HERITABLE RELATIONSHIPS AND VARIABILITY OF YIELD AND YIELD COMPONENTS IN VEGETABLE COWPEA

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ABSTRACT

Six populations from two crosses of vegetable cowpea (*Vigna unguiculata* (L.) Walp) were studied for heritable relationships between yield and yield components. Highly significant differences were observed for all traits. Phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation, indicating the influence of genotype x environment interaction in the expression of all characters. Broad and narrow sense heritability estimates were determined for pod length (71 and 65%, cross 1; 66 and 52%, cross 2), for number of seeds pod^{-1} (74 and 52%, cross 1; 76 and 52% cross 2), and for number of pods $plant^{-1}$ (64 and 49%, cross 1; 69 and 49%, cross 2). Although the heritability values for pod length were relatively high, the non-significant genotypic correlation of pod length with grain yield seems to negate its usefulness as a trait for improvement of yield. The moderate to high heritability values of pods $plant^{-1}$ and seeds pod^{-1} and their highly significant positive correlation with yield suggested that pods $plant^{-1}$ and seeds pod^{-1} are major yield contributing components.

Key Words: Genotype, heritability, phenotype, *Vigna unguiculata*

RÉSUMÉ

Six populations de deux croisements du niébé légume (*Vigna unguiculata* (L.) Walp) ont été étudiées pour leurs relations d'héritabilité en ce qui conserne le rendement et les composants du rendement. Des différences très significatives ont été observées pour tous les caractères. Le coefficient phénotypique de variation, était plus élevé que le coefficient génotypique de variation correspondant, ce qui indique l'influence de l'interaction entre l'environnement et le génotype dans l'expression de tous les caractères. Les estimations au sens large et restreint de l'héritabilité ont été déterminées pour la longueur des gousses (71 et 65% pour le croisement 1; 66 et 52% pour le croisement 2), pour le nombre de graines par gousse (74 et 52%, pour le croisement 1; 76 et 52% pour le croisement 2), et pour le nombre de gousses par plantes (64 et 49%, pour le croisement 1; et 69 et 49% pour le croisement 2). Bien que les valeurs de l'héritabilité pour la longueur de gousses étaient relativement élevées, la corrélation génotypique non-significative de la longueur de gousses et du rendement en graines semble annuler son utilité comme caractère pour l'amélioration du rendement. Les valeurs d'héritabilité modérées à élevées des gousses par plante et des graines par gousse, et leurs corrélations très significatives avec le rendement, laissent penser que le nombre de gousses par plante et graines par gousse sont les éléments importants contribuant au rendement.

Mots Clés: Génotype, héritabilité , phénotype, *Vigna unguiculata*

INTRODUCTION

Vegetable cowpea (*Vigna unguiculata* (L.) Walp) is well adapted to the region of Nigeria south of $10°N$ latitude where it has been reported to have a yield potential of 20 to 26 tonnes ha^{-1} of green pods (Redden, 1981). The high yield could be attributed to increased pod set per peduncle, large seed size, many peduncles per plant, and many seeds per pod. Selection for any of these yield related traits would provide a rapid advance in vegetable cowpea breeding programmes. The heritability and phenotypic and genotypic relationships among these yield related components in vegetable cowpea are lacking in literature and these form the basis of the present study. Recent studies on gene action and inheritance patterns of most of the agronomic traits in vegetable cowpea, however, have been reported (Uguru and Uzo, 1990).

Heritability and its usage in both the broad and narrow sense are described by Poehlman (1987). The F_2 population is used to calculate total phenotypic variance, with mean variances of the F_1 and the parents used to estimate environmental variance. Direct selection for higher yield might provide misleading results because many factors interact to determine cowpea yield (Singh and Jain, 1972). Because individual yield components are less influenced by environmental effects than yield itself, selection for such yield components may be useful in acquiring genotypes with better yield potential (Premsekar and Raman, 1972; Bordia *et al.*, 1973; Jagadish, 1986).

MATERIALS METHODS

Three vegetable cowpea accessions: the determinate AN-16-D, and the climbing AE-36-C and AE-36-S, were selected for this study. The F_1 population of AN-16-D x AE-36-C (cross 1) and AE-36-S x AE-36-C (cross 2) were produced by hand pollination using the method of Utuk (1974). F_2 populations were obtained by allowing natural self-pollination of the F_1. The backcrosses were made during flowering by crossing each F_1 to the respective seed parent (BCP_1) and pollen parent (BCP_2).

The F_1, F_2, BC and parental populations were grown in a randomized complete block design with four replications. Entries were grown in four-row plots 9.0 m long with 90 cm between rows and 30 cm within rows. Data on pod length, number of seeds pod^{-1}, pods $plant^{-1}$, peduncles $plant^{-1}$ and seed yield were collected for each population from the 52 plants in the two middle rows. Seed yield was calculated as the product of the shelling fraction and weight per plant and expressed in tonnes ha^{-1}.

The estimation of the environmental, genotypic, and phenotypic variances, as well as broad sense heritability, were calculated as described by Poehlman (1987). Narrow sense heritability (H_{ns}) was estimated using a slight modification of the method described by Allard (1960).

$$\sigma^2F_2 = 1/2D + 1/4H + E = X$$

$$2\sigma^2F_2 = D + 1/2H + 2E = 2X$$

$$\sigma^2BC_1 + \sigma^2BC_2 = 1/2D + 1/2H + 2E = Y$$

$$2\sigma^2F_2 - (\sigma^2BC_1 + \sigma^2BC_2) = 1/2D = 2X - Y$$

$$H_{ns}(\%) = 1/2D/\sigma^2F_2 = 2X - Y/X1$$

Variance and covariance analyses for the different traits were performed according to Norman *et al.* (1970). Phenotypic correlations, r_{phxy}, were obtained from mean squares and mean products given by Samarawira (1988) as:

$$r_{phxy} = \frac{M(gx \times gy)}{\sqrt{Mgx \times Mgy}}, \text{ where}$$

$Mgx \times gy$ = Mean product of traits X and Y and

Mgx, Mgy = Mean squares of traits X and Y, respectively.

The genotypic correlations between traits X and Y (r_{gxy}) were estimated from components of variance and covariance (Baker, 1986), as the ratio of the genotypic covariance between the two traits and the geometric mean of the genotypic variances. Thus,

$$r_{gxy} = \frac{\sigma_{gxy}}{(\sigma^2gx \times \sigma^2gy)^{0.5}}, \text{ where}$$

gx, gy = genotypic covariance of traits X and Y, respectively;

$\sigma^2 gx$ = genotypic variance of trait X, and

$\sigma^2 gy$ = genotypic variance of trait Y.

Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were estimated using the procedure of Burton and De Vane (1953). Tests for significance of both the phenotypic and genotypic correlations were performed using the Student "t" test:

$$\text{"t"} = \frac{\sqrt{n-2}}{1-r} \text{, where}$$

r = correlation value, and,

n = number of individuals in samples.

RESULTS AND DISCUSSION

Means of the parental, F_1, F_2, BCP_1 and BCP_2 populations are shown in Table 1. Estimates of the variance components for the two crosses are presented in Table 2, and the heritability estimates of the traits and the correlation values between the same traits are included in Tables 3 and 4, respectively.

Parents differed significantly in pod length, pods plant⁻¹, seed pod⁻¹ and seed yield. The similarity in peduncles plant⁻¹ in both crosses (Table 1) suggests that they are capable of producing similar number of reproductive nodes irrespective of their growth habit; the difference being in their respective potential to achieve higher pod set peduncle⁻¹.

The higher heritability estimates for seeds pod⁻¹ and pod length in cross 2 (Table 3) suggest greater additive gene effects. Although the broad sense heritability value for seeds pod⁻¹ was high in cross 1, its narrow sense heritability estimate was identical to the values recorded for pods plant⁻¹, peduncles plant⁻¹ and grain yield. This would appear to imply non-additive genetic and environmental effects or the combined influence of both factors. Because of the usefulness of additive genetic effects to the plant breeder, it is very likely that it would be productive to apply selection pressure to improve pod length in vegetable cowpea.

TABLE 1. Population means for five traits in the P_1, P_2, F_1, F_2, BC_1 and BC_2 populations in two crosses of vegetable cowpea

Traits	Cross I — AN-16-D (P_1) (decumbent) X AE-36-C (P_2) (climbing)						F=LSD (P=0.05)	Cross II — AE-36-S (P_1) X AE-36-C (P_2)						F=LSD (P=0.05)
	P_1	BCP_1	F_1	F_2	BCP_2	P_2		P_1	BCP_1	F_1	F_2	BCP_2	P_2	
Pod length (cm)	14.11	15.61	20.93	17.73	24.00	26.13	0.81	13.50	18.41	20.83	14.94	19.10	26.13	0.43
Pods plant⁻¹	56.75	68.50	79.50	44.75	72.30	47.25	5.42	47.25	43.40	40.75	36.25	43.20	47.25	4.56
Penduncles plant⁻¹	52.50	41.20	36.00	35.75	49.00	48.75	3.96	36.00	35.20	34.25	27.00	23.00	48.75	14.43
Seeds pod⁻¹	11.78	10.50	11.85	9.97	8.60	9.80	0.54	10.40	11.50	12.25	10.75	8.00	9.80	0.31
Grain yield (t ha⁻¹)	2.18	2.46	3.05	1.69	2.12	1.41	0.16	1.08	1.72	1.84	1.79	2.00	1.41	0.14

The phenotypic coefficients of variation were higher than the corresponding genotypic coefficients of variation (Table 3), indicating that all the characters had to some degree interacted with the environment. High phenotypic and genotypic coefficients of variation were observed in pod length and seeds pod⁻¹ and, to some extent, in seed yield. Peduncles plant⁻¹ showed moderate phenotypic and genotypic variations. Because the coefficient of variation measures the magnitude of variability present in a population, selection from a population with such coefficient of variation values is very likely to be effective in improvement of the traits studied.

Although pod length showed relatively high heritability estimates, its low and non-significant genotypic correlation with seed yield, coupled with its unfavourable correlation with pods plant⁻¹ in both crosses (-0.28 and -0.36) (Table 4), seems to nullify its usefulness in improving the yield of vegetable cowpea. The negative association between pod length and pods plant⁻¹ would indicate that selection of genotypes for longer pods would result in plant types that produce fewer pods per plant.

The positive correlations between the other traits indicate simple linear relationships (i.e., selecting to improve one trait seems to improve the other also). Of special note is the highly significant positive relationship between number of pods plant⁻¹ and seeds pod⁻¹. Given the negative relationship between number of pods plant⁻¹ and pod length, selection for increased pod yield implies reduction in seed size. This could improve the vegetative quality of pods.

The highly significant positive correlations between grain yield and (i) pods plant⁻¹ and (ii) seeds pod⁻¹ (Table 4) agrees with the findings of Premsekar and Raman (1972) and Bordia et al. (1973). These associations reinforce the report by Jagadish (1986) that pods plant⁻¹ and seeds pod⁻¹ are the major yield factors. Thus, selection for both could suffice for the improvement of seed yield in vegetable cowpea.

The highly significant variation in peduncles plant⁻¹ among the genotypes may offset the relatively low heritability estimates recorded for this trait in both crosses, thus making it responsive to selection. Therefore, harvesting plants with

TABLE 2. Variance components of five traits in the crosses AN-16-D (P_1) X AE-36-C (P_2) (Cross 1) and AE-36-S (P_1) X AE-36-C (P_2) (Cross II) of cowpea

Trait	Cross I								Cross II							
	$\sigma^2 P_1$	$\sigma^2 BCP_1$	$\sigma^2 F_1$	$\sigma^2 F_2$	$\sigma^2 BCP_2$	$\sigma^2 P_2$	$\sigma^2 E$	$\sigma^2 G$	$\sigma^2 P_1$	$\sigma^2 BCP_1$	$\sigma^2 F_1$	$\sigma^2 F_2$	$\sigma^2 BCP_2$	$\sigma^2 P_2$	$\sigma^2 E$	$\sigma^2 G$
Pod lenght	11.84	24.89	10.14	37.25	25.78	10.83	10.94	26.31	7.08	22.44	8.62	28.06	19.75	10.83	9.50	18.55
Pods plant⁻¹	8.55	24.03	10.01	23.88	22.14	7.27	8.61	15.27	7.64	16.41	8.00	24.34	21.22	7.27	7.64	16.70
Peduncles plant⁻¹	11.11	15.89	11.21	23.10	14.00	11.24	11.19	11.91	14.26	27.04	13.11	31.12	24.23	11.24	12.87	18.25
Seeds pod⁻¹	5.10	14.24	4.86	18.51	13.08	4.29	4.75	13.76	3.18	7.44	4.23	16.52	8.31	4.29	3.90	12.62
Grain yield	0.14	0.32	0.22	0.40	0.26	0.10	0.15	0.26	0.15	0.24	0.08	0.26	0.18	0.10	0.11	0.15

TABLE 3. Estimates of heritability (%), phenotypic coefficient of variation (P.C.V) (%) and genotypic coefficient of variation (G.C.V.) of five traits in two crosses of vegetable cowpea

Trait	AN-16-D x AE-36-C (Cross I)				AE-36-S X AE-36-C (Cross II)			
	Heritability (broad sense)	Heritability (narrow sense)	PCV	GCV GCV	Heritability (broad sense)	Heritability (narrow sense)	PCV	GCV
Pod length	71	65	31.0	26.0	66	52	23.8	19.3
Pods plant[-1]	64	49	8.0	6.4	69	49	11.5	9.0
Peduncles plant[-1]	52	49	11.0	9.0	59	35	16.4	12.6
Seeds pod[-1]	74	52	41.0	36.0	76	52	39.3	34.3
Grain yield (t ha^{-1})	63	55	29.0	23.0	58	38	30.0	23.0

TABLE 4. Phenotypic and genotypic correlation coefficients between traits contributing to yield in the population two crosses of vegetable cowpea

Trait	AV-16-D X AE-36-C (Cross I)		AE-36-S X AE-36-C (Cross II)	
	Phenotypic	Genotypic	Phenotypic	Genotypic
Pod length and				
pods plant[-1]	-0.19	-0.28*	-0.21	-0.36*
penducles plant[-1]	0.48**	0.64**	0.06	0.14
Seeds pod[-1]	0.33*	0.42*	0.32*	0.46
grain yield	0.11	0.24	0.23	0.30
Pods plant[-1] and				
peduncles plant[-1]	0.38	0.47*	0.29	0.36*
seeds pod[-1]	0.54**	0.76**	0.22	0.34*
grain yield	0.68**	0.79**	0.46*	0.48**
Peduncles plant[-1] and				
seeds pod[-1]	0.02	0.12	0.21	0.28
grain yield	0.15	0.22	0.35*	0.44*
Seeds pod[-1] and				
grain yield	0.74**	0.88**	0.61**	0.68**

* Significant at 5% probability
** Significant at 1% probability.

large numbers of peduncles plant[-1] may improve yield in vegetable cowpea because of its effect in determining the number of pods produced by each plant.

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