A note on the heritability of Pod length and number of seeds per pod in Cowpea, *Vigna unguiculata* s.sp. *unguicalata* (L) Walp

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Abstract

KR 91, (a short podded cowpea cultivar) was crossed to Paraquay No. 2, (a long podded cultivar), while Victor (a crowder) was crossed with B_{33} (a non-crowder) to study the inheritance of pod length and seed number respectively in the two crosses. The two parents, P_1, P_2, and the progenies F_1, BC_1, BC_2 and F_2 of each cross were evaluated at the University of Ife Teaching and Research Farm.

Narrow sense heritability estimates of 72.1% and 36.8% were obtained for pod length and number of seeds per pod respectively. About seven and eight pairs of genes control pod length and number of seeds per pod respectively.

Introduction

Aryeetey and Laing (1973) obtained narrow sense heritability estimates of 60.3% and 37.8% for pod length and number of seeds per pod respectively for cowpea *Vigna unguiculata* s.sp. *unguiculata* (L) Walp. They postulated that only a pair of genes control both pod length and number of seeds per pod in contrast to an earlier report (Brittingham, 1950) that eight pairs of genes control pod length. Thus, there is a necessity for further investigation on heritability of pod length and number of seeds per pod in cowpea.

As part of an effort to design appropriate breeding programmes for improving these traits, we have studied their heritability (narrow sense) and the number of genes controlling them. Results of this study are reported in this paper.

Materials and Methods

Four cowpea cultivars, obtained from the Department of Plant Science, University of Ife and the International Institute of Tropical Agriculture, Ibadan (I.I.T.A.), Nigeria were used in this study. Their pertinent characteristics are given in Table 1.

TABLE 1 — CHARACTERISTICS OF COWPEA CULTIVARS USED AS PARENTS

Cultivars	Pod Length (cm)		Number of seeds/pod	
	Range	Mean (± S.E.)	Range	Mean (± S. E.)
KR 91	8.5 - 16.0	9.5 - 0.47	8 - 14	11.6 ± 0.32
Paraquay No. 2	13.1 - 36.1	27.4 ±0.23	6 - 19	12.7 ± 0.30
Victor	12.4 - 15.5	14.2 ±0.10	8 - 18	14.5 ± 0.34
B_{33}	9.9 - 13.4	12.0 ±0.17	5 - 11	7.4 ± 0.25

KR 91, a short podded variety, was crossed to Paraquay No. 2, a long podded variety. Similarly, Victor with many seeds per pod, was crossed to B_{33}, a variety with few seeds per pod. Each F_1 was backcrossed to either parent to obtain backcross to parent one (BC_1) and parent two (BC2) respectively. F_2 generations were obtained from F_1 generations by selfing. Thus apart from the two parents, four generations F_1, BC_1, BC_2, and F_2, were obtained from each cross.

The evaluation of about 50 plants in each parent and F_2 generation, and 25 plants in each of the remaining generations was carried out at the Teaching and Research Farm, University of Ife in the late season of 1979. The field experiment was grown in a randomized complete block with five replicates. A plot consisted of five plants spaced one metre apart in a single row and rows were spaced one metre apart. A space of one metre separated one replicate from the next. The pods of each plant were harvested separately and by use of random numbers, five pods per plant were picked. These pods were evaluated for each trait. Each generation was analysed separately to determine the mean variance of the mean and standard error.

Heritability in the narrow sense (h^2) was computed using the procedure proposed by Warner (1952):

$$\tfrac{1}{2}D = (2\,\sigma^2 F_2 - (\sigma^2 BC_1 + \sigma^2 BC_2)$$
$$h^2_{ns} = \tfrac{1}{2}D/\,\sigma^2 F_2$$

where

$\tfrac{1}{2}D$ = additive component of genetic variance $\sigma^2 F_2$, $\sigma^2 BC_1$, $\sigma^2 BC_2$ = variance of the F_2 and backcross generations respectively.

Estimates of the number of genes controlling each trait were obtained by Wright's (1968) formula:

$$n = \frac{(\bar{P}_1 - \bar{P}_2)^2}{8(2\sigma^2 F_2 - (\sigma^2 BC_1 + \sigma^2 BC_2))}$$

where

n = number of effective factors

$\bar{P}_1$, $\bar{P}_2$ = mean values of the first and second parent respectively.

The observed distribution of F_2 plants in each trait was tested against the normal distribution using Steel and Torries' (1960) approach.

Results and Discussion

Narrow sense heritability estimates of 72.1% and 36.8% were obtained for pod length and number of seeds per pod respectively. These are similar to 60.3% for pod length and 37.8% for seed per pod reported by Aryeetey and Laing (1973). The differences in absolute values are probably due to the different varieties used as parents.

The high narrow sense heritability estimate for pod length suggests that mass selection can be used to improve this trait whereas for number of seeds per pod, pedigree selection will be more appropriate.

The number of genes estimated for pod length and number of seeds per pod in our trials are 6.96 and 7.21 respectively. This is similar to Brittingham's (1950) estimate of eight pairs for pod length, and in contrast to Aryeetey and Laing's (1973) estimate of one pair for both traits. The latter will suggest a qualitative mode of inheritance and this does not conform with the normal distribution observed in this study. Non-significant Chi-square values of 1.20 and 4.54 at 2 degrees of freedom for deviation from normality were obtained for pod length and number of seeds per pod respectively.

TABLE 2 – RANGE, MEAN (± S.E.) AND NUMBER OF PLANTS EVALUATED (IN PARENTHESIS) FOR THE GENERATION MEANS OF POD LENGTH AND NUMBER OF SEEDS/POD.

Trait/Cross	P_1		P_2		F_1		BC_1		BC_2		F_2	
	Range	Mean (± S.E.)	Range	Mean (± S.E.)	Range	Mean (± S.E.)	Range	Mean (± S.E.)	Range	Mean (± S.E.)	Range	Mean (± S.E.)
Pod Length (KR 91 x Paraquay 2)	13.1 - 36.1	27.4 ± 0.23 (48)	8.5 - 16.0	9.5 ± 0.47 (44)	14.3 - 24.4	17.3 ± 0.48 (21)	9.2 - 16.5	23.2 ± 0.63 (22)	17.0 - 27.3	12.7 ± 0.34 (21)	13.4 - 26.8	17.7 ± 0.45 (44)
Number of seeds/pod (Victor x B33)	8 - 18	14.5 ± 0.34 (47)	5 - 11	7.4 ± 0.25 (39)	10 - 15	12.5 ± 0.39 (19)	10 - 17	13.1 ± 0.46 (21)	8 - 14	9.5 ± 0.43 (20)	9 - 17	12.8 ± 0.34 (43)

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