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R Deepa
Department of Spices and
Plantation Crops, HC & RI,
TNAU, Coimbatore, Tamil
Nadu, India

S Balakrishnan
Department of Spices and
Plantation Crops, HC & RI,
TNAU, Coimbatore, Tamil
Nadu, India

V Jegadeeswari
Department of Spices and
Plantation Crops, HC & RI,
TNAU, Coimbatore, Tamil
Nadu, India

G Thiribhuvanamala
Department of Plant Pathology,
TNAU, Coimbatore, Tamil
Nadu, India

N Kumaravadivel
Department of Plant Molecular
Biology and Bioinformatics,
TNAU, Coimbatore, Tamil
Nadu, India

Study of variability, heritability and genetic advance for yield attributing characters in cocoa clones

R Deepa, S Balakrishnan, V Jegadeeswari, G Thiribhuvanamala and N Kumaravadivel

Abstract
Evaluation of variability, heritability and genetic advance of various traits in cocoa clones is an important step to identify the vital characters which attribute to yield. Genetic parameters for yield and its correspondent characters of nine TNAU cocoa clones were estimated low, moderate and high phenotypic coefficient of variations (PCV) and genotypic coefficient of variations (GCV) were observed among the nine clones. Wet bean weight per pod recorded high phenotypic and genotypic coefficient variations, whereas stem girth, number of flowers per tree, number of beans per pod, dry bean weight per pod (g) and dry bean weight per pod (g) showed moderate Genotypic and Phenotypic coefficient of variation. High heritability coupled with high genetic advance was exhibited by number of flower sper tree, number of beans per pod, single dry bean weight per pod and dry bean weight per pod. Hence these characters may be used as major descriptors to select high yielding cocoa clones.

Keywords: GCV, PCV, heritability, genetic advance, cocoa clones, dry bean weight

Introduction

Cocoa (*Theobroma cacao* L.) is one of the economically important agricultural commodity for millions of people worldwide. It is grown by about 6 million farmers globally and livelihoods of more than 40 million people depend on cocoa (Beg *et al*., 2017) [3]. The genus *Theobroma* is a diploid tropical fruit crop species (2n = 2x = 20) and belongs to the family Malvaceae. Cocoa is cultivated in the humid tropical regions of the world, although it originated in the Upper Amazon basin (Motamayor *et al*., 2008) [14]. The largest cocoa-producing region is the Ivory Coast of Africa, where 68% of the world's cocoa is harvested. About 90 - 95 percentage of all cocoa is produced by smallholder farmers (World cocoa foundation, 2014) [21]. Cocoa is grown mostly under shade trees, being either inter-cropped or in a semi-natural agro-forestry system. Farmers have been selecting cocoa genotypes for several years based on disease tolerance and bean quality. Cocoa was traditionally classified into three main groups namely, Criollo, Forastero and Trinitario (Cheeseman, 1944) [6]. However, a new classification based on genetic data was achieved, recognizing upto 10 genetic groups namely Amelonado, Criollo, Contamana, Curaray, Guiana, Iquitos, Marañon, Nacional, Nanay and Purus (Motamayor *et al*., 2008) [14]. Genetic differences among groups may result in differences in yield and size of the pods as well as in disease susceptibility (Clement *et al*., 2003) [8].

Expression of crop diversity is estimated from different indicators of variability especially, the morphological traits which are important for the cataloguing and characterization of genotypes. The variation in the phenotypic expressions is the result of the action of different alleles of genes that occur and control the specific characteristics and the total of the alleles that make up the plant's genotype (Bartley, 2005) [2]. Bioversity International has standardized the descriptor status for cocoa, which comprises of 60 characteristics including plant habit, leaf, floral, fruit, seed traits and special features like reaction to biotic and abiotic stresses.

In India, area expansion under cocoa shows an increasing trend, therefore it is essential to develop high yielding clones and hybrid materials with pest and disease resistance suited to different agro-climatic regions. The TNAU cocoa clones are maintained at Coconut Research Station, Aliyar Nagar as polyclonal garden. The knowledge of genetic variability present in the cocoa clones for the character under improvement is of utmost importance for the success of any plant breeding programme. Heritability estimates along with genetic advance are normally helpful in predicting the gain under selection. The main focus of the study is to analyze the genetic variability and estimate the other associated genetic parameters in the TNAU cocoa

Correspondence
S Balakrishnan
Department of Spices and
Plantation Crops, HC & RI,
TNAU, Coimbatore, Tamil
Nadu, India

types to identify the most relevant yield contributing characters to validate the selection programme.

Materials and methods

The present study was conducted at Coconut Research Station, Aliyar Nagar, Pollachi, Coimbatore District, during July – December, 2018. Nine cocoa plus trees were selected based on yield characters from farmer's field in Pollachi block (Karthikkumar, 2014) [12] and these were multiplied through soft wood grafting (Janani, 2014) [10]. The nine clones were named as TNAU CC 1 to TNAU CC 9 and polyclonal orchard was established at Coconut Research Station, Aliyar Nagar, Pollachi. The experiment was laid out in Randomized Block Design with three replications and observation often yield contributing characters *viz*., plant height, stem girth, number of flowers per tree, number of pods harvested per tree, number of beans per pod, wet bean weight per pod, single fresh bean weight, dry bean weight per pod, single dry bean weight and pod value were recorded. Genotypic, phenotypic, and environmental coefficient of variance, heritability and genetic advance were estimated for all traits. Phenotypic and genotypic coefficients of variation (PCV & GCV) were calculated as suggested by Burton (1952) [5] by estimating the variance components.

The PCV and GCV values were categorized as follows (Sivasubramanian and Menon, 1973) [17].

Table 1: The PCV and GCV Category

PCV and GCV	Category
< 10 per cent	Low
10 – 20 per cent	Moderate
> 20 per cent	High

Heritability and genetic advance were calculated as suggested by Allard (1960) [1] and Johnson *et al.*, (1955) [11].

The heritability per cent was categorized as suggested by Robinson *et al.* (1949) [16].

Table 2: The Heritability Category

Heritability in per cent	Category
< 30 per cent	Low
31 – 60 per cent	Moderate
> 60 per cent	High

The analysis of variance (ANOVA) was executed by using SPSS 16.0 version. Statistical analyses as done based on the standard methods as described by Panse and Sukhamtme (1985).

Result and Discussion

The mean value of TNAU Cocoa Clones showed significant difference for all the observed characters *viz*., stem girth (18.49 cm), number of flowers per tree (324.60), number pods per tree (19.14), number of beans per pod (40.54), fresh bean weight per pod (208.46 g), single fresh bean weight (3.25 g), dry bean weight per pod (28.24 g), single dry bean weight (0.85 g) and pod value (35.75) except plant height (169.71 cm) as presented in table 3. In the present study TNAUCC 5 recorded maximum plant height (177.44 cm) and stem girth (20.69 cm) (Table 3). The maximum stem girth and plant height has indirect influence on the pod yield. Similar result were observed by Sumitha *et al.*, 2018 [19]. The number of flowers per tree (367.05), number pods per tree (21.03),

number of beans per pod (49.81), wet bean weight per pod (302.75 g), single fresh bean weight (3.90 g), dry bean weight per pod (33.58 g) and single dry bean weight (0.90 g) was highest in TNAUCC 5. Flowering is important yield contributing character and it is influenced by genetic make-up of the plant. Nine cocoa clones were developed from a heterogenous population hence showed difference in their performance.

The lowest pod value is observed in the genotype of TNAUCC 5 (29.82). Pod value or pod index is defined as the number of pods required to produce one kg of wet cocoa beans. Pod index is considered as an indirect measurement of pod size (Soria, 1966) [18] and bean size (Wood and Lass, 1985) [20]. The higher pod index was determined by size of the pod and size of the bean.

The result of analysis of variance showed significance difference for all the observed traits except for plant height (Table 4).

Variability (%)

In the present study, the estimates for genotypic and phenotypic coefficient of variation indicated that there is an ample scope for the cocoa crop improvement programme. The results of coefficient of variation (Table 5.) showed that the phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation for all yield and yield contributing characters. Wet bean weight per pod recorded higher phenotypic and genotypic coefficient of variation (33.41% and 33.22% respectively), whereas pod value recorded the lowest GCV (9.61%). In cocoa lower pod value is preferred to have higher bean yield (Karthikkumar, 2014) [12]. High phenotypic coefficient of variation along with high genotypic coefficient of variation indicates that the traits are least influenced by external environmental variation (Binse *et al*., 2009) [4].

Heritability (%)

High heritability were observed for all the characters like stem girth (90.88%), number of flowers per tree (93.38%), number pods per tree (83.53%), number of beans per pod (95.48%), wet bean weight per pod (98.90%), single fresh bean weight (94.23%), dry bean weight per pod (91.01%), single dry bean weight (61.25%) and pod value (91.39%) indicating that these characters are controlled by genetic make-up of the plant and are least influenced by environment. Low heritability was observed for plant height (19.55%) indicating high environmental influence on this trait. These findings were in line with results of Elain Apshara and Nair, 2017. High heritability indicates the scope of genetic improvement of these traits through simple selection (Binse *et al*., 2009) [4].

Genetic Advance as per cent of mean

The genetic advance in the study ranged from 1.38 to 68.06 % (Table 5.). The highest GAM was recorded in wet bean weight (68.06%), number of beans per pod (30.13%), single fresh bean weight (26.44%), number of flowers per tree (24.00%), and dry bean weight per pod (20.07%). Low GAM were observed in plant height (1.38%) and Single dry bean weight (6.56%) whereas stem girth (19.66%), number of pods per tree (13.37%) and pod value (18.93%) had a moderate GAM. Similar findings were also reported by Elain Apshara and Nair, 2017.

Heritability with genetic advance

High heritability value accompanied by high genetic advance percent of mean for number of flowers per tree, number of pods per tree, number of beans per pod, wet bean weight, single fresh bean weight and dry bean weight per pod indicates additive gene action and selection may be effective if it is based on these characters. Single dry bean weight recorded high heritability with low GAM was probably due to the non-additive gene action. Similar results have been reported by Minimol *et al.,* 2014 [13]; Cilas *et al.,* 2010 [7] and Elain Apshara and Nair, 2017.

Table 3: Mean performance of Identified cocoa clones (TNAUCC 1 to 9) for yield and yield contributing characters

Cocoa clones	Plant height (cm)	Stem girth (cm)	No. of flowers per tree	No. pods per tree	No. of beans per pod	Wet bean weight per pod (g)	Single fresh bean weight (g)	Dry bean weight per pod (g)	Single dry bean weight (g)	Pod value
TNAUCC1	167.24	19.64	348.66	19.30	36.21	192.82	2.76	26.73	0.87	37.43
TNAUCC2	170.85	16.26	303.09	18.33	41.37	203.02	2.59	26.73	0.82	37.43
TNAUCC3	166.69	17.89	310.36	19.69	40.40	288.68	3.41	26.46	0.89	37.82
TNAUCC4	174.18	20.07	366.15	20.87	47.48	295.18	3.78	25.94	0.83	38.59
TNAUCC5	177.44	20.69	367.05	21.03	49.81	302.75	3.90	33.58	0.90	29.82
TNAUCC6	168.59	19.36	284.04	19.01	43.73	137.17	3.17	31.18	0.81	32.09
TNAUCC7	164.81	19.79	372.36	19.57	40.54	156.18	3.22	30.96	0.89	32.32
TNAUCC8	167.74	17.56	303.38	17.90	30.31	169.96	2.99	24.94	0.80	40.11
TNAUCC9	169.88	15.17	266.34	16.60	34.98	130.39	3.41	27.67	0.85	36.16
Grand Mean	169.71	18.49	324.60	19.14	40.54	208.46	3.25	28.24	0.85	35.75
SE(d)	4.25	0.47*	1.38*	0.49*	1.07*	5.96*	0.08*	0.74*	0.02*	0.86*
CD (P= 0.05)	9.03	1.02	18.03	1.04	2.29	12.65	0.18	1.57	0.05	1.83

Table 4: Analysis of variance for different characters in cocoa clones

Source of variation	Degree of freedom	Plant height (cm)	Stem girth (cm)	No. of flowers per tree	No. pods per tree	No. of beans per pod	Wet bean weight per pod (g)	Single fresh bean weight (g)	Dry bean weight per pod (g)	Single dry bean weight (g)	Pod value
Replication	2	56.99	0.62	5.57	0.70	3.17	115.30	0.02	1.39	0.0015	2.78
Treatment	8	47.02	10.62*	17.15*	5.90*	112.23*	14442.39*	0.56*	25.79*	0.004*	36.55*
Error	16	27.20	0.34	0.34	0.36	1.745	53.37	0.01	0.82	0.001	1.11

Table 5: Genotypic and phenotypic coefficient of variability (gcv and pcv), heritability (h2) and genetic advance for different characters in TNAU cocoa clones

Traits	PV	GV	EV	PCV	GCV	h^2	GA	GAM
Plant height (cm)	33.81	6.61	27.2	3.43	1.52	19.55	2.34	1.38
Stem girth (cm)	3.77	3.43	0.34	10.50	10.01	90.88	3.64	19.66
No. of flowers per tree	1640.41	1531.86	0.34	12.48	12.06	93.38	77.91	24.00
No. of pods per tree	2.21	1.85	0.36	7.77	7.10	83.53	2.56	13.37
No. of beans per pod	38.58	36.83	1.745	15.32	14.97	95.48	12.22	30.13
Wet bean weight per pod (g)	4849.72	4796.34	53.37	33.41	33.22	98.90	141.88	68.06
Single fresh bean weight per pod (g)	0.20	0.18	0.01	13.62	13.22	94.23	0.86	26.44
Dry bean weight per pod (g)	9.15	8.32	0.82	10.71	10.21	91.01	5.67	20.07
Single dry bean weight (g)	0.00	0.00	0.001	5.20	4.07	61.25	0.06	6.56
Pod value	12.93	11.81	1.11	10.06	9.61	91.39	6.77	18.93

Conclusion

Present study revealed that the TNAU cocoa clones had wide variability for the observed ten traits. Genetic improvement and development of high yielding cocoa clones are dependent upon the volume and nature of genetic variability that are present in the genetic store. Among the nine clones, TNAUCC 5 performed better with higher yield as well as vegetative growth and this clone can be exploited further in crop improvement programme.

Acknowledgement

References

1. Allard RW. Principles of Plant Breeding, J Wiley and Sons, London, 1960, 83-88.
2. Bartley BGD. The genetic diversity of cocoa and its utilization. CABI publishing, UK, 2005, 341.
3. Beg MS, Ahmad S, Jan K, Bashi K. Status, supply chain and processing of cocoa - A review. Trends in Food Science & Technology. 2017; 66:108-116.
4. Binse R, Sarawgi AK, Verulkar SB. Study of heritability, genetic advance and variability for yield contributing characters in rice. Bangladesh J Agril. Res. 2009; 34(2):175-179.
5. Burton GW. Quantitative inheritance in grasses. In: Proc. 6th Int. Grassland Cong., 1952; 1:277-283.
6. Cheesman EE. Notes on the nomenculture. Classification and possible relationship of cocoa populations. Tropical Agriculture. 1944; 21:144-159.
7. Cilas C, Machoda R, Motamayor JC. Relationship between several traits linked to sexual plant reproduction in *Theobroma cacao* L. Number of ovules per ovary, number of seed per pod, and seed weight. Tree Genetic Genomes. 2010; 6:219-226.
8. Clement D, Risterucci AM, Motamayor JC, Goran JN

and Lanaud C. Mapping QTL for yield components, vigor, and resistance to *Phytophthora palmivora* in *Theobroma cacao* L., Genome. 2003; 46:204-212.

9. Elain Apshara S, Nair RV. Genetic analysis in Cocoa (*Theobroma cacao* L.) collections obtained from Nigeria. Journal of Plantation Crops. 2011; 39(1):153-156.

10. Janani P. Studies on certain aspects of crop improvement in cocoa (*Theobroma cacao* L.). Ph.D. (Hort.) Thesis, submitted to Tamil Nadu Agricultural University, Coimbatore, 2014.

11. Johnson WW, Robinson HF, Comstock RE. Genotypic and phenotypic correlation in soybeans and their implications in selection. Agronomy Journal. 1955; 47:477-482.

12. Karthikkumar RB. Performance evaluation and adaptability behavior of plus trees of cocoa (*Theobroma cacao* L.). Ph.D. (Hort.) Thesis submitted to Tamil Nadu Agricultural University, Coimbatore, 2014.

13. Minimol JSB. Suma, Dayalakshmi EM, Jayasree PA. Analysis of genetic parameters of selected cocoa (*Theobroma cacao* L.) hybrids. International Journal of Tropical Agriculture. 2014; 32:825-828.

14. Motamayor JC, Lachenaud P, Mota SJ, Loor R, Kuhn DN, Brown JS, Schnell RJ. Geographic and genetic population differentiation of the Amazonian chocolate tree (*Theobroma cacao* L). PLoS ONE. 2008; 3:10.

15. Panse VG, Sukhatme PV. Statistical methods for agricultural workers, 2nd Edition ICAR, New Delhi, 1961, 361.

16. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. Agronomy Journal. 1949; 41:353-359.

17. Sivasubramanian S, Menon PM. Genotypic variability in rice. Madras Agricultural Journal. 1973; 60:1093-1096.

18. Soria VJ. Principalesvariedades de cacao cultivadas en America Tropical. Turrialba. 1966; 16(3):261-265.

19. Sumitha S, Balakrishnan S, Shoba N, Kumar M, Jeyakumar P, Jegadeeswari V. Performance of identified cocoa clones for morphological and yield traits during initial growth phase. International Journal of Chemical Studies. 2018; 6(5):634-636.

20. Wood GAR, Lass RA. Cocoa, 4thEdn. Longman Scientific and Technical, New York. USA, 1985.

21. World Cocoa Foundation Report: 13, 2014. http://worldcocoafoundation.org/ about cocoa/cocoa-market-statistics/.