ANALYSIS OF GENETIC PARAMETERS FOR BEAN PHYSICAL QUALITY CHARACTERS AND CLUSTERIZATIONS OF ELEVEN GENOTYPES OF ROBUSTA COFFEE (*Coffea canephora*)

*Analisis Parameter Genetik untuk Karakter Kualitas Biji dan Klasterisasi Sebelas Genotipe Kopi Robusta (*Coffea canephora*)*

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ABSTRACT

The genetic parameters of coffee related to their bean physical quality characters are important for breeder to improve the bean quality. Eleven genotypes of robusta coffee were identified and their genetic relationship to the bean physical quality were characterized. The research was conducted at coffee plantation of the Association of Indonesian Coffee Exporters in West Lampung, altitude of 800 m above sea level, Latosol type of soil, and A type of climate, starting from 2010 to 2012. The objectives of this study were to estimate the genotypic coefficient of variation, heritability and genetic advance of the bean physical quality characters, and clusterization analysis of eleven genotypes of robusta coffee. A randomized complete block design with eleven treatments of coffee genotypes and three replications was used in this study. The results showed that the estimated values of genotypic coefficient of variation, heritability and genetic advance for small-size normal bean characters of robusta coffee were very high, so the genetic improvement for these characters has a high probability of success by direct selection. Clusterization of the genotypes resulted three clusters with their respective characteristics. The study implies that future breeding program especially for hybridization should be conducted between genotypes arising from different clusters to obtain the possible high heterosis effects.

[***Keywords*:** *Coffea canephora*, robusta coffee, genetic parameters, clusterization, bean physical quality]

ABSTRAK

Parameter genetik terkait dengan karakter kualitas fisik biji kopi penting bagi pemulia dalam upaya perbaikan kualitas biji. Sebelas genotipe kopi robusta telah diidentifikasi dan hubungan genetik kualitas fisik bijinya telah dikarakterisasi. Penelitian ini dilakukan di perkebunan kopi milik Asosiasi Eksportir Kopi Indonesia di Lampung Barat pada ketinggian tempat 800 m di atas permukaan laut dengan jenis tanah Latosol dan tipe iklim A, mulai 2010 sampai 2012. Tujuannya adalah untuk menduga koefisien keragaman genotipik, heritabilitas, dan kemajuan genetik karakter kualitas fisik biji dan analisis klasterisasi 11 genotipe kopi robusta. Penelitian menggunakan rancangan acak kelompok lengkap dengan 11 perlakuan genotipe kopi robusta dan tiga ulangan. Hasil penelitian menunjukkan nilai duga koefisien keragaman genotipik, heritabilitas, dan kemajuan genetik untuk karakter biji normal berukuran kecil termasuk kategori sangat tinggi, sehingga perbaikan genetik untuk karakter tersebut memiliki peluang keberhasilan yang tinggi melalui seleksi secara langsung. Klasterisasi genotipe menghasilkan tiga klaster dengan karakteristik masing-masing. Hasil ini memberikan implikasi bagi program pemulian berikutnya, terutama dalam proses hibridisasi yang hendaknya dilakukan antargenotipe yang berasal dari klaster yang berbeda untuk memperoleh efek heterosis yang tinggi.

[***Kata kunci*:** *Coffea canephora*, kopi robusta, parameter genetik, klasterisasi, kualitas fisik biji]

INTRODUCTION

The definition of quality of coffee varies along the production level to consumer level. For example, at the exporter or importer level, the quality is determined to bean size, lack of defects, regularity of provisioning, tonnage available, physical characteristics and price. Similarly, the definition of quality of coffee for other levels such as farmers, roasters and consumers has different criteria (Leroy *et al*. 2006).

The expression of quality of coffee, such as bean size and physical characteristics, depends on a multifactorial determinism, including pedoclimatic conditions, postharvest treatments and genetics as well as storage conditions (Yigzaw 2005; Leroy *et al*. 2006; Behailu *et al*. 2008). Among these factors, genotype is the key factor determining the important characters, such as size, shape, color, chemical composition and flavor of the bean. The shape and structure of beans are the result of both genotype

and environment interaction (Wintgens 2004) and can be used as the first step of selection (Leroy *et al*. 2006).

Robusta coffee clones with the initials name of BP (*Besoekisch Proefstation*), i.e. BP 436, BP 534, BP 936, BP 939, BP 42, BP 488, BP 254, BP 358, BP 410 and BP 308 that currently widely used in Indonesia are superior clones from the first generation until the third generation derived from the breeding programs conducted by Indonesian Coffee and Cocoa Research Institute (ICCRI). Parent populations as the base materials for their breeding process are introduced from Congo (Baon 2011). The bean quality characters such as bean size of these clones are highly variable from small to large (Puslitkoka 2003), so it has a very high probability of success in improving the genetic characters of these genotypes. For that purpose, it needs to know their regarding genetic parameters, including the genotypic coefficient of variation (GCV), heritability (H) and genetic advance (GA), for the bean quality characters of the robusta coffee. Mistro *et al*. (2007) argued that the probability and success of coffee breeding are highly depended on the availability of genetic information of breeding materials and the basic knowledge about the genetic parameters allowed the choice of the most suitable selection strategy to reduce time for cultivar development.

In addition to genetic parameters, other basic study which can enrich the information for improving the success of a breeding program is the genotypic clustering. Clustering is grouping of genotypes that are genetically similar or dissimilar. This information is very important as a baseline for subsequent breeding programs through hybridization and other breeding activities to develop superior varieties. In general, a cluster analysis is done to combine observations into homogeneous groups. The role of classification in a crop improvement program has long been well recognized. For different breeding programs or for varietal selection, there is a need to identify genetic materials that contain useful traits. Therefore, it is of great interest to classify the accessions according to their trait scores or genetic structure (Sarkar *et al*. 2011).

The objectives of this study were to estimate the genotypic coefficient of variation, heritability and genetic advance of the bean physical quality characters and clusterization analysis of eleven genotypes of robusta coffee.

MATERIALS AND METHODS

Location and Design of Experiment

The study was carried out at coffee plantation of the Association of Indonesian Coffee Exporters (AICE) in West Lampung with altitude about 800 m above sea level, Latosol type of soil and A type of climate, starting from 2010 to 2012. The experiment was arranged in a randomized complete block design, applying eleven coffee genotype treatments and three replications. The eleven treatments were robusta coffee genotypes consisted of 10 superior genotypes obtained from ICRI, i.e. BP 436, BP 534, BP 936, BP 939, BP 42, BP 488, BP 254, BP 358, BP 410 and BP 308 (Puslitkoka 2003) and one genotype specific of West Lampung (AEGAWA genotype) obtained from individual selections conducted by the AICE. Variables observed were 12 physical bean characters as described in Table 1.

Coffee Bean Collection and Selection

Cherries of the coffee were harvested in June-July 2012 and then bulked and dry processed according to the standard procedures. Measurement of 12 variables was conducted on 100 g samples of cherries which were randomly selected after dry processing. All the 100 g samples were then separated into three criteria according to the Indonesian National Standard (SNI), namely normal beans (N), single beans (S) and defects beans (D). Coffee beans were categorized as “normal” if they had two twin beans in

Table 1. The robusta coffee bean quality character and their codes.

Variable observed	Code of variables
Percentage of number of large-size normal beans	[PN_LS_N]
Percentage of number of small-size normal beans	[PN_SS_N]
Percentage of number of large-size single beans	[PN_LS_S]
Percentage of number of small-size single beans	[PN_SS_S]
Percentage of number of large-size defect beans	[PN_LS_D]
Percentage of number of small-size defect beans	[PN_SS_D]
Percentage of weight of large-size normal beans	[PW_LS_N]
Percentage of weight of small-size normal beans	[PW_SS_N]
Percentage of weight of large-size single beans	[PW_LS_S]
Percentage of weight of small-size single beans	[PW_SS_S]
Percentage of weight of large-size defect beans	[PW_LS_D]
Percentage of weight of small-size defect beans	[PW_LS_D]

a one-fruit set (polyembrionic), whereas the beans were categorized as "single" if there was only one bean in one fruit (peaberry). Coffee beans were categorized as "defect" if there were damages due to broken, rotten and hollow, mixed with other materials and changes in color. Furthermore, beans were categorized as "large" (L) if the fraction of beans retained by screen with 6.5 mm spaces (sieve no. 16); "small" (S) if the fraction of beans retained by screen with 3.5 mm spaces (sieve no. 9). The fractions of beans not retained by screen with 3.5 mm spaces were categorized as "shatter or splinter" (BSN 2008).

Genetic Data Analyses

The genetic parameters analyzed included the genotypic and phenotypic variances, genetic coefficient of variation, heritability and genetic advances based on the methods proposed by Singh and Chaudhary (1979) and Holland *et al.* (2003), and also cited by Maji and Shaibu (2012) and Selvaraj *et al.* (2011) in rice, Tessema *et al.* (2011) and Kitila *et al.* (2011) in coffee, Hefny (2011) in corn, Das *et al.* (2010), Wardiana and Pranowo (2010), and Gohil and Pandya (2009) in physic nut, as well as Khan *et al.* (2008) and Akhtar *et al.* (2007) in *Brassica*, as follows: (1) phenotipyc variance (σ^2_p) = MSt/r, (2) genotypic variance (σ^2_g) = (MSt–MSe)/r, (3) phenotypic covariance (COV_{p1p2}) = MSPt/r, (4) genotypic covariance (COV_{g1g2}) = (MSPt–MSPe)/r, (5) phenotypic coefficient of variation (PCV) = ($\sqrt{\sigma^2_p}/\mu$), (6) genotypic coefficient of variation (GCV) = ($\sqrt{\sigma^2_g}/\mu$), (7) heritability in broad sense (H) = (σ^2_g)/(σ^2_f), (8) expected genetic advance (EGA) = k x H x $\sqrt{\sigma^2_p}$, (9) genetic advance (GA) = (EGA/μ), (10) phenotypic correlation = COV_{p1p2} / $\sqrt{(\sigma^2_{p1})}$ (σ^2_{p2}), and (11) genotypic correlation = COV_{g1g2} / $\sqrt{(\sigma^2_{g1})}$ (σ^2_{g2}), where: μ = average value of character; k = 2,06, value of selection differential at 5% selection intensity; r = number of replications; MSt = value of means square treatment; MSe = value of means square error; MSPt = value of means square product of treatment; and MSPe = value of means square product of error.

Clustering Analysis

Principle Component Analyses (PCA) is one of multivariate analyses widely used in plant breeding, especially in determining genetic parameters, as done by Maji and Shaibu (2012), Khodadadi *et al.* (2011), Eticha *et al.* (2010), Makinde and Ariyo (2010), Wardiana and Pranowo (2010), and Nikhila *et al.* (2008). Clusterization of genotypes was based on the Average Linkage-Between Group of Squared Euclidean Distance method using SPSS version 17, as done by Kawuki *et al.* (2011) and Geleta and Labuschange (2005). This clustering method is the most commonly used statistics for estimating genetic distance between individuals (population or genotype) by morphological data (Mohammadi and Prasanna 2003).

RESULTS AND DISCUSSION

Estimated Values of Genotypic Coefficient of Variation and Heritability

An analysis of variance for all variables showed that the eleven genotypes of robusta coffee varied in phenotypic performances of bean physical quality characters (Table 3). Because the phenotypic performances were affected by genotype and environment interaction, the data were further analysed to separate the values of genotypic, phenotypic, and environmental variances. And then, based on the estimated values of genotypic coefficient of variation (GCV) and genetic advance (GA), five clusters were identified representing very low, low, moderate, high and very high for both genetic parameters, based on Murdaningsih *et al.* (1990) (Table 2).

The estimated values of GCV ranged from 0.15 to 1.81, and classified as very high for characters of PN_SS_N and PW_SS_N (Table 3). It indicates the differences in genotypic value, of individuals in the population, and the magnitude of potency and probability of success of the selection if applied based on those characters. The higher the GCV value, the higher the probability of the success of selection (Falconer and Mackay 1996; Ali *et al.* 2008). The magnitude of genetic variability determines the effectiveness of selection; the greater the variability among the genotypes, the better the chance for

Table 2. Frequency distribution for genotypic coefficient of variation (GCV) and genetic advance (GA) values of eleven genotypes of robusta coffee, West Lampung, 2010-2012.

Categories	Interval class	
	GCV	GA
Very low (VL)	0.15-0.47	0.29-0.93
Low (L)	0.48-0.80	0.94-1.58
Moderate (M)	0.81-1.13	1.59-2.23
High (H)	1.14-1.46	2.24-2.90
Very high (VH)	1.47-1.80	2.91-3.55

Table 3. Values of means square of treatments, range, average, and genetic parameters of 12 beans physical quality characters of eleven genotypes of robusta coffee, West Lampung, 2010-2012.

Code of chahracters	Means square of treatment	Range	Average (%) ± standard error	Genetic parameters				
				Phenotypic variance	Genotypic variance	GCV	H	GA
PN_LS_N	143.20**	22.60 - 52.75	37.69 ± 1.28	47.73	43.30	0.17 VL	0.91	0.34 VL
PN_SS_N	30.26**	0.00 - 15.18	1.77 ± 0.58	10.09	9.19	1.71 VH	0.91	3.36 VH
PN_LS_S	35.95**	2.94 - 16.18	6.08 ± 0.60	11.98	11.62	0.56 L	0.97	1.14 L
PN_SS_S	23.18**	0.00 - 10.97	2.56 ± 0.49	7.73	7.39	1.06 M	0.96	2.15 M
PN_LS_D	148.40**	8.46 - 38.22	25.41 ± 1.25	49.47	46.87	0.27 VL	0.95	0.54 VL
PN_SS_D	226.67**	7.43 - 45.21	26.49 ± 1.60	75.56	70.90	0.31 VL	0.94	0.64 VL
PW_LS_N	137.48**	29.41 - 56.47	45.03 ± 1.22	45.83	42.62	0.15 VL	0.93	0.29 VL
PW_SS_N	17.37**	0.00 - 11.74	1.27 ± 0.44	5.79	5.26	1.81 VH	0.96	3.55 VH
PW_LS_S	44.92**	3.78 - 19.32	7.59 ± 0.68	14.97	14.36	0.50 L	0.91	1.01 L
PW_SS_S	21.66**	0.00 - 10.91	2.41 ± 0.48	7.22	6.83	1.08 M	0.95	2.18 M
PW_LS_D	184.08**	8.83 - 40.90	28.09 ± 1.37	61.36	58.88	0.27 VL	0.95	0.55 VL
PW_SS_D	70.47**	7.71 - 29.05	14.26 ± 0.86	23.49	22.83	0.34 VL	0.97	0.68 VL
Average	-	- - 30.16	28.340.69	0.95	1.37			

** = significant at 1% level, VL = very low, L = low, M = moderate, VH = very high, GCV = genotypic coefficient of variation, H = heritability, GA = genetic advance

further improvement of the crop (Subhaschandra *et al*. 2009). Information on the nature and magnitude of variability is an important prerequisite for systematic breeding programs to improve yield potential of the crop. Progress in improvement of a crop depends on the degree of variability in the desired characters in the base materials (Ganapathy *et al*. 2011). Progress of breeding in quantitative characters is primarily influenced by the magnitude and nature of variation, and success in crop selection, breeding and bio-engineering is also depended on the isolation of genetically superior genotypes based on the amount of variability present in the materials (Akhtar *et al*. 2007).

If the selection is solely based on the value of GCV, it would be difficult to determine the variability decreases. High value of GCV suggested better improvement for selection of traits. However, estimation of heritable variation supported with genetic coefficient of variation alone may be misleading (Roychowdhury and Tah 2011). Therefore, more information on the another genetic parameters is needed, such as H values. The estimated H values for all characters could be categorized as high (> 0.90) (Table 3), indicated that the phenotypic performance of the 12 characters of beans physical quality of robusta coffee was mainly influenced by genetics factors rather than environment factors. H values > 0.90 mean that the value of genotypic variance approximate to the value of phenotypic variance, because mathematically the H value is the ratio of the genotypic and the phenotypic variance (Falconer and Mackay 1996).

The estimated H value provides a broader information about character variation that can be passed to offspring, a good predictor of expected response from the selection, and shows the effectiveness of the selection of genotypes based on their phenotypic performance. It also provides authentic information about the faithfulness by which a particular genetic attribute will be passed down to the successive generation (Akhtar *et al*. 2007; Khan *et al*. 2007; Selvaraj *et al*. 2011; Ghazy *et al*. 2012). The higher the H value, the simpler the selection process and the greater the response on selection (Akhtar *et al*. 2007; Soomro *et al*. 2008; Roychowdhury and Tah 2011). In general, the H concept is very useful for plant breeding because it is applicable to all breeding situation, including selection within randomly-mating cross pollinated population, as well as selection among self-fertilization lines (with or without subsequent random-mating), selection among clones, and selection among test cross progenies in hybrid crops (Holland *et al*. 2003).

Estimated Value of Genetic Advance

Beside the estimated values of GCV and H in the selection process, many breeders considered the magnitude of genetic advance (GA) above the population means. GA is a product of selection differential values

(k), square root of phenotypic variance ($\sqrt{\sigma^2_p}$) as a determinant of the potency of selection progress, while H is a determinant of the efficiency of selection system (Singh dan Chaudhary 1979; Falconer and Mackay 1996). GA can predict the value of expected progress from the selection above the population means (Khan *et al*. 2007; Ghazy *et al*. 2012).

The estimates of H value helps the plant breeder in selection of elite genotypes from divergent populations, but H itself does not provide any indication towards the amount of genetic progress, rather it depends upon the amount of GA (Ganapathy *et al*. 2011). H along with GA should be jointly considered to arrive at a more reliable conclusion (Johnson *in* Chand *et al*. 2008), and availability of good knowledge of both genetic parameters in different yield parameters is a prerequisite for effective plant improvement (Haq *et al*. 2008). Therefore, the selection will be effective when the values of GCV and H are supported by GA. Shukla *et al*. (2005) argued that if the selection was only based on the value of H alone, unsupported by GA, it would not obtain a significant progress.

The estimated values of GA ranged from 0.29 to 3.55 (Table 3). The estimated values of GA for PN_SS_N and PW_SS_N were categorized as very high (Table 3), and it was consistent with the category of GCV for those characters discussed previously. Therefore, based on the value of genetic parameters of GCV, H and GA for PN_SS_N and PW_SS_N characters, improvement of single-size normal bean characters of robusta coffee had high probability of success by selection. Higher GCV value will increase the probability of success in obtaining desired superior genotypes. Furthermore, it was supported by the high value of H which indicated that the two characters observed were mainly controlled by genetic factors so they would easily passed to offspring. Lastly, it was supported by very high value of GA which indicated that the two characters had high response on selection, so the selection will be more effective and efficient.

The high value of GA in one character showed the effectiveness of selection on that character and the GA parameters were controlled by additive genes (Shukla *et al*. 2005; Akhtar *et al*. 2007; Govindaraj *et al*. 2010). Other studies suggested that several plant characters with high values in H and GA were affected by the additive genes, and selection for those characters would be effective and could be applied in early generations. Conversely, if the value of H was high but low in GA, it indicated non-additive gene effect, and selection for improvement of those characters was relatively limited and must be done on the next generation (Ali *et al*. 2008; Govindaraj *et al*. 2010; Hefny 2011; Roychowdhury and Tah 2011).

Clustering Genotypes

Based on Table 3, the estimated values of GCV and GA on the six characters for both percentage value (percentage of number and percentage of weight) were identical. This is also confirmed by the positive significant correlation of the phenotypic and genotypic characters (Table 4). Therefore, the PCA as preliminary analysis for clustering genotypes was performed only on the six characters of percentage of number.

Result of PCA obtained two principal components (PC). The first PC consisted of three characters (PN_SS_D, PN_LS_S, and PN_LS_N) labeled with the small size defect bean and negatively correlated with the large size normal and single bean. The second PC consisted of three characters (PN_LS_D, PN_SS_N, and PN_SS_S) labeled with the large size defect bean and negatively correlated with the small size normal and single bean (Table 5).

Table 4. Phenotypic and genotypic correlation for percentage of number and percentage of weight of eleven genotypes of robusta coffee, West Lampung, 2010-2012.

Correlated characters	Phenotypic correlation	Genotypic correlation
(PN_LS_N) and (PW_LS_N)	0.89**	0.91**
(PN_SS_N) and (PW_SS_N)	0.99**	0.99**
(PN_LS_S) and (PW_LS_S)	0.99**	0.96**
(PN_SS_S) and (PW_SS_S)	0.70*	0.99**
(PN_LS_D) and (PW_LS_D)	0.96**	0.97**
(PN_SS_D) and (PW_SS_D)	0.88**	0.96**

* and ** significant at 5% and 1% level, respectively

Table 5. Loading value for each principle component analysis of eleven genotypes of robusta coffee, West Lampung, 2010-2012.

Code of characters	Principal components	
	1	2
PN_SS_D	**-0.92**	-0.12
PN_LS_S	**0.88**	0.07
PN_LS_N	**0.47**	0.44
PN_LS_D	-0.01	**-0.94**
PN_SS_N	0.12	**0.81**
PN_SS_S	0.61	**0.67**

Bold numbers in the same column are the members of the relevant components.

Cluster analysis by Average Linkage-Between Group of Squared Euclidean Distance method had been applied on the values of factor score for each PC and resulting dendogram for each cluster (Fig.1). By assuming the cut-points in the rescaled distance cluster combined about 5.0 then three clusters were formed. Cluster I consisted of nine genotypes (BP 288, BP 418, BP 936, BP 42, BP 234, BP 534, BP 436, BP 939, and BP 358), and cluster II and III respectively consisted of one genotype (BP 308 and AEGAWA). Each genotype in the same cluster indicated genetic similarities, on the contrary genotypes in different clusters indicated genetic dissimilarities.

All clones of robusta coffee with initial names of BP in cluster I and II are the superior genotypes (first to third generation) derived from the same parent materials introduced from Congo (Baon 2011). The genotype of BP 308 (cluster II) has a specific trait which is resistant to nematodes (Baon 2011; Puslitkoka 2003). While, the genotype of AEGAWA (cluster III) is the specific-location genotype from West Lampung resulted from idividual selection by AICE.

Result of the comparison between clusters based on the percentage of number was identical to the percentage of weight (Table 6) due to the phenotypic and genotypic positive correlation among these characters (Table 4). Therefore, it could be concluded that genotypes in cluster I were highest in large size and small size defect beans, and lowest in small size normal beans; genotypes in cluster II were highest in large size normal beans, highest in large size and small size single beans, and lowest in large size defect beans; and genotypes in clusters III were highest in small size normal and defect beans (Tabel 7). The implication of this analysis for the future coffee breeding program, especially for hybridization, is that the hybridization should be applied between different

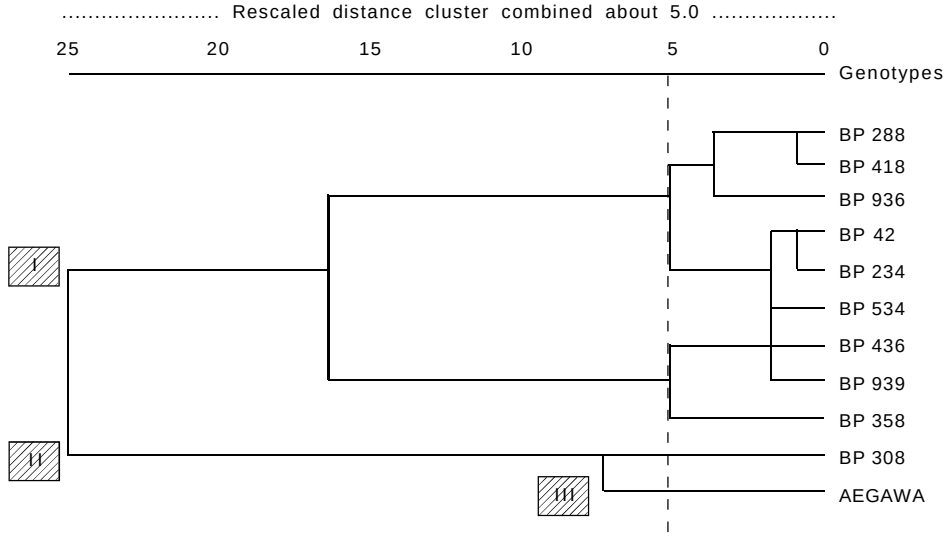

Fig. 1. Dendogram for eleven genotypes of robusta coffee based on the Average Linkage Between Group of Squared Euclidean Distance Method, West Lampung, 2010-2012.

Table 6. Comparison among clusters based on beans physical quality characters of eleven genotypes of robusta coffee, West Lampung, 2010-2012.

Cluster	Percentage of number						Percentage of weight					
	PN_LS_N	PN_SS_N	PN_LS_S	PN_SS_S	PN_LS_D	PN_SS_D	PW_LS_N	PW_SS_N	PW_LS_S	PW_SS_S	PW_LS_D	PW_SS_D
I	36.45b	0.55c	5.80b	1.61b	27.92a	27.67a	44.11b	0.36c	7.25b	1.49b	30.95a	14.74a
II	49.22a	3.76b	9.96a	9.31a	9.59c	18.16b	54.03a	2.44b	12.05a	9.21a	9.67c	9.98b
III	37.30b	10.79a	4.82b	4.34b	18.63b	24.13a	44.31b	8.21a	6.20b	3.90b	20.75b	14.21a
Average	36.41	3.19	7.69	4.36	22.49	26.06	42.51	2.32	9.54	4.16	25.17	14.77

Numbers in each column followed by the same letter are not significantly different based on the Student-t test at 5% level.
Numbers underlined indicate the highest or the lowest percentage value.

Table 7. Characteristics of each cluster of eleven genotypes of robusta coffee based on beans physical quality characters.

Cluster	Beans physical quality characters					
	Large-size normal beans	Small-size normal beans	Large-size single beans	Small-size single beans	Large-size defect beans	Small-size defect beans
I	-	<<	-	-	>>	>>
II	>>	-	>>	>>	<<	-
III	-	>>	-	-	-	>>

Notes: >> the highest percentage; << the lowest percentage

genotypes from different clusters to obtain high heterosis effects.

Factor analysis, cluster analysis and other multivariate statistical methods are useful for estimating the morphological variability within and between germplasm collections. These analysis are also useful to evaluate the value of potential breeding and able to detect the significant differences as well as the magnitude of deviation of germplasm collections (Maji and Shaibu 2012). In crop improvement program, clustering genotypes based on quality and agronomic characters, and then analyzed by multivariate analysis techniques (including PCA) apparently will save time and cost. Similarly, for the stability analysis involving multiple genotypes and different characters in different locations and years (Ethica *et al*. 2010).

CONCLUSION

The estimated values of genotypic coefficient of variation, heritability and genetic advance for small-size normal bean characters of robusta coffee were very high, so the genetic improvement for these characters has a high probability of success by direct selection. Clusterization analysis of the genotypes resulted three clusters with their respective characteristics. It implicates for future breeding program, especially for hybridization, that should be conducted between genotypes from different clusters to obtain high heterosis effects.

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