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GENETIC VARIABILITY AND BREEDING VALUE OF CASTOR GENOTYPES

M. I. Uguru
Department of Crop Science,
University of Nigeria, Nsukka, Nigeria.

ABSTRACT

Six populations consisting of the parents (P_1 and P_2), F_1s, F_2s and backcrosses (BCP_1 and BCP_2) from three crosses of castor (Ricinus communis L.) were studied using randomised complete block design to determine the level of variabilities with a view to ascertaining the improvement potentials through selection. The results show that castor plants are largely heterozygous, an attribute that is highly desirable in plant breeding as they provide heterogeneous populations for a wider spectrum of selection. Genotypic differences were highly significant showing a wide range of variations in many of the characters studied. Phenotypic variations in many of the characters were largely non-genetic and broad sense heritability estimates were relatively low for some of the traits. There were strong indications that improvement of quantitative characters in castor may not be achieved by direct selection from the existing genotypes.

Key words: Variability, Breeding value, castor, *Ricinus communis*.

INTRODUCTION

The widely diverse genetic base of the Nigerian castor germplasm is an important attribute that has made its adaptation to the variable soil and climatic conditions possible. All over the country from latitudes 5 to 13°N the crop can be found growing, unattended to, by the road sides and on refuse heaps. Most castor growers have relied on seeds harvested from impressive plants among these volunteers, and a number of local varieties, diverse in many agronomic characters, have arisen from this selection process.

Following the recent increase in the demand of castor seeds for some industrial applications (Weiss, 1971; Singh and Singh, 1974; Bhatt and Reddy, 1986; and Roetheli *et al.*, 1990) in both local and international markets, the crop is presently being emphasized. As a prelude to meaningful selection for improved agronomic traits, information on the variability of the available genotypes is pertinent. Previous investigations on castor have dealt extensively with correlation studies between yield and yield components (Bhatt and Reddy, 1986). Unfortunately, there are no evidences of sufficient research to determine the degree of variation among castor genotypes with respect to these traits. This is important because crop improvement through selection depends on the magnitude of genotypic variability and the extent to which the desirable characters are heritable. Therefore, survey of the genetic variability with the help of suitable genetic parameters such as phenotypic and genotypic coefficients of variation and heritability estimates is relevant for starting an effective breeding programme. This forms the basis of the present study.

MATERIALS AND METHOD

The experimental materials consist of five genetically diverse genotypes of castor namely; RS_1-0mp, RS_1-0m, RT_1-Owmbp, RN_1-0m and RN_1-

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omp. These were crossed to produce three F_1 populations of RS_1-0mp x RS_1-0m, RS1-0mp x RT_1-0wmbp and RN_1-0m x RN_1-0mp. The F_2 populations were obtained by allowing natural self pollination of the F_1 progenies. The backcrosses were made during flowering by crossing the F_1s to their respective seed parents (BCP_1) and pollen parents (BCP_2).

The F_1, F_2, BC and parental populations were grown in randomised complete block design (RCBD) with three replications. Single row plots of 8 m^2 each were used for the evaluations. Each row consisted of four plants and data on the vegetative and yield characters were taken from all the plants in the row. The data collected were plant height, leaf area, number of leaves, branches, racemes and pods per plant, as well as nodes to primary inflorescence, 100-seed weight and seed yield per plant.

The estimation of the phenotypic, genotypic and environmental variances were calculated according to Poehlman (1987). Phenotypic and genotypic coefficients of variation were estimated according to Burton and De Vane (1953) and heritability in a broad sense was obtained as the ratio of the genotypic variance to the phenotypic variance (Allard, 1960). The population mean, range and standard deviation were calculated as outlined in Little and Hills (1978).

RESULTS AND DISCUSSION

The population mean, range and standard deviation for the nine agronomic traits are shown in Table 1 while the analyses of variance are presented in Table 2. Table 3 shows the variances of the agronomic traits in the three crosses. The estimates of phenotypic, genotypic and environmental variances, and heritability in broad sense are presented in Table 4.

Plant height ranged from 174.3 to 297.4 cm with a mean of 227.66 $\pm$ 0.132. The spread around the mean is indicative of the existence of short internode, normal internode and long internode genotypes. On a general note, however, a greater proportion of the available genotypes are potential trees exceeding 2.0 meters. The cultivars varied greatly with respect to the number and size of leaves produced. Some of the genotypes had few leaves while the others were considerably leafy but the trend appears to suggest that more of the genotypes had profused leaf production potentials. Nodes to primary inflorescence ranged from 8 to 18 as against the 6 to 16 nodes reported in literature (Kittock and Williams, 1968) for the normal internode varieties. The spread around the mean presents a picture of a normal distribution with the greatest proportion of the plants producing the inflorescence at the 13th node. The nodes to primary inflorescence is a varietal characteristic (Weiss, 1971) and a good measure for earliness to flowering

Table 1. Range, mean and standard deviation of the nine characters in castor

Character	Range	Mean	Standard deviation
Plant height (cm)	174.3-297.4	227.66±0.132	30.05
Leaves/plant	40-169	111.96±0.213	33.80
Leaf area/plant (cm^2)	106.6-643.5	308.77±0.446	137.56
Nodes to primary inflorescence	8-18	13.36±0.180	2.40
Branches/plant	12-58	32.24±0.310	10.00
Racemes/plant	2-36	17.65±0.372	6.56
Pods/plant	84-530	305.00±0.410	125.00
100-seed weight (g)	11.9-51.7	24.10±0.510	12.28
Seed yield/plant (g)	90.2-507.2	210.9±0.448	94.57

Table 2. Analysis of variance table for RCBD showing source of variation, degrees of freedom and mean squares only.

Source of variation	D.F.	Plant height	Leaves/plant	Leaf area	Branches/ plant	Nodes to primary inflorescence	Racemes	Pods/plant	100-seed weight	Seed yield
Block	2	87.57*	0.15ns	113.76ns	27.65ns	1.03ns	2.82ns	6.14ns	3.85ns	8.30ns
Genotype	4	4711.5**	2157**	10151.63**	88.68**	5.33**	26.64**	31618.7**	479.9**	3289.0**
Error	8	17.18	28.84	45.87	8.75	1.06	3.26	482.76	20.4	14.6

ns = not significant at $p = 0.05$
** = highly significant ($p = 0.01$)

Table 3. Variances of nine agronomic traits in the crosses RS_1-Omp x RS_1-Om (Cross I), RS_1-Omp x RT_1-*Owmbp* (Cross II) and RN_1-Om x RN_1Omp (Cross III).

	Cross I						Cross II						Cross III					
Character	σ^2P_1	σ^2F_1	σ^2F_2	σ^2P_2	σ^2BCP_1	σ^2BCP_2	σ^2P_1	σ^2F_1	σ^2F_2	σ^2P_2	σ^2BCP_1	σ^2BCP_2	σ^2P_1	σ^2F_1	σ^2F_2	σ^2P_2	σ^2BCP_1	σ^2BCP_2
Plant height	53.3	53.2	87.3	59.6	72.4	70.4	53.3	57.6	66.6	59.2	70.8	78.6	59.6	61.5	74.0	48.4	71.6	60.8
Leaves/ plant	59.6	60.6	88.4	65.6	94.8	100.0	59.6	56.7	75.6	64.8	93.6	84.0	65.6	60.8	98.0	109.6	74.0	114.0
Leaf area	25.7	52.1	82.6	40.3	98.5	63.9	25.7	50.2	58.2	57.1	80.1	72.4	40.3	43.3	92.8	52.0	67.0	86.1
Nodes to primary Inflorescence	1.1	1.6	4.8	2.4	4.4	3.6	1.1	1.2	4.0	2.8	5.2	5.6	2.4	1.4	3.6	1.2	4.8	5.2
Branches plant	19.1	7.7	21.2	17.0	25.0	14.2	19.1	9.6	19.6	11.0	24.6	22.7	17.0	9.4	19.2	12.0	12.0	20.0
Racemes plant	7.8	5.8	17.5	7.4	13.9	10.7	7.8	4.6	13.5	7.1	8.0	9.4	4.4	4.8	8.3	5.4	12.0	13.0
Pods/plant	69.9	68.4	143.5	98.4	121.6	120.8	69.9	74.0	123.0	64.8	109.6	100.0	60.8	84.0	106.4	74.0	107.6	88.4
100-seed weight	16.7	14.5	31.2	16.5	23.0	19.2	16.7	15.1	37.3	17.9	23.2	27.1	19.2	15.1	24.5	15.2	23.1	19.4
Seed yield	37.5	33.6	68.4	27.7	62.1	50.1	37.5	29.3	66.2	31.6	45.2	74.2	46.5	43.4	52.6	48.6	91.7	76.8

Table 4. Estimates of phenotypic, genotypic, and environmental variances, heritability in a broad sense, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV).

Character	*Cross	$\bar{x}$	σ^2 ph	$\sigma^2 g$	$\sigma^2 e$	Herit-ability (%)	PCV (%)	GCV (%)
	I	212.5	187.3	32.0	55.3	37.0	41.0	15.1
Plant height	II	239	66.6	9.9	56.7	15.0	27.9	4.1
(cm)	III	223	74.0	17.5	56.5	24.0	33.2	7.8
	I	145	88.4	26.5	61.9	30.0	61.0	18.3
	II	118	75.6	15.2	60.4	20.0	64.1	12.9
Leaves/plant	III	105	98.0	19.3	78.7	20.0	93.3	18.4
	I	233.7	82.6	43.2	39.4	52.0	35.3	18.5
	II	239.5	58.2	13.9	44.3	24.0	24.3	5.8
Leaf area (cm^2)	III	204.2	92.8	47.6	45.2	51.0	45.4	23.3
Nodes to	I	12	4.8	3.1	1.7	65.0	40.0	25.8
primary	II	15	4.0	2.3	1.7	58.0	26.7	15.3
inflorescence	III	13	3.6	1.9	1.7	54.0	27.7	14.8
	I	40	21.2	6.6	14.6	31.0	53.0	16.5
	II	39	19.6	6.3	13.2	32.5	50.3	16.1
Branches/plant	III	38	19.2	6.4	12.8	33.0	50.5	16.8
	I	19	17.5	10.5	7.0	60.0	44.0	26.3
	II	24	13.5	7.0	6.5	52.0	34.6	18.0
Racemes/plant	III	18	8.3	3.4	4.9	41.0	21.8	8.9
	I	289	143.5	64.6	78.9	45.0	49.7	22.4
	II	294	123.0	53.4	69.6	43.0	41.8	18.2
Pods/plant	III	233	106.4	33.5	72.9	31.0	45.7	14.4
	I	12.6	31.2	15.3	15.9	49.0	248.0	121.0
100-seed	II	23.4	37.3	20.7	16.6	55.0	159.0	88.5
weight (g)	III	19.1	24.5	8.0	16.5	33.0	128.3	44.4
					32.9			
	I	112.1	68.4	35.5	32.8	52.0	60.7	31.5
Seed	II	223.6	66.2	33.4	46.2	50.0	29.6	14.9
yield/plant (g)	III	171.9	52.6	5.8		11.0	30.6	52.7

*I = RS_1-Omp x RS_1-Om; II = RS_1-Omp x RT_1-Owmbp;; III = RN_1-Om x RN_1-Omp.

and pod maturity (Kittock and Williams, 1968).

The number of branches per plant ranged from 12 - 58 with a mean of 32 ± 0.310. The spread around the mean indicates that castor plants are naturally endowed with profused branching habit particularly under tropical humid conditions (Weiss, 1971). The number of branches per plant is an important yield component as the pod bearing raceme terminates each branch. Literally, this agronomic feature would tend to describe profused branching habit as a desirable agronomic development. However, under very humid conditions, large number of branches would cause a prolific increase in the production rates of leaves at the expense of the racemes and pods (Weiss, 1971). Therefore, selection based on prolific branching habit in castor may be unreliable.

The cultivars varied greatly with respect to the number of racemes per plant. Some of the plants produced very few racemes while others produced as much as 36 racemes per plant. However, a greater proportion of the plants produced, on the average, 11 to 23 racemes per plant. Because of the cardinal role as the pod bearing structure, higher number of racemes should be the target in any selection aimed at increased pod yield in castor. The data on number of pods and racemes per plant showed that the plant produced about 17 pods per raceme indicating that higher pod yield can be obtained from plants endowed with higher raceme production.

Seed size as indicated by 100-seed weight varied from 11.9 - 51.7 g with a mean of 24.10 ± 0.510. The distribution suggests the existence of both small-sized and large-sized seeds among the castor genotypes. In many countries, larger seed size attracts higher whole sale price paid to the farmer and increase the predominant repeat sales at the retail market. Under such a situation, selection would be in favour of the large seeded genotypes. Seed yield per plant ranged from 90.2 to 507.2 g. The spread around the mean indicates that the distribution with respect to seed yield appears to be skewed with a greater proportion of the plants producing more than 400 g of seeds per plant.

It is evident from these results that castor plants are very heterozygous. As it is protogynous (Cobley, 1976; Atsmon, 1989), cross pollination is more common and variabilities arising from cross fertilization is not unexpected. Such variabilities are useful in plant breeding as they provide heterogeneous populations for a wider spectrum of selection and additionally such variable populations are usually better buffered against environmental fluctuations. The high variability is further validated by the analysis of variance of RCBD (Table 2) which showed highly significant ($P<0.01$) differences among the genotypes for all the characters.

Estimates of components of variance and coefficients of variation for the different characters in three crosses are shown in Table 4. The phenotypic coefficients of variation were higher than the corresponding genotypic coefficients of variation in all the crosses, indicating that all the characters had to some degree interacted with the environment. Higher phenotypic and genotypic coefficients of variation were observed in 100-seed weight and seed yield/plant (Table 4).

The coefficients of variation in leaf area, plant height, node to primary inflorescence, pods/plant and racemes/plant were moderate. Because the coefficient of variation measures the magnitude of variability present in a population, selection from populations with such high coefficient of variation values in the yield characters is very likely to be effective in the improvement of the traits. Previous reports (Majumder *et al.*, 1969) indicated that genotypic coefficient of variation helps to measure the range of genetic variability in a character and provides a measure to compare the variabilities present in a population. However, this parameter alone does not provide a good estimate of heritable variation except in combination with heritability estimates (Burton, 1952). On this premise, the proposition based on the coefficients of variation is weakened by the relatively low heritability estimates obtained for most of the traits. Of all the characters, nodes to primary inflorescence, racemes/plant, leaf area and seed yield had relatively high heritability estimates. The other characters, plant height, leaves/plant, branches/plant, pods/plant and 100-seed weight had low heritability values, an indication that the characters were subjected to high degree of non-heritable variability.

Crop improvement depends on the magnitude of variabilities and the extent to which the desirable characters are heritable (Uguru, 1994). The results of this study have shown that variations in quantitative traits in castor are high, but the heritable components of these variations are low, indicating less scope for improvement of the characters through straight selection.

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