

A Study of the Genetic Architecture of Some Yield Parameters of Winged Bean Using Model - Fitting Techniques

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ABSTRACT. Five winged bean genotypes were selected to produce three crosses to study the variability observed between the six basic generations of each for the characters, days to flower, pod length, number of pods/plant, 100 seed weight, total seed yield and to evaluate the genetic components of their means using model-fitting techniques of Cavalli (1952). Results revealed that many genes were segregating between the parents, and these genes are mainly in association in the parents. Also, a large additive component and absence of over-dominance indicates that the breeder should be able to extract superior recombinant inbred lines from these crosses for all the characters studied.

INTRODUCTION

Winged bean (*Psophocarpus tetragonolobus* (L.) DC) has been highlighted as a "multi-purpose" crop and as a source of protein, with a high yield potential for the humid tropics. The outstanding nutritive quality of the winged bean seed is based on its high protein content (30-40%) and high oil content (15-20%) which are similar to those of soy bean seed (Cerney, *et al.*, 1971; Claydon, 1975; Ekpenyong and Borchers, 1978; Spata, 1980). Winged bean is thus a crop with a high potential for significant contribution to improving the diets of people in developing countries like Sri Lanka (Hettiarachchi and Sri Kantha, 1980). It therefore needs intensified research in genetic improvement. The hybridization of promising genotypes selected from the germplasm collection available in Sri Lanka (Herath and Iruthayathas, 1981; Ramanayake, 1983) would create additional variability for further improvement of the crop.

Extensive studies on most characteristics of winged bean have been carried out (Erskine and Bala, 1976; Aminah-Lubis, 1978; Senanayake and Thirukeetheswaran, 1978; Wong, 1981). Studies on the genetics of

some quantitative traits have been reported (Erskine, 1981; De Silva and Omran, 1986a, 1986b and 1987) but not as extensively as it should have been for such an important crop. For a breeding programme to be successful, the genetics of all quantitative traits must be well studied and understood.

The present experiment was carried out using 3 crosses, to study the variability observed between the basic generations P_1 , P_2 , F_1 , F_2 , B_1 and B_2 (where P_1 and P_2 are parental generations, F_1 and F_2 are first and second filial generations and B_1 and B_2 are first and second back cross generations) and to evaluate the components of their means. The model-fitting technique of Cavalli (1952) was used for this purpose. Furthermore, evaluation of heterosis and its causes were carried out. The results will provide a breeder with useful information to identify the procedure of his breeding programme for improvement of this crop.

MATERIALS AND METHODS

The following 5 winged bean genotypes were selected to produce 3 crosses as shown:

SLS 44, SLS 60, SLS 72, UPS 53 and UPS 122

Cross I : SLS 44 x UPS 122

Cross II : UPS 122 x SLS 72

Cross III : UPS 53 x SLS 60

All basic generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) were produced for all 3 crosses and grown in the Yala season of 1985 in the field of the International Winged Bean Institute, Pallekele, Sri Lanka.

The number of plants included in each generation were as follows:

Parent 1 (P_1)	=	20
Parent 2 (P_2)	=	20
F_1	=	20
F_2	=	160
Back-cross (B_1)	=	120
Back-cross (B_2)	=	120

The individual plants of each cross were completely randomized within the experimental area using recommended spacing. All normal cultural practices were carried out.

The following characters were considered in this study:

Days to flower (DF) - number of days taken from germination to opening of first flower.

Pod length (PL) - cm

Number of pods/plant (PPP)

100 seed weight (SW) - g

Total seed yield (SY) - kg

The genetical expectations of the generation means according to Mather and Jinks (1971, 1977) are given in Table 1.

RESULTS AND DISCUSSION

The mean performance of the parents, their F_1 hybrids and the results of tests for parental differences and heterosis (t -tests) are given in Tables 2, 3 and 4 for the 3 crosses respectively.

Significant parental differences were observed for all characters in all 3 crosses indicating that a large number of genes are segregating for these characters and the genes have a high degree of association in the parents. Significant heterosis was observed only for PPP and SY of cross I (Table 2). Of the parents, UPS 53 and UPS 122 were the early flowering types.

Longest pods were produced by UPS 122 (27.96 cm) while the shortest were those of UPS 53 (17.88 cm). SLS 72 and UPS 53 gave the largest number of pods despite F_1 of cross I showing heterosis for the character. The heaviest seeds (100 seed wt.) were produced by SLS 44 (56.49 g). Highest seed yields were by SLS 72 (4354.10 kg) and the heterotic hybrid of cross I (4348.70 kg).

Table 1. The genetical expectations of the generation means (Mather and Jinks, 1977).

Generation	m	[d]	[h]	[i]	[j]	[l]
P ₁	1	1	0	1	0	0
P ₂	1	-1	0	1	0	0
F ₁	1	0	1	0	0	1
F ₂	1	0	0.5	0	0	0.25
B ₁	1	0.5	0.5	0.25	0.25	0.25
B ₂	1	-0.5	0.5	0.25	-0.25	0.25

Where m = Mean of all possible homozygotes. All effects are defined as departures from this.

[d] = Net directional value of additive alleles

[h] = Net directional value of dominant alleles

[i], [j], [l] are epistatic components (Mather and Jinks, 1977).

Table 2. Cross I. Mean performances of parents and F₁ and the results of tests for parental differences (P₁ vs P₂) and heterosis (F₁ vs P₁).

Family	DF	PL	PPP	SW	SY
SLS 44	112.00	18.95	19.50	56.49	3907.40
UPS 122	92.90	26.33	22.80	35.57	3481.60
F ₁	94.80	21.92	24.80	43.71	4348.70
P ₁ vs P ₂	***	***	***	***	**
F ₁ vs P ₁	-	-	***	-	**

** Significant at $\bar{P} < 0.01$

*** Significant at $P < 0.001$

Table 3. Cross II. Mean performances of parents and F_1 and results of tests for parental differences (P_1 vs P_2) and heterosis (F_1 vs P_1).

Family	DF	PL	PPP	SW	SY
UPS 122	90.25	27.96	23.95	35.44	3769.10
SLS 72	117.95	19.36	29.00	41.46	4354.10
F_1	95.45	23.33	22.05	38.42	3398.30
P_1 vs P_2	***	***	***	***	***
F_1 vs P_1	-	-	-	-	-

*** Significant at $P < 0.001$

Table 4. Cross III. Mean performances of parents and F_1 and results of tests for parental differences (P_1 vs P_2) and heterosis (F_1 vs P_1).

Family	DF	PL	PPP	SW	SY
UPS 53	89.95	17.88	29.00	38.50	2968.60
SLS 60	124.10	21.78	23.00	44.63	3902.60
F_1	100.20	20.46	25.55	40.54	2959.20
P_1 vs P_2	***	***	***	***	***
F_1 vs P_1	-	-	-	-	-

*** Significant at $P < 0.001$

Table 5. Means of basic generations (upper half) and estimates of the genetical components of these means (lower half) for all three crosses for DF.

Generation	Cross I	Cross II	Cross III
P ₁	112.00 ± 0.59	117.95 ± 0.63	124.10 ± 0.59
P ₂	92.90 ± 0.84	90.25 ± 0.62	89.95 ± 0.51
F ₁	94.80 ± 0.72	95.45 ± 0.51	100.20 ± 0.47
F ₂	93.59 ± 0.85	104.43 ± 0.71	103.61 ± 0.78
B ₁	93.25 ± 0.59	98.36 ± 0.50	92.88 ± 0.42
B ₂	102.53 ± 0.82	106.32 ± 0.65	113.30 ± 0.63
Estimate			
m	85.15	113.74	106.87
[d]	9.49	13.85	17.05
[h]	24.13	-18.24	-6.89
[i]	17.32	-9.60	-
[j]	-	11.91	-7.26
[l]	-14.48	-	-
χ^2	0.06	0.18	1.22
df	1	1	2

Table 6. Means of basic generations (upper half) and estimates of the genetical components of these means (lower half) for all three crosses for PL.

Generation	Cross I	Cross II	Cross III
P ₁	26.33 ± 0.14	27.96 ± 0.33	21.78 ± 0.22
P ₂	18.95 ± 0.15	19.35 ± 0.22	17.88 ± 0.19
F ₁	21.92 ± 0.17	23.33 ± 0.31	20.45 ± 0.19
F ₂	20.62 ± 0.17	22.33 ± 0.29	19.30 ± 0.17
B ₁	22.11 ± 0.17	24.34 ± 0.22	21.27 ± 0.10
B ₂	18.88 ± 0.12	20.67 ± 0.19	19.01 ± 0.12
Estimate			
m	22.65	-	-
[d]	3.60	-	-
[h]	-7.57	-	-
[i]	-	-	-
[j]	-	-	-
[l]	6.85	-	-
χ^2	4.25	-	-
df	2	-	-

Table 7. Means of basic generations (upper half) and estimates of the genetical components of these means (lower half) for all three crosses for PPP.

Generation	Cross I	Cross II	Cross III
P ₁	22.80 ± 0.32	29.00 ± 0.25	29.00 ± 0.44
P ₂	19.50 ± 0.28	23.95 ± 0.26	23.00 ± 0.47
F ₁	24.80 ± 0.28	22.05 ± 0.26	25.55 ± 0.47
F ₂	21.78 ± 0.19	28.07 ± 0.24	25.29 ± 0.28
B ₁	23.39 ± 0.16	25.14 ± 0.25	26.26 ± 0.24
B ₂	19.58 ± 0.15	23.36 ± 0.16	24.33 ± 0.26
Estimate			
m	-	-	26.00
[d]	-	-	3.00
[h]	-	-	-2.38
[i]	-	-	-
[j]	-	-	-2.15
[l]	-	-	1.93
χ^2	-	-	0.00
df	-	-	1

Table 8. Means of basic generations (upper half) and estimates of the genetical components of these means (lower half) for all three crosses for SW (g).

Generation	Cross I	Cross II	Cross III
P ₁	56.49 ± 0.11	41.46 ± 0.14	44.62 ± 0.14
P ₂	35.57 ± 0.11	35.44 ± 0.15	38.50 ± 0.16
F ₁	43.71 ± 0.09	38.42 ± 0.17	40.54 ± 0.16
F ₂	41.23 ± 0.42	39.32 ± 0.18	41.32 ± 0.17
B ₁	49.11 ± 0.25	40.70 ± 0.12	43.20 ± 0.12
B ₂	40.03 ± 0.23	37.32 ± 0.13	39.55 ± 0.10
Estimate			
m	-	39.60	41.55
[d]	-	3.01	3.06
[h]	-	-	-
[i]	-	-1.15	-
[j]	-	0.74	1.57
[l]	-	-1.18	-1.02
χ^2	-	0.01	0.11
df	-	1	2

Table 9. Means of basic generations (upper half) and estimates of the genetical components of these means (lower half) for all three crosses for SY (kg).

Generation	Cross I	Cross II	Cross III
P ₁	3907.40 ± 101.90	4354.10 ± 83.93	3902.60 ± 103.49
P ₂	3481.60 ± 79.72	3769.10 ± 84.14	2968.60 ± 82.22
F ₁	4348.70 ± 77.26	3398.30 ± 58.03	2959.20 ± 81.80
F ₂	3470.10 ± 52.59	4307.80 ± 56.20	3211.50 ± 55.63
B ₁	3502.80 ± 41.69	3825.30 ± 46.58	3545.70 ± 47.68
B ₂	3785.30 ± 48.35	3611.00 ± 34.46	3090.90 ± 42.40
Estimate			
m	-	-	3413.20
[d]	-	-	455.79
[h]	-	-	-
[i]	-	-	-
[j]	-	-	-
[l]	-	-	-464.69
χ^2	-	-	2.96
df	-	-	3

The mean values of basic generations and the estimates of the genetical components of these means for the 5 characters are given in Tables 5, 6, 7, 8 and 9.

Significant epistasis was observed for DF in all 3 crosses (Table 5). Although [h] was greater than [d] indicating over-dominance for DF in cross I, the epistatic component [l] was negative and hence the lack of dominance of F_1 . Also, [i] type of interaction was large and positive. In cross II, again [h] was greater than [d] but there was no [l] type of interaction to give heterosis to F_1 even though [i] was negative. In cross III, [d] was greater than [h] and only [j] type of interaction was present. It should be stated that negative heterosis is preferred in the character days to flowering, so that early flowering types are produced. This was not observed in any of the crosses.

No genetic model fitted the means of the six generations of crosses II and III for pod length (PL) indicating the possibility of higher order interactions operating (Table 6). In cross I, there was no heterosis since [h] was negative, although [d] was small and [l] was large. The only model that fitted the means for PPP was in cross III (Table 7). Both additive and dominance components were small. Both [h] and [i] were negative indicating dominance for decreasing alleles.

No model fitted the means for SW in cross I (Table 8). In crosses II and III there was no significant dominance effect, although interactions were present.

No models fitted the means for SY of crosses I and II (Table 9). In cross III, there was no dominance but very high additive effects. The dominance interaction [l] was also high but negative.

Although heterosis was observed for PPP and SY in cross I, it was not possible to fit a model to these characters. Therefore, heterosis is probably due to higher order interactions. To evaluate this further, more generations will have to be included in the models.

In general, these results indicate that many interactions contributed to the differences in the means of the six generations. There was no evidence to the plant breeder to decide on producing F_1 hybrids for any of the characters.

Over-dominance was present in DF in cross I but it was for increasing alleles i.e. late flowering. In cross II, over dominance was for decreasing flowering time but [d] was also high. Therefore heterosis was not observed. Over-dominance was also observed in PL but, again dominance was for shorter pod length.

The results clearly indicated that many genes were segregating between the parents. Since parental differences were highly significant, it shows that these genes are mainly in association in the parents. Furthermore, in most characters the additive component was much larger than the dominance component. Therefore, under these circumstances a breeder should be able to make recombinant inbred lines from all three crosses in order to produce pure lines superior to the parents for all five characters. There is no evidence for the production of F₁ hybrids.

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