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Early Identification of Genetic Diversity and Distance from Indonesia Cassava Potential as Food, Industrial and Biofuel Based on Morphological Characters

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Abstract

Diversity and genetic distance are required as initial foundations to identify germplasm Indonesian cassava potential for food, industrial, and biofuel resources. This study used 181 cassava *(Manihot esculenta* Crantz*.)* accessions from all islands in Indonesia, i.e. Java, Sumatera, Kalimantan, Sulawesi, Maluku, Nusa Tenggara Timur and Papua Islands. The study was conducted in July 2013 to March 2014. Research experiment design was arranged in Augmanted Design with three control plants per row. There were traits of morphological rod and leaf as parameter, the number of 19 traits. The analysis was using Principal Component Analysis (PCA) and Agglomerative Hierarchical Clustering (AHC). Results of this study are genetic diversity and distance cassava from Indonesia with a wide diversity level of 49.82 % and from 1 to 17 genetic distance spread throughout Indonesia.

Keywords: AHC; distance of genetic; diversity Indonesian cassava potential; *Manihot esculenta* Crantz.; PCA.

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Nomenclature

PCA   Principal Component Analysis
AHC   Agglomerative Hierarchical Clustering
FGE   Fuel Grade Ethanol

1. Introduction

Plant germplasm is the genetic material source for plant breeders to develop an excellent plant cultivar. Cassava is one of plant that largely found in tropical countries, mainly in Africa, Asia, and Latin America [1]. Genetically, cassava is the result of *M.esculenta* subsp. population domestication which located on the outskirt of South Amazon river valley in Acre, Rondonia, and Mato Grosso, Brazil [2]. The domestication happened approximately in 10 000 BC and in the seventh century it was brought to Africa accompanying slavery [3].

Indonesia including the 2A region Indomalayan center, it was showed that Indonesia has potential as a germplasm resources, one of them is cassava. Cassava native to Indonesia is one of the germplasm which has the potential to be developed, particularly the starch. Origin region of cassava that is varied from Aceh to Papua is the natural distance from geographic region of Indonesia. This affects of diversity and genetic distance in cassava was very potential to be developed as comestible, industry and biofuel resources.

Globally, the demand of cassava in various products is increase, mainly flour and starch demand. The content of cassava starch was very high; 30 % in fresh root or 80 % in dry matter, was one of the factors of cassava utilization [4]. In a research conducted the process by Nuwamanya et al. [5] it was concluded that starch content of cassava native to Uganda is 13.78 % to 15.37 %. Recent study, showed that cassava is rich of starch that has potential of comestible, industry, and main commodity of BBN or as producer of FGE [6].

Uncoordinated planting and lack of information related to genetic diversity of cassava is one of the factors to low quality cassava starch. Comprehensive study related to various types of cassava in Indonesia, cultivated or out in the wild was infrequent. Therefore cassava characterization based on morphology be required [7]. Information about accession diversity, morphology and agronomy, may be used as comprehensive database of local cassava diversity in Indonesia for further research. In of plant breeding, genetic diversity and phenotypic are required for further breeding process in breeding selection process [8].

2. Material and method

The research was conducted between July 2013 to March 2014 in Experimental Field Station, Faculty of Agriculture, University of Padjadjaran. The research utilizes 181 accession cassava materials native to Indonesia (Table 1). Research experiment design was arranged in a randomized complete block design (augmented design) [9]. The area was divided into several blocks, no replication for each accession, and varieties of Raweuy, Peuteuy and Jalang native to Jatinangor as controls.

Spacing distance was arranged in 100 cm × 100 cm. Five plants arranged in each row with cassava cutting size 30 cm to 40 cm. Morphological observation of nineteen characters was based on Fukuda descriptors [10] not included for the result character and result component. data collected in the field every three months; three months after planting, six months after planting and nine months after planting. Analysis was using PCA and AHC based on Euclidean distance inequality.

Table 1. Frequency distribution of origin Indonesian cassava clones.

Origin	Number	%
Jawa Barat	111	61.33
Daerah Istimewa Yogyakarta	2	1.10
Jawa Timur	12	6.63
Banten	2	1.10
Nusa Tenggara Timur	9	4.97
Nangroe Aceh Darussalam	3	1.66
Sumatera Utara	7	3.87
Papua	5	2.76
Sulawesi Selatan	5	2.76
Sumatera Barat	4	2.21
Sulawesi Tengah	2	1.10
Kalimantan Barat	3	1.66
Sulawesi Tenggara	4	2.21
Lampung	2	1.10
Bengkulu	3	1.66
Maluku	6	3.31
Sulawesi Utara	1	0.55
Total	181	100.00

3. Result and discussion

3.1. PCA

PCA is one of procedures used to study about genetic variability on multivariate technique [11]. It can also be used for searching which character has high contribution value whether negative or positive contribution in the variation, and it can be used for discovering the distribution of each accession towards biplot graphic. PCA analysis result showed that (Table 2), it resulted four principal component axis that has Eigenvalue for 1.74 to 3.17 which contributes to variation as high as 49.82 %.

Table 2. Eigenvalue, variability and cumulative 181 cassava clones based on 19 morphological characters

	F1	F2	F3	F4
Eigenvalue	3.17	2.43	2.12	1.74
Variability (%)	16.70	12.80	11.16	9.16
Cumulative %	16.70	29.50	40.66	49.82

Percentage value of total diversity in nineteen characters to 181 cassava accession (Table 3) was concluded in main components (PC1, PC2, PC3, PC4) there are (+/- 0,5) more value contribution in each characters. Those characters affect variation in cassava population in accession grouping in biplot graphic. Positive contribution value could affect grouping while characters that has negative contribution value causes accession away from the group.

The main component (PC1) has total diversity value of 16.70 % which was given by pubescence on apical leaves, petiole color, color of leaf vein, length of leaf lobe, ratio of lobe length to lobe width of central leaf lobe (Table 3).

Second component (PC2) has total contribution of 12.80 % elucidated from pollen and flowers characters. Third component (PC3) has total contribution of 11.16 % which elucidated from color of stem cortex, color of stem epidermis and color of stem exterior. Fourth component (PC4) has total contribution of 9.16 % described from number of leaf lobe, presence of pollen and flowers character. Between four main components, only the first and the second component give negative contributions which are pubescence on apical leaves, length of leaf lobe, ratio of lobe length to lobe width of central leaf lobe, presence of pollen and flowers.

Table 3. Factor loadings morphological trait markers contributed to variability

	F1	F2	F3	F4
Pal	-0.61**	-0.25	-0.30	0.07
Sscl	-0.37	-0.47	0.29	-0.30
Nll	-0.29	0.20	0.25	0.51*
Lm	-0.37	-0.11	-0.05	0.07
Op	0.23	-0.03	-0.04	0.09
Fl	0.36	-0.58**	0.25	0.63*
Pol	0.36	-0.58**	0.25	0.63*
Pc	0.72*	0.21	0.25	-0.24
Lc	0.10	0.08	-0.23	-0.01
Clv	0.68*	0.17	0.06	-0.15
Pfs	-0.02	0.16	0.38	-0.09
Csc	0.14	0.02	0.67	-0.22
Cse	0.34	0.02	0.53	-0.09
cse.1	-0.16	0.03	0.53	-0.32
cebap	-0.09	0.02	-0.25	-0.17
Llb	-0.69**	0.32	0.30	0.19
Wll	0.05	0.82*	-0.01	0.41
Rlllw	-0.51*	-0.54**	0.30	-0.23
Pl	-0.49	0.51*	0.48	0.22

Data : pal = pubescence on apical leaves; sscl = shape of central leaflet; nll = number of leaf lobe; lm = lobe margins; op = orientation of petiole; fl = flowering; pol = pollen; pc = petiole color; lc = leaf color; clv = color of leaf vein; pfc = prominence of foliar scars; csc = color of stem cortex; cse = color of stem epidermis; cse.1 = color of stem exterior; cebap = color of end branches of adult plant; llb = length of leaf lobe; wll= width of leaf lobe; rlllw = ratio of lobe length to lobe width of central leaf lobe; pl= petiole length.
*) Characters that has contribution value could affect grouping
**) Characters that has contribution value causes accession away from the group.

Analysis result of main components PC1 and PC2 have total contribution of 29.50 % from variation in 181 accession of cassava. The deployment pattern described in biplot graph and to determine the deployment, the highest Pci value in variation contribution is used. The main component (PC1) and second component (PC2) are component values that give the biggest contribution value towards variations of a character as high as 15.78 % and 13.73 %. Character deployment pattern based on main PCA in biplot graph elucidated in four quadrants in Fig 1. It showed that spread pattern of cassava is wide, there are on four different quadrants. This pattern is the basis of choosing cassava accession that has diverse characters based on diverse morphology of various types of local cassava.
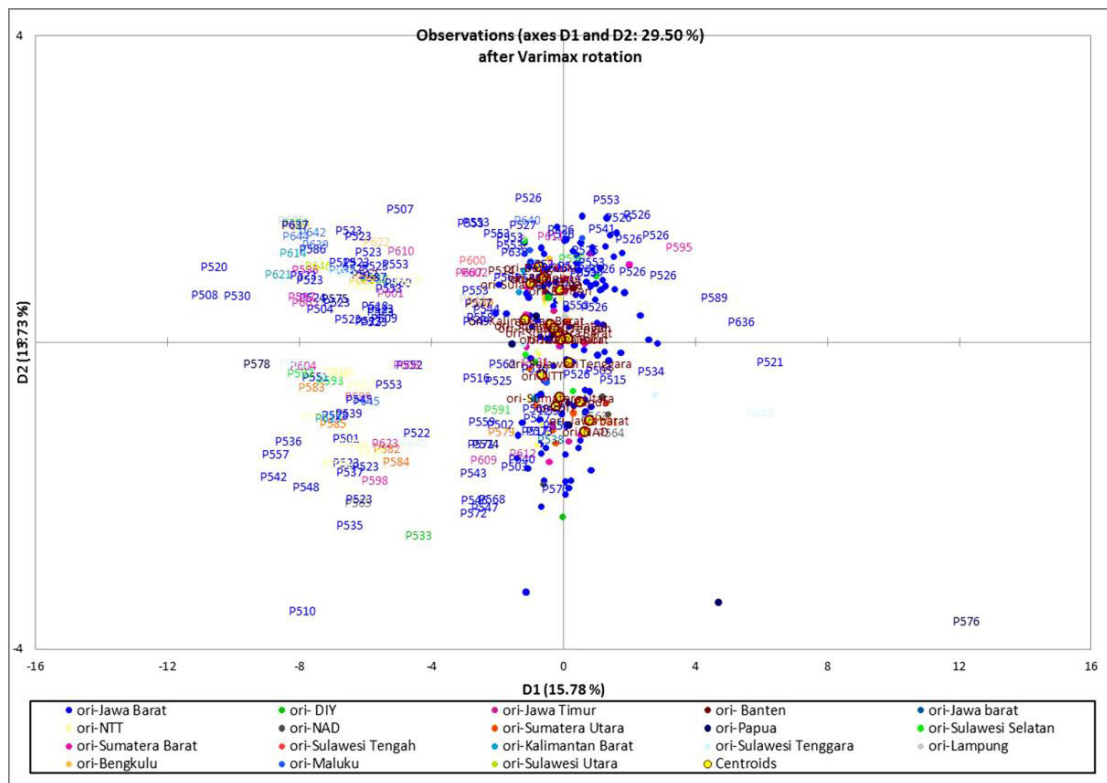
Fig 1. Corresponding cassava clones to the centroids of the origin

3.2. Cluster analysis

AHC in dendogram may illustrate the relationship between accessions [12]. At certain length, several accessions grouped based on analyzed characters. Deployment pattern between 181 plant accessions based on nineteen characters can be seen in Fig 2. Deployment pattern graph consists of two big quadrants. First quadrant consists of 523, 542, 546, 554, 510, 543, 547, and 557. Accessions in quadrant II are accessions excluding eight accessions in quadrant I.

In quadrant II the existing accessions that have various dissimilarities are divided into five groups:

- The first group only consists of accession 576.
- The second group only consists of accession 521,636 and 648.
- The third group consists of accession 534,553,526,589 and 595.
- The fourth group consists of accession 533, 535, 522, 599, 555,585,548, 537, 598, 568, 617, 570, 573, 571, 615, 577, 584, 582, 565, 604, 593, 616, 508, 530, 651, 578, 626, 545, 540, 538, 563, 569, 572, 553, 505, 642, 618, 588, 627, 581, 643, 649, 550, 612, 609, 515, 512, 609, 515, 512, 587, 600, 525, 562, 531, 574, 579, 580, 509, 558, 645, 559, 602, 628, 503, 549, 552, 575, 518, 524, 539, 596, 640, 629, 516, 517 and 502.
- The fifth group consists of accession 611,625,536,608, 605,623, 551, 504, 501, 597, 528, 630, 586, 594, 560, 644, 583, 519,639,601,624,544, 646, 637, 520, 613, 650, 621, 592, 614, 507, 514, 541, 527, 561, 607, 622, 567, 564, 591, 590, 610 and 638.

Accession in quadrant I are the type of cassava from different locations namely Jatinangor, Tanjungsari, Subang, Ciwidey and NTT. While in quadrant are the type of cassava from Jawa Barat, DIY, Jawa Timur, Banten, NTT, NAD, Sumatera Utara, Papua, Sulawesi Selatan, Sumatera Barat, Sulawesi Utara, Kalimantan Barat, Sulawesi Tenggara, Lampung, Bengkulu, Maluku and Sulawesi Tengah. Accession 576 is cassava accession from Papua that is. This is caused by the probability of several characters that give positive effects on variation. For example in PC1

there are only five characters from nineteen characters that give positive effect that is bristle character i.e. pubescence on apical leaves, petiole color, color of leave vein, length of leaf lobe and ratio between width and length in central leaf lobe.

Based on the result of cluster analysis, cassava accession has diversity length of Euclidian length 1-17. The result of main component analysis shows a relatively high contribution value in 181 cassava accession based on nineteen morphological characters. The result of biplot analysis in 181 accession shows that the deployment of 181 cassava accession is very extensive, there are six groups in two quadrants which are formed relatively far between their groups. It shows that the potential of cassava in Indonesia has an extensive diversity considering the geographical condition of Indonesia that is quite extensive. A geographical effect naturally gives the diversity marker in cassava accession itself.
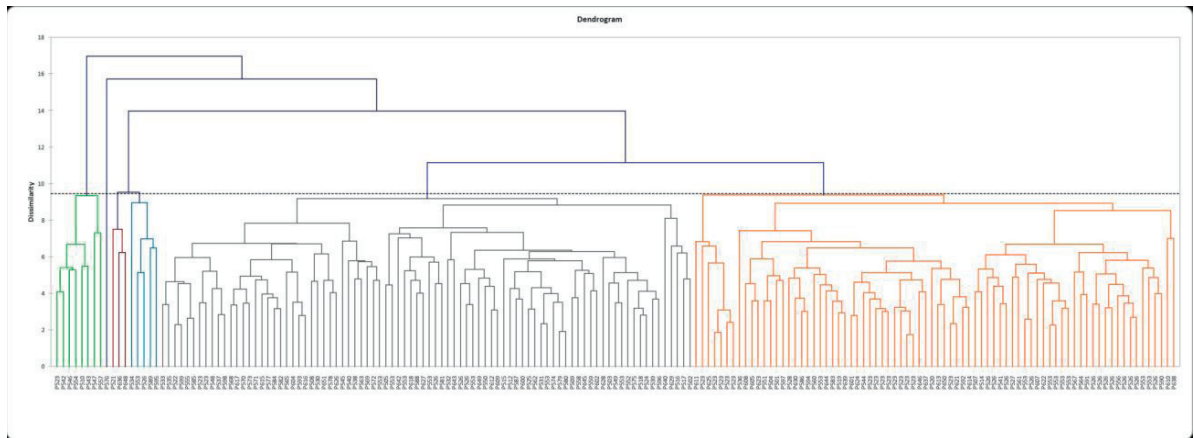

Fig. 2. Dendogram derived from AHC in 181 cassava clones
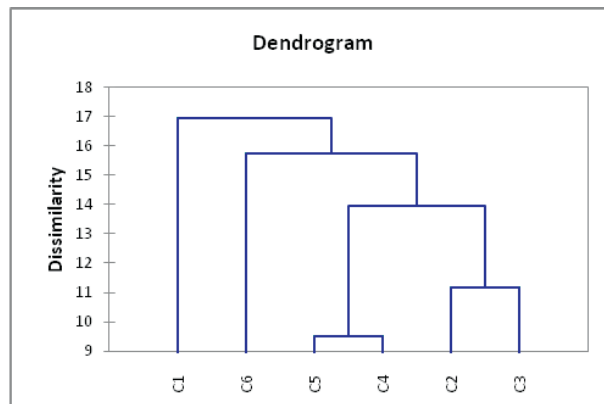based on 19 morphological trait markers

Fig. 3. Dendogram derived from AHC in 181 cassava clones
based on 19 morphological trait markers

4. Conclusion

Diversity and genetic distance of cassava native to Indonesia was extensive in 49.82 % of diversity level and (1 to 17) euclidian of genetic distance which spread across Indonesia. This is an initial capital of choosing cassava potential to be utilized as food, industry, and biofuel.

Acknowledgements

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