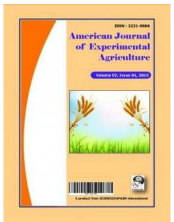

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Combining Ability of Cocoa (*Theobroma cacao* L) Clones and Variability for Morphological Traits among Hybrids

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Authors' contributions

This work was carried out in collaboration between all authors. Authors GUA and DBA designed the study and wrote the protocol. Author GUA wrote the first draft of the manuscript. Authors MOA and DBA reviewed the experimental design. Authors DBA and MOA reviewed all drafts of the manuscript. Authors GUA and DBA managed the analyses of the study. Author DBA identified the plants and performed the statistical analysis. All authors read and approved the final manuscript.

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ABSTRACT

Aims: To estimate the general and specific combining ability (GCA and SCA) of some cocoa clones for some vegetative and pod trait and to quantify the extent of variability among the studied cocoa genotypes.

Place and Duration of Sample: The experiment was performed at Local Clone Trial plot, Cocoa Research Institute of Nigeria (CRIN), Ibadan between June 2013 and April 2014.

Methodology: Three cocoa testers (N38 – T3, T65/7 – T4, and T8/27 – T5) were crossed with two cocoa lines (T12/11 – L1, and T30/13 – L2). Generated pods were evaluated for girth (PG), thickness (PIT) and inner diameter (PIW). Seeds from the selfed and the hybrid pods were sown

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and established in a completely randomized design with three replications. Data on stem girth (SG), plant height (PH), number of leaves (NL), leaf length (LL), leaf width (LW), and petiole length (PTL) were taken at two weeks intervals for twelve weeks on the eleven cocoa genotypes.

Results: Line and tester analysis revealed significant ($P \leq 0.05$) differences for treatment, parents, crosses, lines and line by tester sources of variation. The highest general combining ability (3.83) occurred in T3 for PH. The best (0.46) specific combiner for PG was L2 x T5, while L2 x T3 and L1 x T3 were the best combiners for PIT (0.18) and PIW (3.14) respectively. Analysis of variance also revealed significant ($P \leq 0.05$) differences among the genotypes. T12/11 and T65/7 had the highest genetic similarity (0.86).

Conclusion: Hybrids from the crosses of the parents are new recombinants, adding to the cocoa germplasm size. The observed genotypic diversity forms a good basis for selection of traits to assist a further improvement of cocoa genotypes. Crosses with significant specific combining ability could be selected and use for implementing a more effective cocoa breeding programme.

Keywords: Cocoa; germplasm enhancement; genetic distance; diversity; hybrids.

1. INTRODUCTION

Theobroma cacao tree is a small 4-8 metres tall evergreen tree in the family Malvaceae [1]. It is native to the deep tropical region of South America and grows well as understory plants in humid forest ecosystems. Its seeds are used to make cocoa mass, cocoa powder and chocolate [2].

Breeding success on tree crops is slow; the process of the right parents' choice for generating quality hybrids is another challenge. A concerted breeding effort on tree crops, such as cocoa, often leads to significant improvement in quality, yield and other economic traits [3]. Obtaining plant genetic resources with desirable traits for pairing as male and female parents, to produce superior F_1 progeny over existing genotypes, is a major precondition for designing a model in hybrid breeding program [4]. Therefore, the success in plant breeding through hybridization is dependent on the identification, selection and utilization of the right parents.

Mating designs are meant to generate progenies and estimate genetic variances. The Line × Tester method and analysis by Kempthorne [5] is one. However, it is one of the most relevant tools available to estimate the combining ability to aid selection of desirable parents and crosses for exploitation in pedigree breeding [6]. Adewale et al. [3]; Abrha et al. [7] made used of Line × Tester method in maize and cocoa respectively. The knowledge of combining ability is useful in assessing differences among genotypes and also in elucidating the nature and magnitude of gene actions involved in determining the phenotypic expression of traits in the resultant crosses. Cervantes-Martinez and Brown [8], also reported that, general combining ability and specific combining ability constitutes extremely useful parameters in enabling breeders to make more efficient parental choices, providing information about the potential parental value in crosses as well as describing gene actions.

Variability exists among cocoa genotypes in Nigeria [9,10]. Further identification of proven parents for breeding programs and expansion of existing seed garden hectarage for continuous hybrid pod generation remains a contextual annual objective in the cocoa breeding scheme [3]. Therefore, understanding of the combining abilities and genetic variability of the available genotypes within the germplasm is an indispensable step to the development of breeding strategies.

Germplasm utilization in a breeding program is dependent on the availability of individual information on each genotype. Therefore, the objectives of the present study are: to estimate the general and specific combining ability (GCA and SCA) of five cocoa clones for some vegetative and pod trait, to identify parents with desirable GCA, cross combination with desirable SCA and to quantify the extent of variability among the studied cocoa genotypes.

2. MATERIALS AND METHODS

2.1 Hybridization

In a bid to advance breeding programme and increase the quantity of diversity within the Nigerian cocoa germplasm, the combining ability of some cocoa clones were investigated. Hand crossing among some selected parents was carried out in the Local Clone Trial plot (a twelve year old cocoa plot) at the Cocoa Research Institute of Nigeria (CRIN), Ibadan between June to August, 2013. Choice of parents was based on the initial work of Adewale et al. [10]. The mating design was Line and Tester. Crosses were performed between 2 Lines (L1 - T12/11 and L2 - T30/13) and 3 Testers (T3 - N38, T4 - T65/7 and T5 - T82/27). Selfed pods were equally generated as check materials for the hybrids. Pollination was done artificially. Recipient flowers were tagged and isolated at the bud stage. Selfing and cross pollination was done at anthesis. Progressive developments of cherrelles were monitored to maturation of the pods. By January 2014, uniformly matured ripe pods were harvested as self-pollinated and hybrid pods. Preliminary data were collected on pod girth (PG), pod inner diameter (PIW) and pod thickness (PIT).

2.2 Seedling Establishment

Seedlings from the selfed and hybrid pods were raised in black polythene bags in the nursery from January 2014 to April 2014. The experiment involved eleven genotypes (Six hybrids and five selfed parents). They were laid out in eleven plots per replicate; each plot contained 15 seedlings of a genotype. The experimental layout was completely randomized design of three replications. Data collection started after two weeks of seedling emergence and continued at two weeks interval on stem girth (SG), plant height (PH), number of leaves per plant (NL), leaf length (LL) and width (LW) and petiole length (PTL).

2.3 Statistical Analysis

Data were subjected to Line and Tester analysis following the procedure of Singh and Chaudhary [11]; leading to the estimates of the general and specific combining ability (GCA and SCA) and their standard error. The significance of GCA and SCA were tested following the procedure of Abrha et al. [7] such that corresponding GCA and SCA values were divided by their respective standard error to obtain the t-calculated value. T-calculated was compared with T-tabulated value at error degree of freedom in the Critical Values of the *t* distribution Table.

Further analyses were done to understand the diversity among the eleven genotypes. Data were subjected to Analysis of Variance (ANOVA) in SAS (version 9.2, 2007) to detect the proportional contribution of each sources of variation to the total variation. The significant discriminatory ability of each trait to differentiate the eleven genotypes was tested using STEP DISC procedure in SAS at the probability of 95%. Gower Genetic distance was used to estimate proximity and/or distance among each pair of genotypes and the Principal component analysis was carried out to estimate eigenvectors and eigenvalues. Scores of the first three principal component (PC) axes was used to produce a tri-dimensional figure to reveal the specific grouping of the eleven genotypes within the plane.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance for Lines and Testers

Treatment and the component of treatments (parent, crosses and parent vs. crosses) differed significantly ($P \leq .01$) for all the characters except pod girth and pod thickness in Table 1. However, significant ($P \leq .01$) variation due to treatment and parents respectively occurred in stem girth, plant height, number of leaves, leaf length and leaf width, while that of crosses occurred in plant height, number of leaves, leaf length, leaf width and pod inner diameter. Significant ($P \leq .01$) variation due to parent vs. crosses was limited to three of the eight traits. Significant ($P \leq .05$) differences occurred among lines, tester and line x tester interaction for the traits except SG, NL, PG and PIT for lines, PG and PIT for testers and SG, PG and PIT for line x tester (Table 1). The proportion of the variance of general combining ability (GCA) to specific combining ability (SCA) was higher than one (1.00) in NL. However, GCA/SCA was lower than 1.00 in SG, PH, LL, LW, PG, PIT and PIW (Table 1).

3.2 General Combining Abilities (GCA) of Lines and Testers

Significant ($P \leq .05$) GCA mean square for lines occurred for NL, LL, PG, PIT and PIW (Table 2). Among GCA for tester, a very highly significant but negative variance ($P \leq .001$) was observed in N38 for PIT and T82/27 for SG. Positive and significant ($P \leq .05$) GCA was observed in N38 for PH and T82/27 for PIT and PIW while negative GCA was observed among the testers for PH, NL, LL, LW and PG. The highest (3.83) GCA occurred in N38 for PH (Table 2).

Table 1. Analysis of variance summary of the 2 x 3 lines and testers

SV	**DF**	**Traits/mean squares**							
		SG	**PH**	**NL**	**LL**	**LW**	**PG**	**PIT**	**PIW**
Treatment	10	0.058**	49.14 **	7.74**	16.10**	0.99**	0.932	0.168	1.28
Parent	4	0.189**	14.77**	3.50**	13.51**	0.96**	0.537	0.168	0.51
Crosses	5	0.086	67.38**	12.49**	22.24**	1.17**	0.875	0.168	7.30**
Par vs cr	1	0.071	12.77**	0.69	3.61	0.32**	2.790	0.168	111.70**
Line	1	0.005	7.20*	0.22	13.43**	0.26**	1.800	0.168	3.20*
Tester	2	0.155**	133.12**	24.39**	19.19**	0.43**	0.290	0.168	3.72*
Line x Tester	2	0.058	31.733**	6.72**	29.69**	2.36**	0.995	0.168	1.29**
Error	20	0.018	8.85	3.08	8.23	0.61	0.072	0.168	0.21
σ^2gca		0.004	4.99	9.54	0.59	-0.095	0.009	0.168	-0.36
σ^2sca		0.013	7.63	1.21	7.15	0.583	0.308	0.168	4.24
σ^2gca/ σ^2sca		0.131	0.65	7.87	0.08	-0.163	0.031	0.168	-0.08

, **, * – significant at 0.05, 0.01 and 0.001 level of significance*

NB: SG = Stem girth, PH = Plant height, NL= numbers of leaves, LL = Leaf length, LW= Leaf width, PG = Pod girth, PIT = Pod thickness, PIW= Pod inner diameter, Par vs Cr = Parents vs crosses

Table 2. Estimates of general combining abilities (GCA) of lines and testers

Components	SG	PH	NL	LL	LW	PG	PIT	PIW
GCA for lines								
L1	4.33	0.86	-0.42*	-0.422*	0.24	0.31**	-0.11 ***	-0.42*
L2	-4.33	-0.851	0.42*	0.422*	-0.29	- 0.31 **	0.11***	0.42*
S.E(g)	2.37	0.42	0.15	0.153	0.26	0.08	0.01	0.15
S.E (g_1-g_1)	3.36	0.59	0.21	0.216	0.37	0.12	0.02	0.21
GCA for testers								
T3	0.09	3.83**	1.55	-0.202	0.05	0.23	-0.17***	-1.17**
T4	0.089	1.42	0.72	1.88	0.24	-0.19	0.03	0.37
T5	-0.187***	-5.26	-2.28	-1.67	-0.29	-0.04	0.13 ***	0.52*
S.E(g)	0.05	1.21	0.71	1.17	0.32	0.11	0.02	0.18
S.E (g-g)	0.07	1.71	1.01	1.65	0.45	0.15	0.03	0.26

*, **, *** *- significant at 0.05, 0.01 and 0.001 level of significance*

NB: SG = Stem girth, PH = Plant height, NL= numbers of leaves, LL = Leaf length, LW= Leaf width, PG = Pod girth, PIT = Pod thickness, PIW= Pod inner diameter

3.3 Specific Combining Abilities (SCA) of Lines and Testers

Result of the specific combining ability (SCA) of each line and each tester is presented in Table 3. Positive and significant (*P* ≤ .01) SCA estimates were observed in L1 x T3 for PIW, L1 x T4, L1 x T5, L2 x T3 respectively for PIT and PIW and L2 x T5 for PG. However, negative and significant (*P* ≤ .05) SCA values occurred in L1 x T3 for PIT, L1 x T5 for SG and PG, L2 x T4 for PIT and PIW and L2 x T5 for PIT and PIW. The best specific combiner for optimum PG was L2 x T5, while L2 x T3 and L1 x T3 was the best combiner for PIT and PIW respectively (Table 3).

3.4 Analysis of Variance Summary for Vegetative and Pod Characteristics

The result for analysis of variance is presented in Table 4. From Table 4, there were significant (*P* ≤ .05) differences among the eleven genotypes for all the traits measured from 2nd to the 12th weeks after planting (WAP) except for plant height at 2WAP, leaf length at 4, 8 and 10 WAP, leaf width at 12WAP and petiole length at 12WAP. Means of each trait increased progressively from 2WAP to 12WAP. Significant (*P* ≤ .01) differences for pod characteristics was limited to Pod girth (PG) and Pod thickness (PIT) The means for PG and PIT was 7.54 cm and 1.08 cm respectively. In general, the least CV of 4.36 occurred in pod girth while the highest (19.42) occurred in plant height (Table 4).

3.5 Stepwise Selection of Discriminatory Traits

The Summary of the Stepdisc procedure for Stepwise Selection of traits in SAS is presented in Table 5. Eight most discriminatory traits were selected based on the 0.05 level of probability from the analysis. The traits are: SG 4 WAP, PTL 10 WAP, SG 2 WAP, PTL 2 WAP, NL 6 WAP, LL 1 WAP, PG, PIT (Table 5).

3.6 Similarity Matrix between the Eleven Cocoa Genotypes

Pairs of Gower genetic distance between the 11 genotypes is presented in Table 6. From the table, T12/11 (Selfed) and T65/7 (Selfed) had the highest genetic similarity of 0.860. The lowest genetic similarity (0.296) occurred between Hybrid 1 and Hybrid 3 (Table 6).

3.7 Percentage of Total Variation, Eigen Values and Eigen Vectors for the Principal Component Axes

Table 7 presents the eigenvalues and the eigenvectors of the eight traits for the principal component (PC) axes. The total variation explained by the first three PC axes was 90.03%. By the magnitude, SG 2 WAP (0.48) and PIT (- 0.29) had the highest and least vector loading for PC1, PTL10 WAP (0.57) and NL 6 WAP (- 0.06) for PC 2 and LL 2 WAP (0.57) and SG 2 WAP (- 0.03) for PC3.

3.8 Tri-dimensional Grouping of the Eleven Cocoa Genotypes

Four basic clustering groups were visible in Fig. 1. Clusters 1 and 2 had four (Hybrid 1, T12/11 (selfed), N38 (selfed), and T65/7 (selfed) and two (Hybrid 2 and Hybrid 5) genotypes respectively. Clusters 3 and 4 had three (T30/13 selfed, T82/27 selfed and hybrid 4) and two (Hybrid 6 and Hybrid 3) genotypes.

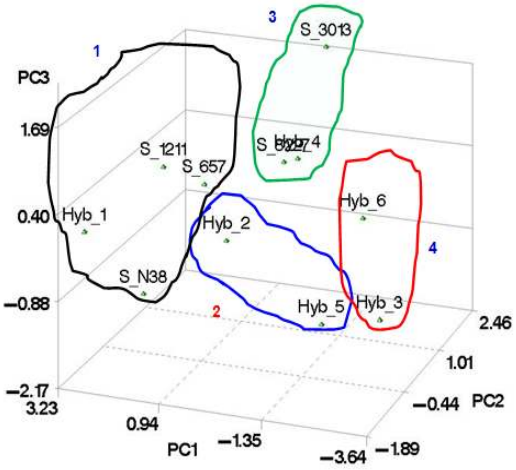

Fig. 1. Tri-dimensional graph showing the grouping of the eleven cocoa genotypes

NB: Hyb_1 = Hybrid 1, Hyb_2 = Hybrid 2, Hyb_3= Hybrid 3, Hyb_4= Hybrid 4, Hyb_5= Hybrid 5, Hyb_6 = Hybrid 6, S_1211 = T12/11 self, S_657 = T65/7 self, S_N38 = N38 self, S_30/13 = T30/13 self, S_82/27 = T82/27 self

4. DISCUSSION

The selection of the five parents was justified by the observed variation among the lines and the testers. Using parents with wider genetic distance for hybridization helps in the generation of new variants and the increase of genetic resources in the germplasm [10]. This is reflected in the identified significant differences among the parents and their respective hybrids for most of the characters studied. Genetic similarity among the parents was quite high, ranging from 0.296 to 0.860, despite the fact that new distinctive variants with significant heterotic characteristics were generated for an addition to the cocoa genepool in Nigeria.

As explained by Abrha et al. [7], the non-significant difference observed in this study for some traits in the line and tester indicates that the line and tester used had comparable potential for the studied traits. The greater than one (1.00) value obtained from the proportion of variance of GCA/SCA for number of leaves agrees with the result of Singh et al. [12], Gansen and Ran Gaswamy [13]. With reference to the remarks of Sarker et al. [14] and Rashid et al. [6], the responsible gene action for the number of leaves in this study is additive. Number of leaves per plant, which has positive correlation with floral initiation and photosynthetic capacity of plant [15] may hence become a very relevant trait for cocoa seedling selection. Hladni et al. [16] had remarked that the identification of additive gene action makes selection of progeny very effective because heritability of those traits will be reliable.

The identified significant variation among stem girth, plant height, number of leaves, leaf length, leaf width, petiole length, pod girth and pod thickness presents a justified platform for selection for the traits in subsequent breeding program. The continuous increase in size and number of the measured vegetative traits from two weeks after planting to twelve weeks indicates the presence of ontogenetic drift. Vascular plants increases in both size and complexity during vegetative growth and reproductive development showing changes in growth indices that are characteristics of ontogenetic drift [17]. The moderately low coefficient of variation observed for most of the traits makes them more reliable to be selected for breeding as it is obvious that the reliability of a trait to be selected for breeding programme among other factors is dependent on the magnitude of its coefficient of variation.

General combining ability denotes the fixable component of genetic variance and it is of great importance in the development of superior genotype. SCA which represent the non-fixable component provides information on hybrid performance [18]. The result of the GCA and SCA in this study agrees with that of Hladni et al. [4], in which they observed significant differences among the GCA for testers and SCA for crosses. While negative GCA is undesirable, the positive and significant GCA effect of N38 for plant height, T82/27 for pod diameter and pod thickness makes both potential parents for the identified traits. Many workers [18]; [19]; [20]; [3] had reported positive and negative GCA and SCA in many crops. The significant variation observed in the SCA may indicate a distinct deviation from the full performance of the parents used in making the crosses. Significant SCA effect among the crosses indicates a significant deviation from predictable parental performance [7]. The crosses with positive and significant SCA could be selected and used in cocoa breeding programs.

Table 3. Specific combining ability of each line and tester

Crosses	SG	PH	NL	LL	LW	PG	PIT	PIW
L1 x T3	0.03	1.78	1.23	-1.654	--0.60	0.28	-0.18***	3.14***
L1 X T4	-0.05	1.04	-0.61	2.53	0.65	0.18	0.09**	0.85**
L1 X T5	-0.17*	-2.83	-0.61	-0.874	-0.05	-0.46**	0.09**	0.83**
L2 X T3	-0.06	-1.79	-1.22	1.65	0.60	-0.28	0.18***	1.69***
L2 X T4	-0.06	-1.10	0.61	-2.52	-0.65	-0.18	-0.09**	-0.89**
L2 X T5	0.09	2.83	0.61	0.874	0.05	0.46**	-0.09**	-0.83**
S.E(g)	0.07	1.71	1.01	1.65	0.45	0.15	0.03	0.26
S.E(S_{ij}-S_{kj})	0.11	2.42	1.43	2.34	0.64	0.21	0.04	0.37

, **, * - significant at 0.05, 0.01 and 0.001 level of significance*

NB: SG = Stem girth, PH = Plant height, NL= numbers of leaves, LL = Leaf length, LW= Leaf width, PG = Pod girth, PIT = Pod thickness, PIW= Pod inner diameter

Table 4. Analysis of variance summary for vegetative and pod characteristics of the eleven cocoa genotypes

SV	Df	2 WAP	4 WAP	6 WAP	8 WAP	10 WAP	12 WAP
Stem girth							
Genotype	10	1.89***	2.95**	3.01**	7.59***	8.61***	0.06*
Error	18	0.22	0.03	0.58	1.23	1.60	3.07
Mean		4.03	6.03	8.10	9.90	12.13	13.90
Cv %		11.66	12.92	9.40	11.29	10.43	12.61
Plant height							
Genotype	10	I5.35ns	7.56*	10.09*	14.40**	27.67*	49.07**
Error	18	11.14	2.89	3.27	3.12	6.26	16.795
Mean		17.18	19.33	20.93	22.70	26.64	30.58
Cv %		19.42	8.78	8.63	7.78	19.07	13.40
Number of leaf							
Genotype	10	1.89***	2.95**	3.00**	7.59***	8.61***	0.05*
Error	18	0.22	0.03	0.57	1.23	1.60	3.07
Mean		4.03	6.03	8.09	9.83	12.12	13.90
Cv %		11.66	12.92	9.39	11.28	10.43	12.60
Leaf length							
Genotype	10	2.68*	2.56ns	5.45**	4.17ns	7.74ns	17.00*
Error	18	0.79	1.36	1.46	2.22	4.52	7.00
Mean		9.89	12.29	14.29	17.07	19.34	21.64
Cv %		8.97	9.49	8.438	8.77	10.98	12.23
Leaf width							
Genotype	10	0.7 9***	0.61**	0.89**	0.57**	0.54*	0.88ns
Error	18	0.14	0.13	0.17	0.22	0.52	0.57
Mean		3.74	4.70	5.45	6.18	6.87	7.78
Cv %		9.98	7.67	7.57	7.50	10.53	9.74
Petiole length							
Genotype	10	0.06*	0.17**	0.58**	0.49**	0.93**	1.00 ns
Error	18	0.01	0.03	0.12	0.11	0.23	0.47
Mean		1.20	1.60	2.15	2.88	3.62	4.54
Cv %		11.50	11.67	16.22	11.93	13.37	15.11
Pod characteristics							
		PG	PIT	PIW			
Genotype	10	0.69**	0.11**	17.93ns			
Error	11	0.11	0.01	33.19			
Mean		7.54	1.08	5.73			
Cv%		4.36	9.01	10.50			

, **, * - significant at 0.05, 0.01 and 0.001 level of significance*

NB: SV = Source of variation, DF = Degree of freedom, WAP = Weeks after planting, PG = Pod girth, PIT = Pod thickness, PIW= Pod inner diameter

The observed less than 1 (< 1.0) GCA:SCA proportion of variance for stem girth, plant height, leaf length, leaf width, pod girth, pod thickness and pod diameter implicated the non-additive gene action. Non-additive genetic component according to Hladin et al. [4] was responsible for the inheritance of plant length and leaf area in sunflower. Sanghera and Hussain [21] strongly recommended that the identification of non-additive genetic variance could be a primary justification for initiating a hybrid program in plants.

Wider crosses in sesame was advocated by Kumaresan et al. [22], such according to them could lead to heterosis in hybrids and the production of new recombinants for desired trait. Genotypes belonging to clusters with high inter cluster distance are genetically more diverse. However, generating reliable grouping of genotypes is a prerequisite for selection of genotypes (within clusters) for subsequent cross breeding programme. Moreover, the identification of the most discriminatory phenotypic traits for the grouping protocol is primary. In our study, the

Table 5. Summary of the Stepdisc procedure for Stepwise Selection of traits in SAS

S/N	Variables	F-values	Pr > F
1	SG 4 WAP	15.43	<.0001
2	PTL 10 WAP	5.51	0.0005
3	SG 2 WAP WAP	3.60	0.0071
4	PTL 2 WAP WAP	3.07	0.0172
5	NL 6 WAP	3.03	0.0196
6	LL 1 WAP	2.66	0.0364
7	PG	3.86	0.0128
8	PIT	9.22	0.0001
9	NL 1 WAP	2.32	0.0646
10	NL 8 WAP	1.94	0.1191
11	PTL 8 WAP	1.69	0.1798
12	PTL 6 WAP	1.18	0.3789
13	PTL 4 WAP	0.77	0.6517
14	LW 8 WAP	1.78	0.1581
15	LW 6 WAP	0.76	0.6665
16	LW 4 WAP	0.64	0.7607
17	LW 2 WAP	1.09	0.4268
18	LL 12 WAP	1.22	0.3573
19	LL 6 WAP	0.71	0.7020
20	NL12 WAP	0.51	0.8596
21	NL10 WAP	1.25	0.3411
22	NL 4 WAP	0.99	0.4953
23	PH 12 WAP	1.26	0.3388
24	PH10 WAP	0.85	0.5916
25	PH 8 WAP	0.58	0.8039
26	PH 6 WAP	1.18	0.3781
27	PH 4 WAP	0.92	0.5403
28	SG 12 WAP	0.95	0.5203
29	SG 10 WAP	0.36	0.9430
30	SG 8 WAP	0.51	0.8568
31	SG 6 WAP	0.33	0.9589
32	PIW	0.60	0.7893

NB: SG = Stem girth, PTL = Petiole length, NL = Numbers of leaves, LL = Leaf length, LW = Leaf width, PH = Plant height, WAP = Weeks after planting, PIT = Pod thickness, PG = Pod girth, PIW= Pod inner diameter. 2,4,6,8, 10, 12 are weeks of data collection

Table 6. Similarity matrix between genotypes by Gower genetic distance

Genotypes	Hybrid 1	Hybrid 2	Hybrid 3	Hybrid 4	Hybrid 5	Hybrid 6	T12/11 selfed	T30/13 selfed	N38 Selfed	T65/7 selfed
Hybrid 2	0.705									
Hybrid 3	0.296	0.390								
Hybrid4	0.595	0.716	0.587							
Hybrid 5	0.527	0.750	0.544	0.761						
Hybrid 6	0.428	0.545	0.776	0.737	0.644					
T12/11Selfed	0.773	0.730	0.469	0.715	0.571	0.585				
T30/13Selfed	0.529	0.671	0.458	0.753	0.695	0.683	0.604			
N38 Selfed	0.754	0.671	0.538	0.614	0.563	0.616	0.827	0.538		
T65/7 Selfed	0.780	0.848	0.456	0.803	0.711	0.589	0.860	0.723	0.787	
T82/27Selfed	0.473	0.593	0.698	0.757	0.641	0.810	0.696	0.646	0.660	0.659

Table 7. Eigen values, percentage of total variation and eigen vectors for the principal components axes

PC-Axes	Eigen-value	Percentage of total variation	Cumulative percentage	Eigen vectors for the principal components axes							
				SG 2 WAP	SG 4 WAP	NL6 WAP	LL2 WAP	PTL2 WAP	PTL10 WAP	PG	PIT
PC 1	4.05	50.63	56.63	0.48	0.47	0.45	0.11	0.37	0.23	0.36	-0.29
PC 2	1.92	23.55	74.63	0.05	-0.07	-0.06	0.52	0.42	0.57	0.12	0.45
PC 3	1.27	15.85	90.48	-0 .03	-0 04	-0.1	0.57	-0.60	-0.11	0.51	0.17

NB: PC = Principal component, WAP = Weeks after planting, SG = Stem girth, NL =Numbers of leaves, LL = Leaf length, PTL = Petiole length, PG = Pod girth, PIT = Pod thickness selection of eight out of the 32 phenotypic traits presented to the STEPDISC procedure in SAS revealed that each trait have different discriminatory ability for a set of genotypes meant for classification. The use of many phenotypic traits for classification of genotypes without initial selection (based on their discriminatory potentials) may lead to the employment of redundant traits whose effect could mask reliable classification, thus leading to misleading conclusion.

5. CONCLUSION

Hybrids from the crosses of the parents are new recombinants, adding to the cocoa germplasm size. The observed genotypic diversity forms a good basis for selection of traits to assist a further improvement of cocoa genotypes. Crosses with significant specific combining ability could be selected and use for implementing a more effective cocoa breeding programme.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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