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PHENETIC ANALYSIS OF CULTIVATED TARO (*Colocasia esculenta* [L.] Schott) ACCESSIONS BASED ON MORPHOLOGICAL CHARACTERS

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SUMMARY

Taro (*Colocasia esculenta* L. Schott; Araceae) is a cultivated plant originating from Southeast Asia. Taro accessions are widespread in Java, Indonesia, and are known to have high morphological diversity. However, information about the phenetic relationships between taro genotypes is lacking. The present study aimed to determine the phenetic relationships and intraspecies classification of taro genotypes from Java on the basis of morphological characters. Seventy-three accessions of taro were obtained from existing collections and through exploration in Central Java and Yogyakarta, Indonesia. On the basis of morphological traits, the variations in taro accessions were mainly shown by roots, corms, and leaf parts. Generally, the leaves of taro accessions from Java, Indonesia, were peltate. Results revealed that leaf organs had the highest variation, especially in terms of color characteristic patterns. In the analysis of phenetic relationships by using the Gower Similarity and Unweighted Pair Group Method with Arithmetic Mean Method, the taro genotypes were classified into two groups (pink and white) on the basis of root color, tip color, leaf exudates, and ring color on the midrib base. On the basis of primary leaf veins, the white group of the taro accessions was further subdivided into two groups, i.e., dark green and light green. Dendrograms showed that all the accessions were divided into two main clusters at the similarity index of 0.58. Observations based on morphological variations and phenetic analysis can be used as a basis for the intraspecies classification of taro germpalsm.

Keywords: *Colocasia esculenta*, group accessions, morphology, phenetic analysis, intraspecies

Key findings: This research will provide basic information about Indonesian taro accessions, which have the potential to be utilized in commercial breeding programs.

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INTRODUCTION

Taro (*Colocasia esculenta* L. Schott; Araceae) has been cultivated since ancient times in Oceania, Asia, and Africa for its edible corms and leaves (Kuruvilla and Singh, 1981; Coates *et al.,* 1988; Chair *et al*., 2016). Taro is an important food crop in the tropical areas of Africa, Asia, and Latin America. However, its germplasm is being lost because of its replacement by cereals; drought; and human interference, such as deforestation (Beyene, 2013). According to Prana *et al*. (2010), taro can be found in most of the Indonesian archipelago. In Java, Indonesia, although several taro accessions are still cultivated and some survive on riverbanks and around moist ponds, a larger pool of taro germplasm is found in farmers' fields and forest areas (Prana, 2007; Beyene, 2013).

The intraspecies classification of cultivated plants is increasingly needed to identify genetic diversity within a population of species. Past studies on taxonomy intended to produce nonformal classification, and classification below the species level is a problem in cultivated plants in the intraspecies classification of wild and cultivated genotypes (Hawkes, 1986; Kreike *et al*., 2004). On the basis of the morphological characterization and scoring of different taro accession groups, phenetic analysis can be performed in terms of the similarity of the characters in each group. Phenetic relationship analysis is a numerical taxonomic method that interprets the similarity of organisms in a group (Sokal and Sneath, 1972; Singh and Jain, 1981).

Different studies on morphological variations and diversity among Indonesian taro species have been conducted on existing germplasm (Hartati *et al*., 2001) and American taro/arrow leaf elephant ear (*Xanthosoma sagittifolium* L.) from West Java, Indonesia (Maxiselly and Karuniawan, 2011). Past studies on the phenetic analyses of taro genotypes in Kalimantan, Indonesia, reported great genetic diversity (Oktavianingsih *et al*., 2019). The highest morphological variations in phenetic analysis were recorded for local taro accessions from Java Island studied for agronomic purposes and the selection of superior accessions (Prana and Tatang, 2002; Andarini and Risliawati, 2018). Pitoyo *et al*. (2018) examined variability in taro accessions based on morphological, anatomical, and izosyme characters. Significant differences were observed in the form of quantitative characters.

In phenetic analysis, the relationship among taro accessions is illustrated by similarity index values (Oktavianingsih *et al*., 2019). Phenetic analysis is also related to plant breeding in that it can be used to determine the genotypes of potential parentals for crossing programs and to identify the best taro genotype. Phenetic analysis can provide information on intraspecies diversity through cluster analysis showing phenotypic and genotypic relationships in plant species (Purnomo *et al*., 2012, 2017; Oktavianingsih *et al*., 2019). Therefore, the present study aimed to

Figure 1. Sampling locations for taro accessions in Java with black rectangular code: a. Banten Province, b. West Java Province, c. Central Java Province, d. Yogyakarta Province, e. East Java Province.

determine morphological variations and phenetic relationships to assess taro groups in Java, Indonesia.

MATERIALS AND METHODS

Materials and procedures

A total of 73 taro accessions were provided by the Center for Research and Development of Agricultural Biotechnology and Genetic Resources, Bogor, Indonesia. These taro genotypes were further studied for different traits at the Research Garden in Pacet, Cianjur, West Java, Indonesia. Samples were also collected from different sites in Central Java (Banyumas, Magelang, and Purworejo Regencies), East Java (Kediri, Malang, Sidoarjo, and Pasuruan Regencies), and Yogyakarta (Sleman District) (Figure 1, Table 1). The morphological characterization of the taro accessions was carried out by following the taro descriptors developed by IPGRI with some modifications (IPGRI, 1999).

Data analysis

A total of 33 vegetative and morphological traits of taro germplasm were observed and studied (Table 2). Morphological data were analyzed descriptively to determine the morphological variation shown by taro accessions from Java, Indonesia. The morphological scoring of taro accessions in the form of operational taxonomic units (OTUs) was performed on the basis of binary and multi states. Then, data were standardized in accordance with the presence and absence of the different traits. On the basis of scoring, the similarity index values between OTUs were calculated by using the Gower formula. On the basis of the similarity matrix between OTUs, cluster analysis was carried out by using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) algorithm to create a dendrogram describing the relationship between OTUs by using Multivariate Statistical Package software (Kovach, 2007). Moreover,

Table 1. List of accession numbers, BB-Biogen accession numbers, accession names, and locations of taro accessions observed.

No.	Acc. Nos.	Acc. Nos. BB-Biogen	Local name of Accessions	Location of taro accessions	No.	Acc. Nos.	Acc. Nos. BB-Biogen	Local name of Accessions	Location of taro accessions
1	DIY-01	CO-002	*Bogor*	Gunungkidul, Yogyakarta	38	JBR-31	CO-194	*Baban*	Cianjur, West Java
2	DIY-02	CO-003	*Sutera*	Gunungkidul, Yogyakarta	39	BTN-07	CO-149	*TalasHijau*	Lebak, Banten
3	JBR-01	CO-013	*Mangkubumi*	Ciamis, West Java	40	BTN-08	CO-150	*Margaluyu*	Lebak, Banten
4	JTG-01	CO-015	*LumbuSawah*	Banjarnegara, Central Java	41	BTN-09	CO-155	*TalasBodas*	Lebak, Banten
5	JTG-02	CO-019	*Buntil*	Banyumas, Central Java	42	BTN-11	CO-163	*TalasHijau*	Lebak, Banten
6	BTN-01	CO-027	*Leuwidamar*	Lebak, Banten	43	JBR-33	CO-168	*Hariang*	Sumedang, West Java
7	JBR-02	CO-037	*Ketan*	Bogor, West Java	44	JBR-34	CO-184	*SutinarajaSadang*	Garut, West Java
8	JTG-03	CO-058	*Batang*	Batang, Central Java	45	JBR-35	CO-186	*Paris*	Garut, West Java
9	JBR-03	CO-110	*Cilawu*	Garut, West Java	46	JBR-36	CO-188	*Bayongbong*	Garut, West Java
10	JTG-04	CO-139	*Mekarsari*	Banjarnegara, Central Java	47	JTG-09	CO-210	*Kebumen*	Kebumen, Central Java
11	JBR-06	CO-203	*Bogor*	Majalengka, West Java	48	BTN-12	CO-025	*TalasHijau*	Lebak, Banten
12	JTG-05	CO-213	*Jahe*	Wonogiri, Central Java	49	JTG-12	CO-054	*Lesmana*	Banyumas, Central Java
13	JBR-07	CO-030	*Pacet*	Cianjur, West Java	50	JTG-13	CO-059	*Cilopadang*	Cilacap, Central Java
14	JBR-08	CO-033	*Cilawu*	Garut, West Java	51	JBR-37	CO-060	*Cibadak*	Sukabumi, West Java
15	JBR-09	CO-035	*Sente*	Bogor, West Java	52	JBR-38	CO-115	*Sente*	Kuningan, West Java
16	JBR-10	CO-036	*Bentul*	Bogor, West Java	53	JBR-39	CO-119	*Kimpul*	Bogor, West Java
17	JBR-11	CO-051	*Nagreg*	Bandung, Jawa Barat	54	JTG-14	CO-140	*TalasPutih*	Banjarnegara, Central Java
18	JTG-06	CO-062	*Bandar*	Batang, Central Java	55	JBR-40	CO-181	*Surade*	Sukabumi, West Java
19	JBR-12	CO-072	*LahunAnak*	Bogor, West Java	56	JBR-41	CO-101	*Sukamulya*	Kuningan, West Java
20	JBR-13	CO-076	*BalongHejo*	Bogor, West Java	57	JBR-43	CO-183	*SutinarajaWaru*	Garut, West Java
21	JBR-15	CO-082	*BalongBodas*	Bogor, West Java	58	JBR-44	CO-189	*Beulang*	Garut, West Java
22	JBR-16	CO-103	*Sente*	Kuningan, West Java	59	JTM-02	CO-207	*BentulKuning*	Trenggalek, East Java
23	JBR-17	CO-104	*TalasBodas*	Kuningan, West Java	60	JBR-46	CO-259	*Semir*	Sumedang, West Java t
24	JTG-07	CO-112	*Palado*	Batang, Central Java	61	JTG-15	CO-048	*Cilesung*	Batang, Central Java
25	JBR-19	CO-113	*Kuningan*	Kuningan, West Java	62	JTM-04	CO-217	*BentulKuning*	Banyuwangi, East Java
26	JBR-20	CO-116	*Loma*	Bogor, West Java	63	JTM-05	CO-219	*Sente*	Banyuwangi, East Java
27	JBR-21	CO-120	*TalasSawah*	Bogor, West Java	64	JTG-16	CO-016	*LumbuIreng*	Banjarnegara, Central Java
28	JBR-22	CO-127	*Ronyok*	Sukabumi, West Java	65	DIY-03	CO-010	*Playen*	Gunungkidul, Yogyakarta
29	BTN-02	CO-130	*Lampung*	Lebak, Banten	66	DIY-04	-	*LompongIreng*	Sleman, Yogyakarta
30	BTN-03	CO-131	*TalasHijau*	Lebak, Banten	67	DIY-05	-	*Banyu*	Sleman, Yogyakarta
31	JBR-24	CO-185	*KarangMulya*	Garut, West Java	68	JTM-06	-	*Talas*	Sidoarjo, East Java
32	JBR-25	CO-196	*SirihHiJau*	Cianjur, West Java	69	JTM-07	-	*LompongIreng*	Sidoarjo, East Java
33	JTG-08	CO-021	*Salak*	Banjarnegara, Central Java	70	JTG-17	-	*Benak*	Magelang, Central Java
34	JBR-26	CO-028	*TalasHijau*	Sukabumi, West Java	71	JTM-08	-	*Bentul*	Kediri, East Java
35	JBR-27	CO-038	*Bogor*	Bogor, West Java	72	JTM-11	-	*Bentul*	Pasuruan, East Java
36	JBR-28	CO-102	*Kutil*	Kuningan, West Java	73	JTG-20	-	*Krempyang Mas*	Banyumas, Central Java
37	JBR-30	CO-109	*Bentul*	Garut, West Java	-	-	-	-	-

Table 2. Scoring of the morphological characters of taro accessions from Java based on Anonymous (1999) with slight modifications.

Code	Characters	Scoring
H01	Plant high	0: 100 cm; 1: >100 cm
A01	Root color	0: white; 1: pink
A02	Uniformity of root color	0: uniform; 1: nonuniform
R01	Rhizome shape	0: conical; 1: rounded; 2: cylindrical; 3: elliptical; 4: halter; 5: lengthwise
R02	Rhizome skin surface	0: smooth; 1: stringy; 2: scaly, 3: stringy and scaly
R03	Rhizome skin thickness	0: thin; 1: thick
R04	Rhizome cortex color	0: white; 1; pink; 2: orange; 3: yellow
R05	Rhizome flesh color	0: white; 1; pink; 2: orange; 3: yellow
R06	Rhizome flesh fiber color	0: yellow; 1: brown; 2: purple
R07	Bud color	0: white; 1: light green; 2: pink; 3: purple
R08	Stolon number	0: none; 1: 1–5; 2: 6–10; 3: >10
R09	Sucker number	0: none; 1: 1–5; 2: 6–10; 3: >10
D01	Leaf length and width ratio	0: ≤1.5; 1: >1.5
D02	Leaf position	0: drooping; 1: cup with flat tip, 2: cup with drooping tip, 3: erect
D03	Leaf symmetry	0: asymmetrical; 1: symmetrical
D04	Upper leaf blade color	0: green; 1: dark green
D05	Surface condition of the upper leaf blade	0: dull, 1: shiny
D06	Color of the sap on the leaf tip	0: white; 1: red/pink
D07	Leaf margin	0: flat, 1: wavy, 2: undulate
D08	Leaf edge color	0: light green/yellowish, 1: green, 2: purple
D09	Secondary leaf nerve color	0: light green/yellowish; 1: green; 2: purple; 3: purple yellow spots; 4: dark purple
D10	Primary leaf nerve color	0: light green/yellowish; 1: green; 2: dark green
D11	Pigmentation of the leaf nerve on the lower leaves	0: none; 1: V shape; 2: I shape; 3: Y shape; 4: expanding Y shape
D12	Ratio of leaf length and leaf petiole length	0: ≤1.5; 1: >1.5
D13	Color of leaf petioles 1/3 over adaxial part	0: white; 1: light green; 2: green; 3: purple; 4: dark purple; 5: purplish green
D14	Color of leaf petioles 1/3 over the abaxial part	0: white; 1: light green; 2: green; 3: purple; 4: dark purple; 5: purplish green
D15	Color of the leaf petioles 1/3 middle	0: white; 1: light green; 2: green; 3: purple; 4: dark purple; 5: purplish green
D16	Color of the leaf petioles one third bottom	0: white; 1: light green; 2: green; 3: purple; 4: dark purple; 5: purplish green
D17	Lines on leaf petioles	0: none; 1: purple present; 2: light green present
D18	Color of the ring at the base of the leaf sheath	0: white; 1: red/pink
D19	Leaf sheath color	0: light green; 1: dark green; 2: purple; 3: dark purple; 4: purplish green
D20	Color of the edge of the leaf sheath	0: brown continuous; 1: brown broken
D21	Length sheath and leaf ratio	0: ≤1.5; 1: >1.5

scoring data were analyzed through principal component analysis (PCA) to identify the morphological characters that play an important role in the formation of different clusters. Logical clusters, which formed at a similarity index between 0.70 and 0.90, in the dendrogram were used to describe the number of groups below the species level (Sokal and Sneath, 1972; Stace, 2000).

RESULTS

Morphological variation

The taro accessions collected in Java were evaluated and compared on the basis of vegetative and morphological characters (Table 2). The morphological variations in taro accessions were mainly based on roots, corms, and leaf parts. Leaf organs have the highest variation principally based on color distribution. Variations in root organs were found in terms of root color. Taro roots could be divided into two groups, i.e., pink (Figure 2A.a and Figure 2A.c) and white (Figure 2A.b) in accordance with color. Variations in the corms of the taro accessions included shape, skin thickness, surface condition, cortex color, and flesh fiber (Figure 2C).

The main components of the taro leaf structure were a blade with prominent veins, long petioles, and sheaths. Some of the accessions exhibited patterns of green or purple stripes on their leaf sheaths. The color characteristic and edge color of the leaf sheath varied (Figure 3). The base of the leaf sheath formed a pseudo stem, and the color pattern of the base of the pseudo stem (ring color) was a good identifier of white and pink taro accession groups (Figure 2A).

Taro leaf blades showed the greatest variation compared with other leaf parts. Variations in taro accession characters included leaf shape, leaf tip, color, margin, leaf veins, and sap color. Color patterns were found on the surfaces (Figure 3) and sheaths (Figure 2.B) of the leaf blades. In general, the petiole had the same shape, and the ratios of the length of petioles and leaf sheath were the same. The taro leaf blades were rounded, and the positions of the leaf blades and the petioles were peltate or hastate. The leaves of taro accessions from Java, Indonesia, were generally peltate. The leaf blades of taro accessions generally had three primary veins with a Y arrangement with varying angles and 9 to 13 secondary veins in a pinnate arrangement (Figure 3C). The leaf vein color pattern under the leaf surface was an important characteristic for the identification of taro accessions from Java, Indonesia.

Phenetic analysis

Morphological characters were scored in accordance with the descriptors of taro with some modifications (IPGRI, 1999). In this study, 33 vegetative and morphological characters were used qualitatively and quantitatively (Table 2). The similarity index between OTUs was calculated by using the Gower formula through clustering with the UPGMA algorithm to produce a dendrogram. The phenetic analysis of the OTUs of 73 taro accessions generated a dendrogram that described the similarity relationships among different accessions from Java (Figure 4). The similarity indexes of

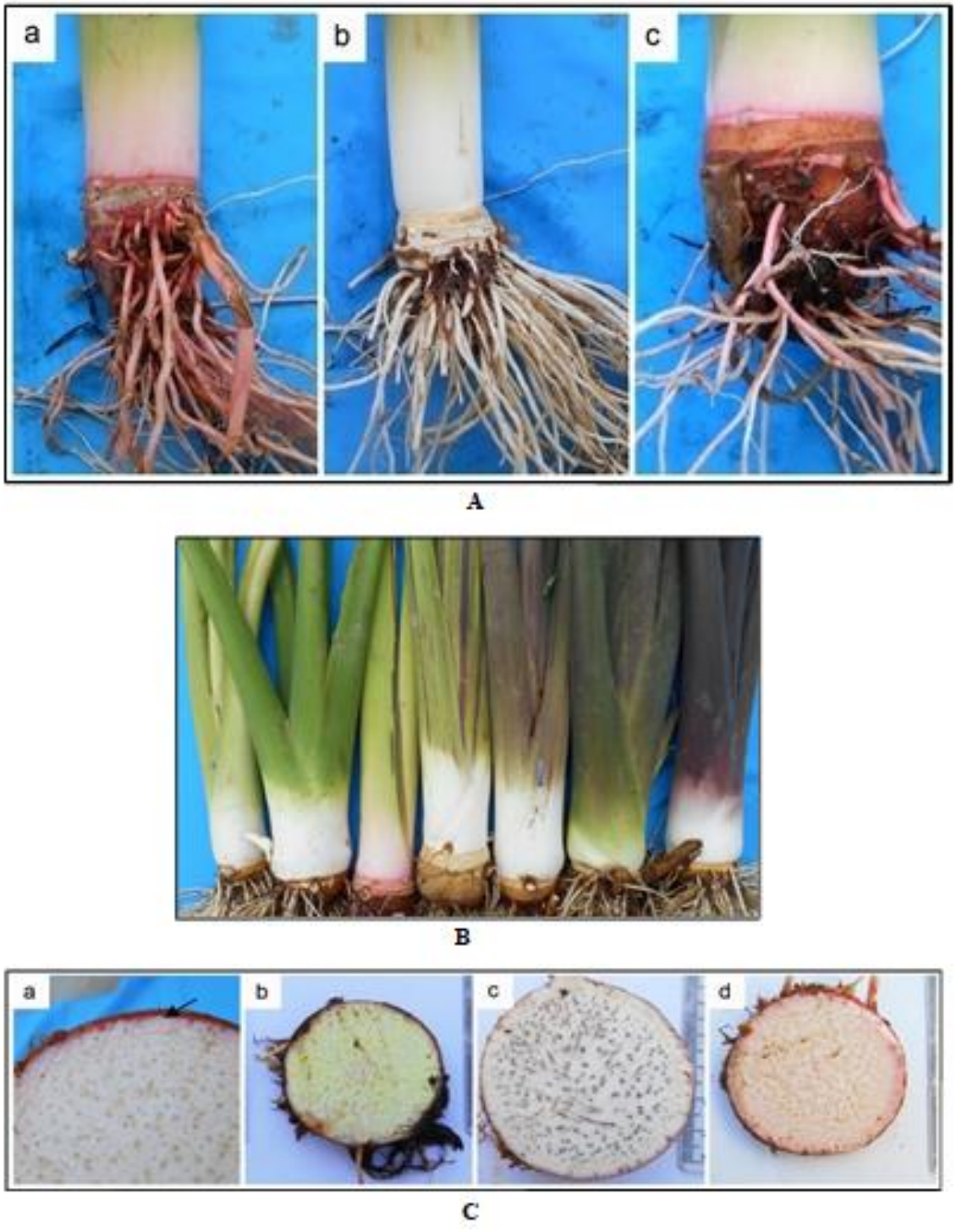

Figure 2. Root, corm, and corm flesh (rhizome) of taro: A. Root and corm; a and c. Corm with pink-fiber roots, b. Corm with white-fiber roots. B. Color variation in leaf petiole and sheath. C. Color variation in corm cortex, flesh, and fiber; a. Red cortex, b. yellow flesh corms, c. purple fibers, d. orange flesh and pink fibers.

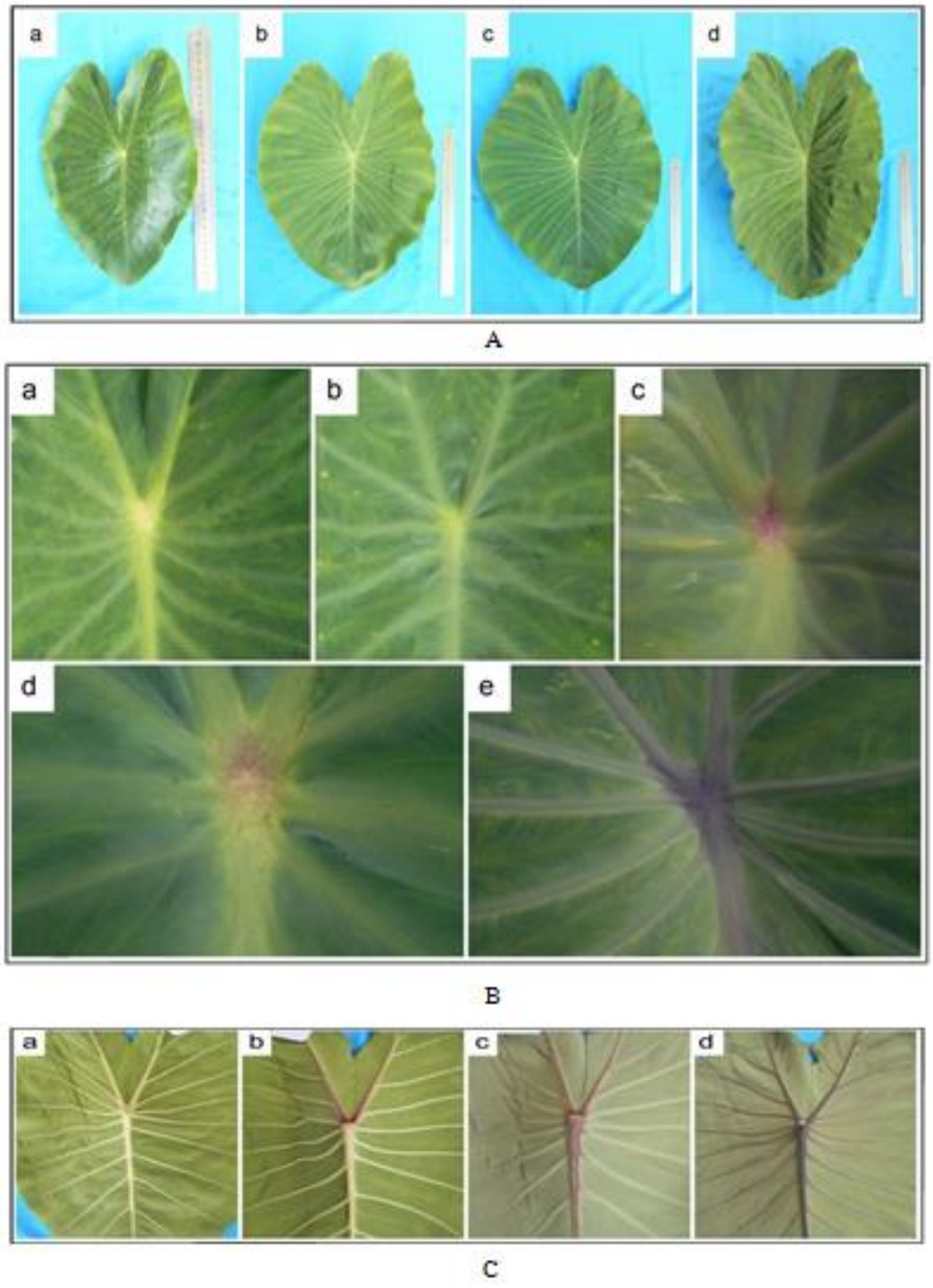

Figure 3. Symmetry and color variation of taro leaves and pigmentation pattern on the lower surfaces of taro leaves. A. Blade (lamina) symmetry: a–c asymmetry, d. symmetry. B. Color variation shown by branching veins on the upper surfaces of taro leaves: a. light green, b. green, c. purple, d purple with yellow spots, e. dark purple (black). C. Variation in lower leaf vein pigmentation: a. without pigmentation, b. letter V pattern, c. letter Y pattern, d. letter Y pattern extending to the secondary leaf veins.

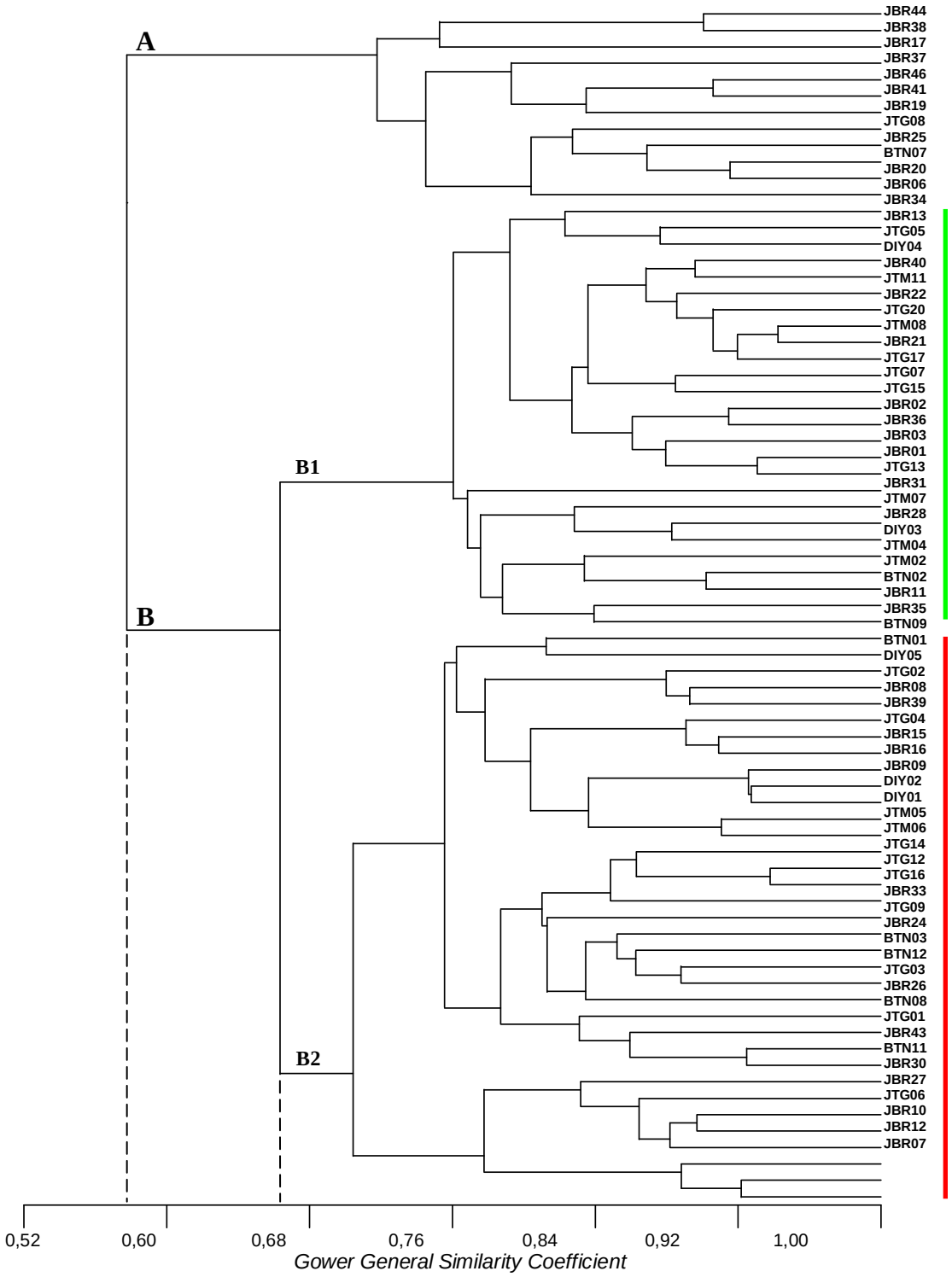

Figure 4. Dendrogram of the 73 taro accessions from Java generated by using the UPGMA method.

the taro accessions from Java, Indonesia, ranged from 0.57 to 0.94.

The dendrogram showed that all the accessions with a similarity index of 0.58 were subdivided into two main clusters, namely, cluster A (blue box line) and cluster B (black box line). Then, cluster B with a similarity index of 0.66 was subdivided into clusters B1 (green box line) and B2 (red box line) (Figure 4). Cluster analysis further revealed that the dendrogram had the main clusters A (blue line) and B (black line), and clusters A and B were separated with the similarity index of 0.578. Accessions in Cluster A showed variations in root color, sap color at the leaf tip, and ring color at the base of the leaf (Figure 5). This group was considered as the pink group of taro accessions, i.e., JBR-44, JBR-38, JBR-17, JBR-37, JBR-46, JBR-41, JBR-19, JTG-08, JBR-25, BTN-07, JBR-20, and JBR-06 (Table 3). Accessions in Cluster B showed variations in roots, sap at the leaf tip, and white rings at the base of the leaf sheaths.

Cluster B was subdivided into two clusters, i.e., B1 (green line) and B2 (red line), and both subgroups were separated with the similarity index of 0.66. Accessions in Cluster B1 had dark yellow or purple spots on their secondary leaf veins, and the color of primary leaf veins was dark green. Cluster B1 consisted of accessions JBR-34, JBR-13, JTG-05, DIY-04, JBR-40, JTM-11, JBR-22, JTG-20, JTM-08, JBR-21, JTG-17, JTG-07, JTG-15, JBR-02, JBR-36, JBR-03, JBR-01, JTG-13, JBR-31, JTM-07, JBR-28, DIY-03, JTM-04, JTM-02, BTN-02, and JBR-11. This group was considered as the white taro group with dark green leaf veins. By contrast, accessions in the B2 group showed secondary veins that were light green or purple and primary veins that were light green to green. This group consisted of accessions JBR-35, BTN-09, BTN-01, DIY-05, JTG-02, JBR-08, JBR-39, JTG-04, JBR-15, JBR-16, JBR-09, DIY-02, DIY-01, JTM-05, JTM-06, JTG-14, JTG-12, JTG-16, JBR-33, JTG-09, JBR-24, BTN-03, BTN-12, JTG-03, JBR-26, BTN-08, JTG-01, JBR-43, BTN-11, JBR-30, JBR-27, JTG-06, JBR-10, JBR-12, and JBR-07 and was considered as the white taro group with light green to green leaf veins.

PCA based on 33 vegetative and morphological characters produced a scatter diagram of taro accessions with two main components (Figure 6). The role of morphological characters in the grouping of taro accessions was based on the value of variable loadings presented in Table 4. The analysis of the two main components of the 73 taro accessions based on 33 morphological characters produced a scatter diagram of taro accessions. As shown in Table 5, 14 characters played an important role in grouping taro accessions through PCA (italic writing). Eight characters, namely, A01, A02, D06, D08, D09, D16, D18, and D19, were jointly capable of separating all the accessions from PC1 and PC2. By contrast, the other six characters were capable of separating the accessions from one axis only. The characters D10, D13, and D15 separated the accessions from PC1 only, whereas the characters R06, D11, and D20 separated the samples from PC2 (Table 5).

DISCUSSION

In taro (*C. esculenta* L.) genotypes, corm shape varies and can be conical, round, cylindrical, elliptical, dumbbell,

or elongated (IPGRI, 1999). The shape and size of taro corms are influenced

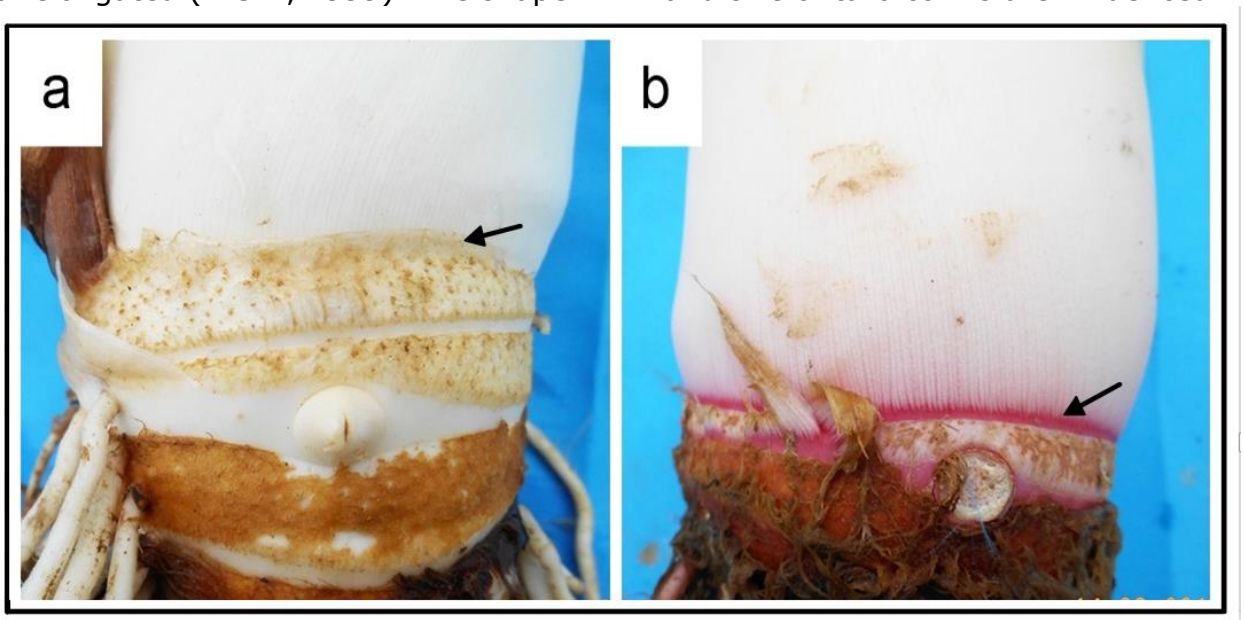

Figure 5. Ring color of the base of taro leaf sheath (black arrow): a. white, b. pink.

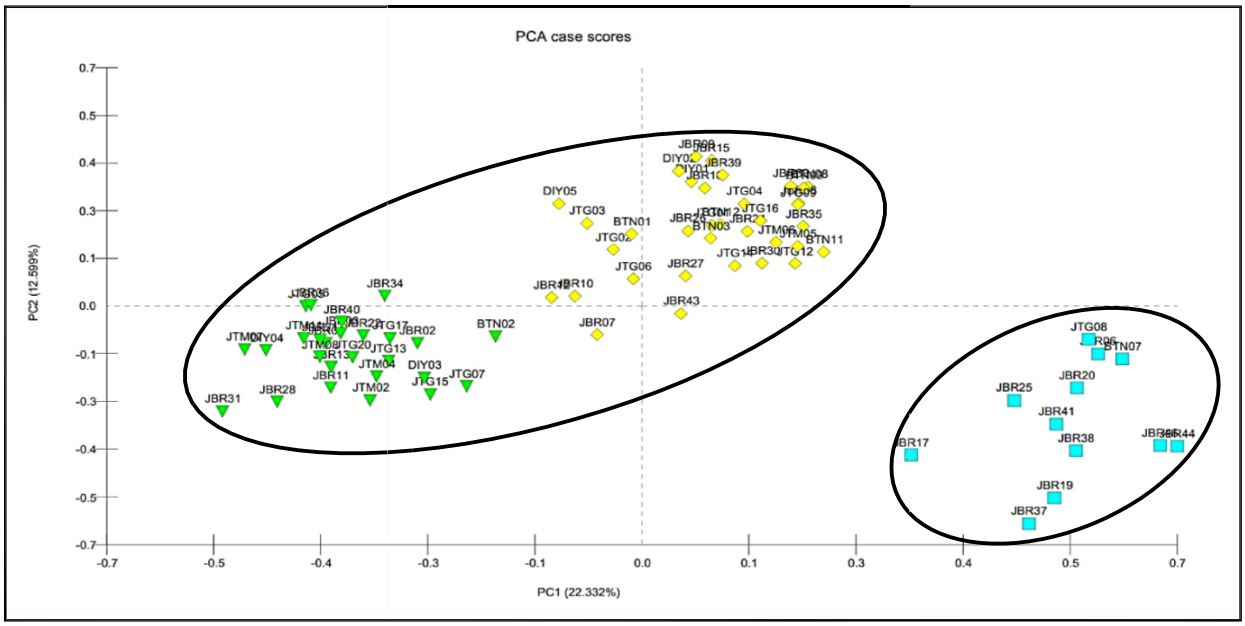

Figure 6. PCA projection of 73 accessions of taro in the first two components (PC1 vs. PC2) on the scatter diagram. Note: Accessions with blue color represent cluster A, those with green color represent cluster B1, and those with yellow color represent cluster B2.

Table 3. Nonformal intraspecies classification of taro from Java, Indonesia.

Groups	Subgroups	Accessions Number
A Pink group accessions	–	JBR-44, JBR-38, JBR-17, JBR-37, JBR-46, JBR-41, JBR-19, JTG-08, JBR-25, BTN-07, JBR-20, JBR-06
B White group accessions	B1 Subgroup with dark green primary leaf veins	JBR-34, JBR-13, JTG-05, DIY-04, JBR-40, JTM-11, JBR-22, JTG-20, JTM-08, JBR-21, JTG-17, JTG-07, JTG-15, JBR-02, JBR-36, JBR-03, JBR-01, JTG-13, JBR-31, JTM-07, JBR-28, DIY-03, JTM-04, JTM-02, BTN-02, JBR-11
	B2 Subgroup with light green primary leaf veins	JBR-35, BTN-09, BTN-01, DIY-05, JTG-02, JBR-08, JBR-39, JTG-04, JBR-15, JBR-16, JBR-09, DIY-02, DIY-01, JTM-05, JTM-06, JTG-14, JTG-12, JTG-16, JBR-33, JTG-09, JBR-24, BTN-03, BTN-12, JTG-03, JBR-26, BTN-08, JTG-01, JBR-43, BTN-11, JBR-30, JBR-27, JTG-06, JBR-10, JBR-12, JBR-07

Note: The accession number refers to that in Table 1.

Table 4. PCA variable loadings of the first two components of main component extraction.

Codes	Characters	PC1	PC2
H01	Rhizome shape	0.189	−0.158
A01	Rhizome skin surface	0.269	−0.293
A02	Rhizome skin thickness	0.227	−0.223
R01	Rhizome cortex color	0.033	0.052
R02	Rhizome flesh color	0.009	0.109
R03	Color of rhizome flesh fiber	0.063	−0.041
R04	Shoot color	0.155	−0.097
R05	Stolon number	−0.039	−0.105
R06	Sucker number	0.173	−0.291
R07	Leaf length and width ratio	0.163	−0.172
R08	Leaf position	0.094	−0.062
R09	Leaf symmetry	−0.113	0.154
D01	Upper leaf blade color	−0.009	0.072
D02	Surface condition of the upper leaf blade	−0.019	0.147
D03	Color of the sap on the leaf tip	0.116	0.042
D04	Leaf margin	−0.192	−0.090
D05	Color of leaf margin	−0.014	0.191
D06	Color of secondary nerves	0.269	−0.293
D07	Color of primary nerves	0.054	0.059
D08	Pigmentation of the leaf nerves on the lower leaves	−0.248	−0.241
D09	Length and wide Leaf petiole Ratio	−0.296	−0.232
D10	Color of 1/3 petioles, upper leaf adaxial	−0.286	−0.169
D11	Color of 1/3 petioles, upper leaf abaxial	−0.135	−0.220
D12	Color of 1/3 petiole, central	0.016	0.004
D13	Color of 1/3 petiole, bottom	−0.258	−0.119
D14	Leaf petiole lines	−0.149	−0.164
D15	Color of the basal ring of the leaf sheath	−0.278	−0.190
D16	Color of leaf sheath	−0.257	−0.229
D17	Leaf sheath margin color	0.034	−0.008
D18	Length of leaf sheath and petiole ratio	0.269	−0.293
D19	Rhizome shape	−0.213	−0.207
D20	Rhizome skin surface	−0.043	0.223
D21	Rhizome skin thickness	−0.045	−0.045

Table 5. Characters that play a role in grouping taro accessions.

Code	Character	PC1	PC2
A01	Root color	0.269	−0.293
A02	Uniformity of root color	0.227	−0.223
R06	Color of rhizome flesh fiber	-	−0.291
D06	The color of the sap at the leaf tips	0.269	−0.293
D08	Leaf edge color	−0.248	−0.241
D09	Color of secondary leaf nerves	−0.296	−0.232
D10	Leaf vein color	−0.286	-
D11	Pigmentation of veins on the leaf lower surface	-	−0.220
D13	Color of petiole 1/3 above the adaxial part	−0.258	-
D15	Color of petiole 1/3 middle	−0.278	-
D16	Color of petiole 1/3 bottom	−0.257	−0.229
D18	Color of the ring at the base of leaf sheath	0.269	−0.293
D19	Leaf sheath color	−0.213	−0.207
D20	Color of leaf sheath edge	-	0.223

by the type, humidity, and fertility of the soil. The genotypic expression of the skin color and rhizome (corms) of taro is based on their adaptation to sunlight in open or shaded sites (Lebot *et al*., 2017; Mandal *et al*., 2013). In taro, phenotypic factors were likely more influential than genotypic factors because size (quantitative variable) was influenced by environmental factors. Past studies have proven that phenotypic variations interact with genotypic variations and the environment, and in general, the phenotypic coefficient of variation is greater than the genotypic coefficient of variation in taro germplasm (Singh *et al*., 2000; Singh *et al*. 2012; Singh *et al*., 2017; Mandal *et al*., 2013). The main components of the taro leaf structure are a blade with prominent veins, long petiole, and sheath. Oktavianingsih *et al*. (2019) found that the division of taro accession groups is based on the variation in leaf sheaths. Taro leaf blades have the greatest variation compared with other leaf parts. Taro leaf blades are rounded, and the positions of the leaf blades and petioles are peltate or hastate. Lebot and Aradhya (1991) and Lebot (2009) revealed that taro leaves are peltate or hastate.

The results showed that the leaf blade of the taro accessions had three primary veins in a Y arrangement with varying angles and 9 to 13 secondary veins in a pinnate arrangement. The vein color pattern under the leaf surface played an important role in the identification of taro accessions from Java, Indonesia. The importance of the color pattern of taro leaf veins for identification and selection was also stated by Mandal *et al*. (2013) and Ezeabara *et al*. (2015). The distribution of color pigmentation in leaf veins on the underside of the leaf blade also varied across accessions, and past studies reported the same findings for taro germplasm (Prana *et al*., 2000, 2010).

The dendrogram divided the taro accessions into clusters A and B, and cluster B was further divided into B1 and B2. The determination of the existence of these three clusters on the dendrogram was based on the similarity index of 0.60 to 0.80 for intraspecies categories (Sokal and Sneath, 1972; Stace, 2000). In this study, the three clusters could be

distinguished on the basis of color characteristics, i.e., root color, leaf tip sap color, and leaf base color (Prana *et al*., 2010; Rodriguez-Manzano *et al*., 2010). Pitoyo *et al*. (2018) reported that taro accessions from Southeastern Central Java, Indonesia can be divided into two distinct clusters on the basis of morphological characters. According to Lebot *et al*. (2004), taro accessions from Southeast Asia and Oceania form unclear dendogram structures and produce groups with continuous variations. Oktavianingsih *et al*. (2019) reported the highest diversity and found five groups for diploid taro germplasm. Rodriguez-Manzano *et al*. (1999) reported a positive correlation among shoot color, corms (rhizome), and roots with corm taste in Cuba. Taro accessions with pink organs have corms with superior taste.

Cultivated plants are often subjected to nonformal classification. Hasan *et al*. (2006a, 2006b) divided water yam (*Dioscorea alata*) accessions from Malaysia into six groups based on morphological and molecular characters by using RAPD analysis. Purnomo *et al*. (2012) divided water yam (*D. alata*) accessions from Indonesia into seven groups and the lesser yam (*Dioscorea esculenta*) from Indonesia into three accession groups on the basis of morphological characters (Purnomo *et al*., 2017). The dendrogram showed that taro accessions from Java, Indonesia, had the highest diversity. Previous findings also illustrated that taro germplasm originating from Indonesia has the greatest genetic diversity (Lebot and Aradhya, 1991; Kreike *et al*., 2004; Lebot *et al*., 2004) likely because Indonesia in general, and Java in particular, include the natural distribution area of taro (Mathews, 2006; Govaerts, 2012). According to Lebot (2009), the highest variation was reported in taro accessions collected in Indonesia. According to Das *et al*. (2015), research on the karyotype and ploidy is important to taro cultivation.

The role of morphological characters in the grouping of taro accessions revealed that the main components produced a total variation on axis 1 (PC1: 22.332%) and axis 2 (PC2: 12.559%). In past studies, the values of PC1 and PC2 represent approximately seven and four morphological characters, respectively (Bro and Smilde, 2014). The analysis of the main components was found to be useful for phenetic analysis, showing that morphological characters have an important role in cluster formation (Ochsmann, 2004). Vegetative characters are widely used for the intraspecies identification and classification of taro. Somantri *et al*. (2004) and Hafsah *et al*. (2014) reported that the color character of taro has the highest diversity. In particular, the color of vegetative organs plays an important role in the classification and intraspecies identification of taro.

Observations based on morphological variations and phenetic analysis can be used as a basis for the intraspecies classification of taro. In this study, the taro accessions were divided into two groups, i.e., pink and white. The distribution of accessions in the pink and white groups was mainly based on the color of roots, color of the sap at the tips of the leaves, and the color of the rings at the base of the leaves. Past studies anticipated the nonformal classification of wild and cultivated genotypes (Hawkes, 1986; Kreike *et al*., 2004). Taro germplasm from Java, Indonesia, can also be

classified in accordance with the principle of nonformal classification (Hanelt, 1986).

CONCLUSION

Taro accessions revealed the highest diversity for leaf color patterns, including leaf veins and leaf midribs, with a similarity index of 0.57 to 0.96. Taro accessions were classified into pink and white accessions. The white accession group was subdivided into two groups i.e., dark green and light green veins.

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