AJSR
AFRICAN JOURNAL OF SCIENCE AND RESEARCH

African Journal of Science and Research,2014,(3)5:18-24
ISSN: 2306-5877
Available Online: http://ajsr.rstpublishers.com/

GENETIC RELATIONSHIP AND VARIABILITY AMONG INDONESIAN PURIFIED LOCAL LINES OF BAMBARA GROUNDNUT (*Vigna subterranea* (L.) Verdc.) BASED ON MORPHOLOGICAL CHARACTERS.

Nuryati[1*], Andy Soegianto[2] and Kuswanto[2]
1)Center of Plant Variety Protection and Agriculture Permit, Ministry of Agriculture, Jl. Harsono RM No.3, Ragunan, Jakarta Indonesia.
2) Faculty of Agriculture, University of Brawijaya, Jl. Veteran Malang East Java Indonesia.
Email: sekar_volvox@yahoo.com

Received:16,Aug,2014 ***Accepted: 30,Sep,2014***

Abstract
Bambara groundnut is one of alternative food in Indonesia. This research was conducted to evaluate genetic relationship and variability among 50 purified local lines based on morphological characters. The local lines were collected from plantation center areas. Purification of collected lines was done based on pod and seed characters. Evaluation of genetic relationship and variability were conducted using 50 purified local lines.Twenty plants from each line were planted in polybag without replication. Observation on individual plant based on IPGRI guidelines with some improvements. Genetic relationship on qualitative characters was analyzed by cluster analysis based on simple matching coefficient. Whereas variability analysis on quantitative characters was done based on genetic coefficient of variation. Evaluation of genetic relationship showed that at genetic similarity level 0.695, fifty purified local lines of bambara groundnut have been divided into two groups, each consisted of 45 lines and 5 lines respectively. The cluster analysis in the line showed no uniform lines. Variability analysis among 50 purified local lines showed that genetic variation was narrow. Furthermore, genetic variation within lines showed that 50 purified local lines had narrow variability on 21 characters and had narrow to broad genetic variation on 3 characters that have been observed. High variability on qualitative characters was found both within and among the purified local lines.

Keywords: *Bambara groundnut, Vigna subterranea, Relationship, Variability.*

INTRODUCTION

Bambara groundnut is one of alternative food in Indonesia. It is well-known as 'kacang bogor' in West Java and 'kacang kapri' in East Java. Mayes *et al.* (2009) in Podulosi *et al.* (2011) stated that bambara groundnut (*Vigna subterranea*) is one of underutilized crops.This crop plays its role in adapting to climate changes, this plant is known as a drought tolerant plant. It becomes the genetic resources to improve plant variety which has resistance to biotic and abiotic stress. Underutilized crop can increase food security by eliminating the risk of over dependency on the limited main crops. Besides that it could support plant diversification effort and increase sustainable agricultural development by reducing cultivation input such as reducing the application of nitrogen fertilizer so as can diminish agricultural sector contribution in increasing of greenhouse gas effect (Mayes *et al*., 2011).

Bambara groundnut contains high protein. It has 17.78% protein, 59.67% carbohydrate and 5.82% fat contents (Kuswanto, 2013). Bambara groundnut also contains high lysine and it will complete low lysine content of cereal if they are consumed simultaneously (Redjeki, 2007).

In accordance to Regulation of The Health Ministry, The Republic of Indonesia Number 75 in 2013, the average protein requirements for Indonesian people is 57 grams per people per day at the consumption level (Ministry of Health, 2013). According to Hardinsyah *et al.* (2012), in order to obtain better quality of protein and micronutrients, 25% of the protein sufficiency requirement value has been fulfilled from animal protein and 75% from vegetable protein. Based on the census in 2010, numbers of the adults (15-64 years old) were 157,053,112 people or are approximately 66% of the whole population in Indonesia (National Family Planning Coordinating Board, 2013). Based on the data, it is assumed that the requirements of vegetable protein per year for the adults are about 2.45 x 10^6 ton $year^{-1}$. In fact, the amount of protein requirements would be higher in view of population of baby, children and pregnant women who require higher protein. Therefore bambara groundnut could become one alternative protein sources.

Bambara groundnut usually consumed with boiled or fried. Bambara groundnut has potential to be used as materials for industry. It can be used as material for milk production (Brough *et al*., 1993). It is also can be use for tempe production. Tempe is a traditional Indonesian food. Amadi *et al.* (1999) showed that tempe made from bambara groundnut has the same taste and texture as tempe made of soybean.

One of the obstacles in developing bambara groundnut in Indonesia is unavailable superior varieties for the farmers. At present, they just grow local variety that has low yield. Redjeki (2007) stated that 'Bogor lines' which has been grown in Gresik by population of 250,000 plants/ha have produced 0.86 ton/ha. Bambara groundnut which has been grown in Gresik during dry season without fertilizer application, has produced 0.77 ton/ha dry seeds. Besides that, bambara groundnut breeding program in Indonesia has not been well developed.

A research on evaluation of genetic variation toward 38 local lines in University of Brawijaya has shown high variation within and among local lines (Kuswanto et al., 2012). This indicates that the local lines are highly potential as material in breeding of bambara groundnut.

By considering the potency of bambara groundnut and the constraints of their development, improvements in local lines are required through purification process and selection of potential lines to get new varieties or as parental of crossing.

Objective of the research was to determine genetic relationship and variability of purified local lines of bambara groundnut.

MATERIAL AND METHODS

The research was conducted from April 2013 to February 2014. This research started by collecting seeds from the farmers in plantation center of bambara groundnut in Indonesia particularly in West Java Province and East Java Province. Denomination of collected local lines was done by using first letter of the place origin of the seed. Purifying collected local lines was done at Plant Breeding Laboratory, Faculty of Agriculture, Brawijaya University based on pod characters such as the pod shape, texture, color and number of seeds per pod, as well as the seed characters, such as the shape, color and texture of the seed surface. Fifty purified local lines were selected as material for field evaluation.

Field evaluation was carried out at University of Brawijaya Research Station in Jatikerto village, Malang District of Indonesia with altitude of 330 m above sea level. Bambara groundnut seeds were planted in polybag, each line consisted of 20 plants, one poybag was planted one plant and placed in two rows. Cultivation was done based on bambara groundnut standard cultivation technique. Ten plants were observed in relation to days of fresh harvest and fresh weight of pod, while ten other plants were observed until the harvest time of the seeds.

Observation on quantitative and qualitative characters of every individual plant was done following the IPGRI descriptors for bambara groundnut (2000) with some improvements. Quantitative characters that were recorded are plant height, canopy width, number of leaves, petiole length, terminal leaflet length, terminal leaflet width, internode length, days of the first flowering, peduncle length, banner length, number of flowers per plant, days of fresh pod harvest, fresh pod weight per plant, days of the seed harvest, number of pods per plant, pod length, pod width, number of stems, number of nodes per stem, shell thickness, seed length, seed width, 50 seeds weight and shelling percentage. While qualitative characters were observed are pigmentation on hypocotyls, growth habit, terminal leaflet shape, color of terminal leaflet, pigmentation on banner, pigmentation on wing, stem hairiness, pod shape, pod color, pod texture, seed shape, seed color and seed surface texture.

Genetic relationship evaluation within and among lines were done toward qualitative characters by cluster analysis based on *simple matching coefficient*. Dendogram was constructed using *Unweightted Pair-Group Method with Arithmetic* (UPGMA) through *Multivariate Statistical Package* MVSP 3.12d Program (Kovach, 2007). Variability of quantitative characters within and among lines were analyzed based on Genetic Coefficient of Variation determination according to Singh and Chaudhary (1979). Genetic coefficient of variation category is determined according to Murdaningsih *et al.* (1990).

RESULTS AND DISCUSSION

Ten local lines of bambara groundnut had been collected successfully from several places in West Java and East Java. Purification process had been done based on pod and seed characteristics. Pod and seed characteristic from every local lines had high variability. Shape, color and texture of pods from one location showed considerable variation. The same thing happened in the shape, color and texture of seed. This variability on pod and seed characteristics can be used as material for breeding program in developing new varieties. List of originated location, altitude and codes of denomination of the local lines and number local lines each locations are presented in Table 1.

Table (1). List of originated location, altitude, codes of the name of collected local lines and number of purified local lines each location.

No.	Originated Location (Village, District, Regency, Province)	Altitude (m) above sea level	Codes	Number of lines
1.	Wanakerta, Situraja, Sumedang, West Java.	257	WSS	50
2.	Cijedil, Cugenang, Cianjur, West Java.	688	CCC	28
3.	Brengkok, Brondong, Lamongan, East Java	21	BBL	36
4.	Melirang, Bungah, Gresik, East Java	24	MBG	28
5.	Gedangan, Sidayu, Gresik, East Java	20	GSG	37
6.	Candih, Kamal, Bangkalan, East Java	15	CKB	2
7.	Labang, Labang, Bangkalan, East Java	52	LLB	2
8.	Jukong, Labang, Bangkalan, East Java	33	JLB	2
9.	GiliTimur, Kamal, Bangkalan, East Java	21	GTKB	2
10.	Telang, Kamal, Bangkalan, East Java	6	TKB	2

Selection was conducted among 189 lines to get 50 lines that have distinct characters and a sufficient number of seeds as material for evaluating genetic relationship and variability. The description of 50 purified local lines selected are presented in Table (2).

Table(2). List of the fifty purified local lines and it is description were used in field experiment.

No.	Name of lines	Pod shape	Pod texture	Intensity of brown color of pod	Seed color	Seed shape	Seed texture	No. of seed per pod
1	WSS 1.1.2	without point	smooth	light	cream	oval	smooth	1
2	WSS 1.2.2	without point	smooth	light	brown	oval	smooth	1
3	WSS 1.3.2	without point	smooth	light	dark brown	oval	smooth	1
4	WSS 1.4.2	without point	smooth	light	dark purple	round	smooth	1
5	WSS 2.2.2	ending in a point,	smooth	light	brown	oval	smooth	1
6	WSS 2.3.2	ending in a point,	smooth	light	dark brown	oval	smooth	1
7	WSS 3.1.2	without point	rough	light	cream	oval	smooth	1
8	WSS 3.2.2	without point	rough	light	brown	oval	smooth	1
9	WSS 4.3.2	without point	slightly rough	rather dark	dark purple with spot	oval	smooth	1
10	WSS 6.3.2	ending in a point,	slightly rough	rather dark	dark purple with spot	oval	smooth	1
11	WSS 8.2	two-seeded pod	mixture	mixture	dark purple	other	smooth	2
12	CCC 1.1.1	without point	slightly rough	rather dark	black	round	smooth	1
13	CCC 1.3.1	without point	slightly rough	rather dark	dark purple	round	smooth	1
14	CCC 1.4.1	without point	slightly rough	rather dark	dark purple	round	rough	1
15	CCC 1.5	without point	slightly rough	rather dark	brown	mixture	smooth	1
16	CCC 2.1.1	without point	rough	rather dark	black	round	smooth	1
17	BBL 2.1.1	without point	smooth	dark	black	round	smooth	1
18	BBL 2.3.1	without point	smooth	dark	dark brown	round	smooth	1
19	BBL 2.4	without point	smooth	dark	brown	mixture	smooth	1

No.	Name of lines	Pod shape	Pod texture	Intensity of brown color of pod	Seed color	Seed shape	Seed texture	No. of seed per pod
20	BBL 5.3.1	without point	slightly rough	rather dark	dark brown	round	smooth	1
21	BBL 5.3.2	without point	slightly rough	rather dark	dark brown	oval	smooth	1
22	BBL 6.1.1	without point	slightly rough	dark	black	round	smooth	1
23	BBL 6.2.1	without point	slightly rough	dark	dark purple with spot	round	smooth	1
24	BBL 6.3.1	without point	slightly rough	dark	dark brown	round	smooth	1
25	BBL 10.1	two-seeded pod	mixture	mixture	black	other	smooth	2
26	MBG 1.1.2	without point	smooth	light	black	oval	smooth	1
27	MBG 1.2.1	without point	smooth	light	black with spot	round	smooth	1
28	MBG 3.1.1	without point	Slightly rough	light	black	round	smooth	1
29	MBG 3.3.1	without point	Slightly rough	light	dark purple	round	smooth	1
30	MBG 5.1.1	without point	rough	light	black	round	smooth	1
31	MBG 5.3.1	without point	rough	light	dark purple	round	smooth	1
32	MBG 7.1	two-seeded pod	mixture	light	black	other	smooth	2
33	GSG 1.1.1	without point	smooth	light	black	round	smooth	1
34	GSG 1.4	without point	smooth	light	black	mixture	rough	1
35	GSG 1.5	without point	smooth	light	dark purple	mixture	rough	1
36	GSG 1.6	without point	smooth	light	brown	mixture	smooth	1
37	GSG 2.1.1	ending in a point,	smooth	light	black	round	smooth	1
38	GSG 2.2.1	ending in a point,	smooth	light	black with spot	round	smooth	1
39	GSG 2.4	ending in a point,	smooth	light	black	mixture	rough	1
40	GSG 2.5	ending in a point,	smooth	light	dark purple	mixture	rough	1
41	GSG 3.1.2	without point	slightly rough	light	black	oval	smooth	1
42	GSG 3.2.1	without point	slightly rough	light	black with spot	round	smooth	1
43	GSG 3.3.1	without point	slightly rough	light	dark brown	round	smooth	1
44	GSG 3.3.2	without point	slightly rough	light	dark brown	oval	smooth	1
45	GSG 3.5	without point	slightly rough	light	brown	mixture	smooth	1
45	CKB 1*	-	-	-	black	-	smooth	1
47	GTKB 1*	-	-	-	black	-	smooth	1
48	LLB 1*	-	-	-	black	-	smooth	1
49	JLB 1*	-	-	-	black	-	smooth	1
50	TKB 1*	-	-	-	black	-	smooth	1

Notes: *) data of shape, texture and color of pod and shape of seed are not available

Genetic relationship of 50 purified local lines

Cluster analysis to determine relationship within and among purified local lines was done based on the qualitative characters. Qualitative character is a character that controlled by monogene, the different qualitative character controlled by different gene, and therefore differences among characters were presumed as genetic differences.

Cluster analysis within each line showed that there have not been found lines whose group members had genetic similarity coefficient of 1, this implied that the lines derived from purification process were not uniform yet, so the selection process could be done to get uniform lines.

Analysis of genetic relationship among 50 purified local lines presented in the following dendogram (Figure 1).

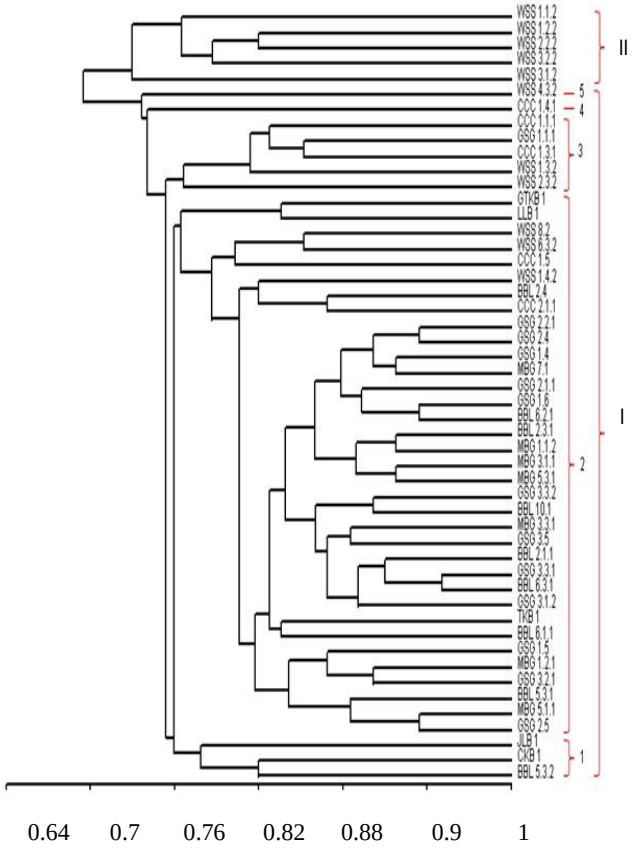

Figure1. Dendogram of 50 purified local lines based on qualitative characters.

A dendogram showed that at genetic similarity level 0.695, fifty purified local lines were divided into two groups. Group I comprised of 45 lines and Group II comprised of 5 lines. Both groups had significant differences, such as pigmentation on hypocotyls on lines that belonged to Group II.

The result of cluster analysis also showed that the line originated from the same location not always be joined in a group. For example, sub-group 1 from the Group I consisted of JLB 1, CKB 1 and BBL 5.3.2 derived from some regency, such as Bangkalan and Lamongan, East Java Province. The same results as reported by Pabendon *et al*. (2003) in grouping 37 genotypes of maize that based on molecular marker showed that genotypes in the same group are not always derived from the same location. This research showed that there were lines from West Java which joined with the lines from East Java in the same group or had close genetic relationship. This explained by the fact that the seeds planted by the farmers were not only obtained from their own fields, but also bought from the market; meanwhile, based on information from the farmers in Gresik, some of bambara groundnut seeds in the market in East Java come from West Java, particularly in specific months when the farmers in East Java have not gone in the harvest time.

Genetic variability of 50 purified local lines

Evaluation of genetic variability within 50 purified local lines was done on 24 quantitative characters. Result of this research showed that genetic variation of each line had narrow variability for plant height, canopy width, number of leaves, petiole length, terminal

leaflet length, terminal leaflet width, internode length, days of the first flowering, banner length, peduncle length, banner length, days of fresh harvest, days of seed harvest, pod length, pod width, number of stems, number of nodes per stem, seed length and seed width, 50 seed weight and shelling percentage. Three other characters include number of flowers per plant, weight of fresh pod per plant and number of pod per plant showed that there were lines which had narrow variability and there were lines that had broad variability. GSG 3.5, GSG 2.4 and WSS 2.2.2 line has broad variability in number of flowers per plant character. There were 32 purified local lines had broad genetic variability and 18 purified local lines had narrow genetic variability in fresh pod weight per plant character. While for number of pods per plant, there were 37 purified local lines had narrow genetic variability and 13 lines with broad genetic variability. Genetic coefficient of variation of each character of the fifty purified local lines are presented in Table (3).

The genetic coefficient of variation among purified local lines ranged from 0% - 23.021% or relatively low. It showed that among 50 bambara groundnut lines had narrow genetic variability based on 21 quantitative characters that had been observed.

Table (4). Data for Mean, environmental variance, phenotypic variance, genotypic variance, heritability and GCV among the lines

Characters	Mean	σ_e^2	σ_p^2	σ_g^2	h² (%)	GCV (%)
Plant height (cm)	31.744	5.604	5.365	-0.239	0	0
Canopy width (cm)	41.821	10.710	21.661	10.951	50.555	7.913
Number of leaves	30.060	8.300	53.659	45.359	84.532	22.405
Petiole length (cm)	17.257	1.942	3.430	1.489	43.394	7.071
Internode length (cm)	2.076	0.040	0.193	0.153	79.356	18.839
Terminal leaflet length (cm)	8.262	0.344	0.599	0.255	42.562	6.109
Terminal leaflet width (cm)	3.027	0.063	0.314	0.251	79.947	16.561
Days of the First Flowering (das)	47.499	8.553	15.854	7.301	46.054	5.689
Peduncle length (mm)	11.197	0.913	2.763	1.850	66.968	12.148
Banner length (mm)	7.008	0.177	0.072	-0.105	0	0
Days of fresh pod harvest (das)	116.076	36.651	162.100	125.449	77.390	9.649
Days of seed harvest (das)	128.38	77.388	48.908	-28.400	0	0
Pod length (mm)	14.301	0.792	2.219	1.427	64.303	8.353
Pod width (cm)	10.902	0.417	0.878	0.461	52.518	6.228
Stem number	7.345	0.300	1.438	1.134	79.086	14.499
Internode number per stem	5.831	0.215	0.563	0.347	61.714	10.103
Shell thickness (mm)	0.340	0.001	0.004	0.003	78.663	15.569
Seed length (mm)	10.785	0.502	1.118	0.617	55.131	7.284
Seed width (mm)	8.014	0.238	0.342	0.104	30.446	4.024
50 seed weight (gr)	20.497	2.012	24.275	22.264	91.713	23.021
Shelling percentage (%)	27.852	3.846	8.454	4.608	54.505	7.707

Notes: GCV: 0% - 25% = relatively low, 25% - 50% = semi low, 50% - 75% = high enough, 75% - 100% = high.

Broad heritability of 21 characters observed ranged from 0% - 91.713%. Negatively heritability was observed on plant height, peduncle length and harvest date traits. Characters that have negative heritability values presumed as zero. These characters had low heritability. Low heritability implies that environmental effect is bigger than genetic effect. Seed width, petiole length, leaf length and day of the first flowering had heritability 30.446%, 43.394%, 42.562% and 46.054% respectively. Those characters had medium heritability. Characteristics which had heritability more than 50% or had high heritability were canopy width, number of leaves, internode length, terminal leaflet width, peduncle length, fresh harvesting date, pod length, pod width, stem number, number of internode per stem, shell thickness, seed length, 50 seed weight, and shelling percentage. Character that has the highest heritability value was 50-seed weight for about 91.713%. Characters that has high heritability value showed higher effect of the genetic factor than the environment factor on the phenotypic appearance. Research on heritability of some morphological characters on bambara groundnut has been conducted by Karikari (2000) on nine accessions derived Botswana, Zimbabwe dan Tanzania in which weight of 100 seeds and shelling percentage had medium heritability.

The variability of qualitative characters within and among purified local lines showed high variation. The variability of qualitative traits represented the difference of genetic trait. This research showed that growth habit and leaf shape within the lines was still varies. The growth habit in one purified local line had bunch, semi bunch and spreading. There were 35 lines had lanceolate terminal leaflet shape, whereas the shape of terminal leaflet of the other 15 lines was varied. Besides lanceolate, the other shape of terminal leaflet shape on these lines is oval and elliptic. High variability also showed in shape, color and texture of the pod and seed that resulted from one plant in one line. Most of the color of seeds that producing by the fifty purified lines is dark colored seed testa. There were seven colors of seed that have been observed in this research. Those colors are cream, brown, black, black with brown spot, dark brown, dark purple and dark purple with spot. Redjeki *et al*. (2011) stated that Indonesian farmers prefer to plant seed having dark colored testa and a white hilum. This research also showed that there were 5 lines WSS 3.1.2, WSS 3.2.2, WSS 2.2.2, WSS 1.2.2 and WSS 1.1.2 from Sumedang Regency had distinct characteristics. These lines had pigmentation on hypocotyls, while the 45 lines did not have pigmentation on the hypocotyls.

The variability of the qualitative characters within 50 purified local lines and among 50 purified local lines showed genetic differences. Qualitative character is a character that not affected by the environment, the selection in early generations would be more efficient if it is done based on qualitative characters.

In this study, the progenies of purified local lines were not completely identical with the parents. For instance, BBL 5.3.2 line had without point pod shape. While the progenies did not only had without point pod shape (same as its parent), but they also had pods with ending in a point, round on the other side shape, even it had pods with two seeds. The same condition also occurred on pod color and texture characters and seed shape and color characters. CCC 1.1.1 lines had black color of seed. The progenies of this line had seed with cream color (1.31%), brown (4.34%), black (59.57%), black with brown spots (10.56%), dark brown (11.86%), dark purple (12.36%). This could happen because there was segregation of heterozygous genotype. The same thing was described by Karikari *et al.* (1997) as quoted by Ouedraogo *et al.* (2008) in which the farmers in Burkina Faso who used seeds from prior plantation period, stated that the color of the seed change year-by-year, because there were still segregation that occurred in the progenies.

Most of the purified local lines examined in this study derived from one seeded pod. There were three lines had seed from two-seeded pod parent i.e. MBG 7.1, BBL 10.1 and WSS 8.2. The progenies from these lines are mostly one-seeded pod, while the two-seeded pod of each line has 1.89%, 3.95% and 1.43%. This suggests that the effectiveness of the two-seeded pod characters as criteria of selection in this study was still low.

CONCLUSION AND SUGGESTION

Conclusion

1. The fifty purified local lines at 0,695 genetic similarity levels divided into two groups, each consisting of 45 lines and 5 lines with pigmentation on hypocotyls as distinctive character.
2. There was high variability on qualitative characters within or between the lines.
3. In the early stages, selection based on qualitative characters will be more efficient.
4. The effectiveness of two-seeded pod character as criteria of selection was still low (maximum only 4%).

Suggestion

Further selection based on qualitative characters is required in order to obtain uniform lines.

ACKNOWLEDGEMENTS

Partly of financial support received from the Faculty of Agriculture Brawijaya University for the present study is gratefully acknowledged.

REFERENCES

1. Amadi, E.N., R. Uneze., I. S Barimalaa and S.C. Achinewhu. 1999. Studies on the production of bambara groundnut (*Vigna subterranea*) tempe. *Plant Foods for Human Nutrition*. 53: 199-208.
2. Brough, S.H., S.N. Azam-Ali and A. J. Taylor. 1993. The potential of bambara groundnut (*Vigna subterranea*) in vegetable milk production and basic protein functionality systems. *Food Chemistry*. 47:277-283.
3. Hardinsyah., H. Riyadi and V. Napitupulu. 2012. *The adequacy of energy, protein, fat and carbohydrates* (in Indonesia). Department of Nutrition Faculty of Human Ecology.Bogor Institute of Agriculture. 26p.
4. IPGRI, IITA, BAMNET. 2000. *Descriptors for bambara groundnut* (*Vigna subterranea*). International Plant Genetic Resources Institute, Rome, Italy; International Institute of Tropical Agriculture, Ibadan, Nigeria; The International Bambara Groundnut Network, Germany.
5. Karikari, S.K. 2000. Variability between local and exotic bambara groundnut landraces in Botswana. *African Crop Science Journal*. 8(2):145-152.
6. Kovach, W.L., 2007. *MVSP - A MultiVariate Statistical Package for Windows, ver. 3.1*. Kovach Computing Services, Pentraeth, Wales, U.K.
7. Kuswanto.2013. *The result of Seed Laboratory Test of Bambara Groundnut* (in Indonesia). Faculty of Agriculture, Brawijaya University. Malang.
8. Kuswanto., B. Waluyo., R. A. Pramantasari and S. Canda. 2012. *Collection and Evaluation Local Lines of Bambara Groundnut* (*Vigna subterranea*) (in Indonesia).Faculty of Agriculture, Brawijaya University. Malang.
9. Mayes, S., F.J. Massawe, P.G. Alderson, J.A. Roberts, S.N. Azam-Ali and M. Hermann. 2011. The potential for underutilized crops to improve security of food production. *Journal of Experimental of Botany*.1-5
10. Ministry of Health.2013. *Mininsterial Regulation of Health Republic of Indonesia Number 75 Year 2013 about Recommended Daily Intake for Indonesian Nation* (in Indonesia). Ministry of Health. 10p.
11. Murdaningsih, H.K., A. Baihaki., G. Satari., T. Danakusuma and A. H. Permadi.1990. Genetic variation of several garlic traits in Indonesia (in Indonesia). *Zuriat*.1 (1): 2-36
12. National Family Planning Coordinating Board. 2013. *Profile Population and development in Indonesia Year 2013* (in Indonesia). National Family Planning Coordinating Board. Jakarta. 108p
13. Ouedraogo, M., J. T. Ouedraogo, J. B. Tignere, D. Balma, C. B. Dabire and G. Konate. 2008. Characterization and evaluation of accessions of bambara groundnut (*Vigna subterranea* (L.) Verdcourt) from Burkina Faso. *Science & Nature*.5 (2): 191-197.
14. Pabendon, M. B., E. Regalado, Sutrisno, M. Dahlan and M. L. George. 2003. The clustering recuiring of maize genotypes based on SSR (*Simple Sequence Repeat*) Markers (in Indonesia). *Journal of Penelitian Pertanian Tanaman Pangan*. 22(1):23-30
15. Padulosi, S., V. Heywood., D. Hunter., A. Jarvis. 2011. *Underutilized species and climate change: Current Status and Outlook in Crop Adaptation to Climate Change* First edition. John Wiley @ Sons, Ltd
16. Redjeki, E.S. 2007. Growth and Yield of Bogor and Gresik Local lines of bambara groundnut on various seed color (in Indonesia). Paper presented at *the proceedings of the national seminar on research funded by Competitive Grant.* Bogor. 114-118.
17. Redjeki, E.S., S. Mayes and S. Azam-Ali. 2011. Evaluating the stability and adaptability of bambara groundnut (*Vigna subterranea* (L.) Verd) landraces in different agroecologies. Paper presented at *2nd International symposium on underutilized plant species*. Kuala Lumpur. Malaysia.
18. Singh, R. K. and B. D. Chaudhary.1979. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers. New Delhi. 304p.

Appendix

Table (3). Genetic coefficient of variation (GVC) of quantitative characters of the fifty purified local lines

No.	Name of Lines	GVC per characters (%)																						
		PH	CW	NL	PL	TLL	TLW	IL	FFD	PDL	BL	FHD	SHD	POL	POW	NS	IN	ST	SL	SW	50SW	SP	NF	FPW	NP
1	BBL 5.3.2	5.60	7.49	6.79	3.13	9.54	6.83	7.99	3.57	28.65	11.11	6.27	11.32	8.17	5.40	26.37	14.39	14.17	7.75	5.40	22.75	19.99	23.99	60.97	41.75
2	CCC 1.4.1	6.34	8.74	13.65	9.86	18.54	17.92	7.92	10.36	31.97	11.09	3.83	8.35	8.63	6.47	23.39	10.05	14.80	9.63	6.70	22.62	26.69	22.60	44.22	47.95
3	GSG 2.5	7.79	5.78	25.35	6.79	0.00	21.51	16.77	4.29	0.00	6.17	3.85	5.84	5.18	4.39	19.75	20.25	9.38	4.10	2.09	15.30	20.70	0.00	72.80	45.65
4	MBG 5.1.1	8.76	12.58	21.63	7.46	9.10	17.53	19.34	7.28	15.31	3.15	3.14	5.50	8.26	7.59	14.41	9.87	13.74	9.91	8.81	29.91	16.37	37.91	40.38	34.72
5	WSS 2.3.2	6.50	14.25	20.96	13.57	5.39	15.59	30.14	2.64	34.49	6.13	14.79	1.32	11.91	9.13	6.73	29.64	14.91	12.70	11.27	42.24	30.56	41.03	158.26	31.14
6	JLB 1	4.66	9.84	17.10	11.01	4.32	7.34	9.50	6.88	19.35	6.01	8.62	14.03	10.67	9.27	18.13	7.17	20.98	9.95	7.13	30.89	16.18	28.04	66.18	34.62
7	BBL 6.1.1	0.00	10.09	15.73	8.68	15.48	16.05	11.06	3.70	30.08	9.74	0.00	4.79	7.33	5.65	18.38	11.52	15.16	5.27	2.44	9.00	6.67	35.02	38.05	55.22
8	CCC 1.5	8.96	17.18	24.37	7.87	8.80	13.70	33.60	24.89	21.36	3.73	8.05	3.39	10.08	8.41	10.69	16.88	21.60	10.62	9.68	32.31	7.73	12.66	31.93	40.23
9	GSG 3.1.2	6.15	9.59	22.00	7.70	4.97	6.04	20.84	5.22	11.46	7.17	10.87	6.63	4.85	3.96	10.11	16.03	0.00	5.44	4.55	9.07	0.00	25.13	66.06	32.92
10	MBG 5.3.1	3.86	7.36	8.30	5.76	7.56	10.29	10.89	6.01	10.36	7.22	9.88	4.44	0.83	0.87	12.09	3.78	10.18	2.58	0.00	5.30	17.55	37.06	65.31	33.23
11	WSS 3.1.2	5.48	9.67	19.44	7.12	7.07	12.02	17.11	7.83	17.40	5.56	5.34	3.24	5.11	4.05	17.79	15.32	7.97	6.73	5.03	18.17	12.86	37.95	36.27	45.55
12	TKB 1	8.02	6.48	14.12	9.11	12.40	12.37	14.34	4.73	18.58	6.58	11.31	3.36	4.88	2.39	32.42	12.69	13.65	3.54	0.58	8.03	16.38	43.18	64.57	29.74
13	BBL 6.2.1	5.50	4.63	17.03	7.24	6.73	8.38	12.45	8.24	12.03	1.86	13.40	8.67	4.31	3.41	20.65	12.42	8.48	4.24	3.28	9.56	10.52	22.63	85.83	36.53
14	CCC 2.1.1	6.66	13.58	20.64	11.02	3.77	9.15	11.56	3.58	14.34	9.53	9.30	8.33	4.60	4.14	26.03	10.69	7.33	4.11	2.64	18.42	22.58	39.20	78.25	34.17
15	GSG 3.2.1	11.75	20.81	34.10	15.34	8.89	6.91	22.58	2.88	18.86	8.05	7.14	7.08	4.69	4.80	20.57	26.28	14.52	4.41	4.18	15.72	22.35	39.19	35.24	52.40
16	MBG 7.1	8.44	6.82	14.28	0.00	10.91	10.13	10.86	7.17	10.89	4.86	3.41	7.77	4.34	4.68	19.44	0.00	19.01	5.45	3.91	11.99	27.31	38.00	60.10	45.72
17	WSS 3.2.2	6.61	0.00	24.68	5.92	13.26	5.18	12.49	15.25	25.63	2.61	12.67	8.67	5.72	4.91	21.80	12.29	13.43	5.59	4.69	15.64	18.05	46.08	90.33	38.11
18	BBL 6.3.1	8.88	10.89	25.01	9.48	10.16	9.62	11.98	4.22	19.25	5.66	8.14	3.30	5.74	6.03	12.18	11.36	12.27	5.33	4.42	15.72	21.30	17.42	50.15	61.96
19	GSG 3.3.1	6.71	6.21	14.96	7.59	10.11	10.38	15.81	1.22	12.54	5.84	8.84	6.69	12.43	8.16	9.46	15.90	9.03	6.69	4.49	16.50	12.50	22.07	36.39	44.81
20	WSS 4.3.2	8.18	9.75	8.98	13.12	7.70	10.67	28.90	1.83	24.72	9.23	6.92	7.14	5.49	4.97	13.97	18.71	11.52	7.64	5.63	17.26	8.39	42.96	95.54	54.35
21	BBL 10.1	4.55	12.98	30.03	6.88	7.64	10.58	14.07	3.35	9.16	4.91	3.87	6.87	11.23	5.60	13.87	12.33	8.68	6.99	6.13	20.44	32.77	37.82	71.49	44.60
22	GSG 3.3.2	5.49	15.06	48.77	9.54	10.32	6.79	13.40	12.20	7.26	5.96	13.92	10.68	7.82	6.03	29.35	15.45	13.30	6.55	7.48	18.55	34.36	38.16	73.88	50.69
23	WSS 6.3.2	14.30	9.37	18.72	11.49	19.85	21.09	18.01	5.00	13.84	5.29	5.03	7.55	11.83	10.40	12.71	23.54	12.55	10.98	9.20	26.35	15.14	41.02	103.15	69.53
24	GSG 3.5	13.97	16.81	44.59	16.27	25.15	16.33	28.95	7.79	17.52	2.75	3.51	6.03	12.14	9.32	29.25	20.20	15.84	8.96	8.60	23.80	6.84	68.86	83.21	51.14
25	WSS 8.2	7.95	6.33	12.72	4.09	11.12	21.27	23.39	8.06	18.89	7.32	10.44	9.54	9.42	11.82	0.00	12.50	20.67	7.99	9.54	30.48	8.65	44.08	42.20	34.91
26	GSG 2.4	10.52	17.33	16.50	12.12	20.22	33.51	25.12	8.98	15.48	8.12	9.75	0.00	9.29	8.00	35.24	23.63	8.56	7.78	8.10	28.94	16.99	57.47	36.15	42.85

No.	Name of Lines	GVC per characters (%)																						
		PH	CW	NL	PL	TLL	TLW	IL	FFD	PDL	BL	FHD	SHD	POL	POW	NS	IN	ST	SL	SW	50SW	SP	NF	FPW	NP
27	WSS 2.2.2	10.22	29.47	27.67	11.39	18.01	35.29	42.23	3.96	21.85	5.64	21.75	8.17	9.51	12.62	17.79	29.91	16.72	9.83	11.31	30.45	14.46	64.64	39.89	69.15
28	GSG 2.2.1	10.60	15.62	32.61	13.34	13.59	13.93	33.79	15.72	19.72	6.84	14.83	6.45	11.91	8.13	27.92	21.48	9.38	6.77	6.26	21.54	20.40	30.12	55.45	55.92
29	WSS 1.4.2	7.91	8.11	23.09	7.44	9.94	13.77	29.22	4.03	8.03	5.39	20.79	4.93	5.96	6.50	17.81	21.16	18.50	7.63	6.51	22.87	6.32	44.05	99.62	45.00
30	GSG 2.1.1	4.65	4.55	13.94	6.33	8.08	3.23	14.16	9.26	13.96	5.47	11.78	7.99	4.76	2.84	14.56	17.36	8.82	4.94	3.97	9.48	16.92	37.72	28.59	35.66
31	MBG 3.1.1	12.01	5.11	9.45	8.92	14.05	14.44	19.53	10.71	9.94	5.61	13.27	5.94	5.01	5.84	17.76	14.51	14.83	6.11	6.78	15.81	16.63	30.32	50.33	36.76
32	GSG 1.6	6.44	2.56	19.70	7.51	6.89	4.88	14.80	5.38	18.60	6.27	13.48	8.67	4.83	5.37	19.05	12.91	29.15	4.16	2.60	5.32	13.66	31.66	51.33	37.53
33	BBL 5.3.1	9.93	5.76	15.96	7.71	6.31	3.36	18.19	5.02	13.07	3.62	0.50	7.85	2.92	2.05	17.60	10.37	18.90	3.52	1.06	2.51	20.41	48.36	48.09	25.02
34	LLB 1	11.22	6.38	6.39	13.26	2.66	0.00	18.62	8.61	30.21	0.93	0.00	\5.22	5.24	5.02	6.06	12.33	7.97	0.00	1.44	3.77	18.91	33.90	185.87	56.16
35	WSS 1.3.2	8.49	11.84	18.60	12.19	11.64	17.73	27.67	5.53	16.84	5.57	9.42	4.70	6.07	4.64	13.07	10.48	15.69	6.00	4.67	16.93	12.92	40.92	64.71	49.56
36	MBG 1.2.1	8.79	9.94	16.04	8.38	8.19	16.97	0.00	11.59	20.86	6.66	0.00	7.05	5.22	3.65	27.74	7.65	17.56	3.69	2.81	12.95	17.61	29.01	36.58	51.22
37	GSG 1.5	6.01	7.13	0.00	4.62	6.76	12.73	13.70	12.37	40.47	6.09	8.40	5.40	5.61	5.21	1.36	14.18	14.37	5.63	3.20	18.36	35.62	13.49	81.82	69.56
38	BBL 2.4	9.79	4.83	15.53	7.69	7.87	18.11	12.92	7.81	12.52	4.00	5.19	3.74	4.76	3.94	11.40	8.18	7.90	4.90	4.96	15.18	10.40	26.65	33.36	48.69
39	GTKB 1	4.71	10.20	6.54	4.86	15.19	19.04	10.12	10.34	29.31	3.81	0.00	5.62	5.07	5.60	21.29	5.29	9.42	6.53	6.48	12.59	37.42	46.04	88.98	40.85
40	WSS 1.2.2	5.37	12.90	17.66	7.17	8.60	2.18	20.42	4.87	13.38	2.96	15.23	10.91	4.50	5.63	23.05	33.61	20.73	5.15	6.39	19.71	14.74	31.66	64.41	38.58
41	MBG 1.1.2	8.49	16.68	34.12	9.66	13.33	12.83	25.64	12.89	23.46	4.27	11.99	6.04	0.00	1.39	19.83	5.30	9.62	2.27	0.60	14.72	14.34	27.05	72.39	35.72
42	GSG 1.4	10.40	13.53	10.26	9.14	6.05	16.28	20.81	7.30	16.36	7.55	14.72	7.39	3.32	3.51	34.91	11.15	16.40	4.69	3.50	22.15	30.20	22.54	65.88	22.08
43	CCC 1.3.1	1.94	10.88	26.68	15.11	5.33	12.59	12.46	5.12	18.22	6.30	4.04	4.81	5.83	5.46	1.84	11.01	21.78	7.63	6.63	21.93	15.76	17.81	59.87	10.51
44	BBL 2.3.1	8.16	7.42	17.47	11.60	6.84	13.38	14.51	5.57	18.75	2.30	0.32	8.81	3.67	2.60	4.58	15.36	11.49	5.57	3.16	0.00	11.93	26.41	40.24	20.83
45	CKB 1	4.89	10.08	21.96	8.21	11.17	9.18	27.39	7.00	19.83	5.53	8.01	7.48	1.80	0.00	18.64	13.30	8.76	3.08	1.83	11.91	23.86	25.33	43.69	42.69
46	WSS 1.1.2	6.35	12.41	24.55	7.09	6.98	12.03	20.57	0.89	7.03	6.21	12.32	9.19	7.68	4.97	12.49	19.80	11.61	8.14	4.88	22.16	46.79	28.37	71.96	29.07
47	MBG 3.3.1	2.81	11.70	32.36	12.31	11.65	20.37	24.28	5.68	18.87	0.00	0.43	9.62	9.19	8.54	19.58	16.35	21.63	9.42	8.87	21.11	28.13	31.13	51.48	47.60
48	GSG 1.1.1	9.62	18.27	20.17	8.28	9.76	15.52	23.63	16.32	15.04	5.58	7.12	8.89	7.89	11.01	19.24	17.50	7.58	8.61	8.96	21.27	30.67	44.51	49.29	65.91
49	CCC 1.1.1	7.22	3.50	10.29	7.41	1.82	6.65	12.83	4.77	17.66	6.45	4.77	5.18	7.09	6.66	20.04	3.27	21.25	6.55	4.98	26.21	14.79	2.44	0.00	0.00
50	BBL 2.1.1	9.36	13.66	14.14	9.60	5.86	15.22	15.91	0.00	18.98	9.07	0.00	8.80	5.22	4.50	16.49	12.58	30.47	5.61	4.83	14.48	17.82	23.75	77.26	38.59

Notes: PH = Plant Height, CW = Canopy width, NL = Number of leaves, PL= Petiole Length, TLL= Terminal Leaflet Length, TLW (cm)= Terminal Leaflet Width (cm), IL = Internode Length, FFD = Days of the First Flowering, PDL = Peduncle Length, BL = Banner length, FHD= Days of fresh pod harvest, SHD = Days of seed harvest ,POL = Pod Length, POW = Pod width, NS = Number of Stem IN= Internode number Per Stem, ST= Shell Thickness, SL= Seed Length, SW= Seed Width, 50SW = 50 Seed Weight, SP = Shelling Percentage, NF = Number of Flowers per Plant, FPW = Fresh pod weight per plant, NP = Number of pod per plant. GCV: 0%- 25% = relatively low, 25% - 50% = semi low, 50% - 75% = high enough, 75% - 100% = high, > 100% = very high.