Evaluation of genetic purity on Bambara groundnut lines (*Vigna subterranean* L. Verdcourt) *based on qualitative and quantitative characters*

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ABSTRACT

Evaluation of Genetic Purity Bambara groundnut hope line is very important to maintain genetic purity before being released into new varieties. The purpose of this research to examine 12 lines of local Bambara groundnuts. The experiment consisted of 12 unit, each containing 30 plants. The data results are analysed of cluster test forvariables qualitative, quantitative variables by counting the mean, variance, standard deviation and coefficient of diversity. The results showed that the 7 populations lines of hope were uniform because they had a similarity matrix value above 0.80 and the remaining 5 populations of lines of hope were not uniform because they had a similarity matrix value below 0.80. The results of data analysis on quantitative characters showed that age of germination, flowering, and harvest. Terminal leaf length and width, number of internodes, and number of branches had low diversity. Character number of leaves and, diameter of thecrown at the age of 3, 4, 5, 6, 7 and 10 WAP, petiole length, internode length, weight of wet stover, weight of dry stover, length and width of seeds had moderate diversity. Characters of wet pod weight, pod weight dryness, skinthickness, number of seeds and seed weight varied from high to veryhigh.

Keywords: *Bambara groundnuts, genetic purity, diversity coefficient, cluster test*

INTRODUCTION

Bambara groundnuts is a legume which well-known for its wide adaptation and ability to remain productive on less fertile soils. This nut comes from the African region. This is based on the status of this plant in Africa as an important food crop after maize and peanuts (Bhakti *et al.*, 2018). The spread of this bean originated from the Arabian who brought the Bambara bean to Madagascar. At the beginning of the 17th century, these nuts arrived in Suriname and Brazil, then spread to the Philippines and Indonesia (Adhi,2018). In the world this nut is known as Bambara groundnut. Planting around Bogor causes this plant to be called kacang bogor, while in Gresik it is usually called peas. Along with its development, bambara bean plants spread to Sukabumi and Bandung. Some people call this bean the name Bandung bean (Kuswanto., etal., 2012).

Bambara beans are suitable for dry climates, especially in Madura. Whereas soils with limestone as the parent material have a higher soil pH when compared to soils derived from parent material or sand, this is due to the low alkaline leaching, especially if the soil is fine-textured (Supriyadi,2007).

Existing local bambara groundnut lines is a genetic source in breeding programs that provide great opportunities for the establishment of superior varieties. These local lines have the potential as selection materials that can be used as cross parents as well as the main ingredients in assembling superior varieties (Hamid, 2009). The superior bambara groundnut varieties are desirable include high yields, tolerance the pests and diseases, early maturity, high nutrition. If a line can be released as a new superior variety, then the conditions that must be met by the line concerned are populations of different, unique, uniform and stable lines. The problem faced is the development of local bambara bean lines which are still diverse and farmers are still planting adaptive local cultivars whose genotypes are still mixed so that yields are still low because the national bambara bean variety is not yet available (Yuliawati *etal.*, 2019).

The bambara peanut breeding program begins with the selection and evaluation of existing local lines. Selection and evaluation of existing local strains is an important alternative solution to obtain uniform superior strains and the desired properties. Selection is one way of assembling new high-yielding varieties from mixed populations, with the aim of increasing the homogeneity (homosigosity) of the lines. Assembling superior varieties through selection methods, evaluation of the purity of the expected lines has an important role (Fatimah, et al., 2020).

MATERIALS AND METHODS

This research was carried out in the experimental garden of the Agrotechnology Study Program, Faculty of Agriculture, University of Trunojoyo Madura in August 2020–January 2021. The research located at an altitude of ± 2 –10 m above sea level, with the Grumusol soil type. This research were used some tools included hoes, sprayers, nameplates, labels, rulers, markers, digital scales, plastic bags and cameras, also Urea, Ultradap and KCL for the fertilizer.

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The planting material used comes from research results in Pamekasan in 2019 including G1 (Madura Local), G2(Gresik Local), G3 (BBL6.1.1), G4 (GSG1.1.1), G5 (CKB-1), G6(TKB-1), G7(GSG2.4), G8(BBL2.1.1), G9(GSG 3.1.2), G10(JLB-1), G11(CKB-1 US), G12(TKB-1US).

The study was carried out without using an experimental design in which all lines were grown together in the same planting environment without repetition. Planting is done by planting one strain in one bed. So each genotype consists of 30 plants, so there are 360 plants in total. Qualitative variables include plant growth type, leaf shape, leaf color, hypocotyl color, flowering, pod shape, pod color, pod texture, seed shape, seed color, hairs on the stem, and pods filled with two seeds. Quantitative variables observed included, germination age, flowering age, number of leaves, crown width, harvest age, petiole length, terminal leaf length, terminal leaf width, internode length, number of internodes, number of branches, number of pods per plant, fresh pod weight per plant. plants, fresh stover weight, dry pod weight per plant, dry stover weight, pod width, pod length, skin thickness, number of seeds per plant, seed weight per plant, shell weight per plant, seed width and seed length.

Evaluation of purity was analyzed based on qualitative characters using a cluster test with the Simple Matching Coefficient and creating a dendrogram using the Unweightted Pair Group Method with Arithmetic (UPGMA), MVSP3.22 (Multi Variate Statistical Package) software application. According to Pandin, (2010) the degree of similarity using a genetic matrix can be divided into 4 categories, namely very close resemblance (very good) r>0.9 ; good 0.8<r<0.9; not good 0.7<r<0.8; bad r<0.7. Diversity is analyzed based on quantitative characters by calculating the mean value, variance (σ^2), deviation standard (σ) and the coefficient of variation (KK).

Variety of each strain with formula $(\sigma^2)=\frac{\Sigma(x-x)^2}{n-1}$,

Deviation Standard $(\sigma)=\sqrt{\frac{\Sigma(x-x)^2}{n-1}}$,

Coefficient of variation (KK) $=\frac{\sigma}{x}x\ 100\%$.

Note x: the average of each population x: the average of the entire population for each plant characteristic n: the number of populations.

The criteria for the value of the coefficient (KK) according to (Napitupulu & Kuswanto, 2020; Nugraha et al., 2017) Low diversity of CC values 0–25%, Moderate diversity of CC values 25–50%, High diversity of CC values 50–75%, Very diversity high KK 75–100%.

RESULT AND DISCUSSION

The Purity of Genetic

The purity evaluation of each expected lines from bambara groundnut selection was an important step that must be carried out because it aims to find out whether the expected lines were truly uniform or diverse.

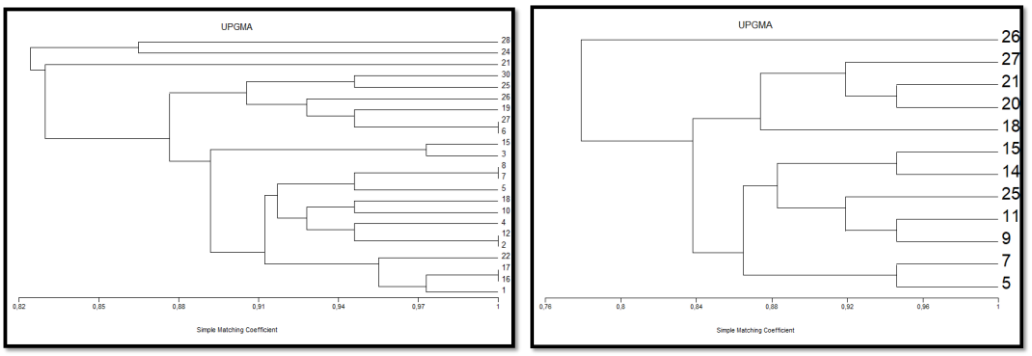
The results of bambara groundnut plant conducted in the Agroecotechnology experimental garden showed that the expected lines of the bambara groundnut were well planted and still maintained their purity. This is proven by the results of the cluster analysis in the form of a dendogram which showed the similarity matrix values of the eight expected lines above 0.80. Lines that have a similarity value below 0.80 were thought to be the result of heterozygous genotype segregation.

When viewed from the similarity value, the lines that have purity were in the poor category (0.7<r<0.8) but it still had a lot in common. If it assumed, the similarities in the strains were around 0.7-0.8, then 0.2 - 0.3 were the difference. This showed the frequency of homozygous genotypes was higher than heterozygous genotypes (Nugraha *et al.*, 2017).

Table 1. The Similarity Value of 12 Expected line of Bambara Groundnut

KodeGalur	KodeGenotip	Nilaikemiripan
G1	LokalMadura	0,78-1,00.
G2	LokalGresik	0,83-1,00
G3	BBL6.1.1	0,81-1,00
G4	GSG1.1.1	0,74-1,00
G5	CKB-1	0,86-1,00
G6	TKB-1	0,83-1,00
G7	GSG2.4	0,875-1,00
G8	BBL2.1.1	0,79-1,00
G9	GSG3.1.2	0,78-0,95
G10	JLB-1	0,84-1,00
G11	CKB-1(US)	0,82-1,00
G12	TKB-1(US)	0,85-1,00

Note : Very Good (r > 0,9), Good (0,8 < r < 0,9), poor (0,7 < r <0,8), Very Poor (r<0,7)



Picture 1.DendogramTKB-1 and GSG3.1.2

Table 2. The value of mean, variance (σ2), standard deviation (σ) and coefficient variation (KK) on quantitative characters

Quantitative Characters	mean	σ^2	σ	KK	
				score	criteria
Age of Germinate (HST)	6-8	0,21-2,18.	0,46-1,48	7,48-22,61	all similar
Age of Flowering (HST)	53-61	7,05-140,46	2,65-11,85	4,46-21,47	all similar
Age of harvest (HST)	118-139	3,48-749,19	1,87-27,37	1,51-23,18	all similar
Number of leaf 3 MST(Helai)	3,03-5,27	0,86-1,75	0,75-1,32	17,92-38,21	7 lines of moderate diversity
Number of Leaf 4 MST(Helai)	6,27-10,33	2,52-9,68	1,59-3,11	18,47-45,76	8 lines of moderate diversity
Number of Leaf 5 MST(Helai)	10,50-19,93	13,17-25,22	3,63-5,57	21,44-47,53	8 lines of moderate diversity
Number of Leaf 6 MST(Helai)	16,97-38,13	40,23-141,37	6,34-11,89	20,57-47,94	8 lines of moderate diversity
Number of Leaf 7 MST(Helai)	26,97-64,47	104,88-558,81	10,24-23,64	23,60-60,36	2 lines high KK
Number of Leaf 10MST(Helai)	68,30-140,43	351,09-3434,20	18,74-58,60	20,85-69,38	2 lines high KK
Crown Width 3 MST(cm)	14,47-28,73	4,92-56,05	3,13-7,49	10,67-48,60	2 lines of moderate diversity
Crown Width 4 MST(cm)	24,17-36,20	9,57-59,31	3,09-7,70	9,94-28,67	2 lines of moderate diversity
Crown Width MST(cm)	28,90-43,93	26,58-84,40	5,16-9,19	12,15-27,28	1 lines of moderate diversity
Crown Width 6 MST	34,17-50,00	16,48-101,37	4,06-10,07	8,41-26,35	2 lines of moderate diversity
Crown Width 7 MST	37,53-56,33	19,10-141,51	4,37-11,90	8,41-33,30	3 lines of moderate diversity
Crown Width 10 MST	44,96-58,63	12,59-193,00	3,55-13,89	6,57-30,90	1 lines of moderate diversity
Length of petiole 10MST(cm)	11,79-18,11	1,27-10,77	1,13-3,28	7,03-26,75	1 lines of moderate diversity
Length internode10MST(cm)	1,08-1,82	0,02-0,17	0,15-0,42	13,50-33,12	4 lines of moderate diversity
Length of terminal leaf 10MST(cm)	6,48-8,35	0,35-2,21	0,59-149	8,93-21,87	all lines similar
Width of terminal leaf 10MST(cm)	2,05-2,92	0,04-1,47	0,21-1,21	6,65-45,25	2 lines of moderate diversity
Number of internodes	6,98-8,96	0,95-2,57	0,97-1,60	11,79-21,36	all lines similar
Number of branch	6,17-7,41	0,82-2,12	0,91-1,46	12,56-21,83	all lines similar
Weight of wet stover (g)	72,68-156,95	961,98-3168,87	31,02-56,29	29,81-55,33	3 lines of High Diversity
Weight of dry stover (g)	40,69-62,09	113,98-368,52	10,68-19,20	21,09-40,89	10 lines of moderate diversity
Weight of wet pod (g)	1,08-7,12	0,44-99,15	0,66-9,96	59,67-139,91	9 lines of very high diversity
Weight of dry pod (g)	0,18-1,50	0,02-3,56	0,14-1,89	55,64-184,98	11 lines of very high diversity
Number of Pod	1,50-5,24	0,50-38,09	0,71-6,17	41,65-136,85	9 lines of very high diversity
Length of Pod (mm)	8,72-11,43	4,70-9,08	2,17-3,01	19,13-33,78	6 lines of moderate diversity
Width of pod (mm)	5,91-8,44	3,03-5,25	1,74-2,29	21,19-32,44	8 lines of moderate diversity
Skin Thickness (mm)	0,29-0,39	0,00-0,17	0,05-0,41	17,53-103,70	1 lines of very high diversity
Weight Skin(g)	0,11-0,66	0,01-0,63	0,08-0,80	66,77-120,69	10 lines of very high diversity
Weight Skin (g)	0,16-0,92	0,01-1,37	0,12-1,17	52,83-126,91	9 lines of very high diversity
Number of seeds	1,40-5,28	0,53-39,27	0,73-6,27	41,99-118,74	4 lines of very high diversity
Length seeds (mm)	6,92-8,98	1,45-5,46	1,20-2,34	15,14-29,35	5 lines of moderate diversity
Width seeds (mm)	4,93-6,75	1,29-3,33	1,3-1,82	17,85-31,92	6 lines of moderate diversity

The highest similarity in observed qualitative characters was related to the genetic purity of each genotype tested, the more diverse the plant characters in one genotype, the more pure the plant is from that genotype. This confirmed that variations occured in each individual would not affect to the group of the lines (Mustofa*etal.*,2013).

The differences in the qualitative characters could be assumed due to differences in plant genetic factors. However, this assumption was not always used as a reference in assessing purity. Not all morphological traits could be used as stable characters because there were plant traits that strongly influenced by environmental changes. The same thing also showed the pods character of these Bogor beans. There was a very wide variation in the character of the color of the pods, and the color of the seeds. Character differences in Bogor beans were due to genetic factors but also those caused by the growth and development phases of plants (Pratama & Saptadi, 2017). The position and depth of the pods under soil surface determined the final character of the pods. This results in a very wide variability, so that these variables were not observed (Nugraha *et al*., 2017).

Variety of Gen

The diversity strain of Bambara groundnut was described by means, variance (σ2), standard deviation (σ) and coefficient of variation (KK) for each character. The quantitative characters observed were age of germination, age of flowering, age of harvest, number of leaves at the age 3, 4, 5, 6, 7 and 10 MST, the width of crown by age 3,4,5,6,7 and 10MST, The length of petiole, internode, terminal leaf, width of terminal leaf, number of internodes, branches, also number of wet stover, dry stover, weight of wet pod, dry pod, number of pods, pod length, pod width, skin thickness, skin weight, weight seeds, number of seeds, width and length of seeds.

Characteristic of age of germination, age of flowering, age of harvest, number of leaves at the age 3, 4, 5, 6, 7 and 10 MST, crown width at 3, 4, 5, 6, 7 and 10 WAP, petiole length, internode length, length terminal leaf, width of terminal leaf, number of nodes, number of branches, wet grafts, dry stover, wet pod weight, dry pod weight, number of pods, pod length, pod width, skin thickness, skin weight, seed weight, number of seeds, seed width and seed length tested on 12 bambara bean genotypes showed low to very high variability.

Quantitative character observations were carried out for each line to determine the value of the coefficient of diversity. The KK value was used to display the variation or diversity of character. The low to moderate value of the coefficient diversity indicated that the diversity of these plants could be said almost same or similar (Napitupulu & Kuswanto, 2020). Based on Nugraha *et al.*, (2017) Low KK value indicated low environmental influence. This result showed that the environment did not have a significant influence on the phenotypes of plants. The high coefficient of variation indicated that there was a significant role for environmental factors which caused on variety appearance of these parameters.

CONCLUSION

The results shows that there are seven expected bambara groundnut lines tested already similar and five lines are not similar or not pure. Characteristics of wet pod weight, dry pod weight, skin thickness, number of seeds, seed weight have a high to very high coefficient of variation, while the characters of germination age, flowering age, harvesting age, length and width of terminal leaves, number of internodes, and number of branches, has a low diversity coefficient. The characters of number of leaves, crown diameter, petiole length, node length, wet stover, dry stover, length and width of the seeds have a moderate diversity coefficient.

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