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1. The Application of Green Manure *Azolla pinnata* L. to Reduce Dosage of N Fertilizing on Irrigated Rice Field (Sugiyanta and Septi Rinasusanti) 1
2. Effect of Watering on Growth and Yield of Buckwheat (Yonny Koesmaryono, Rokim, Muhammad Erwin Choron and Hideki Sugimoto) 7
3. The Effectiveness of Microbial Inoculant Originated from Wamena Biological Garden and Compost Augmentation to Stimulate the Growth of *Pterocarpus indicus* Jacq. (Suliasih, H.J.D. Latupapua and Sri Widawati) 12
4. Soil Temperature Response of Buckwheat as Characterized by Mulching and Population Densities (Yonny Koesmaryono, Fibrianty and Hideki Sugimoto) 16
5. The Application of Soil Microbes from Wamena Botanical Garden (WBiG) as Bio-Fertilizer on Purple Eggplant (*Solanum melongena* L.) (Sri Widawati and Suliasih) ... 20
6. Mesh Selectivity of Sweeping Trammel Nets for Croaker (*Argyrosomus amoyensis* Bleeker) and Moustached Thryssa (*Thryssa mystax* Bloch & Schneider) in The Northern Coast of Central Java (Ari Purbayanto) 25
7. Viability of Cashew Nut Seed (*Anacardium occidentale* L.) at Different Handling Methods and Storage Periods (Sukarman and Devi Rusmin) 30
8. Quantitative Trait Loci Analysis for Seed Protein and Oil Content and their Epistatic Interaction in Soybean (Teuku Tajuddin) 35
9. Study on The Relationship of 73 Introduced and Indigenous Banana Accessions Based on Qualitative Morphological Characters (Sobir, Memen Surahman and Hanik Rohmah Robi'ah) 39

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STUDY ON THE RELATIONSHIP OF 73 INTRODUCED AND INDIGENOUS BANANA ACCESSIONS BASED ON QUALITATIVE MORPHOLOGICAL CHARACTERS

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ABSTRACT

*In order to characterize the potential of banana (*Musa spp*) germplasm, 73 accessions consisting of 27 accessions introduced from INIBAP (International Initiative of Banana and Plantain) and 46 accessions of indigenous banana are subjected to relationship analysis through 22 qualitative morphological characters, including pseudostem, petiole, and lamina. Characterization based on scoring method of banana descriptor of IPGRI (International Plant Genetics Resources Institute). Similarity analysis reveals that distance among banana accessions genetics ranges at 0.0-1.0 of similarity value. Highest genetics similarity (1.0 level of similarity) is shown by banana accessions introduced from INIBAP (International Initiative of Banana and Plantain) or FHIA25 group. On the contrary, lowest genetics similarity (0.0 level of similarity) is shown by INIBAP accession of AA cv Rose with indigenous accession of Ambon Amerika B, and Triolin. Dendrogram generated by using SAHN-UPGMA (Sequential, Agglomerative, Hierarchical, and Nested -Unweighted pair-group method, arithmetic average) indicates that the evaluated accessions separates at 0.21 coefficient of similarity, subsequently at 0.38 coefficient of similarity, the accessions are divided into seven groups. Among those groups, two groups are exclusively, consisting of INIBAP accessions, one group consists of indigenous accessions, and the other four groups shared by INIBAP accessions and indigenous bananas.*

Key words : *Musa spp*, genetics relationship, morphological characters

INTRODUCTION

Current commercial banana (*Musa spp*) presumably originates from *Musa acuminata* Colla ($2x=22$) and *Musa balbisiana* Colla ($2x=22$). Mutation, domestication, and selection play important role in banana evolution [1]. Ploidy and genome derives from *M. acuminata* denoted with A symbol, and those derives from *M. balbisiana* denoted with B symbol. Crossing between wild banana of *M. acuminata* and *M. balbisiana* produce hybrids of diploid AB, triploid AAB and ABB as well as tetraploid AAAB, AABB and AB BB [2].

Base consumption pattern banana is separated into desert bananas and cooking bananas. Genome composition of the banana showed correlated to the grouping of use. Bananas derived from *M. balbisiana* genome are cooking banana, and bananas derived from *M. acuminata* genome are dessert banana. However, bananas developed from crossing of *M. acuminata* with *M. balbisiana* produce both of desert and cooking bananas [3]. Plantain is a sub group of cooking banana that should be processed prior to be consumed [2].

Most of wild banana is located in Southeast Asia (4), therefore Indo-Malaysia region (Indonesia, Malaysia, Philippines, and New Guinea) is the center of origin of banana, lately distributed to tropical and subtropical countries in Asia, America, Africa, and Australia [1]. Southeast Asia region is reported to have rich banana diversity [3]. Indonesia as a part of Southeast Asia Region also has rich bananas cultivars [5], however, characterization and identification of Indonesian banana is lack behind.

Characterization and identification of banana germplasm in Indonesia are very important, since the same banana cultivar has several local names. On the contrary, the same local name refers to a different banana cultivar. Characterization based on morphological marker is common to be utilized to resolve duplication problem of germplasm. Genetics relationship studies by using morphological characters have been widely used [6;7;8;9;10].

This study aims to characterize banana collections in Center of Tropical Fruit Studies (CETROPS) based on their morphological markers, and to elucidate relationship among the accessions. Obtained data are necessary to optimize their potentiality for banana improvement and develop phenotypic markers for commercial use.

MATERIALS AND METHODS

Plant Materials

Banana collections of CETROPS (Center for Tropical Fruit Studies) including 27 accessions introduced from INIBAP (International Initiative of Banana and Plantain) and 46 accessions of indigenous banana grows in Tajur Field Station located 250 m above sea level. List of evaluated accessions is presented in Table 1.

Morphological Analysis

Field observations are conducted from August to September 2004, based on 22 vegetative characters as described by Banana Plant Descriptor of International Plant Genetics Resources Institute [11] by slight modification [12]. Observed characters in-

clude six leaf characters (shape of leaf blade base, edge of petiole margin, insertion point of leaf blade on petiole, color of cigar leaf dorsal surface, color of midrib ventral surface, color of midrib dorsal surface), eight petiole characters (canal shape, edge of petiole margin, wax on petiole, edge petiole margin, wing type, color of petiole, color of petiole margin, color of edge petiole margin), and nine pseudostem characters (pseudostem blotch, sap color, pigmentation of the upperlying pseudostem, pigmentation of the underlying pseudostem, pseudostem appearance, predominant upperlying color of the pseudostem, predominant underlying color of the pseudostem, upperlying color of the pseudostem base, underlying color of the pseudostem base).

Data Analysis

The observed data are scored based on Banana Plant Descriptor method (IPGRI, 1996). Subsequently, characters similarity analysis is conducted based on Simple matching coefficient (SM) of Sokal and Sneath [13]. Cluster analysis is conducted by using Sequential Agglomerative Hierarchical and Nested - Unweighted Pair Group Method Arithmetic average (SAHN-UPGMA) of Sneath and Sokal [13]. The analyses is performed by using program of NTSYSpC (Numerical Taxonomy and Multivariate Analysis System) version 2.02 [13].

RESULTS AND DISCUSSION

Results

Visual observations of vegetative characters indicates that banana accessions with similar name tends to have similar vegetative performance, as demonstrated in group of Pisang Kepok, Pisang Siam, F25 and C2. However, banana accessions in Pisang Ambon group shows slight discrepancy for several characters.

Scoring of observed characters by using Banana Plant Descriptors standard [11] reveals that the variance among accession of each character ranges 0-6. Subsequently, similarity analysis of scored data shows that among evaluated accessions have phenotypic similarity ranging at 0.0-1.0.

The highest genetics relationship (1.0 of similarity value) is shown by banana accessions introduced from INIBAP (International Initiative of Banana and Plantain) or FHIA25 group. In contrast, the lowest genetics relationship (0.0 of similarity value) is shown by INIBAP accession of AACV Rose with indigenous accession of Ambon Amerika B, and Triolin.

Table I. List of banana accession subjected in the study. Accessions no 1-27 and accessions no 28-73 are the introduction banana from INIBAP and indigenous banana.

No	Accession Code	No	Accession Code
1	PJB 5 (P5)	38	EMAS (BOGOR) (EMAS B)
2	PJB 7.2 (P7)	39	EMAS (PURBALINGGA) (EMAS P)
3	FHIA-02 (F2)	40	EMAS 40 HARI (JOGJA) (EMAS 40)
4	FHIA-02. 4.5 (F45)	41	EMBOK (JOGJA) (EMBOK)
5	FHIA-02. 7.5 (F75)	42	ICE (JOGJA) (ICE JOG)
6	FHIA-03 (F3)	43	JAMBE
7	CACHACO (CA)	44	JEPANG
8	AACV ROSE (ACV)	45	KAPAS
9	GROS-MICHEL (GM)	46	KEPODANG
10	YANGAMBI Km 5 (YKM)	47	KEPOK
11	FHIA-17 (F17)	48	KEPOK AMERIKA (KEPOK A)
12	FHIA-23 (F23)	49	KEPOK KUNING (KEPOK K)
13	GCTV-119 (GCT)	50	KEPOK MANGGALA (KEPOK M)
14	SH 3436-9 (SH9)	51	KLUTUK SUKUN (KLUTUK S)
15	TMBX -6.1 (T6)	52	KUTES (WONOSOBO)
16	TMBX 5295-1-10.2 (T10)	53	LAMPENENG (LAMPEN)
17	FHIA-18 (F18)	54	LIDI
18	FHIA-21 (F21)	55	MADURA
19	CRBP 39.2 (C2)	56	MANDAR
20	CRBP 39.2.1 (C21)	57	MAULI (JOGJA)
21	CRBP 39.2.2 (C22)	58	PAPAN
22	CRBP 39.3 (C3)	59	PONTHO (JOGJA)
23	SH 3640 (S40)	60	PONTHO BUNTHEK (PONTHOB)
24	FHIA-25. 1.1 (F251)	61	RAJA BULU (RBULU)
25	FHIA-25. 3.2 (F253)	62	RAJA GENDEROWO (RGROWO)
26	FHIA-25. 5 (F255)	63	RAJA SABLENG (RSABLENG)
27	PISANG CEYLAN (PC)	64	RAJA SEREH (RSEREH)
28	AMBON	65	ROTAN HARI (ROTAN H)
29	AMBON AMERIKA B (AMAB)	66	SABULAN
30	AMBON BADAQ (AMBAD)	67	SIAM
31	AMBON HIJA U (AMHIJ)	68	SIAM MANGGALA (SIAM M)
32	AMBON LUMUT A (AMLUMA)	69	SIAM PARIS (SIAM P)
33	AMBON LUMUT B (AMLUMB)	70	SIGUNG
34	AMBON PUTIH (AMPUT)	71	SRI NYONYA (SRI NY)
35	AMBON WARANGAN (AMWARJ)	72	SUSU
36	ANJASMORO (JOGJA) (ANJASJ)	73	TRIOLIN JOGJA (TRIOLIN)
37	BANGKA HULU (BANGK)		

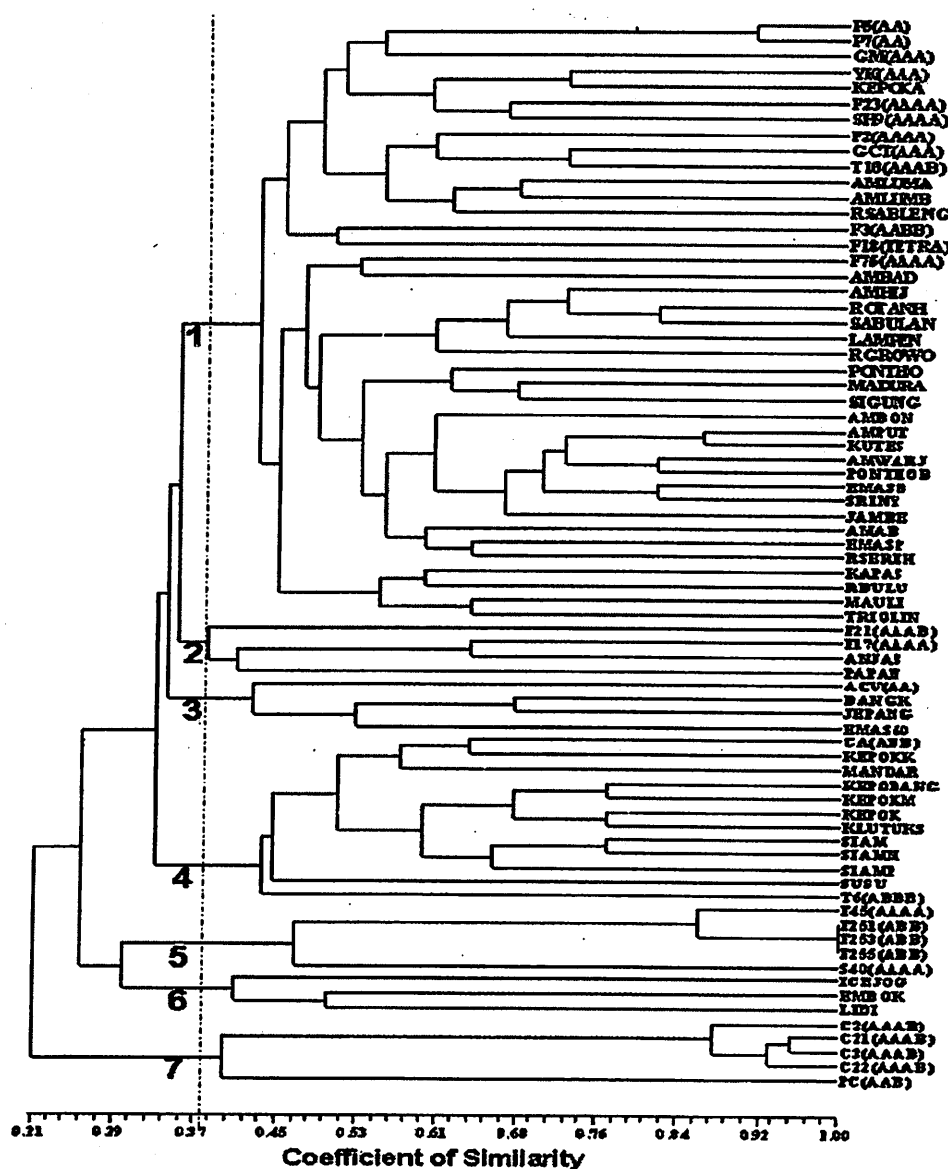


Figure 1. A Dendrogram generated by Sequential Agglomerative Hierarchical and Nested - Unweighted Pair Group Method Arithmetic average (SAHN-UPGMA) based on scored data of 22 vegetative characters.

A dendrogram generated by Sequential Agglomerative Hierarchical and Nested - Unweighted Pair Group Method Arithmetic average (SAHN-UPGMA) shows that genetics variability is detected at range of 0.21 – 1.0 of similarity coefficient (Figure 1). At 38% of similarity coefficient, the evaluated accessions separates into seven groups. Based on member of each group, it reveals that two groups exclusively consist of INIBAP accessions, one group consists of indigenous accessions, and the other four groups shares by INIBAB accessions and indigenous bananas (Table 2).

Group I, the biggest group, consists of 40 accessions including 12 introduced accessions and 28 indigenous accessions, famous local banana Ambon and Pisang Raja clustered in this group. Group II

consists of two introduced accessions of tetraploid banana F1 (AAAB) and F7 (AAAA) together with local banana of Anjasmara and Papan. On Group III, introduced accession ACV (AA) clustered with indigenous banana accessions of Bangkahulu, Jepang, and Erias 40 Hari, this group shows similarity at dominant red to dark red of pseudostem pigmentation.

Clustering results show that two introduction accessions CA (ABB) and T6 (ABBB) grouped with indigenous accessions of Siam, Kepok, and Klutuk Sukun in Group IV. Group V exclusively consists of five introduced accessions, in contrast with Group VI exclusively consists of three indigenous accessions. Moreover, Group VII exclusively consists of five introduced accessions.

Table 2. Grouping of 73 introduced and indigenous banana accessions, separated at 38% of similarity coefficient.

Group	Number	Members
I	40	<i>P6 (AA), P7 (AA), GM (AAA), YK (AAA), KEPOK A, F23 (AAAA), SH9 (AAAA), F2 (AAAA), GCT (AAA), T10 (AAAB), AMLUM A, AMLUM B, R SABLENG, F3 (AABB), F18 (TETRA), F75 (AAAA), AMBAD, AMHIJ, ROTAN H, SABULAN, LAMPEN, R GROWO, PONTHO, MADURA, SIGUNG, AMBON, AMPUT, KUTES, ANWAR J, PONTHO B, EMAS B, SRINY, JAMBE, AMAB, EMAS B, R SEREH, KAPAS, R BULU, MAULI, TRIOLIN</i>
II	4	<i>F21 (AABB), F17 (AAAA), ANJAS, PAPAN</i>
III	4	<i>ACV (AA), BANGKA, JEPANG, EMAS 50</i>
IV	12	<i>CA (ABB), KEPOK K, MANDAR, KEPODANG, KEPOK M, KEPOK, KLUTHUK S, SIAM, SIAM M, SIAM P, SUSU, T6 (ABBB)</i>
V	5	<i>F45 (AAAA), F251 (ABB), F253 (ABB), F255 (ABB), S40 (AAAA)</i>
VI	3	<i>ICEJOG, EMBOK, LIDI</i>
VII	5	<i>C2 (AAAB), C21(AAAB), C3 (AAAB), C22 (AAAB), PC (AAB)</i>

Introduced banana accessions denoted in *italic*

DISCUSSIONS

- Wide range of similarity among evaluated accession indicates that the banana collections of CETROF are vary in genetics properties, especially the variation in genome composition, as exhibited by diploid ACV (AA), triploid CA (ABB) and tetraploid F1 (AAAB). Subsequently, clustering group reveals that based on 22 morphological characters several introduced banana from INIBAP clustered in same group with indigenous banana, that rise possibility that they share common ancestors in their later genome development, as indicated in Pisang Ambon that clustered in Group I with Gros Michel (AAA).
- Several introduced accessions show high similarity (1.0 value of similarity) among them, as found in Group V by FHIA25.1.1, FHIA25.3.2, and FHIA25.5 indicate that they share the same morphological characters as detected in this study. This results are confirmed by previous study [12] that found similar results under 71 vegetative characters. However, genetically they show slight differences as detected by RAPD analysis in the same study [12]. Meanwhile, the lowest similarity (0.0 coefficient of similarity) is shown by AAcv Rose in Group III with Ambon Amerika B and Triolin in Group I, that visually they are different, especially as shown in pseudostem and petiole characters.
- Grouping in this study solely based on vegetative characters, therefore, do not completely represent genome composition of the accessions. Several accessions the with the same genome composition clustered in different group, as exhibited by F23 (AAAA) of FHIA-23 in Group 1 with T45 (AAAA) of TMBX-45 in Group 5, and T10 (AAAB) in Group 1 with C22 (AAAB) in Group VII. This discrepancy, due to genome composition mostly refers to fruit characters, and based on classical method for genome identification used 15 characters, 13 characters out of them are

reproductive characters, and two others are vegetative characters [2]. Both two vegetative characters shape of leaf blade base and pseudostem blotch were used in this study already.

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