RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
58 (1) 215-226, 2026
http://doi.org/10.54910/sabrao2026.58.1.20
http://sabraojournal.org/z
pISSN 1029-7073; eISSN 2224-8978

MORPHOLOGICAL AND ISSR MARKER-BASED DIVERSITY OF LOCAL TARO (*COLOCASIA ESCULENTA* L.) IN SOUTH SULAWESI, INDONESIA

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SUMMARY

Taro (*Colocasia esculenta* L.) is an important local crop supporting Indonesia's food diversification. This study assessed the morphological and genetic diversity of 103 accessions collected from nine districts across low, middle, and high elevations in South Sulawesi. Morphological evaluation employed 34 qualitative and 13 quantitative traits, while genetic variation analysis used 16 inter simple sequence repeat (ISSR) primers. Cluster and principal component analyses (PCA) revealed wide morphological variation, particularly in leaf and corm traits, but no clear grouping by elevation, suggesting a strong influence of environment and seed exchange practices. ISSR markers displayed high polymorphism (89%–100%), with the primer UBC856 showing the highest informativeness (PIC = 0.426). Analysis of molecular variance (AMOVA) indicated most genetic variation resided within populations (85% at the district level and up to 98% across altitudinal zones), whereas among-population variation was scarce. A molecular dendrogram and PCA supported the absence of distinct genetic structuring by elevation. Overall, the findings imply the shaping of taro diversity is more by vegetative propagation and socio-cultural seed exchange than geographic barriers. These results provide a valuable basis for germplasm conservation, breeding strategies, and the development of improved cultivars to enhance local food security.

Keywords: Taro (*Colocasia esculenta* L.), diversity, domestication, ISSR primers, morphological traits, vegetative propagation, geographic isolation

Key findings: Genetic variation-based morphological traits and ISSR markers emphasize the potential of local taro (*C. esculenta* L.) germplasm as a crucial genetic resource for breeding cultivars adaptable to diverse agroecological environments.

Communicating Editor: Dr. Kamile Ulukapi

Manuscript received: July 23, 2025; Accepted: September 19, 2025.

Citation: Syahril W, Miftahudin, Giat MR, Sjahril R (2026). Morphological and ISSR marker-based diversity of local taro (*Colocasia esculenta* L.) in south Sulawesi, Indonesia. *SABRAO J. Breed. Genet. 58 (1) 215-226. http://doi.org/10.54910/sabrao2026.58.1.20*.

INTRODUCTION

The substantial reliance on rice as Indonesia's primary staple food boosts the vulnerability of the national food system to production and distribution variations. Thus, food diversification is essential to reduce structural food insecurity risks. Taro (*Colocasia esculenta* L.), a monocotyledonous member of the Araceae family, subfamily Aroideae, can serve as a promising alternative carbohydrate source due to its adaptability to diverse agroecological conditions and competitive nutritional profile (Talang *et al.,* 2025). Taro propagation vegetatively can be through tubers, stolons, and crowns. Moreover, it provides higher levels of protein, vitamin B, and calories and lower fat than cassava and sweet potato (Club, 2022).

For some communities in Indonesia, taro was one of the staple foods before choosing rice as their primary food source (Rotinsulu *et al.,* 2024). Taro development continues by local communities in South Sulawesi Province, Indonesia. Several taro accessions with morphological variations emerged to be widely planted, ranging from lowlands to highlands in North Toraja Regency, South Sulawesi Province, Banggai Islands Regency, and Central Sulawesi Province, Indonesia (Septianti and Sahardi, 2018).

South Sulawesi is an area traversed by the Wallace Line, a major biogeographical boundary that enhances regional biodiversity. This position contributes to the exceptionally high taro diversity observed in South Sulawesi, resulting in the highest level of taro variety. Although taro has become a popular food alternative in several regions of South Sulawesi, information related to its genetic diversity and distribution remains limited. Previous research revealed taro exhibited the optimum level of morphological diversity indicated by leaf tip characters, tuber size, and tuber shape (Thakur *et al.*, 2021). However, diversity analysis based on morphological traits has a low level of consistency because such types of quantitative traits can mostly gain influences from environmental factors (Medeiros *et al.,* 2020). Therefore, it was essential to carry out diversity analysis of local taro accessions based on molecular markers in the South Sulawesi Province.

In plant genetics studies, inter simple sequence repeats (ISSR) are one of the most widely used markers due to their superiority in elucidating genetic variation. As a dominant polymerase chain reaction (PCR)-based marker, ISSR has the highest level of reproducibility and polymorphism, proving to be an effective primer in evaluating DNA bands on gel electrophoresis that can be interpreted as alleles (Amiteye, 2021). The ISSR markers, which do not require prior sequence information, are effective for detecting dominant traits, identifying duplicate accessions in germplasm collections, and establishing genetic relationships among species (Morillo *et al.,* 2022).

Information on genetic diversity is useful for plant breeders; therefore, the said study has a sound scientific basis for determining taro accessions for further development into superior cultivars. Additionally, genetic diversity information can serve as a reference for local taro conservation strategies in South Sulawesi. The improvement of local taro into superior ones will become a companion food in achieving food security for the people of South Sulawesi, in particular, and the people of Indonesia, in general. Thus, the presented study aimed to analyze the genetic diversity of local taro distributed across different altitude zones using ISSR markers in South Sulawesi, Indonesia.

MATERIALS AND METHODS

Genetic material

The collection of 103 taro accessions used for morphological and molecular analysis came from eight different districts in South Sulawesi, Indonesia, i.e., Bantaeng (9.12–2.006 meters above sea level [masl]), Bulukumba (3.75–1.523 m), Sinjai (10.69–1.996 m), Enrekang (49.54–2.028 m), Toraja (231.4–2.291 m), North Toraja (563–2.299 m), Luwu (10.51–1.833 m), Palopo City (6.89–79 m), and from

Bogor District (371.57 m), West Java, Indonesia. These elevation data were direct recordings during field sampling using GPS devices.

Taro exploration stage

Taro exploration, as conducted in eight districts of South Sulawesi, Indonesia, utilized purposive sampling, with environmental data recorded for each accession. Such data included location, coordinates, altitude, temperature, humidity, sample status, and taro presence, following the International Plant Genetic Resources Institute (IPGRI) Colocasia descriptor (Figure 1) (IPGRI 1991). Applying the altitudinal classification (<400 m, 400–700 m, >700 m) continued within each district, meaning that sampling sites in a single district could represent lowland, mid-altitude, and highland zones depending on their local topography.

Morphological analysis

Collected corms growing in five replications were under uniform greenhouse conditions at the Hasanuddin University, Makassar, Indonesia. Morphological observations progressed from 3.5 months to maximum growth for 34 qualitative traits (leaf, petiole, and corm) and 13 quantitative traits, including leaf dimensions, plant height, and corm attributes.

Molecular analysis

DNA isolation

Genomic DNA extraction from young taro leaves followed the protocol of the Genomic DNA Mini Kit Plant (Geneaid Biotech Ltd., Taiwan). DNA concentration and purity assessment continued with a UV spectrophotometer at 260/280 nm, with the

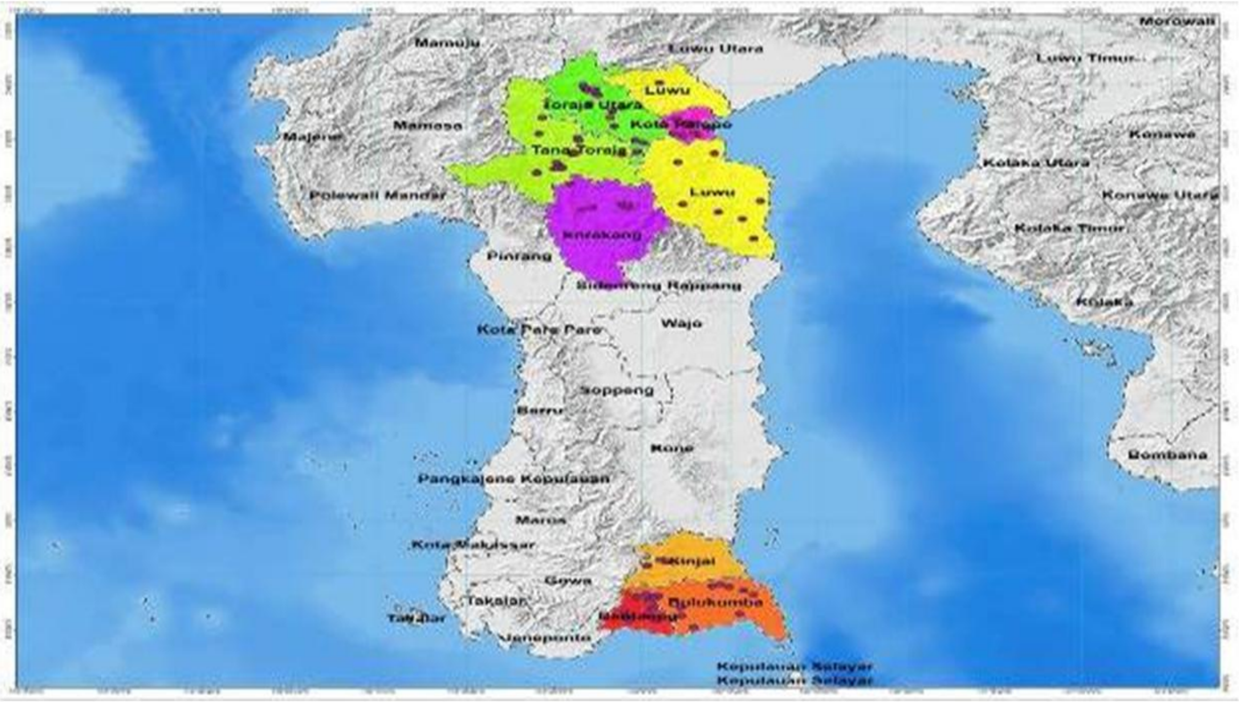

Figure 1. Distribution map of taro (*Colocasia esculenta* L.) cultivation in South Sulawesi, Indonesia, showing the sampling districts: Bantaeng (red), Bulukumba (orange), Sinjai (light orange), Enrekang (purple), Toraja (light green), North Toraja (green), Luwu (yellow), and Palopo City (pink).

quality evaluated by electrophoresis on 1.5% agarose gel in 1× TAE buffer stained with GelRed at 120 V for 60 min. Gels reached visualization under a UV transilluminator, using the purified DNA as a PCR template.

ISSR DNA amplification

DNA amplification with ISSR primers took place in a 25 µL reaction containing 3 µL DNA template, 2 µL primer, 12.5 µL GoTaq Green Master Mix (Promega, USA), and 7.5 µL ddH$_2$O, resulting in a total volume of 25 µL per reaction. PCR conditions included initial denaturation at 95 °C for 3 min; 35 cycles of denaturation at 95 °C for 30 s; annealing at 54 °C for 50 s and extension at 72 °C for 60 s; followed by a final extension at 72 °C for 10 min, and cooling at 4 °C for 5 min. Electrophoresed amplicons were on 2% agarose gel in 1× TAE buffer, stained with GelRed (Vivantis, Malaysia), and visualized using a 100 bp DNA ladder (Geneaid, Taiwan).

Data analysis

Morphological and molecular data based on the taro accessions underwent analysis using NTSYs-PC ver.2.02 for the cluster analysis (Kaur *et al.,* 2023) and PAST ver.4.03 for the principal component analysis (PCA) of the qualitative traits (Noor *et al.,* 2023). Qualitative and quantitative morphological traits received scoring as multistate data to construct similarity matrices and the unweighted pair group method with arithmetic mean (UPGMA)-based dendrogram. Genetic diversity assessment used ISSR binary data (presence = 1 and absence = 0), while evaluating profile markers and calculating the analysis of molecular variance (AMOVA) employed GenAlEx (Peakall and Smouse, 2012).

Polymorphic information content (PIC) calculation had the formula $PIC_i = 2f_i(1-f_i)$, where f_i represents the amplified allele frequency and $(1-f_i)$ as the null allele frequency (Roldán-Ruiz *et al.,* 2000). The effective multiplex ratio (EMR), reflecting the proportion of polymorphic bands, used the computation $EMR = n \times \beta$, with n as the total number of bands and β as the number of polymorphic bands (Grativol *et al.* 2011). Marker index (MI), representing the overall utility of each marker, resulted from multiplying PIC and EMR (Powell *et al.,* 1996).

RESULTS

Taro distribution in South Sulawesi

Collected taro accessions totaled 103, coming from eight districts in South Sulawesi and a comparison region (Bogor Regency). These included six accessions from Sinjai, 11 from Enrekang, 17 from Tana Toraja, 21 from North Toraja, 10 from Bantaeng, 14 from Bulukumba, eight from Luwu, 12 from Palopo City, and four from Bogor, Indonesia. The highest accession numbers recorded resulted in North Toraja (21), followed by Tana Toraja (17), Bulukumba (14), Palopo City (12), and Enrekang (11), reflecting regions with broader taro distribution (Figure 1).

Genetic distance analysis

Intracluster genetic distance of six taro clusters based on morphological characters ranged from 0.45 (Cluster V) to 0.54 (Cluster II), indicating the highest diversity within Cluster II and greater homogeneity in Cluster V (Table 1). Intercluster distances ranged from 0.28 to 0.91, with the topmost value in Cluster III, reflecting substantial genetic divergence, while Cluster V showed the closest proximity with other clusters. Cluster VI, with only two accessions, exhibited constant intra- and intercluster diversity values (0.51).

Clustering analysis

The UPGMA dendrogram based on 13 quantitative and 34 qualitative morphological characters of 103 taro accessions formed six distinct clusters (Figure 2). Accessions procured from Bogor, Indonesia, provided clustering with those from various South

Table 1. Preliminary genetic distance summary among the taro (*Colocasia esculenta* L.) clusters based on multistate morphological traits.

Cluster	Number of Accessions	Average Intra G.D.	Minimum G.D. Inter	Maximum G.D. Inter
I	8	0.51	0.36	0.68
II	26	0.54	0.34	0.77
III	33	0.53	0.34	0.91
IV	13	0.49	0.34	0.68
V	21	0.45	0.28	0.70
IV	2	0.51	0.51	0.51

G.D. = Genetic distance

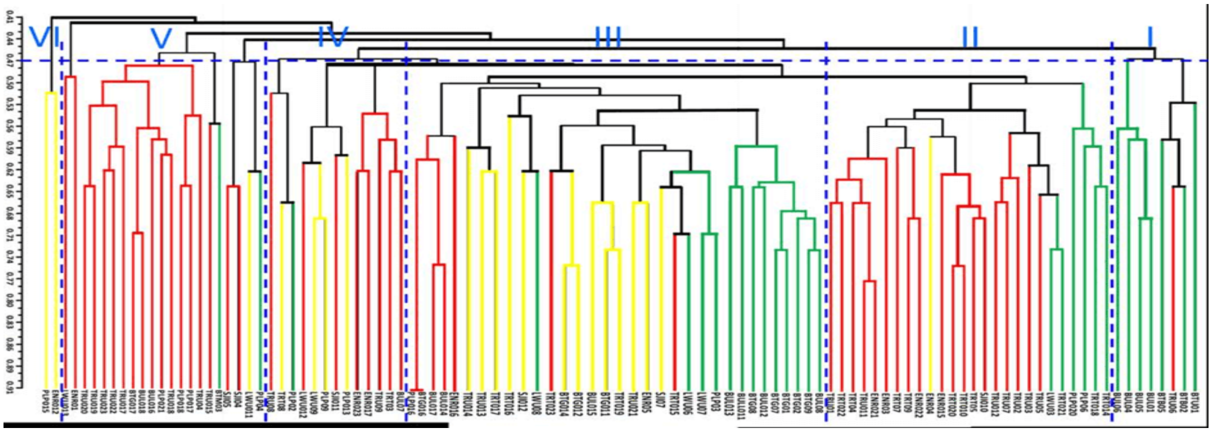

Figure 2. Dendrogram of 103 taro (*Colocasia esculenta* L.) based on quantitative and qualitative morphological characters in South Sulawesi, Indonesia. Red: highland zone >700 masl, yellow: midland zone 400–700 masl, and green: lowland <400 masl zone.

Sulawesi regions, likely due to similarities in cultivation practices, especially in flooded fields.

Taro genetic diversity

Principal component analysis (PCA) revealed principal component 1 (PC1) accounted for 83.72% of the variation, while PC2 explained 10.37%, together representing over 94% of the total qualitative morphological variations (Figure 3a). This effectively captured most morphological diversity among the taro accessions. Leaf and petiole color traits, including leaf main vein color (LMVC), color of basal third (CoBT), color of middle third (CoMT), and color of top third (CoTT), contributed substantially to PC1, indicating their substantial discriminatory power. In contrast, corm cortex color (CCC) and corm flesh color of the central part (CFCoCP) were the major contributors to PC2. The accession BTG017 from Suli Boro, Bantaeng Regency (highlands), exemplified these variations (Figure 3b), showing uniformly dark green leaves, a purple upper petiole, and a light cream corm with a white cortex. The broad corm cortex color variation (white, yellow, pink, brown, and purple) underscores the significant taxonomic value of underground tissue colors in classifying taro accessions.

ISSR marker polymorphism

The annealing temperatures (Tm) of the 16 ISSR primers ranged from 46.1 °C to 57.2 °C, indicating variations in primer stability during amplification. The number of amplified bands

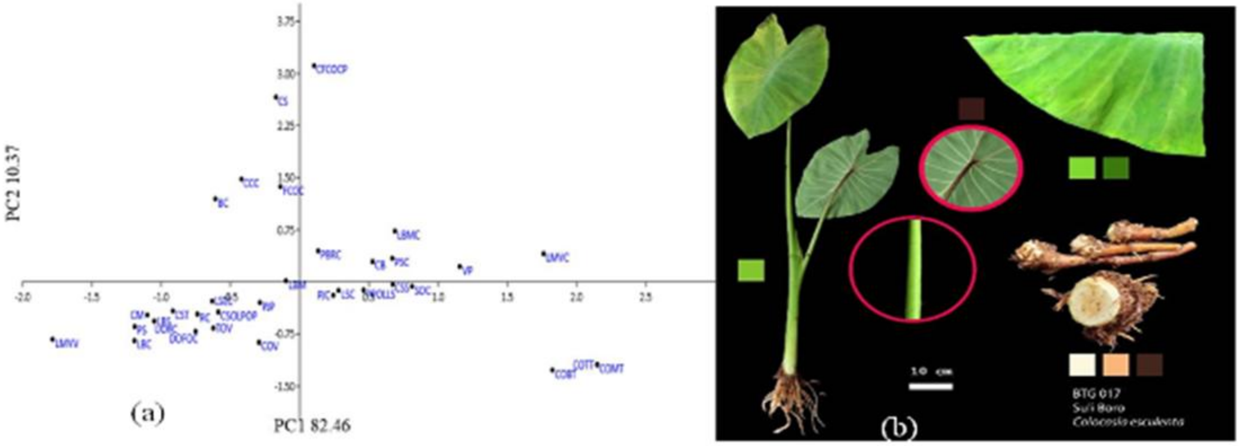

Figure 3a. Principal component analysis (PCA) of 34 qualitative morphological characters of taro (*Colocasia esculenta* L.) in South Sulawesi, Indonesia. b: The observed qualitative morphological characters of taro plants.

Table 2. Information on 16 ISSR primers used in taro (*Colocasia esculenta* L.) diversity in South Sulawesi, Indonesia.

Primer	Sequences	Na	Np	PPB (%)	H	I	PIC	EMR	MI
UBC807	(AG)8T	19	19.00	100	0.352	0.530	0.361	19.00	6.856
UBC809	(AG)8G	9	9.00	100	0.372	0.555	0.314	9.00	2.829
UBC810	(GA)8T	18	16.00	89	0.333	0.510	0.296	14.22	4.216
UBC811	(GA)8C	16	16.00	100	0.346	0.524	0.332	16.00	5.311
UBC817	(CA)8A	13	12.00	92	0.393	0.579	0.276	11.07	3.062
UBC824	(TC)8G	17	17.00	100	0.386	0.570	0.364	17.00	6.182
UBC825	(AC)8T	16	16.00	100	0.287	0.454	0.286	16.00	4.582
UBC834	(AG)8YT	16	16.00	100	0.384	0.567	0.291	16.00	4.651
UBC836	(AG)8YA	14	14.00	100	0.347	0.527	0.337	14.00	4.720
UBC840	(GA)8YT	20	20.00	100	0.252	0.413	0.234	20.00	4.677
UBC841	(GA)8YC	19	19.00	100	0.342	0.522	0.312	19.00	5.925
UBC847	(CA)8RC	20	20.00	100	0.402	0.589	0.387	20.00	7.731
UBC848	(CA)8RG	19	19.00	100	0.413	0.601	0.395	19.00	7.508
UBC856	(AC)8YA	19	19.00	100	0.455	0.646	0.426	19.00	8.086
UBC873	(GACA)4	14	14.00	100	0.353	0.536	0.311	14.00	4.357
UBC889	DBD(AC)7	12	12.00	100	0.363	0.544	0.314	12.00	3.774
Minimum		9	9.00	89	0.252	0.413	0.234	9.00	2.829
Maximum		20	20.00	100	0.455	0.646	0.426	20.00	8.08
Average		16.3	16.12	98	0.361	0.542	0.327	15.95	5.275

Note: Na = Number of bands, Np = Number of polymorphic bands, PBB = Percentage of polymorphic bands, H = Nei's gene diversity, I = Information (Shannon), PIC = Polymorphism information content, EMR = Effective multiplex ratio, and MI = Marker index.

(Na) varied between nine and 20, with polymorphic bands (Np) ranging from nine to 20, and an average of 16.12 bands per primer (Table 2). All the ISSR primers exhibited the highest polymorphism (89%–100%), confirming their effectiveness in evaluating taro genetic diversity. Nei's heterozygosity (H) ranged from 0.252 (UBC840) to 0.646 (UBC856), averaging 0.361, indicating moderate to high genetic variability among the taro accessions.

Table 3. Molecular diversity analysis of 103 taro (*Colocasia esculenta* L.) accessions using ISSR markers.

Source of variation (different zone altitudes)	d.f.	SS	MS	Est. Var.	Percentage
Among populations	2	1.448	0.724	0.008	2
Within population	100	46.280	0.463	0.463	98
Total	102	47.728		0.471	100
Source of variation (different district)					
Among populations	8	890.999	111.375	6.601	15
Within population	94	3539.525	37.655	37.655	85
Total	102	4430.524		44.256	100

Note: df = degrees of freedom, SS = sum of squares, MS = mean squares, Est. Var. = estimated variation, and % = percentage of variation.

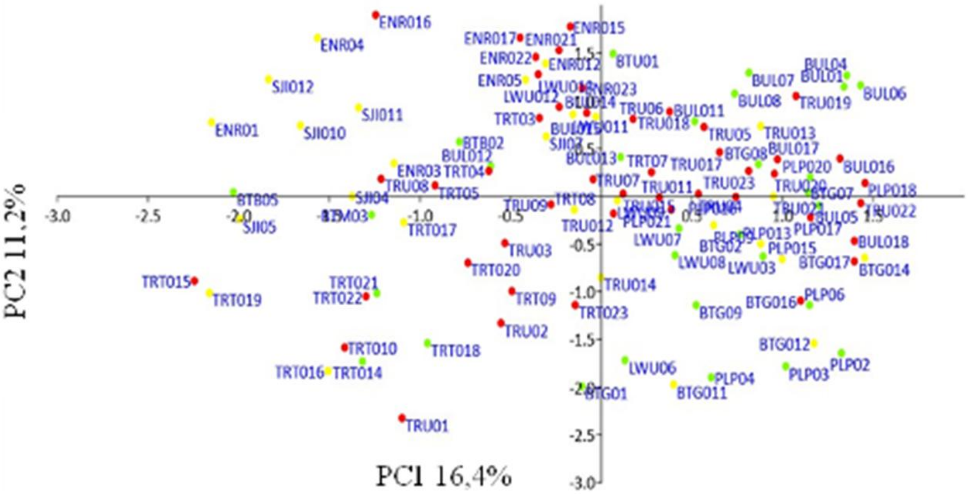

Figure 4. Matrix plot for principal component analysis (PCA) based on ISSR markers of taro (*Colocasia esculenta* L.), South Sulawesi, Indonesia. Red: highland zone >700 masl, yellow: midland zone 400–700 masl, and green: lowland <400 masl zone.

Molecular-based genetic diversity

Analysis of molecular variance (AMOVA) revealed most genetic variation in taro accessions occurred within populations, with 98% variations within and only 2% between altitude-based populations (PhiPT = 0.017, p = 0.030) (Table 3). For nine districts and locations, 85% of variation was within populations, while 15% was among the populations (PhiPT = 0.149, p = 0.001).

Principal component analysis

PCA based on ISSR markers in 103 taro accessions showed no obvious grouping by altitude zones (lowland, midland, or highland), and most accessions displayed a scattering across the PC1 (16.4%) and PC2 (27.6%) axes (Figure 4). Although several lowland, midland, and highland accessions (TRU01, TRU02, TRU09, TRU20, TRT014, TRT015, TRT021, and TRT022) clustered on the left side, the distribution pattern was insufficient to form distinct groups.

Genetic diversity within and between taro groups

According to the genetic diversity of six taro clusters, with intracluster genetic distances (Intra-GD) ranging from 0.66 (Cluster VI) to

Table 4. Intra- and Inter-genetic distance among clusters of taro (*Colocasia esculenta* L.) in South Sulawesi, Indonesia.

Cluster	Number of Accessions	Average Intra G.D.	Minimum G.D. Inter	Maximum G.D. Inter
I	14	0.69	0.61	0.68
II	6	0.70	0.63	0.82
III	27	0.70	0.58	0.84
IV	27	0.69	0.59	0.85
V	11	0.72	0.65	0.81
IV	18	0.66	0.57	0.79

G.D: Genetic distance

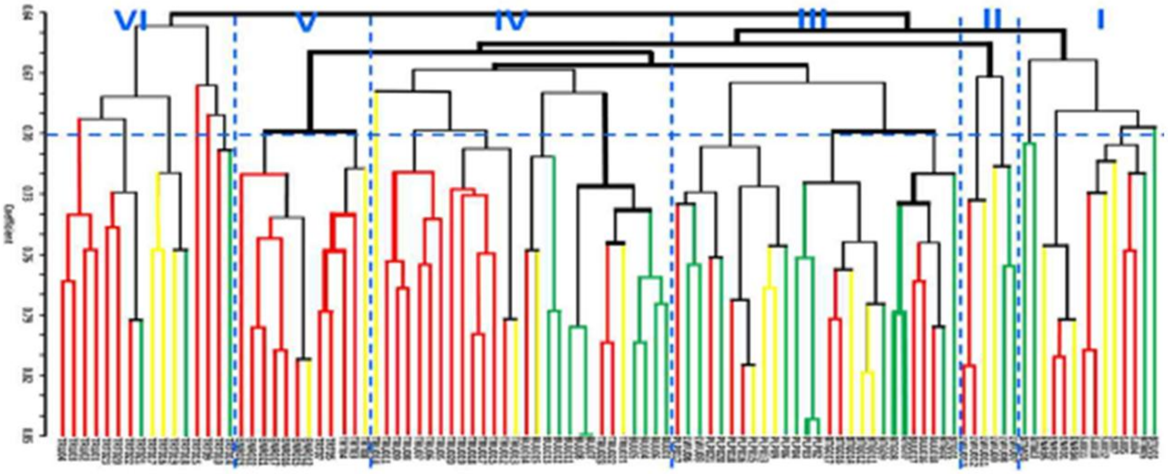

Figure 5. Dendrogram of 103 taro species of *Colocasia esculenta* L. of South Sulawesi, Indonesia, based on ISSR molecular markers. Red: highland zone >700 masl, yellow: midland zone 400–700 masl, and green: lowland <400 masl zone.

0.72 (Cluster V), this indicates moderate to high genetic variability (Table 4). Cluster V exhibited the greatest intracluster diversity, whereas intercluster distances ranged from 0.57 to 0.85, reflecting substantial genetic differentiation.

ISSR marker-based clustering

The dendrogram analysis of 103 taro accessions using ISSR markers revealed no obvious grouping pattern based on altitude zones in South Sulawesi, Indonesia. Taro accessions from the districts, viz., Bantaeng, Bulukumba, Sinjai, Enrekang, Toraja, North Toraja, Luwu, and Palopo City, and a reference from Bogor Regency, incurred dividing into six clusters at the similarity coefficient of 0.70 (Figure 5).

DISCUSSION

Based on the exploration across nine locations in South Sulawesi, taro was most abundant in North Toraja, Tana Toraja, Bulukumba, Palopo City, and Enrekang (Figure 1). Beyond its role as an alternative food source, taro is also beneficial as animal feed and as raw material for the food and pharmaceutical industries (Maretta *et al.,* 2021). Its cultural and dietary importance predates the New Order era, although agricultural modernization shifted its use. Nutritionally, taro is rich in carbohydrates

(86.11% ± 0.6%), starch (70%–80%), and protein (1.4%–3.0%), surpassing many other tuber crops and being highly recommended for diabetic and low-income diets (Shah *et al.,* 2022; Ferdaus *et al.,* 2023). Morphological diversity analysis revealed six distinct clusters, with intracluster distances ranging from 0.45 to 0.54 and intercluster distances from 0.28 to 0.91 (Table 1). Cluster II exhibited the highest internal variability (0.54), whereas cluster III showed the greatest divergence from other groups (0.91). These findings, consistent with Abate *et al.* (2021), highlight substantial genetic variation. Though clustering was not strictly altitude-driven, micro-ecological conditions and cultivation practices likely shaped diversity. Leaf morphology, elevation-related adaptation, and mechanisms, such as somatic mutations, transposons, and epigenetic variation, further contribute to taro's phenotypic plasticity (Adamidis *et al.,* 2021; Pillay, 2024).

PCA of qualitative morphological traits showed PC1 and PC2 together explained 92.83% of the total variations, demonstrating its effectiveness in simplifying complex data and revealing diversity patterns among taro accessions (Figure 3a). Similar observations came from Tripathi *et al.* (2022), who noted that a few PCs can capture most genotypic variation. In this study, PC1 dominance was mainly by leaf and petiole color traits (LMVC, CoBT, CoMT, CoTT), while PC2 reflected tuber characteristics (CCC, CFCoCP), which varied from white to purple. Leaf and petiole colors, though environmentally influenced, provide useful markers for accession identification, whereas tuber color represents a stable genetic trait with direct implications for consumer preference, nutritional quality, and market acceptance (Krstić *et al.,* 2024; Vinutha *et al.,* 2024).

ISSR analysis further confirmed substantial diversity, producing clear banding patterns across accessions, consistent with findings in other Araceae genera (Sousa *et al.,* 2024). The primers' efficiency gained support from the effective multiplex ratio (EMR) and marker index (MI) values (Table 2), which ranged from 9.00 to 20.00 and 2.829 to 8.086, respectively. UBC856 showed the highest MI (7.46), followed by UBC847, indicating a strong discriminatory power. As highlighted by Chňapek *et al.* (2024), primers with high PIC, EMR, and MI values provide greater reliability in genetic analysis.

The genetic diversity analysis disclosed a predominance of intrapopulation variation, with AMOVA showing 98% within-population variation and only 2% for among populations across altitudinal zones (Table 3). When populations entailed groupings by districts, intrapopulation variation remained high (85%), while interpopulation variation accounted for 15%. These results indicate maintaining most genetic diversity in taro is within districts and across elevation gradients, with relatively low differentiation among populations. Similar findings came from Wang *et al.* (2023), who emphasized reproductive systems and micro-environmental variations managing the plant genetic diversity more than geographic barriers. Despite vegetative propagation (Chauhan *et al.,* 2021), taro maintained the highest genetic diversity due to interregional gene flow (Salgotra and Chauhan, 2023), supported by extensive seed exchange practices within South Sulawesi's Austronesian-like communities (Endardi *et al.,* 2023).

The PCA results further confirmed the absence of obvious clustering by elevation, with only a few mid- and high-altitude accessions (TRT015, TRU01, and ENR01) deviating from the cluster center. The UPGMA analysis grouped the taro accessions into six clusters, with the greatest genetic distance (0.85) observed between clusters IV and III. Cluster III comprised accessions with superior tuber yield and large corm size, whereas cluster IV contained accessions with strong vegetative vigor and distinctive leaf/petiole color traits. Crossing these two clusters would therefore combine yield-related characteristics with adaptive and morphological diversity, offering promising opportunities for generating novel genotypes with both agronomic and market relevance. These findings align with Doggalli *et al.* (2024), who also reported clustering often reflects genetic differentiation shaped by domestication, ecological adaptation, and seed exchange rather than strict geographic boundaries in maize.

The PCA revealed overlapping distributions among altitude zones, with no clear clustering, although several mid- and high-altitude accessions (TRU01, TRU02, TRU09, TRU20, TRT014, TRT015, TRT021, and TRT022) diverged from the cluster center. These accessions exhibited distinctive petiole and corm traits, likely reflecting both unique alleles and adaptations to waterlogged environments, as commonly observed in Toraja and North Toraja, where taro cultivation prevails under flooded conditions. Such traits highlight their potential as valuable breeding resources for improving performance in suboptimal soils.

Consistent with these findings, genetic distance analysis grouped the 103 accessions into six clusters, with intracluster distances ranging from 0.66 to 0.72 (Table 4). Cluster V displayed the highest diversity (0.72), comprising accessions from Toraja and Enrekang cultivated across contrasting altitudes, suggesting the presence of genotypes from multiple districts and ecological zones contributed to this diversity. In contrast, cluster VI exhibited the lowest diversity (0.66), reflecting the genetic uniformity expected under clonal propagation (Muktar *et al*., 2023). The largest intercluster distance (0.85) was evident between clusters III and IV, which represent contrasting agronomic traits—high-yielding accessions with large corms versus vigorous types with distinctive leaf and petiole coloration—indicating strong potential for crossbreeding to expand genetic variability.

The UPGMA dendrogram supported these clustering patterns, dividing the accessions into six major groups at the 0.70 cutoff (Figure 4). Highland accessions clustered tightly and homogeneously, likely constrained by low temperatures that restrict genetic variation, a trend also reported in taro and other root crops cultivated in cooler environments (McCulloch *et al.,* 2025). Conversely, lowland accessions showed more dispersion, reflecting heterogeneous growing conditions and higher levels of gene flow. Interestingly, accessions from Bogor and the highland districts of Enrekang, Luwu, and Sinjai grouped with the lowland cluster, underscoring taro's ecological adaptability across diverse environments (Sabdanawaty *et al.,* 2021). Elevation shapes genetic structure without reducing overall genetic diversity.

CONCLUSIONS

The study revealed the highest morphological and genetic diversity in 103 local taro accessions procured from South Sulawesi, Indonesia. Petiole color, corm skin color, and corm flesh color were the key differentiating traits, while ISSR markers showed the highest polymorphism (89%–100%), with the primer UBC856 being the most informative. The AMOVA indicated most genetic variations occurred within populations. The results suggested vegetative propagation, ecological adaptation, and seed exchange manage the taro's genetic structure, providing a sound genetic base for conservation, germplasm management, and breeding programs supporting sustainable food security.

ACKNOWLEDGMENTS

This study took place as part of the Future-fit Tropical Food Crops Research Group, with funding from the TRG Batch I Grant from Universitas Hasanuddin, Indonesia (Fiscal Year 2025). The authors sincerely thank Universitas Hasanuddin for the financial support through this research contract.

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