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Genetic diversity in Eddoe Taro (*Colocasia esculenta* var. antiquorum) from Indonesia based on morphological and nutritional characteristics

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Abstract. *Maretta D, Sobir Helianti I, Purwono, Santosa E. 2020. Genetic diversity in Eddoe Taro (*Colocasia esculenta *var antiquorum) from Indonesia based on morphological and nutritional characteristics. Biodiversitas 21: 3525-3533.* Low yield uniformity and quality due to genetic performance become negative incentives to farmers in Eddoe Taro production. However, genetic evaluation is rarely been reported in this taro type in Indonesia. In this study, 14 eddoe genotypes collected from different regions in Indonesia were evaluated to develop a diversity map for crop improvement and future breeding activities. The genotypes were planted in the open field from September 2018 to March 2019 at the experimental station belonging to LAPTIAB-BPPT, PUSPITEK at South Tangerang District, Indonesia. Morphological and nutritional characters were accessed on the shoot and underground parts. The genotypes exhibited variation in 38 out of 48 characters in which 12 quantitative characters were distinct including oxalate level. The study revealed three findings: (i) Characters related to growth and yield had high genotypic variance coefficients, i.e., sheath length, total petiole length, plant height, number of suckers, corm and cormels weight, (ii) Genotypes clustered into two separate groups as introduced and landraces, and (iii) Landraces had high genetic variation leading to speculation of high clonal variation. Considering the findings, accession S6, S7, S18, S30, and S36 are recommended for further studies in crop improvement purposes.

Keywords: Crop improvement, Eddoe Taro, genetic properties, glucomannan, oxalate

INTRODUCTION

Taro (*Colocasia esculenta* (L.) Schott) is an important food in many localities in the humid tropics and subtropics (Chaïr et al. 2016). The corm is rich of nutrients such as carbohydrate, protein, elements (Fe, Ca, P, Mg, Na, and K) and vitamins (A, B1, B2, B3, and C) (Ezeabara et al. 2015, Mergedus et al. 2017); the protein level is higher than cassava and sweet potato tubers (Temesgen and Retta 2015). Taro tubers are also important sources of anthocyanins, cyanidin 3-glucoside, and flavonoids that act to improve blood circulation, antioxidants, and inhibit cancer development (Rashmi et al. 2018).

Morphologically, taro has two forms according to the corm and cormel developments, i.e., dasheen and eddoe types that botanically called as *Colocasia esculenta* var esculenta and *Colocasia esculenta* var antiquorum, respectively and var esculenta distributes widely in the globe, while var antiquorum predominantly distributes in China and Japan (Plucknett 1983). For this reason, var antiquorum to some extend is called Satoimo or Japanese taro.

In Indonesia, the production of Eddoe Taro is getting popular to fulfill the high demand for export. Since 2013, about 6,300 tons of frozen taro have been exported to Japan (ITPC 2014). For such reason, intensive cultivation has been being developed in some districts like Bantaeng (South Sulawesi), Banggai Kepulauan (Central Sulawesi) (Laosa et al. 2016), Kapahiang (Bengkulu) (Amelia and Yumiati 2016) and provinces such as East and West Java (Astuti et al. 2017) and Aceh (Rosdanelly et al. 2018). The Indonesian Government also provides seeds and subsidies to farmers.

However, in the field, many farmers face problems on quality and productivity leading to the low economic benefit of the business. In Eddoe Taro, the quality of cormels is determined by glucomannan and oxalate content. Glucomannan content in taro has been intensively studied (Njintang et al. 2011; Ekowati et al. 2015). The glucomannan is explored in concern to health and beauty (Bateni et al. 2013; Tester and Al-ghazzewi 2016). Glucomannan is a neutral, fermentable and viscous dietary fiber that has been proven to reduce obese (Zalewski et al. 2015), to relieve physiological disorders especially diabetes and cardiovascular diseases (Shah et al. 2015), to reduce blood lipid and cholesterol (Behera and Ray 2016), and to extend storage in the frozen form of processed meat and fish products (Yang et al. 2017). Thus, it is desirable to produce cormels with high glucomannan content. On the other hand, oxalate content as anti-nutrient should be low

(Akalu and Geleta 2017). The mucilage of the fresh taro causes irritation (Yu et al. 2015), stimulates kidney stones, and impairs the absorption of minerals such as iron and calcium in the body (Hang et al. 2013). High oxalate content causes itching in the mouth, burning sensation, and skin irritation (Kaushal et al. 2012; Dewi et al. 2017), leading to low palatability.

One effort to improve quality and yield of the taro is through genetic improvement (Banjaw 2017). Instead of many improved skills on general taro breeding, the diversity of eddoe type in Indonesia is still unknown. Since genotype characterization is a fundamental step onto selection of candidate parents for future breeding programs (Pitoyo et al. 2018). Thus, the study aimed to evaluate morphological and nutritional characters of Eddoe Taro in Indonesia.

MATERIALS AND METHODS

Study site and plant materials

The experiment was conducted in rainy season from September 2018 to January 2019 in the open field at Experimental Station of Laboratory for Development of Industrial Technology for Agricultural and Biomedicine (LAPTIAB), Research Center for Science and Technology (PUSPIPTEK) Setu subdistrict, South Tangerang, Banten, Indonesia. The site had altitude 60 m above sea level (6°21'26.5"S 106°39'56.2"E) with clay soil (Red Yellow Podzolic). The soil had pH 6.1, low C/N ratio (C/N=10), high available phosphorus (67 mg P2O5/100 g; HCl 25% extraction), low available potassium (32 mg K2O/100 g; HCl 25% extraction) and high cation exchangeable capacity 14.58 me/100 g by NH4CH3CO2 extraction.

Fourteen Eddoe Taro genotypes were obtained from six provinces (Table 1). The type had been verified in the preliminary experiment and coded following the official record. All genotypes are conserved in the LABTIAB facilities with copy genotypes that are maintained at Bogor Agriculture University, Indonesia.

Cultivation method

All genotypes were planted in two blocks, to minimize the variation of soil fertility. The first block was located at higher soil level, than that of the second block. In each block, the arrangement of the genotype was randomized. Each genotype was planted 5 plants in each block.

Before planting, the soil was plowed and harrowed twice; and the planting site was designed using a raised bed about 15 cm from the soil level. The width of the planting bed was one meter, and each bed only planted a single line. Soil liming at rate 2 $t.ha^{-1}$ was applied after bedding.

Seed planting used cormlet, seized 2.5-3.5 cm in diameter, and 30-50 g in weight depending on genotype. Among genotypes, planting distant applied 100 cm, while 60 cm in a row within a particular genotype. In each planting hole, a single cormlet was used. At planting, the cormlet had no leaf was exist. Organic manure from cow dung was applied at a week before planting, about 1 kg for each planting hole. NPK fertilizers were applied twice. The first application was conducted four weeks after planting (WAP) using one-third of the total NPK dose. The second application using the rest of the dose was conducted at 12 WAP. NPK fertilizer derived from single fertilizer, i.e., 120 $kg.ha^{-1}$ Urea (46% N), 50 $kg.ha^{1}$ SP36 (36% P_2O_5) and 150 $kg.ha^{-1}$ KCl (60% K_2O)/. Weeding used manual and pesticide spraying using common chemicals according to field conditions.

Morphological evaluation

Morphological data were obtained at maximum vegetative growth (14 WAP) and at harvesting time (20 WAP). Morphological description followed IPGRI (1999), and nutritional characters focused on chlorophyll, oxalate, and glucomannan contents. Thus, a total of 48 characters were evaluated.

The morphological evaluation focused on plant habit, leaf, petiole, corm, cormel, and root (Figure 1). Plant habits included plant height (Ph), plant span (Ps), and the number of suckers. Leaf characters included leaf base, predominant position of leaf lamina surface, leaf blade margin, leaf blade color, leaf blade margin color, leaf lamina appendages, leaf main vein color, vein pattern, lamina length, lamina width, sheath length, leaf sheath edge color, and leaf waxiness. Petiole characters included petiole junction pattern, petiole junction color, petiole stripe, petiole stripe color, petiole basal-ring color, the cross-section of the lower part of petiole, and total petiole length. Corm characters included corm manifestation, length, corm branching, shape, weight, cortex color, flesh color of the central part, corm flesh fiber color, skin surface, skin thickness, degree of fibrousness of corm, and bud color. Cormel characters included weight, number, shape, flesh color of cormels, and root characters included color and uniformity of color.

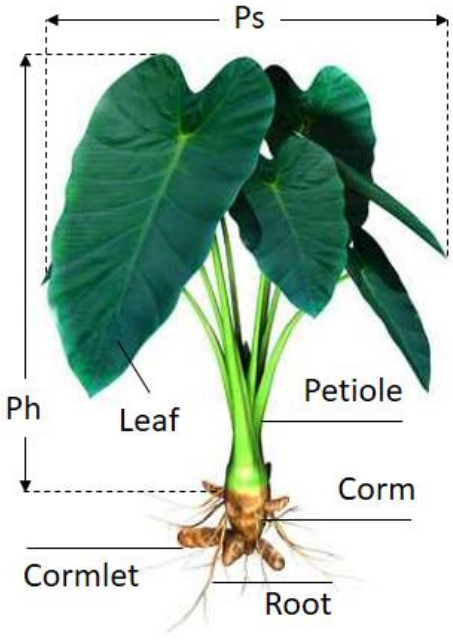

Figure 1. Part of the eddo taro plant. Note: Ph-plant height, Ps-Plant span (Picture adopted from https://www.seedsofindia.com)

Nutritional analysis

Glucomannan and oxalate were analyzed from mixed flour of corm and cormlets. The preparation followed to Chairul and Chairul (2006). After cleaning, corm/cormlets were peeled, thin-sliced and oven-dried at 80°C for 20 hours continuously. The dried-chips then were made into flour using a blender (Madato type) and then shieved using 80 mesh before preparing the analysis.

Glucomannan analysis used the gravimetric method of Widjanarko and Megawati (2015). Five-gram taro flour was added to preheated 50 mL distilled water (75°C) plus 0.5 g $Al_2(SO_4)_3$ (10% of sample weight) in Erlenmeyer glass inside the water bath. The mixture was kept at 75°C while stirring for 35 min, then the solution was transferred into falcon tube 50 mL and centrifuged at 2000 rpm (25°C for 30 min). The supernatant was transferred to a new falcon tube and then added isopropyl alcohol 1:1 (v/v). The supernatant was inverted until coagulated. The pellet was then filtered using filter paper (Whatman No 1 qualitative ∅125 mm) equipped with a vacuum pump (Rocker 300 type). Finally, the pellet was oven-dried at 60°C for 24 hours. Percentage glucomannan content on dry basis was estimated from ratio final weight to sample weight.

Oxalate analysis referred to Naik et al. (2014). Initially, taro flour weighed 0.25 g was transferred in to test tube, added 10 mL 0.25 N HCl, and then heated at 85-90°C for 15 min in the water bath. After cooling in room temperature, the volume was adjusted into 25 mL with 0.25 N HCl and mixed gently. The supernatant (1 mL) was then used for oxalic acid measurement using spectrophotometric.

Before measurement, the fresh stock solution was prepared. For this purpose, 1000 ppm standard solution was developed from 139.6063 g oxalic acid ($C_2H_2O_4.2H_2O$) diluted in 100 distilled water. The second stock was 0.02 M $KMnO_4$, it was prepared by dissolving 3.1606 g $KMnO_4$ into 1 L distilled water. The third stock was 2 N H_2SO_4, it was made by dissolving 27.8 mL concentrate H_2SO_4 with distilled water into a final volume of 500 mL. The standard solution was made for 0, 5, 10, 15, 20, 25, 30, 35, 40, 45 and 50 ppm of the oxalic acid standard solution. In each 1 mL solution was added 5 mL 2 N H_2SO_4 and 2 mL of 0.003 M $KMnO_4$, then incubated at room temperature (27±2°C) for at least 10 min. The measurement used UV-1800 spectrophotometric Shimadzu at 528 nm.

Data analysis

Analysis of variance (ANOVA) was performed by F-test to investigate the presence of statistically significant differences among genotypes for quantitative characters. Duncan's multiple range test $p<0.05$ was addressed to estimate genotypic differences by optimizing the block as replication.

Cladogram analysis used DARwin 6 (http://darwin.cirad.fr) by utilizing all quantitative and qualitative data. In the clustering process, the software was set in dissimilarity mode, unweighed neighbor-joining and bootstrap 1000 times.

The relationships among genotypes was estimated using STRUCTURE 2.3.4, using combining data of quantitative and qualitative characters. The calculation used the admixture model, length of period 100,000, number of MCMC repeat after burned 100,000, K=3, and the number of iteration 20. Optimum K was determined by using Structure Harvester (Earl et al. 2012) through online (http://taylor0.biology.ucla.edu/structureHarvester).

Genotypic and phenotypic variances estimation and the calculation of the variance coefficient followed Syukur et al. (2015). The formulas as follows: Genotypic variance (σ^2g) = MSg-MSe; Genotypic variance coefficient (GVC): $[\sqrt{\sigma^2g}/x]$ x 100; Phenotypic variance (σ^2p) = σ^2g + MSe; Phenotypic variance coefficient (PVC): $[\sqrt{\sigma^2p})/x]$ x 100; Here, MSg and MSe denoted genotypic and error means square, respectively. The 'r' represented replication (n=2) and 'x' represented mean value. Deshmukh et al. (1986) classified PVC and GVC as high (> 20%), medium (10 to 20%), and low (< 10%). Estimate of broad-sense heritability (h^2) was calculated based on variant value of genetic and phenotypic follow Stansfield (1983), $h^2 = \frac{\sigma^2\xi}{\sigma^2r}$; ; the h^2 was classified as high ($h^2 > 0.50$), medium ($0.20 \leq h^2 \leq 0.50$), and low ($h^2 < 0.20$).

Table 1. Site of origin of 14 Eddoe Taro accessions

Code	Local name	Collecting site (Subdistrict, District, Province)	Habitat*	(Altitude m asl)	Origin
S6	Safira	Bontadaeng, Bantaeng, South Sulawesi	AF	750	LR
S7	Satoimo	Bontadaeng, Bantaeng, South Sulawesi	AF	750	IN
S15	Satoimo	Lembah Seulawah, Aceh Besar, Aceh	AF	150	IN
S17	Dempel	Trowulan, Mojokerto, East Java	HG	30	LR
S18	Talas Oshikawa	Kepung, Kediri, East Java	AF	60	IN
S20	Bentul	Batu, Malang, East Java	RG	445	LR
S24	Talas Oshikawa	Lamongan, Lamongan, East Java	AF	6	IN
S26	Salak	Karang Asem, Karang Asem, Bali	HG	88	LR
S28	Bentul	Pesantren, Kediri, East Java	HG	60	LR
S30	Keladi	Belitang, Belitang, South Sumatra	AF	40	LR
S33	Brentel	Sooko, Mojokerto, East Java	HG	30	LR
S34	Japanese taro	Lilirilau, Soppeng, South Sulawesi	AF	90	IN
S35	Japanese taro	Batulappa, Pinrang, South Sulawesi	AF	50	IN
S36	Ngariung Indung	Santana, Kuningan, West Java	AF	760	LR

Note: ***** AF-agriculture farmer field**,** HG-homegarden, RG-grow wild in the experimental field garden; ** LR-landrace, IN-Recently introduced according to farmer information, but dating unknown

RESULTS AND DISCUSSION

Morphological and nutritional characters

Eddoe genotypes collected from Indonesia showed variation in leaf, petiole, corm, and cormels (Figure 2). Among 48 characters used in the genotyping, 38 characters showed variation including qualitative and quantitative characters. Twelve out of 15 quantitative characters exhibited significant variation among genotypes (Table 2). There was no significant difference for corm diameter, number of cormlet and glucomannan content. Table 2 shows characters related to plant growth and production like chlorophyll content, leaf size, plant size, number of the sucker, corm size, and cormlet weight had variation among genotypes.

Moreover, oxalate content in the corm and cormlets significantly varied among genotypes (Table 2). Low oxalate level is an important indicator for taro palatability affected by genotype (Nurilmala and Mardiana 2019); the level of the oxalate content could be reduced by cooking (Hang et al. 2013). We confirmed here that genotype had a different level of oxalate. This fact could be an important consideration in crop improvement to address farmer's problems in cormel quality.

From 33 qualitative characters observed, 28 characters showed variation among genotypes. The variation was found in leaf blade margin, leaf lamina appendages, leaf blade margin color, leaf sheath color, and vein pattern. Here, seven characters were presented; these characters could be easily distinguished for genotyping including by farmers (Table 3). Among leaf morphological characters, sheath color and vein patterns were easily recognized. Three accessions had red-purple sheath, i.e., S26, S28, and S33 genotypes, while the others were light green. The common vein pattern was V-pattern, followed by Y-pattern extending to secondary vein and Y-pattern. Y-pattern was found in single accession S20 from Malang District (Table 1).

Petiole varied in whole color, junction, stripe, and basal-ring color. Here, the whole petiole color was the most prominent character compared to other petiole characters. The whole petiole mostly was light green, but brown existed for S26 and S30, and purple was found in S28 and S33 genotypes (Table 3). Rudyatmi and Rahayu (2014) reported that taro with purple petiole was known as black taro.

Corm exhibited variation in shape, cortex color, flesh color of the central part, flesh fiber color, skin thickness, fibrousness degree of corm and bud color; with corm shape and bud color were the most discernible characters. S28 was the only genotype with cylindrical corms (Table 3). Corm with dumb-bell shape existed in two genotypes, conical shape in four and round shape in seven genotypes. Corm dumb-bell and round shape was also found in *C. esculenta* characterized by Sinaga et al. (2017). Bud color was yellow-green in S20, S28 and S33 genotypes, and pink-red in the other 11 accessions. Table 3 shows that all genotypes with round corm had pink-red corm bud. Corm commonly had a big size and located at the central such as in S6, S20, and S36 genotypes. However, for some genotypes like S18, S34 and S35 had the corm size almost the same size as its cormlets (Figure 2C).

Table 2. ANOVA for quantitative characters of 14 Eddoe Taro genotypes from Indonesia

Characters	Mean±SD	SS	MS	F Value	R-Square	CV	Sig
Leaf lamina							
Length (cm)	36.1±8.6	1607.76	123.67	5.81	0.86	12.79	**
Width (cm)	12.7±2.8	158.99	12.23	4.89	0.84	12.49	**
Sheath length (cm)	22.1±5.5	688.66	52.97	6.81	0.88	12.64	**
Total petiole length (cm)	62.1±23.1	12285.81	945.06	8.24	0.90	17.24	**
Plant width (cm)	93.7±23.7	10208.65	785.28	3.25	0.79	16.58	*
Plant height (cm)	81.8±27.8	17775.32	1367.33	8.28	0.90	15.71	**
Number of sucker	5.7±3.4	214.69	16.51	3.34	0.79	39.27	*
Corm							
Length (cm)	61.0±13.5	4232.96	325.61	7.08	0.88	11.12	**
Diameter (cm)	56.5±7.2	885.72	68.13	1.87	0.66	10.69	ns
Weight (g)	95.5±36.9	1375410.69	105800.82	5.97	0.81	24.04	**
Cormlet							
Number	24.3±10.1	1705.90	131.22	1.91	0.67	34.17	ns
Weight (g)	425.8±47.3	1375410.69	105800.82	5.97	0.87	31.27	**
Chlorophyll (mg/g)	57.6±5.2	520.89	40.07	2.58	0.72	6.84	*
Oxalate (ppm)	94.8±32.8	15738.99	1210.69	3.47	0.85	19.69	*
Glucomannan (%)	5.7±1.5	39.40	3.03	2.23	0.69	20.43	ns

Note: SD-Standard Deviation; SS-Sum of Squares; MS-Mean Square; CV-coefficient of variant; ** : significant ($p<0.01$); * : significant ($p<0.05$), ns : not significant

Figure 2. The appearance of leaf lamina (A), petiol (B), corm (C), and cormlets (D) of 14 Eddoe Taro genotypes from Indonesia

Table 3. Selected morphological data of 14 Eddoe Taro genotypes from Indonesia

Characters	Genotype code													
	S6	**S7**	**S15**	**S17**	**S 18**	**S20**	**S24**	**S 26**	**S28**	**S30**	**S 33**	**S34**	**S35**	**S 36**
Sheath color	1	1	1	1	1	1	1	2	2	1	2	1	1	1
Vein pattern at leaf base	3	3	3	3	3	1	3	2	2	2	2	3	3	3
Whole petiole color	3	3	3	3	3	3	3	1	2	1	2	3	3	3
Corm shape	4	4	4	4	4	3	4	3	1	3	3	2	4	2
Bud color	2	2	2	2	2	1	2	2	1	2	1	2	2	2
Cormlet shape	4	4	4	4	4	3	4	2	3	1	3	4	4	4
Root color	2	2	2	2	2	1	2	2	1	2	1	2	2	2

Note: Sheath color (1-light green, 2-red purplish), Vein pattern at leaf base (1-Y pattern, 2- Y-pattern extending to the secondary vein, 3-V pattern), Whole petiole color (1-brown, 2-purple, 3-light green), Corm shape (1-cylindrical, 2-dumb-bell, 3-conical, 4-round), Bud color (1-yellow green, 2-pink-red), Cormlet shape (1-conical, 2-elongated, 3-elongated-curved, 4-elliptical), Root color (1-pinkish white, 2-white)

Genetic properties

GVC and PVC for important quantitative characters significantly varied from low to high (Table 4). Six characters had high criteria GVC, i.e, sheath length, total petiole length, plant height, number of sucker, corm and cormlets weight. Chlorophyll content contributed to low GVC, and it was the lowest among characters. On the other side, all PVC was high, except for the character of chlorophyll content. In the present study, all PVC values were higher than the GVC. This finding is a common case in the genotypic evaluation such as in other crops (Effendy et al. 2018).

In the breeding process, genotype selection based on characters with high heritability and high genetic variation is desirable. Heritability value would determine the selection method of plant characters because it gives a portion of genetic and phenotypic variation that is inherited (Sleper and Poehlman 2006). According to Jalata et al. (2011), broad genetic diversity would speed the success of the selection and breeding progress. Effendy et al. (2018) pointed out that high genetic variation of particular characters within a population reflected the span of genetic control and the high genetic control means expected product of the breeding process could be estimated more precisely. In the present experiment, the estimate of broad-sense heritability and PVC of all characters showed high, except the chlorophyll content that showed medium and low. High GVC found in characters sheath length, total petiole length, plant height, number of suckers, weight of corm, cormlets weight and oxalate content (Table 4). The high genetic diversity would enlarge chances of success selection in plant breeding due to the higher frequency of

genes (Hapsari 2014). Confirmable to Eze and Nwofia (2016) that plant height, number of suckers, length, and weight of corm and cormlet weight has high heritability. This research result reveals additional information that oxalate content also has a high value of heritability, PVC and GVC. It indicates that the quantitative characters as listed in Table 4 could be used in the selection program.

On the contrary, Mulualem and Michael (2013) reported that the quantitative characters of *Colocasia esculenta* had low or medium PVC, GVC, and heritability. Low heritability value indicated a character inherited complicatedly and influenced by environment factors (Meydina et al. 2015). Refers to Sleper and Poehlman (2006) the effectiveness of selection depends on the variability of the individual in the population and the variability among plants due to the environment. For that reason, the selection of these all Eddoe Taro genotypes highly recommended to be examined in multi-location or different season conditions to find out which genotypes perform consistently in a wide range of environments.

Genotype grouping

Genotypes separated into two groups with seven-member in each group, Group-1 (S18, S20, S26, S28, S30, S33, and S36) and Group-2 (S6, S7, S15, S17, S24, S34, and S35) (Figure 3). Group-2 represented the 'satoimo group' judge from the local name, except Safira (S6) and Dempel (S17). Cladogram showed S6 separated to other members including S7. Unexpectedly, S6 and S7 genotypes that geographically close (Table 1), were separated distantly in the cluster Group-2.

According to farmers that cultivated the S7 accession, they received the seed from the local government of South Sulawesi province. The local government imported seeds from Japan through a trading company. The seeds were propagated by the trading company and then distributed to some Districts within South Sulawesi, including other provinces such as Aceh and East Java, so farmers maintained the accessions name as 'satoimo' of Japanese. Therefore, it is presumable that Satoimo group shared similar ancestor based on morphological characters; and the ancestor was likely derived from S7 in Bantaeng District, South Sulawesi. In Aceh, Eddoe Taro was reintroduced around 2014 almost the same time reintroduction to Buleleng District in Bali (Taufiq 2015); thus it supported that Aceh accession S15 clustered in Satoimo group.

High genetic variation within satoimo group as shown in Figure 3, indicated that clonal variation could be high in eddoe type. There probably was genetic distant between S6 and S7 although geographically close due to clonal variation. On the other side, Group-1 represented the local landrace. It is still unclear, S18 that had a similar name with S24 'Talas Oshikawa' clustered to a different group. In general, morphological variation within Group-1 was larger than the variation within Group-2 (Figure 3). It needs further evaluation using molecular markers the reliability in this grouping.

Genotype grouping using a cladogram was consistent with grouping based on population assessment using STRUCTURE (Figure 4). The population grouped into two types, Type-1 and Type-2. The Type-1 was indicated by light grey color consisted of eight genotypes (S6, S7, S15, S17, S18, S24, S34, S35, S36) and shows high uniformity. The type-1 population included all accessions in the Group-2 cladogram (Figure 3), and the clustering was exactly matched with a local name especially S18 that unable to be resolved using the cladogram. Here, almost all accessions under Type-1 were taken from the commercial field at which based on farmer interview the parent seeds were imported except for S6, S17, and S36 that obtained from local farmers. Considering these genotypes shared the same ancestor, this finding envisages the hypothesis that clonal variation could be high in Eddoe Taro.

Type-2 had five members, i.e., S20, S26, S28, S30, and S33 indicated by a mixture of black and dark grey colors (Figure 4). Type-2 accessions corresponding to Group-1 in the cladogram. This type, most probably as original landraces in Indonesia.

Table 4. Genotypic and phenotypic variances and it's coefficient for 12 quantitative characters of Eddoe Taro in Indonesia

Character	σ^2g	σ^2p	h^2		GVC (%)		PVC (%)	
Leaf lamina								
Length	51.20	72.48	0.71	***	19.84	**	23.60	***
Width	4.86	7.37	0.66	***	17.42	**	21.44	***
Sheath length	22.59	30.38	0.74	***	21.54	***	24.97	***
Total petiole length	415.18	529.88	0.78	***	32.80	***	37.06	***
Plant size								
Plant span	271.96	513.32	0.53	***	17.60	**	24.18	***
Plant height	601.09	766.24	0.78	***	29.96	***	33.83	***
Number of suckers	5.79	10.73	0.54	***	42.50	***	57.87	***
Corm								
Length	139.82	185.80	0.75	***	19.40	**	22.36	***
Weight	878.63	1,406.01	0.62	***	31.03	***	39.25	***
Cormlets weight	44,036.55	61,764.27	0.71	***	49.28	***	58.36	***
Chlorophyll content	12.26	27.80	0.44	**	6.08	*	9.15	*
Oxalate content	431.12	779.57	0.55	***	21.90	**	29.45	***

Note: GVC-Genotypic variance coefficient; PVC-phenotypic variance coefficient; ***high, **medium, *low

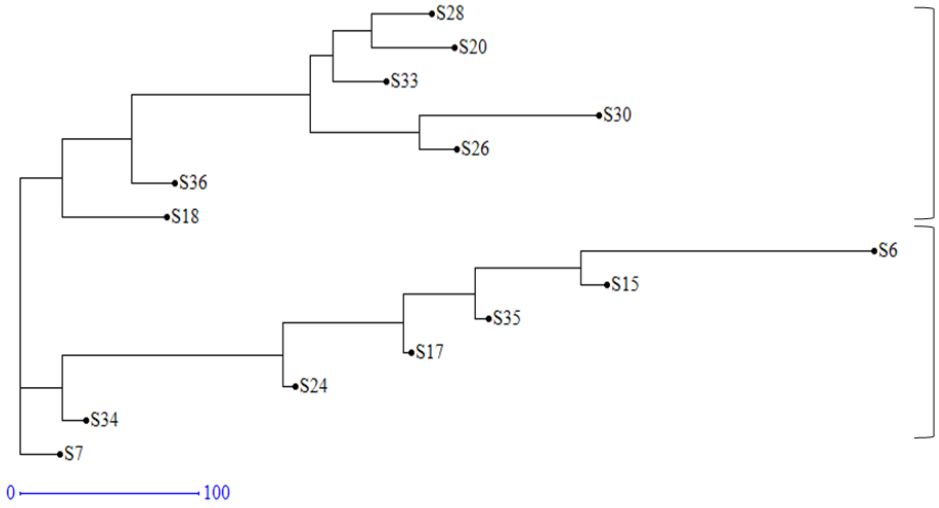

Figure 3. Cladogram of 14 Eddoe Taro genotypes collected from Indonesia. Bar indicates dissimilarity distant. The genotype name is presented in Table 1

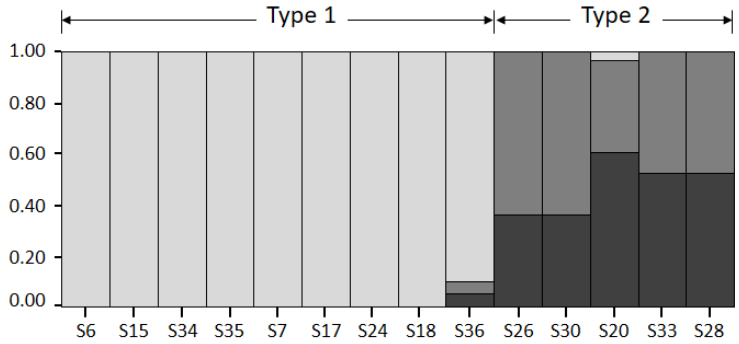

Figure 4. The genetic population structure of Eddoe Taro in Indonesia is drawn by STRUCTURE

Figure 4 shows that genetically, S36 seemed as an intermediary type between Type-1 and Type-2 clusters. Since S36 contained many share characters from population Type-1 lead to join the Type-1 in the present analysis. Considering that Type-1 just recently introduced, it is difficult to conclude that S36 was a result of breeding Type-1 and Type-2 genotypes. Moreover, based on genetic composition it is likely that Type-2 genotypes were clonal variant from S36 in Kuningan District.

Source of genetic variation

We speculated that morphological and nutritional variation in Eddoe Taro from Indonesia arose from a combination of multiple introduction and clonal variation. The first introduction could be around the 1940s or before. This assumption based on information from Prana (2007) where the eddoe type is only found at an isolated site like 'Talas bithek' in Tana Toraja District and 'Talas salak' in Buleleng District, Bali, in which these sites had intense interaction with Japanese in the past time. Fortunately, we incorporated 'Talas salak' from Karangasem District, Bali (code S26) that geographically less than 100 km; it was involved in Group-1 and Type-2. Here, Group-1 or Type-2 was represented as the first introduction. According to information from senior farmers (> 80-year old) in Sooko village, Mojokerto, he claimed that the seeds of 'Brentel' (S33) were introduced by the Japanese army in around 1940s to support their logistic in East Java. His information was confirmed in the cladogram dan dendrogram (Figures 3 and 4). It is confident to note that S20, S26, S28, S30, and S33 arisen from the first introduction.

The second introduction was represented by genotypes belongs to Group-2 cladogram or Type-1 dendrogram such as S6, S7, S15, S17, S24, S34 and S35 (Figures 3 and 4). The introduction could be around the 2000s through South Sulawesi after the establishment of the 'Satoimo Consortium Project in 2004' involving Japanese and Indonesian companies (Kallo et al. 2019). According to Das et al. (2015), Eddoe Taro has diversity in chromosome numbers. Thus, it is probable that the Japanese introduced different cultivars for the first and second periods.

Presence of genetic variation within-cluster group in Figure 3 probably due to clonal variation after generations. According to Vandenbroucke et al. (2016), clonal variation in taro was about 3%. After the first phase of the introduction, the development of Eddoe Taro could be

restricted by unknown reasons. The success of the Green Revolution in Indonesia leading to the high availability of rice (Poerwanto et al. 2012, Yunus et al. 2016), could be one explanation Eddoe Taro became less utilized. During the survey, many farmers in East Java stated that Eddoe Taro was abandoned ones, even sometimes called a weed. The eddoe underwent dormant during the dry season; the dormancy might limit continuous availability, unlike dasheen type that available throughout the year. The case nearly similar to clonally propagated *Amorphophallus paeoniifolius* as a neglected crop in Java after the green revolution (Santosa et al. 2017).

As a result, eddoe genotypes such as S36 were cultivated in a limited area at highland in Kuningan District, West Java along the edge of a vegetable field close to Ceremai Mt. Locally, S36 called Ngariung indung or lahun indung means 'mother carrying the son'. Sometimes the boiling cormlets were available in the local market. According to Kuningan people, particular cormlets have been known available in the market since the 1970s.

S36 was an exceptional genotype. According to the clade diagram, it is grouped with genotypes into the first phase of introduction (Figure 3) but genetic composition indicated a high proportion of the second phase of introduction (Figure 4). Judgment from the timeline, the S36 was most likely as descendent from the first phase of introduction but underwent genetic manipulation. The genetic manipulation is less likely from natural mating because flowering on eddoe type in the field was a rare case. According to Susepah (2018), Sundanese in Kuningan is a famous retailer that travels across Indonesian cities. The Kuningan genotype probably originated from clonal variation, like in clonally propagated *A. paeoniifolius* (Santosa et al. 2010). Nevertheless, the hypothesis needs further evaluation because in the present experiment the original variety of satoimo from Japan was not incorporated.

To develop better cormlets quality and production, it is important to consider this genetic diversity and historical data. After years, first introduced-genotype probably has adapted with Indonesian agro climate, while second introduced-genotype has superiority in the palatability and global acceptance. Therefore, it is recommended to use genotype S6, S7, S18, S30 and S36 for further breeding purposes. In conclusion, genetic diversity based on morphological characters was considered high in eddo taro in Indonesia as representing by major characters such as sheath and petiole color, vein pattern at the leaf base, leaf size, plant size, cormels size and oxalate content. On the other hand, the cormlets number and glucomannan content were statistically similar. The cause of such high diversity is presumably caused by multiple introductions from Japan and variation in clonal propagation. However, it needs further clarification using a robust genotyping method such as a molecular marker. Based on distinct grouping, five genotypes, i.e., S6, S7, S18, S30, and S36 could be considered as parents in the future breeding program and a multi-location examination is recommended to determine the consistency perform of genotypes.

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