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MORPHOLOGICAL DIVERSITY OF COTTON GERMPLASM IN DEVELOPING SELECTION METHODS TO BREED SUPERIOR COTTON VARIETY

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ABSTRACT

Cotton fiber supports the textile industry, folk weaving, and Indonesian paper money. The land suitable for the development of cotton should possess a dry climate. Balittas has 945 cotton germplasm accession derived from the introduction which belongs to the species *Gossypium hirsutum*, *G. Barbadense*, *G. Arboreum*, and *G. herbaceum*. It is very crucial to determine germplasm characteristic. The research was carried out at KP. Karangploso, Balittas altitude of 515 masl, climate type D (moderate) Smith Ferguson, rainfall of 1500 mm/year, and type of soil Gleysol Gleik / Inceptisol. The material used is 85 accessions, planted March 23, 2016. Fertilizer dosage: 97 kg N + 30 kg P₂O₅ + 30 kg K₂O / ha and insecticides (Confidor, Furadan, Organeem. Each accession was planted 10 m in length, 150 cm X 25 cm space. The study aims to analyze the diversity of morphological characters and cotton germplasm categorizing to ensure it can be used as a basis for selecting genetic resources in assembling new superior varieties. The results of quantitative observations at the age of 120 days exhibited high diversity. The featured characters are: budding age, flowering age, blooming age, generative branch length, number of generative branch joint, and generative branch internode length, number of vegetative branches, number of generative branches, generative branch height, canopy width, number of fruit, length of segment, weight of 40 seeded cotton. KK value were 39%, 59%, 34, 24%, 22%, 24%, 67.22%, 22%, 28%, 24% respectively. As the coefficient of diversity > 20%, the assessment result exhibited significantly different character.

KEY WORDS

Cotton, identification, morphological character

The development of cotton was mainly carried out to support the textile industry, folk weaving, and Indonesian paper money. Suitable land for the development of cotton in Indonesia is widely available, especially in Central and Eastern Indonesia, which is dominated by dry land and climates. The main obstacle in developing national cotton has generally been caused by biotic factors such as pests and diseases, as well as abiotic factors in the form of water shortages (drought) causing low national productivity. Lewis (1982) states that plant productivity could be improved in two ways, namely by changing the environment (amelioration) or improving plant genotypes. Nevertheless conducting environmental improvements is very expensive and may generate negative impacts. On the other hand, improving plant genotypes is relatively cheaper, and does not cause negative impacts on the environment. This approach is conducted by assembling superior varieties. The 'Gene pool' with extensive genetic diversity is needed for building superior cotton varieties. Cotton germplasm stored in Balittas to date is 945 accessions originating from introduction through the exchange of varieties with several cotton research institutions abroad, from germplasm banks such as IRCT France, USDA America United, ICAR India, as well as from several cotton management companies. Most of the germplasm is classified as *Gossypium hirsutum* species, some are included in *G. Barbadense*, *G. Arboreum*, and *G. herbaceum*.

However, until recently the collection of cotton germplasm with genetic information for the traits needed for breeders is lacking, therefore it is necessary to explore as much genetic information as possible from each existing accession through germplasm characterization and screening/evaluation activities. In the effort to improve cotton plants, a diverse

population is needed, especially in the nature of breeding purposes. Assembly of varieties to obtain new superior varieties with desirable traits needs to be supported by germplasm with high genetic diversity (Akhtar et al. 2007). According to Bari & Musa (1974). The availability of genetic resources with several characters that have been identified is information regarding the genetic diversity of germplasm. This aspect is crucial as it is very important to distinguish between genotypes required in the development of plant breeding programs (Bennett, 1993). According to Sumarno (2002), germplasm is a collection of genetic diversity of types of organisms. Bermawi (2005) argues that characterization is an activity to obtain morpho-agronomic characteristics or data which aims to distinguish phenotype from each accession. The characterization uses instructions from The International Union For The Protection Of New Varieties Of Plants (UPOV 2002). The following step is determining genetic diversity by grouping germplasm. The grouping method is an indispensable step in the utilization of the germplasm collection (Bozokalfa et al. 2009; Lule et al. 2012). The degree of variation in the genetic material will determine genetic diversity. Grouping germplasm collections is a strategy in the effort to utilize germplasm collections (Bozokalfa et al. 2009; Lule et al. 2012). The success of crop selection in breeding depends on genetic variation from existing germplasm accessions (Akhtar et al. 2007). Germplasm collections need to be characterized to ensure their properties are known as genetic information in the variety assembly program. This study aims to analyze the diversity of morphological characters and grouping of cotton germplasm of the Balittas collection to ensure it could be utilized as a basis for selecting genetic resources in the assembly of new superior varieties.

MATERIALS AND METHODS OF RESEARCH

The research activities were carried out at KP. Karangploso, Balittas with an altitude of 515 masl possessing type D (moderate) climate Smith Ferguson, rainfall 1500 mm / year, and type of Gleyamosol Gleik / Inceptisol soil, from January to December 2016. Research material used were 100 cotton germplasm accessions (Table 1), planted on March 23, 2016. The fertilizer dosage used is 97 kg N + 30 kg P₂O₅ + 30 kg K₂O / ha. Insecticides – Confidor, Furadan, Organeem. Each accession was planted in one row for 10 m. Planting distance of 150 cm X 25 cm, one plant per hole. Fertilization was done twice, 1/3 dose of N and all doses of P₂O₅ and K₂O at the time of planting, and 2/3 doses of N on 30 days after planting. Observation of morphological characters referred to the cotton descriptor list from International Union for the Protection of New Varieties of Plants (UPOV 2001).

The results of correlation analysis exhibited a positive or negative correlation between (1) plant height with canopy width, flowering age, and weight of 100 fruits (2) number of epidermis with flowering age (3) budding age with number of fruits and fiber length (4) flowering age with plant height, budding age, and fiber length (5) number of plant/ fruit with weight of 100 fruits (6) weight of 100 fruits with plant height, flowering age, and number of fruit / plant. It indicates that the characters observed above are related to each other. The descriptive Statistics quantitative character of cotton germplasm referred to (Descriptor list) from the International Union For The Protection of New Varieties of Plants (UPOV 2012), as presented in (Table. 3).

Method of germplasm accession grouping utilized cluster analysis with Euclidian distance and average linkage method (Suhartini & Sutoro 2007; Setyowati et al. 2009; Furat & Uzun 2010). The variables used in the grouping are variables that are mutually independent. In the initial phase, quantitative character data were analyzed using the Pearson correlation coefficient. If there is a correlation, the observed variables are transformed into the main component variables. The main component analysis was done after the quantitative data is standardized by dividing each variable with its standard deviation, therefore it is within the commensurate range due to different data units (Joliffe 2002; Tresniawati & Randriani 2008). The results of the main component analysis were followed by cluster fingerprint analysis. Data analysis was carried out using Minitab 15 software.

The diversity of cotton germplasm based on morphological characters could be predicted through the value of the Diversity Coefficient (CV) of each parameter observed. Nilasari et al. 2013 and Hadi et al. 2014), argues that to estimate the level of difference in the observed germplasm population, CV Value could be utilized. (Table 3). The results of the quantitative morphological characterization exhibited a high diversity in the number of epidermises on the leaves, flowering age, plant height, and canopy width.

Table 1 – 100 cotton germplasm accessions Research material

NO.	Accession/Var	Population	Origin	NO.	Accession/Var	Population	Origin
1	Kanesia 8	Var	Var	51	KI 123	USA	AMERICA
2	Kanesia 10	Var	Var	52	KI 124	USA	AMERICA
3	Kanesia 14	Var	Var	53	KI 240	USA	AMERICA
4	Kanesia 15	Var	Var	54	KI 845	BRAZIL	AMERICA
5	Kanesia 16	Var	Var	55	KI 846	BRAZIL	AMERICA
6	Kanesia 20	Var	Var	56	KI 847	BRAZIL	AMERICA
7	KI 2	USA	AMERICA	57	KI 848	BRAZIL	AMERICA
8	KI 15	USA	AMERICA	58	KI 849	BRAZIL	AMERICA
9	KI 17	USA	AMERICA	59	KI 850	BRAZIL	AMERICA
10	KI 19	USA	AMERICA	60	KI 851	BRAZIL	AMERICA
11	KI 20	USA	AMERICA	61	KI 409	Nicaragua	AMERICA
12	KI 23	USA	AMERICA	62	KI 30	Yugoslavia	EUROPE
13	KI 74	USA	AMERICA	63	KI 40	Yugoslavia	EUROPE
14	KI 75	USA	AMERICA	64	KI 51	Yugoslavia	EUROPE
15	KI 76	USA	AMERICA	65	KI 38	Bulgaria	EUROPE
16	KI 77	USA	AMERICA	66	KI 46	Bulgaria	EUROPE
17	KI 82	USA	AMERICA	67	KI 44	USSR	EUROPE
18	KI 85	USA	AMERICA	68	KI 448	FRENCH	EUROPE
19	KI 86	USA	AMERICA	69	KI 951	INDONESIA	ASIA
20	KI 88	USA	AMERICA	70	KI 952	INDONESIA	ASIA
21	KI 89	USA	AMERICA	71	KI 339	PHILIPINA	ASIA
22	KI 90	USA	AMERICA	72	KI 47	INDIA	ASIA
23	KI 92	USA	AMERICA	73	KI 151	INDIA	ASIA
24	KI 94	USA	AMERICA	74	KI 320	INDIA	ASIA
25	KI 95	USA	AMERICA	75	KI 351	INDIA	ASIA
26	KI 96	USA	AMERICA	76	KI 48	PAKISTAN	ASIA
27	KI 97	USA	AMERICA	77	KI 58	PAKISTAN	ASIA
28	KI 98	USA	AMERICA	78	KI 62	CHINA	ASIA
29	KI 99	USA	AMERICA	79	KI 688	CHINA	ASIA
30	KI 102	USA	AMERICA	80	KI 689	CHINA	ASIA
31	KI 103	USA	AMERICA	81	KI 691	CHINA	ASIA
32	KI 104	USA	AMERICA	82	KI 693	CHINA	ASIA
33	KI 105	USA	AMERICA	83	KI 36	CAMERON	AFRICA
34	KI 106	USA	AMERICA	84	KI 39	UGANDA	AFRICA
35	KI 107	USA	AMERICA	85	KI 43	UGANDA	AFRICA
36	KI 108	USA	AMERICA	86	KI 45	UGANDA	AFRICA
37	KI 109	USA	AMERICA	87	KI 135	USA	AFRICA
38	KI 110	USA	AMERICA	88	KI 168	USA	AFRICA
39	KI 111	USA	AMERICA	89	KI 268	USA	AFRICA
40	KI 112	USA	AMERICA	90	KI 289	EGYPT	AFRICA
41	KI 113	USA	AMERICA	91	KI 711	EGYPT	AFRICA
42	KI 114	USA	AMERICA	92	KI 364	NIGERIA	AFRICA
43	KI 115	USA	AMERICA	93	KI 453	NIGERIA	AFRICA
44	KI 116	USA	AMERICA	94	KI 502	AUSTRALIA	AUSTRALIA
45	KI 117	USA	AMERICA	95	KI 509	AUSTRALIA	AUSTRALIA
46	KI 118	USA	AMERICA	96	KI 510	AUSTRALIA	AUSTRALIA
47	KI 119	USA	AMERICA	97	KI 564	AUSTRALIA	AUSTRALIA
48	KI 120	USA	AMERICA	98	KI 569	AUSTRALIA	AUSTRALIA
49	KI 121	USA	AMERICA	99	KI 629	AUSTRALIA	AUSTRALIA
50	KI 122	USA	AMERICA	100	KI 633	AUSTRALIA	AUSTRALIA

The results analyzed by the correlation of quantitative observations are presented in (Table 2).

Table 2 – Correlations between quantitative variables

n/n		TT	LK	JB	UK	UB	JBH	B100	PS
TT	Pearson Correlation	1	.523**	0.168	0.013	.341**	-0.043	-.269**	-0.132
	Sig. (2-tailed)		0	0.096	0.902	0.001	0.672	0.007	0.189
	N	100	100	100	100	100	100	100	100
LK	Pearson Correlation	.523**	1	-0.075	0.074	0.146	0.042	-0.052	0.087
	Sig. (2-tailed)	0		0.458	0.467	0.147	0.675	0.61	0.388
	N	100	100	100	100	100	100	100	100
JB	Pearson Correlation	0.168	-0.075	1	.277**	0.039	0.009	-0.1	-0.048
	Sig. (2-tailed)	0.096	0.458		0.005	0.697	0.927	0.322	0.638
	N	100	100	100	100	100	100	100	100
UK	Pearson Correlation	0.013	0.074	.277**	1	.296**	0.087	-0.047	.239*
	Sig. (2-tailed)	0.902	0.467	0.005		0.003	0.39	0.643	0.017
	N	100	100	100	100	100	100	100	100
UB	Pearson Correlation	.341**	0.146	0.039	.296**	1	0.007	-.380**	0.165
	Sig. (2-tailed)	0.001	0.147	0.697	0.003		0.946	0	0.101
	N	100	100	100	100	100	100	100	100
JBH	Pearson Correlation	-0.043	0.042	0.009	0.087	0.007	1	-.236*	0.131
	Sig. (2-tailed)	0.672	0.675	0.927	0.39	0.946		0.018	0.193
	N	100	100	100	100	100	100	100	100
B100	Pearson Correlation	-.269**	-0.052	-0.1	-0.047	-.380**	-.236*	1	-0.105
	Sig. (2-tailed)	0.007	0.61	0.322	0.643	0	0.018		0.297
	N	100	100	100	100	100	100	100	100
PS	Pearson Correlation	-0.132	0.087	-0.048	.239*	0.165	0.131	-0.105	1
	Sig. (2-tailed)	0.189	0.388	0.638	0.017	0.101	0.193	0.297	
	N	100	100	100	100	100	100	100	100

** Correlation is significant at the 0.01 level (2-tailed).

* Correlation is significant at the 0.05 level (2-tailed).

Notes:

TT: Plant Height (cm); UB: Flowering age (hr); LK: Canopy Width; JBH: Fruit/plant; JB: Number of epidermis (mm²); B100: Weight of 100 fruits (gram); UK: Flower bud age(day); PS: % fiber.

CV values of the characters were 65%, 59%, 42%, and 45% respectively. The coefficient of diversity was 20% Alnopri & Hermiati (1992). High diversity values indicate that these characters have a wide variety. This provides an opportunity for breeders to make a selection to choose superior accession. The budding age, number of fruits/plants, weight of 100 fruits and percentage of fiber with CV values of 17%, 14%, 5.3%, and 9.4%. These possess low diversity coefficient as the CV value is below 20%.

Table 3 – Descriptive Statistics of quantitative characters of cotton germplasm

n/n	N	Range	Minimum	Maximum	Mean	Std. Error	Std. Deviation	Variance	CV (%)
	Statistic	Statistic	Statistic	Statistic	Statistic		Statistic	Statistic	Statistic
TT	100	118.8	86.2	205	1.42E+02	2.57794	25.77937	664.576	65
LK	100	161.5	12.5	174	1.14E+02	2.36365	23.63647	558.683	17
JB	100	296	0	296	40.376	6.21773	62.17734	3.87E+03	59
UK	100	19	40	59	44.5	0.26419	2.64193	6.98	42
UB	100	29	51	80	55.36	0.38938	3.89384	15.162	45
JBH	100	355.6	10.4	366	25.931	3.48925	34.89251	1.22E+03	14
B100	100	468	294	762	5.40E+02	10.18266	101.82656	1.04E+04	5.3
PS	100	37.76	16.67	54.42	37.7625	0.40043	4.00431	16.034	9.4
Valid N (listwise)	100								

The density of epidermis is often used by plant breeders to control the attack of sucker piercing insects. *Amrasca biguttula* (Empoasca sp.) is the main cotton plant pest in Indonesia, which is very detrimental because it can attack cotton plants starting from young plants to old plants. Great attacks occur if the environmental conditions are dry due to lack of rain. These pests attack the plant by sucking the leaf liquid, the plants attacked the leaves

become curly and curved downward. In heavy attacks the leaves are red-brown, dry, then the expression is influenced by the genes H_2 , H_3 , H_4 , and H_5 , (Hendrizzi et al., 1984). The density of epidermis on Ballitas cotton germplasm varied from 0 - 587 trichomes per 25 mm². The density of epidermis was calculated using the Robinson method, et al., (1980), 5 mm x 5 mm square was carved on the lower leaf lamina, the number of the epidermises (trichomes) was calculated based the square. The trichome number category per square centimeter (cm²) according to Kartono (1991), is: <121 = no epidermis; 121 - 240 = small number of epidermis; 241 - 360 = medium epidermis; 361 - 480 = large number of epidermis; > 480 = huge number of epidermis. Cotton varieties with epidermisless properties possess high tannin and terpene content. It is capable to reduce *Helicoverpa armigera* pest attacks up to 50% (Benedict et al., 1992). The diversity of epidermis from 100 accessions observed exhibited a diversity of CV 59%.

Table 4 – Qualitative characteristics of cotton germplasm

Qualitative Characters		Percentage (%)
1. Flower position	Clustered	2
	Not Clustered	98
2. Leaf color	Green	97
	Light Green	0
	Green	0
	Dark Green	1
	Reddish Purple	2
3. Leaf shape	Palmate	8
	Normal	84
	Twisted Normal	5
	Palmate Normal	2
	Twisted	1
4. Nectar	Exist	90
	Nonexistent	9
	Exist/Nonexistent	1
5. Crown color	Beige	87
	Yellow	4
	Beige/Yellow	1
	Yellow/Purple	8
6. Spots on the flower crown	Exist	4
	Non Existent	96
7. Pollen colour	Beige	72
	Yellow Beige	1
	Purple Beige	0
	Yellow	27
	Purple Yellow	0
8. Pistil Position	Above	76
	Parallel	24
9. Petal shape	Twisted	1
	Normal	99
10. stem color	Reddish Green	95
	Dark Green	2
	Purplish Red	3
11. plant shape	Compact	35
	Cylindric	5
	Prostrate	60
12. fruit shape sharpness	Pointy	5
	Spiky	92
	Sharp	1
	Blunt	3
13. Fruit skin texture	Smooth	3
	Medium	82
	Coarse	15
14. Fiber color	White	96
	Light Brown	2
	Light Green	1
	Brown	1

The density of the epidermis is one of the characteristics of a variety of options as accessions resistant to sucker piercing pests, which are the main cotton plant pest in Indonesia. Great attacks occur if the environmental conditions are dry due to lack of rain. Hendrizzi et al., (1984), suggested that the *Amasca biguttula* attacks plants by sucking in leaf fluid. Attacked plants leaves become curly and curved downward. In heavy attacks the leaves are red-brown, dry, then their expression is influenced by genes H_2 , H_3 , H_4 , and H_5 . The density of epidermis in Ballitas cotton germplasm varies from 0 - 587 trichomes per 25 mm². The density of epidermis was calculated using the Robinson, et al., (1980) method, a square of 5 mm x 5 mm was carved in the lower leaf lamina, the number of the epidermises (trichomes) was calculated based on existing epidermis in the square.

Germplasm plasma is observed as a qualitative character, carried out if the conditions have met the requirements in accordance with the reference (Suratman & Setyawan, 2000). The results of the observations exhibited a diversity of all characters observed (Table 4). The observation of the character of the 100 accessions observed: 98% is not clustered and 2% are clustered, meaning that the diversity is very low. The color characteristics of the leaf diversity are very low, such as green (97%), light green (0%), green (0%), dark green (1%), and reddish purple (2%). Plant shape characters are compact (35%), cylindrical (5%), and Prostrate (60%).

From the observation of the character of cotton, leaf shape varies, namely: palmate (8%), normal (84%), normal twisting (5%), normal palmate (2%), and twisting (1%). exhibited that the diversity is quite high. Leaf shape is an important character in the classification of varieties. Wilson and George (1982), suggested that the nature of the okra leaf leaves can reduce the egg deposit of *Helioverpa armigera*, increase resistance to *Peptinopora gossypiella*, and reduce fruit rot disease. On average the cotton on the leaves has the nectar glands. Out of the 100 accessions observed, only one accession which nectar existence is unclear, 99% exist and 9% of accessions nonexistent. Wilson (1976), suggested that the nectar is one of the important properties for resistance to flower buds and fruit piercer. The color of the flower crowns on 100 accessions was varied: beige (57%), yellow (3%), yellow/beige (1%) and yellow/purple (8%). The crown color of the *Gossypium* tetraploid species is controlled by the duplication of Y1 and Y2 Hutchison and Silow genes, 1939. In Kohel and Lewis (1984), it is suggested that yellow is all allotetraploid except yellow in G. From this gene Y1 is controlled by Y2 gene according to Stephens (1954 b In Kohel and Lewis, 1984). Y1 gene in sub-genomics possesses chromosome 18 D Y2 gene. The genome is D. The yellow flower crown is usually found in *G. barbadense*, (Endrizzi, 1975 In Kohel and Lewis, 1984), but often found in Pima cotton (Turcottte and Feaster, 1963 In Kohel and Lewis, 1984). The beige-colored flower crown is found in *G. hirsutum* cultivars which are controlled by the y1y1y2y2 gene but also found in yellow flower crowns on wild relatives. The spots on the flower crown possess low diversity. The spotted ones were (5%) and no spot(95%). The color of pollen is quite varied which includes: beige (72%), yellow beige (1%), purple beige (0%), yellow (27%), and purple yellow (0%). Harlan (1929) In Kohel and Lewis (1984), suggested that pollen color is controlled by a pair of P and p genes. Whereas the yellow color is dominant in beige. The position of the pistil is above (76%) and parallel (24%). The petal shape diversity is very low: twisted (1%) and normal (99%). The stem color character diversity is very low: reddish green (95%), dark green (2%) and purplish red (3%). Stephenss, (1974 a), suggested that the red color of the stem was caused by the presence of anthocyanin substances which pigmentation was expressed on the tissues of the leaf sertain on the base of the flower crown which usually occurs in cotton breedd in Asia. The sharpness of the fruit shape, spiked fruit reached (92%), pointy fruit (5%), sharp (1%) and blunt (3%). The fruit skin coarseness exhibited: smooth (3%), medium (82%) and coarse (15%). The variation of fiber color character is also very low, the dominant color is white which reaches 96%, light brown (2%), light green (1%) and brown 1%. Fruit skin texture diversity is smooth (3%), medium (82%), and coarse (15%).

The genetic relationship is an effort to find out the relationship between genotypes in the accession of cotton plants. Furthermore, based on the genetic similarities the character will be classified, by describing the level of genetic variability, used for genetic analysis

based on morphological characters. Prior to carrying out a cluster analysis for germplasm grouping, it is important to determine whether the variables observed are mutually independent. Maji & Shaibu (2012), suggests that if there is a correlation between the variables observed, it is necessary to analyze the main components first, before conducting a cluster analysis. The results of the correlation analysis exhibited no real correlation between the characters observed. Subsequent cluster analysis was carried out using characters that contributed to the diversity of the first six main components because the proportion of diversity reached more than 80% and eigenvalues > 1. Joliffe (1967) gave the limitation that cluster analysis was carried out using characters the proportion of diversity > 80% and eigenvalues > 1. The results of the cluster analysis exhibited that the Balittas cotton germplasm collection was divided into VI levels of similarity that had a relatively high diversity. At the level of similarity I of germplasm is divided into 3 major groups, at the level of similarity II is divided into 4 groups, in similarity III is divided into 5 major groups, in similarity IV is divided into 2 major groups, in similarity V is divided into 2 major groups and in similarity VI is divided into 6 large groups (Figure 1). Grouping based on the country of origin of germplasm consists of Indonesian commercial varieties, United States of America (USA), South America, Europe, Asia, Africa, and Australia with a diversity of 84.90%. Categorized germplasm diversity can be used as an important source of information to assess potential accession. Accession from different groups possess significantly different character, therefore a high diversity of morphological characters in the managed population provides wider opportunities for the improvement of plant varieties. To obtain information on the diversity of crucial agronomic traits, which can later be used as elders selected in cultivation programs. Accessions possessing a genetic distance from different groups can be selected, information on the diversity of morphological characters also opens up opportunities for improved varieties with resistance to biotic and abiotic stresses. Cluster analysis method could be used to determine the characters that contribute to population diversity (Khodadadi et al. 2011). Tresniawati & Randriani (2008), stated that germplasm grouping can describe genetic relationships between accessions. This may provide information regarding character traits from each accession group formed.

Figure 1 – Dendrogram average linkage, euclidian distance

CONCLUSION

The results of the qualitative morphological characterization exhibited diverse characters: low (flower position, spots on the flower crown, pollen color, fiber color, and petal shape), medium (nectar, crown color, stem color, and fruit shape sharpness) and height (position of pistil, plant shape and fruit skin coarseness).

The results of the quantitative morphological characterization exhibited high diversity with CV values: number of leaves (65%) flowering age (59%), plant height (42%), and canopy width (45%).

The results of the cluster analysis indicate that the Balittas germplasm collection is divided into 6 large groups of similarity level and possess relatively high diversity. At the level of similarity I of germplasm is divided into 3 major groups, at the level of similarity II is divided into 4 groups, in similarity III is divided into 5 major groups, in similarity IV is divided into 2 major groups, in similarity V is divided into 2 major groups, and in the similarity VI is divided into 6 large groups (Figure 1). Based on country of origin grouping, germplasm consists of Indonesian commercial varieties, United State of America (USA), South America, Europe, Asia, Africa, and Australia with a diversity value of 88.90%.

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