.1	90%	90%	ID														
4	*Amorphophallus hirtus*	AF387396.1	90%	89%	100%	ID													
5	*Amorphophallus ochroleucus*	AF387409.1	90%	89%	100%	100%	ID												
6	*Amorphophallus bulbifer*	MT850190.1	90%	89%	99%	99%	99%	ID											
7	*Amorphophallus symonianus*	AF387419.1	90%	89%	100%	100%	100%	99%	ID										
8	*Amorphophallus yunnanensis*	AF387423.1	90%	89%	99%	99%	99%	98%	99%	ID									
9	*Amorphophallus henryi*	AF387394.1	90%	89%	99%	99%	99%	98%	99%	99%	ID								
10	*Amorphophallus konjac*	AF387398.1	90%	89%	99%	99%	99%	98%	99%	99%	99%	ID							
11	*Amorphophallus pulchellus*	KU523488.1	90%	89%	99%	98%	98%	99%	98%	98%	98%	99%	ID						
12	*Amorphophallus lanuginosus*	KU523463.1	90%	89%	99%	99%	99%	99%	99%	99%	98%	99%	99%	ID					
13	*Amorphophallus amygdaloides*	KU523411.1	90%	89%	99%	99%	99%	98%	99%	100%	99%	99%	98%	98%	ID				
14	*Amorphophallus pilosus*	KU523483.1	90%	89%	99%	99%	99%	99%	99%	98%	98%	98%	99%	100%	98%	ID			
15	*Amorphophallus brevispathus*	AF387384.1	90%	89%	99%	99%	99%	98%	99%	99%	99%	99%	98%	99%	99%	99%	ID		
16	*Amorphophallus cicatricifer*	KU523427.1	90%	89%	99%	99%	99%	99%	99%	98%	98%	98%	99%	99%	98%	98%	99%	ID	
17	*Arisaema triphyllum*	OR464987.1	87%	86%	96%	96%	96%	95%	96%	96%	95%	97%	95%	95%	96%	95%	95%	96%	ID

The phylogenetic tree presented in Figure 5 illustrates the genetic relationships between the Porang plant samples from Sita Village, Indonesia, and various *Amorphophallus* species from different countries. Based on genetic sequence analysis, both Porang samples (1 and 2) show a close relationship with multiple species within the genus *Amorphophallus*, such as *Amorphophallus bulbifer* (Brazil) and *Amorphophallus muelleri* (Netherlands), with DNA sequence similarity reaching 94%. In this phylogenetic tree, both Porang samples from Sita Village cluster within the same clade as other *Amorphophallus* species, indicating a high level of genetic similarity between them. The clade divisions observed in the tree reveal two major groups based on genetic proximity: Porang Plant 1 from Sita Village is more closely related to *Amorphophallus bulbifer*, whereas Porang Plant 2 from Sita Village is more closely related to *Amorphophallus muelleri*.

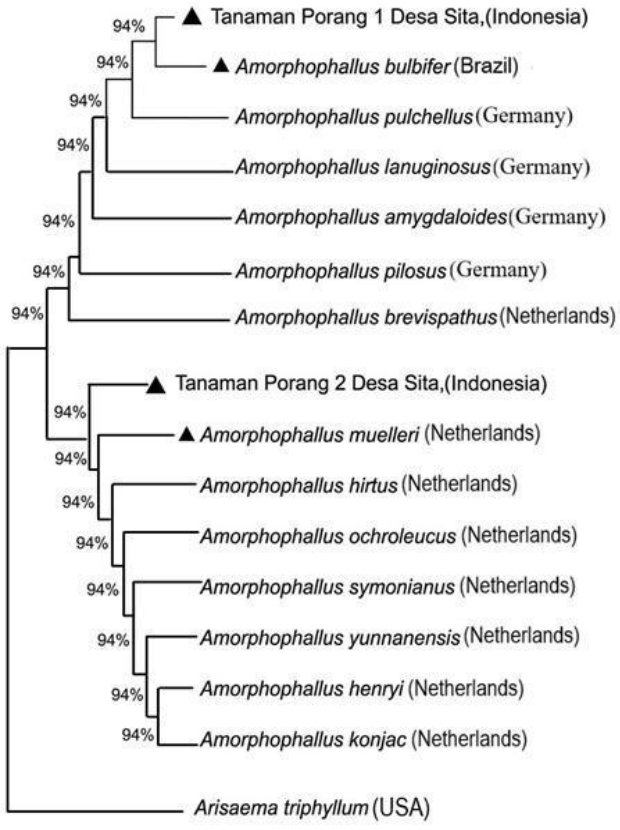


Figure 5. Phylogenetic Tree of Porang Plant Samples 1 and 2 Constructed Using the Maximum Likelihood Method with 1000 Bootstrap Replications.

IV. DISCUSSION

Morphological observations of Porang leaves revealed variations in vegetative development that can serve as indicators of growth stage and physiological adaptation. The palmate leaves of Porang 2 exhibited a younger growth phase compared to Porang 1, as indicated by the lighter leaf coloration due to incomplete chloroplast differentiation, a common condition in young leaves with high photosynthetic activity but still-developing chlorophyll reserves (Putri *et al*., 2021). Slightly undulating leaf margins increase the photosynthetic surface area without significantly increasing tissue biomass, whereas the attenuate leaf base supports mechanical load distribution in large compound leaves, reflecting a structural adaptation for energy efficiency and mechanical strength (Sari *et al*., 2021). Moreover, the uniformity of leaf venation patterns suggests genetic stability of leaf morphology, making this trait a relevant preliminary parameter for taxonomic identification prior to molecular analysis.

Morphological analysis of Porang stems provides insights into vegetative growth strategies and structural adaptations supporting photosynthetic function and mechanical stability. The presence of a pseudostem reflects a characteristic morphological feature of the Araceae family, in which the true stem develops underground as a corm, while the leaf stalk functions as vegetative support (Nugraha *et al*., 2022). The cylindrical shape and smooth stem surface indicate mechanical adaptation to support large compound leaves while minimizing pathogen colonization on the epidermis, whereas the dominance of parenchyma tissue underscores the stem's physiological role as temporary water storage during early vegetative growth. Differences in stem dimensions among individuals suggest distinct growth strategies: Porang 1, with a shorter stem and larger diameter, reflects vegetative stability and optimal support for the leaf crown, whereas Porang 2, with a taller stem and smaller diameter, prioritizes vertical growth as a response to light competition in its growing environment (Mutaqin *et al*., 2024; Lestari *et al*., 2024). The consistent mottled coloration observed in both individuals indicates a conserved trait within the genus *Amorphophallus*, while variation in stem dimensions appears more influenced by environmental conditions than by major genetic changes (Ardhani *et al*., 2023).

Morphological analysis of Porang corms provides critical insight into vegetative adaptation strategies and energy storage capacity that support plant regeneration in the following growth season. The corm-type tuber is an adaptive structure characteristic of the genus *Amorphophallus*, functioning as a center for energy reserve storage and a regenerative organ (Kurniawan *et al*., 2022). The broad distribution of corm mass reflects uniform accumulation of photosynthates during prior growth phases, while the larger corm size in Porang 2 indicates a higher capacity for nutrient storage and a positive correlation with subsequent vegetative vigor (Prasetyo & Nugroho, 2022). The presence of an apical depression with a clearly visible shoot meristem marks an active growth point capable of developing into a pseudostem and leaves in the next growth season, simultaneously serving as an indicator of physiological dormancy (Fauzi & Nugroho, 2022). Dark corm skin coloration is associated with physiological maturity and the accumulation of phenolic compounds as protection against soil microorganisms, whereas a coarse texture enhances mechanical resistance to environmental stress (Setianingsih *et al*., 2021; Lee *et al*., 2021).

Phylogenetic analysis revealed that both Porang samples from Sita Village cluster into two separate clades based on their genetic proximity to other *Amorphophallus* species. High bootstrap values (94%) in the phylogenetic tree indicate strong confidence in the species grouping, consistent with modern phylogenetic standards using multi-locus approaches (Moss *et al*., 2020). The sequence similarity of Porang 1 to *Amorphophallus bulbifer* from Brazil and Porang 2 to *Amorphophallus muelleri* from the Netherlands demonstrates that both samples have close phylogenetic relationships with species known outside Indonesia. Porang 1 shows affinity to *Amorphophallus bulbifer* and several other species from Germany, such as *Amorphophallus* lanuginosus and *Amorphophallus* pulchellus, consistent with findings by Cusimano *et al*. (2021), which indicated high diversity within the genus *Amorphophallus* and differential adaptation under local environmental selection pressures. Porang 2 is closely related to *Amorphophallus muelleri* and *Amorphophallus* konjac, which share morphological traits and industrial applications (Jansen *et al*., 2020).

These findings support the hypothesis that Porang plants in Indonesia may belong to widely distributed *Amorphophallus* species, with potential for development in food and health industries. The observed clade division indicates that samples fro m Sita Village, despite showing proximity to foreign species such as *Amorphophallus bulbifer* (Brazil) and *Amorphophallus* konjac (Netherlands), reflect data repository locations rather than natural species distribution. As noted by Zhang *et al*. (2022), in phylogenetic analyses based on public databases such as GenBank, country labels do not necessarily correspond to the species' natural geographic origin. Therefore, interpretation of species origin in this study should also consider morphological and ecological evidence. The close relationship of Porang with *Amorphophallus muelleri*, which is widely cultivated in Indonesia, suggests comparable economic potential for Sita Village Porang in food and pharmaceutical industries due to its high glucomannan content (Jansen *et al*., 2020). Research by Puspita *et al*. (2021) highlights the substantial potential of Indonesian Porang as a premium commodity in international markets, especially as a source of food and health products based on glucomannan. The genetic proximity observed in this study is significant. Further research involving multi-locus or whole-genome analyses will be

crucial to enhance phylogenetic resolution and provide a deeper understanding of relationships among *Amorphophallus* species. As Zhang *et al*. (2022) emphasized, genomics-based approaches can yield more accurate phylogenetic trees and reveal complex species relationships.

V. CONCLUSION

Porang plants exhibit variation in leaf, stem, and corm morphology, reflecting structural adaptations to their environment and growth stages. Meanwhile, molecular identification through phylogenetic analysis indicates that Porang Plant 1 from Sita Village is genetically closer to *Amorphophallus bulbifer*, whereas Porang Plant 2 shows a closer genetic relationship to *Amorphophallus muelleri*.

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