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Morphological Variation in Arabica Coffee (*Coffea arabica* L.) Growing in North Sumatra Indonesia

Variasi Morfologi Kopi Arabica (Coffea arabica L.) yang Tumbuh di Sumatera Utara Indonesia

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ABSTRACT

*Genetic variation is important in plant breeding. However, information on the genetic variability of Arabica coffee especially in coffee field of North Sumatra was not yet available. Magnitude of morphological variation, genotypic variation, phenotypic variation, heritability, genetic advance, genetic correlation, and phenotypic correlation of plant vigors and yield components of 28 genotypes were evaluated using nested design. This research showed morphological and genetic variations of the genotypes in the field. Based on the research locations as operational taxonomic unit, the genotypes were separated into three clusters. Most of the parameters had low to moderate genotypic variation, while phenotypic variation was moderate to high. Heritability and genetic advance were low, moderate, and high. Several plant vigors and yield components had a positive significant genetic and phenotypic correlation one another, and several had negative ones. Coffee berry borer infestation (CBBI) had a highly significant negative genetic correlation with leaf width (r_G = -0.309**), leaf weight (r_G = -0.671**), fruit diameter (r_G = -0.320**), and bean length (r_G = -0.175**). CBBI showed a significant positive genetic correlation with mesocarp pH (r_G = 0.134*). To reduce CBBI, selection for higher leaf weight is better. Selection on lower pH of mesocarp could be considered to decrease CBBI.*

Keywords: cluster analysis, genetic correlation, genetic heritability, variability

ABSTRAK

*Variasi genetik merupakan dasar bagi pemuliaan tanaman. Akan tetapi, informasi tentang variabilitas genetik kopi Arabica yang ditemukan di ladang kopi di Sumatera Utara belum tersedia. Variasi morfologi, variasi genotipik, variasi fenotipik, heritabilitas, kemajuan genetik, korelasi genetik, dan korelasi fenotipik dari vigor tanaman dan komponen produksi dari 28 genotipe kopi Arabica diteliti dengan menggunakan rancangan tersarang. Penelitian ini menunjukkan variasi morfologis dan genetik dari genotipe. Berdasarkan lokasi penelitian sebagai unit taksonomi operasional, genotipe menyebar ke dalam tiga kluster. Hampir semua parameter mempunyai variasi genetik yang rendah hingga sedang, sedangkan variasi fenotipik sedang hingga tinggi. Heritabilitas dan kemajuan genetik rendah, sedang dan tinggi. Beberapa vigor tanaman dan komponen produksi mempunyai korelasi genetik dan fenotipik yang positif dan signifikan satu dengan lainnya, sedangkan beberapa lainnya memiliki korelasi yang negatif. Infestasi penggerek buah kopi (CBBI) menunjukkan korelasi genetik yang sangat signifikan dan negatif dengan lebar daun (r_G = -0.309**), bobot daun (r_G = -0.671**), diameter buah (r_G = -0.320**), dan panjang biji (r_G = -0.175**). CBBI mempunyai korelasi genetik yang signifikan dan positif dengan pH daging buah (r_G = 0.134*). Untuk mengurangi CBBI, lebih baik memilih tanaman dengan bobot daun yang berat. Tanaman dengan pH daging buah yang rendah dapat dipilih untuk mengurangi CBBI.*

Kata kunci: analisis kluster, heritabilitas, keragaman genetik, korelasi genetik

INTRODUCTION

Arabica coffee (*Coffea arabica* L.) was cultivated for the first time around 120 years ago in North Sumatra. In Indonesia, North Sumatra is one of the most important production center of Arabica coffee. Indonesia produced 189,834 tons of Arabica coffee beans in 2016, of which North Sumatra contributed 53,237 tons green beans per year (DGEC, 2017). A total of 63,339 ha of Arabica coffee growing areas are located in North Sumatra, which become source of livelihood for 143,061 coffee farmers. In recent years, Arabica coffee cultivation is facing climate change (Sudradjat, 2010) which can be seen at coffee plantation in nine districts of North Sumatra with the altitude between 800 to 1,600 m above sea level (asl). This environmental

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pressures might create genetic mutation lead to genetic variation.

Although Indonesian Goverment has released several commercial cultivars, empirical facts showed that many of coffee farmers are still using traditional seeds from unknown resources for their new cultivation field which might cause low coffee productivity (1.14 ton ha^{-1} of green bean), and might cause genetic variation among farmers' land. Low productivity could also be affected by soil fertility (Hanisch *et al*., 2011) and coffee berry borer (CBB) attact which is considered as one of the most destructive pest of Arabica coffee in North Sumatra.

Plant breeders require genetic variability of desirable characters to carry out the breeding programs (Mayo, 1987; Mishra and Slater, 2012; Constantin *et al*., 2017). Genetic variation of Arabica coffee can be found not only in cultivated cultivars (Setotaw *et al*., 2010; Tessema *et al*., 2011; Geleta *et al*., 2012; Fatimah *et al*., 2014; Randriani *et al*., 2014; Dani *et al*., 2016), but also in wild populations (Schmitt *et al*., 2009; Aerts *et al*., 2013; Atinafu *et al*., 2017). Previous studies done by Silvestrini *et al*. (2008) and Kathurima *et al*. (2012) exhibited that genetic variation in commercial coffee cultivar was narrow. However, another study conducted by Geleta *et al*. (2012) revealed broad genetic variation in the collection of Arabica coffee cultivars. Genetic diversity was shown to be correlated with morphological diversity (Yuan *et al*., 2015). However, information on genetic diversity of Arabica coffee derived from North Sumatra was not yet available. The aim of this research was to determine morphological and genetic variations of Arabica coffee at coffee plantations in North Sumatra.

MATERIALS AND METHODS

The research was carried out in District Tapanuli Utara, Toba Samosir, Humbang Hasundutan, Samosir, Simalungun, Pakpak Bharat and Dairi, North Sumatra Province. Data was collected in July 2014. The nested design with three factors was used for data analysis (Quinn and Keough, 2002). The first step was to select 7 districts, then 2 sub-districts were chosen in each district, and the final step was to select 2 coffee farms in each sub-district. These selected coffee farms were treated as genotypes (G). Each farm consisted of 200-300 plants of variety Sigarar Utang which is Arabica coffee. The plants were 6-7 years old, with the characteristics of having a shot of bronze-colored leaves, ripe fruits, and harvest frequency of once in two weeks. Ten plants were selected randomly in each farm. In total, twenty eight genotypes of Arabica coffee were used to determine morphological and genetic variation in this study. Mesocarp pH was measured using pH meter (Amtast KS-05 vergara). A fruit showing the frass on the entrance hole is a CBB infected fruit which is caused by females of CBB live inside the fruit after boring a hole at dictus or near the dictus (Vega *et al*., 2009). All fruits were checked. Coffee berry borer infestation (CBBI) was the ratio of the number of infected fruits to the total number of fruits (%).

Tree morphology comprises plant vigor (plant height, leaf length, leaf width, leaf weight), yield components (100 fruits weight, fruit length, fruit diameter, mesocarp thickness, mesocarp pH, 100 parchments weight, parchment length, parchment width, parchment thickness, 100 beans weight, bean length, bean width, bean thickness), and coffee berry borer infestation (CBBI) (Wahyudi *et al*., 2016). All data were analyzed with the hierarchical cluster analysis using nearest neighbour cluster method measured with squared Euclidean distance. In the analysis, research location was used as operational taxonomic unit (OTU) while coffee morphology were treated as variables.

The additive effect model for the nested design with three factors was $Y_{ijkl} = \mu + D_i + S_{j(i)} + G_{k(j(i))} + E_{l(k(j(i)))}$ where Y_{ijkl} = *ijkl*th observation, μ = general mean, D_i = effect for *i*th districts, $S_{j(i)}$ = effect for *j*th sub-districs within *i*th districts, $G_{k(j(i))}$ = effect for *k*th genotype within *j*th sub-districts within *i*th districts, and $E_{l(k(j(i)))}$ = error (Quinn and Keough, 2002). Estimated variance component (EVC) for phenotype = $s^2_P = s^2_G + s^2_E$ (Table 1). Genotypic coefficient of variation (GCV) = $((s^2_G)^{0.5}/m) \times 100\%$, and phenotypic coefficient of variation (PCV) = $((s^2_P)^{0.5}/m) \times 100\%$ where m = mean of phenotype (Mayo, 1987). Coefficient of heritability in broad sense (H^2_{bs}) = $H^2_{bs} = s^2_G/s_P{}^2$. Estimated genetic advance (GA) = $i \times (s^2_P)^{0.5} \times H^2_{bs}$. Then, GAM as expression of GA in percentage of mean (m) = (GA/m) x 100% where i = 2.063 at selection intensity 5% (Mayo, 1987). GCV, PCV and GAM were stated as low (<5%), moderate (5-10%), and high (>10%). H^2_{bs} was defined as low (40%), moderate (40-60%), and high (>60%). Genetic correlation coefficient r_{Gxy} between two phenotypes (x and y) = $r_{Gxy} = cov_{G(xy)}/(\sigma^2_{Gx} \times \sigma^2_{Gy})^{0.5}$ while phenotypic correlation coefficient r_{Pxy} between two = $cov_{p(xy)}/(\sigma^2_{Px} \times \sigma^2_{Py})^{0.5}$ whereby cov_{Gxy} was genetic covariance between phenotypes x and y, and cov_{Pxy} was phenotypic covariance between phenotypes x and y (Mayo, 1987). The significance of the correlation coefficients r_{Gxy} and r_{Pxy} was compared to critical r tabular value at $\alpha = 0.05$ and $\alpha = 0.01$ using the degree of freedom of the error (Quinn and Keough, 2002). IBM SPSS version 19 and Microsoft Excel version 2007 was used for data analysis.

RESULTS AND DISCUSSION

The cluster dendrogram showed morphological variation among research locations (Figure 1). Gichimu and Omondi (2010) found the correlation between morphological variation with genetic variation of coffee genotypes. Genotypes were significantly different in plant vigor, yield components, and CBBI (Table 2).

This research found low and moderate genetic variation in several plant vigor and yield components while high one in CBBI (Table 3). The results of this research might be generally in line with Kitila *et al*. (2011) and Beksisa and Ayano (2016) who found low, moderate and high genetic variation in fruit length and fruit diameter, plant height, bean length, and bean width. Tessema *et al*. (2011) found the similar result in bean weight but Kitila *et al*. (2011) revealed high genetic variation in bean weight. Low and moderate genotypic variation in most of the parameters might indicate the nature of self-fertilized coffee plants. Broad genetic variability must be obtained through hybridization.

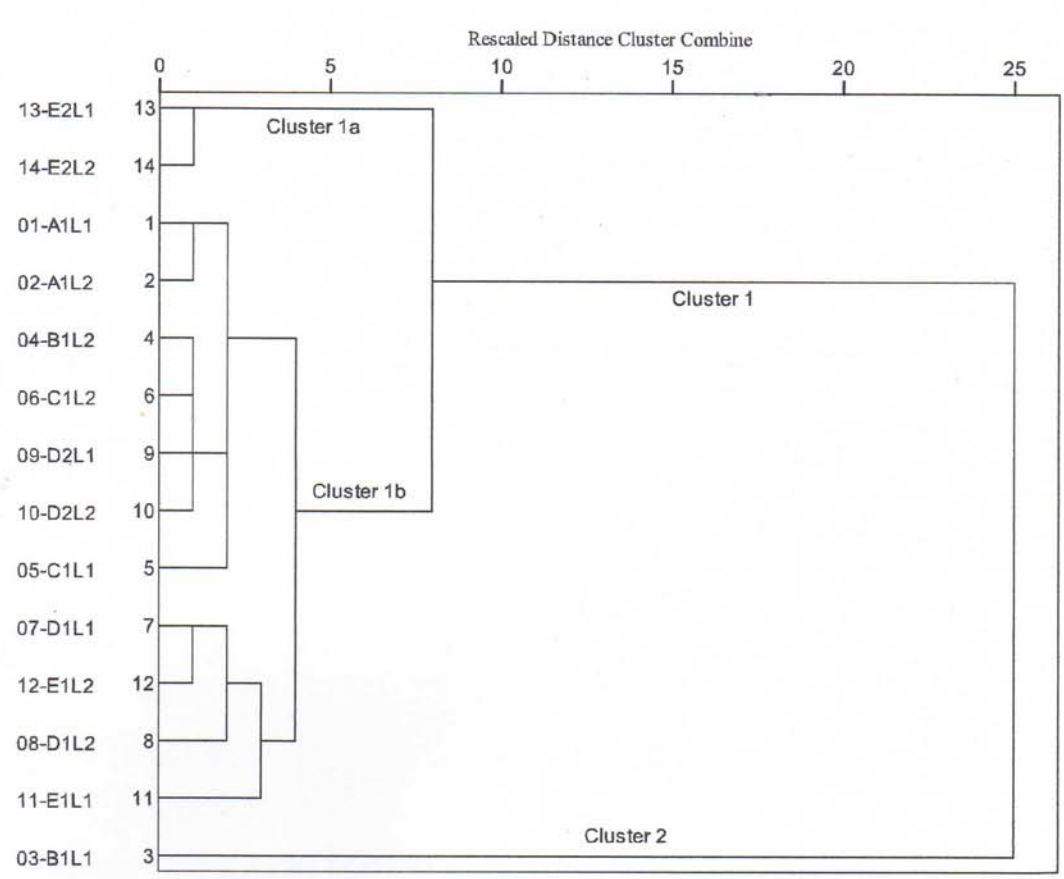

Figure 1. Cluster analysis based on 14 locations using 18 morphological variables of the genotypes of Arabica coffee

Note: 01-A1L1 = Location 1 (Sub-district Parlilitan 1 in District Humbanghas), 02-A1L2 = Location 2 (Sub-district Parlilitan 2 in District Humbanghas), 03-B1L1 = Location 3 (Sub-district Dolok Pangaribuan in District Simalungun), 04-B1L2 = Location 4 (Sub-district Tanjung Dolok in District Simalungun), 05-C1L1 = Location 5 (Sub-district Kerajaan in District Pakpak Bharat), 06-C1L2 = Location 6 (Sub-district Tinada in District Pakpak Bharat), 07-D1L1 = Location 7 (Sub-district Pangururan in District Samosir), 08-D1L2 = Location 8 (Sub-district Ronggur Nihuta in District Samosir), 09-D2L1 = Location 9 (Sub-district Parbuluan 1 in District Dairi), 10-D2L2 = Location 10 (Sub-district Parbuluan 2 in District Dairi), 11-E1L1 = Location 11 (Sub-district Siborong-borong in District North Tapanuli), 12-E1L2 = Location 12 (Sub-district Sipaholon in District North Tapanuli), 13-E2L1 = Location 13 (Sub-district Uluan in District Tobasa), 14-E2L2 = Location 14 (Sub-district Sigumpar in Tobasa)

Plant vigor and yield components showed moderate to high phenotypic variation (Table 3). The results of this research supported Kittila *et al*. (2011) and Beksisa and Ayano (2016) who found moderate to high phenotypic variation in plant height, fruit diameter, bean length and bean width. In contrary to this research, low phenotypic variation in fruit length and high phenotypic variation in bean weight were found by Kitila *et al*. (2011) and Tessema *et al*. (2011).

This research showed low, moderate, and high heritability in several plant vigor component and yield components (Table 3). High heritability was manifested by leaf weight, fruit weight, mesocarp pH, parchment weight, and CBBI. These research results were in line with Kitila *et al*. (2011) who found high heritability in plant height, fruit length, fruit diameter, bean weight, bean length and bean width. However, Kitila *et al*. (2011) found high heritability in plant height, fruit length, fruit diameter, bean weight, bean length and bean width while Bekisa and Ayono (2016) revealed low heritability in plant height, and Tessema *et al*. (2011) found high heritability in bean weight.

This research revealed low to high genetic advance in several plant vigor components and yield components (Table 3). In contrary to this result, Kitila *et al*. (2011) and Bekisa and Ayono (2016) found moderate genetic advance in several plant vigor and yield components. Kitila *et al*. (2011) and Tessema *et al*. (2011) found high genetic advance bean weight. Two-thirds (66.7%) of the parameters had low to moderate genetic advance. This might relate to narrow genotypic variation of the existing coffee cultivars as self-fertilized coffee plants.

This research found that all plant vigor components (plan height, leaf length, leaf width, leaf weight) had a high significant genetic correlation (Table 4). Genetic correlation between several vigor parameters one another and with yield components was also found by Kitila *et al*. (2011). Selection for leaf weight would be the first priority to increase resistance of plant against CBB. The selection could be possible to be carried out successfully due to high heritability. The lower pH of mesocarp was the less CBBI was. Consequently, selection for lower pH of mesocarp could decrease CBBI. The selection could be conducted

Table 1. Estimation of variance analysis for nested design with factors district (p = 7 levels), subdistrict within district (q = 2 levels) and genotype within subdistrict within district (r = 2 levels) and sample (n = 10)

Source of variation	df	MS	F-ratio	EMS	EVC
District (D)	p -1	MS_D	$MS_D/MS_{S(D)}$	$\sigma^2_E + n\sigma^2G + nr\sigma^2_S + nrq\sigma^2_D$	$s^2_D = (MS_D - MS_{S(D))}/nrq$
Subdistrict nested in District (S(D))	p(q-1)	$MS_{S(D)}$	$MS_{S(D)}/MS_{G(S(D))}$	$\sigma^2_E + n\sigma^2_G + nr\sigma^2_S$	$s^2_S = (MS_{S(D)} - MS_{G(S(D))}/nr$
Genotype nested subdistrict nested in district (G(S(D)))	pq(r-1)	$MS_{G(S(D)}$	$MS_{G(S(D))}/MS_{Error}$	$\sigma^2_E + n\sigma^2_G$	$s^2_G = (MS_{G(S(D))} - MS_{Error)}/n$
Residual	pqr(n-1)	MS_{Error}		σ^2_E	$s^2_E = MS_{Error}$

Note: df = degree of freedom, MS = mean square, EMS = expected mean square, EVC = estimated variance component, s^2_D = EVC for districts, s^2_S = EVC for sub-districts, s^2_G = EVC for genotypes, s^2_E = EVC for error = MS_{Error}. Hence, EVC for phenotype = $s^2_P = s^2_G + s^2_E$

Table 2. Analysis of variance of district, subdistrict, genotype and estimated variance components of parameters

	MS district (p = 7; df = 6)	MS subdistrict (q = 2; df = 7)	MS genotype (r = 2; df = 14)	MS error (df = 252)	F-ratio for district	F-ratio for subdistrict	F-ratio for genotype	s^2_D	s^2_S	s^2_G	s^2_E	s^2_P
PH	0.05	0.04	0.04	0.01	1.23ns	1.08ns	3.91**	0.000	0.000	0.003	0.01	0.01
LL	50.05	11.52	11.42	0.72	4.35*	1.01ns	15.96**	0.96	0.01	1.07	0.72	1.79
LWi	4.20	2.17	1.94	0.20	1.94ns	1.12ns	9.91**	0.05	0.01	0.17	0.20	0.37
LWe	1.49	0.27	0.15	0.01	5.44*	1.88ns	16.44**	0.03	0.01	0.01	0.01	0.02
HFW	6,888.10	1,101.50	786.30	48.08	6.25*	1.40ns	16.35**	144.70	15.76	73.82	48.08	121.90
FL	0.80	0.09	0.08	0.02	9.00**	1.10ns	3.26**	0.02	0.000	0.01	0.02	0.03
FD	0.11	0.02	0.02	0.01	5.22*	1.01ns	2.20**	0.002	0.000	0.001	0.01	0.01
MT	0.90	0.19	0.11	0.03	4.70*	1.81ns	3.26**	0.02	0.004	0.01	0.03	0.04
MpH	3.14	2.25	1.92	0.09	1.39ns	1.17ns	21.55**	0.02	0.02	0.18	0.09	0.27
HPW	814.8	167.20	155.70	8.22	4.87*	1.07ns	18.95**	16.19	0.57	14.75	8.22	22.97
PL	0.19	0.03	0.02	0.004	6.12*	1.47ns	5.30**	0.004	0.001	0.002	0.004	0.01
PWi	0.16	0.02	0.004	0.003	8.30**	4.33**	1.43ns	0.003	0.001	0.000	0.003	0.003
PT	0.02	0.01	0.01	0.003	4.47*	1.02ns	1.84*	0.001	0.000	0.000	0.003	0.003
HBW	38.77	9.16	4.70	0.80	4.23*	1.95ns	5.84**	0.74	0.22	0.39	0.80	1.19
BL	0.04	0.01	0.01	0.003	2.79ns	1.44ns	3.35**	0.001	0.000	0.001	0.003	0.003
BWi	0.01	0.003	0.003	0.001	3.74ns	1.03ns	3.00**	0.000	0.000	0.000	0.001	0.001
BT	0.01	0.002	0.001	0.001	3.40ns	1.94ns	1.16ns	0.000	0.000	0.000	0.001	0.001
CBBI	6,146.50	1,077.80	1,011.70	16.31	5.70*	1.07ns	62.03**	126.70	3.30	99.54	16.31	115.90

Note: PH = plant height (m), LL = leaf length (cm), LWi = leaf width (cm), LWe = leaf weight (g), HFW = 100 fruits weight (g), FL = fruit length (cm), FD = fruit diameter (cm), MT = mesocarp thickness (cm), MpH = mesocarp pH, HPW = 100 parchments weight (g), PL = parchment length (cm), PWi = parchment width (cm), PT = parchment thickness (cm), HBW = 100 beans weight (g), BL = bean length (cm), BWi = bean width (cm), BT = bean thickness (cm), CBBI = coffee berry borer infestation (%). For districts, F-table at α 0.05 = 3.87 and at α 0.01 = 7.19. For sub-districts, F-table at α 0.05 = 2.77, and at α 0.01 = 4.28. For genotypes, F-table at α 0.05 = 1.73 and at α 0.01 = 2.15, ns = not significant, * = significant at α 0.05, ** = highly significant at α 0.01

successfully due to moderate genetic variation. This selection may be combined with selection for yield in the first high-yield year (Oliveira *et al*., 2010).

This research revealed that several plant vigor and yield components phenotypically correlated each others (Table 4). Kitila *et al*. (2011), Rodrigues *et al.* (2012), and Gessese *et al*. (2015) found a phenotypic correlation between several plant vigor parameters and yield components.

In the future research, it would be necessary to examine how pH of mesocarp could affect CBBI. Lower pH might cause an unpleasant taste for CBB. Lower pH might affect certain chemical substances in coffee fruit so that the pest

Table 3. Genetic components of parameters

Parameter	Minimum	Maximum	Mean	s_d	GCV (%)	PCV (%)	H^2_{bs} (%)	GA	GAM (%)
PH	1.41	1.72	1.63	0.03	3.3	7.0	22.6	0.05	3.3
LL	10.73	16.32	14.40	0.27	7.2	9.3	59.9	1.65	11.5
LWi	4.54	6.54	5.69	0.14	7.4	10.7	47.1	0.59	10.4
LWe	1.16	1.87	1.57	0.03	7.4	9.6	60.7	0.19	12.0
HFW	141.24	201.19	166.40	2.19	5.2	6.6	60.6	13.79	8.3
FL	1.34	1.96	1.63	0.05	4.6	10.7	18.4	0.07	4.1
FD	1.17	1.44	1.31	0.03	2.6	7.9	10.8	0.02	1.8
MT	0.75	1.52	1.15	0.06	7.5	17.4	18.4	0.08	6.6
MpH	4.19	5.42	4.80	0.09	8.9	10.9	67.3	0.72	15.1
HPW	40.65	59.87	50.53	0.91	7.6	9.5	64.2	6.35	12.6
PL	1.19	1.45	1.30	0.02	3.2	5.8	30.1	0.05	3.6
PWi	0.81	1.08	0.87	0.02	1.3	6.5	4.2	0.00	0.6
PT	0.59	0.61	0.57	0.02	2.8	9.9	7.7	0.01	1.6
HBW	13.81	14.38	13.96	0.28	4.5	7.8	32.6	0.74	5.3
BL	0.85	1.04	0.94	0.02	2.7	6.2	19.0	0.02	2.5
BWi	0.66	0.77	0.70	0.01	2.1	5.1	16.7	0.01	1.8
BT	0.34	0.39	0.37	0.01	1.0	8.0	1.6	0.001	0.3
CBBI	0.31	61.87	17.33	1.28	57.6	62.1	85.9	19.08	110.1

Note: PH = plant height (m), LL = leaf length (cm), LWi = leaf width (cm), LWe = leaf weight (g), HFW = 100 fruits weight (g), FL = fruit length (cm), FD = fruit diameter (cm), MT = mesocarp thickness (cm), MpH = mesocarp pH, HPW = 100 parchments weight (g), PL = parchment length (cm), PWi = parchment width (cm), PT = parchment thickness (cm), HBW = 100 beans weight (g), BL = bean length (cm), BWi = bean width (cm), BT = bean thickness (cm), CBBI = coffee berry borer infestation (%), sd = standard deviation, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, H^2_{bs} = coefficient of heritability in broad sense, GA = genetic advance, GAM = genetic advance in percentage of mean

would stop drilling the fruit of coffee. Coffee genotypes and species might be different in chemistry whereby some of the chemotypes were shown to be insecticidal (Green *et al*., 2015). It would be also important to examine whether this pest could adapt to lower pH. This pest could evolve to high caffeine content so that caffeine was no longer toxic to this pest (Filho and Mazzafera, 2003).

Table 4. Genetic (r_G) and phenotypic (r_p) correlation coefficient

		LL	LWi	LWe	HFW	FL	FD	MT	MpH	HPW	PL	PWi	PT	HBW	BL	BWi	BT	CBBI
PH	rG	-0.180 **	-0.322 **	-0.260 **	0.439 **	0.064 ns	-0.564 **	0.824 **	0.296 **	0.506 **	-0.148 *	0.320 **	0.521 **	0.475 **	0.324 **	0.363 **	0.189 **	0.327 **
PH	rP	-0.051 ns	-0.109 ns	-0.089 ns	0.146 *	0.064 ns	0.032 ns	0.248 **	0.049 ns	0.211 **	0.015 ns	0.017 ns	0.030 ns	0.149 **	0.058 ns	0.127 *	0.065 ns	0.132 *
LL	rG	1	0.868 **	0.284 **	0.188 **	0.901 **	0.310 **	0.040 ns	0.110 ns	0.346 **	0.146 *	0.900 **	0.175 **	0.224 **	0.163 **	0.205 **	0.339 **	-0.017 ns
LL	rP	1	0.590 **	0.217 **	0.091 ns	0.395 **	0.050 ns	0.076 ns	0.085 ns	0.224 **	0.045 ns	0.103 ns	0.024 ns	0.056 ns	0.042 ns	0.023 ns	-0.008 ns	-0.013 ns
LWi	rG		1	0.370 **	0.108 ns	0.705 **	0.573 **	0.092 ns	0.244 **	0.349 **	-0.124 *	0.534 **	-0.076 ns	0.167 **	0.056 ns	-0.095 ns	-0.487 **	-0.309 **
LWi	rP		1	0.228 **	0.061 ns	0.242 **	0.096 ns	0.052 ns	0.151 **	0.232 **	-0.046 ns	0.175 **	-0.043 ns	0.063 ns	0.011 ns	-0.016 ns	0.046 ns	-0.222 **
LWe	rG			1	0.190 **	-0.188 **	0.142 *	-0.074 ns	-0.206 **	-0.278 **	-0.147 *	0.235 **	-0.659 **	0.077 ns	0.241 **	0.060 ns	0.575 **	-0.671 **
LWe	rP			1	0.103 ns	-0.057 ns	0.047 ns	-0.028 ns	-0.122 *	-0.155 **	-0.078 ns	0.014 ns	-0.200 **	0.051 ns	0.020 ns	0.030 ns	0.024 ns	-0.491 **
HFW	rG				1	0.168 **	-0.380 **	0.457 **	0.079 ns	0.550 **	0.204 **	0.798 **	0.712 **	0.967 **	0.610 **	0.404 **	0.433 **	0.222 **
HFW	rP				1	0.041 ns	-0.062 ns	0.132 *	0.067 ns	0.377 **	0.111 ns	0.235 **	0.170 **	0.452 **	0.218 **	0.130 **	-0.025 ns	0.159 **

Table 4. Genetic (r_G) and phenotypic (r_p) correlation coefficient (*continued*)

		LL	LWi	LWe	HFW	FL	FD	MT	MpH	HPW	PL	PWi	PT	HBW	BL	BWi	BT	CBBI
FL	rG					1	0.507 **	0.032 ns	0.256 **	0.457 **	0.266 **	0.640 **	0.747 **	0.376 **	0.472 **	0.101 ns	-0.473 **	0.176 **
FL	rP					1	0.162 **	0.059 ns	0.066 ns	0.205 **	0.086 ns	0.126 *	0.034 ns	0.085 ns	0.063 ns	0.093 ns	0.066 ns	0.073 ns
FD	rG						1	-0.280 **	0.139 *	0.172 **	-0.085 ns	-0.320 **	-0.332 **	-0.513 **	0.622 **	-0.210 **	-0.196 **	-0.320 **
FD	rP						1	-0.103 ns	0.030 ns	0.041 ns	-0.160 **	-0.101 ns	-0.029 ns	-0.061 ns	0.108 ns	0.037 ns	0.155 **	-0.101 ns
MT	rG							1	0.353 **	0.566 **	-0.786 **	0.014 ns	0.519 **	0.520 **	-0.067 ns	-0.036 ns	0.105 ns	0.160 **
MT	rP							1	0.105 ns	0.261 **	-0.155 **	0.027 ns	0.008 ns	0.115 *	0.002 ns	0.007 ns	0.018 ns	0.070 ns
MpH	rG								1	0.374 **	-0.470 **	-0.435 **	-0.544 **	-0.089 ns	0.038 ns	-0.026 ns	-0.845 **	0.134 *
MpH	rP								1	0.236 **	-0.251 **	-0.137 *	-0.112 ns	-0.015 ns	0.014 ns	0.059 ns	-0.069 ns	0.130 *
HPW	rG									1	-0.109 ns	0.392 **	0.969 **	0.382 **	0.275 **	0.000 ns	0.364 **	0.357 **
HPW	rP									1	-0.071 ns	0.186 *	0.216 **	0.211 **	0.016 ns	0.038 ns	0.077 ns	0.272 **
PL	rG										1	0.472 **	0.329 **	0.286 **	0.524 **	0.557 **	0.527 **	0.159 **
PL	rP										1	-0.024 ns	-0.009 ns	0.019 ns	0.226 **	-0.050 ns	-0.011 ns	0.084 ns
PWi	rG											1	0.398 **	0.951 **	0.229 **	0.162 *	0.338 **	0.668 **
PWi	rP											1	0.974 **	0.172 **	-0.04 ns	0.050 ns	0.045 ns	0.126 *
PT	rG												1	0.951 **	0.229 **	-0.087 ns	0.162 ns	0.668 **
PT	rP												1	0.172 **	-0.004 ns	-0.089 ns	0.050 ns	0.126 *
HBW	rG													1	0.502 **	0.116 *	0.344 **	0.146 *
HBW	rP													1	0.128 *	0.276 **	0.188 **	0.069 ns
BL	rG														1	0.731 **	0.385 **	-0.175 **
BL	rP														1	0.074 ns	0.024 ns	-0.109 ns
BWi	rG															1	0.064 ns	0.071 ns
BWi	rP															1	0.237 **	0.025 ns
BT	rG																1	0.127 *
BT	rP																1	0.011 ns

Note: Degree of freedom = 252, r tabular at α 0.05 = 0.113, ns = not significant, * = significant at α = 0.05, r tabular α 0.01 = 0.148, ** = highly significant at α 0.01; PH = plant height (m), LL = leaf length (cm), LWi = leaf width (cm), LWe = leaf weight (g), HFW = 100 fruits weight (g), FL = fruit length (cm), FD = fruit diameter (cm), MT = mesocarp thickness(cm), MpH = mesocarp pH, HPW = 100 parchments weight (g), PL = parchment length (cm), PT = parchment thickness (cm), HBW = 100 beans weight (g), BL = bean length (cm), BWi = bean width (cm), CBBI = coffee berry borer infestation (%)

CONCLUSION

This research revealed morphological and genetic variation of the genotypes of Arabica coffee. The genotypes morphologically separated in three clusters based on the research locations. Leaf length, leaf width and leaf weight, hundred fruit weight, mesocarp thickness, mesocarp pH and hundred parchment weight showed moderate genetic variation. Plant height, fruit length, fruit diameter, parchment length, parchment width, parchment thickness, hundred bean weight, bean length, bean width and bean thickness had low genetic variation. Because leaf weight had significant negative genetic correlation with coffee berry borer infestation, selection for higher leaf weight

would be the best selection criterion to improve resistance of coffee against coffee berry borer. In future research, it could be needed to examine how pH of mesocarp could affect CBBI. Coffee hybridization is needed to obtain broad genetic diversity and big genetic advance.

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