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NOTE

In the name of Allah

ESTIMATES OF INBREEDING DEPRESSION AND HERITABILITY FOR YIELD AND YIELD COMPONENTS FROM THE F_2 GENERATION OF A COMMON BEAN DIALLEL CROSS[1]

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ABSTRACT

Data obtained from a diallel cross involving four common bean (*Phaseolus vulgaris* L.) cultivars (two from each of the Pinto and Kidney commercial groups) and their F_1 and F_2 generations were analyzed and estimates of inbreeding depression (I.D.) and heritability (h^2) were calculated for seed yield, pods per plant, seeds per plant, seeds per pod, and 100-seed weight. The F_2's were significantly higher than the parents and lower than the F_1's in seed yield and pods and seeds per plant. Average I.D. was highly significant for these three characters and for seeds per pod and seed weight. Most of the heterosis in the F_1 for seed yield, pods and seeds per plant, and seeds per pod disappeared after one generation of natural selfing. Large values of

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بنام خدا

تخمین ضعف خودگشنی وقابلیت توارث عملکرد و اجزاء عملکرد در نسل دوم حاصل از تلاقیهای دی آلیل در لوبیا

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خلاصه

مشاهدات حاصله از تلاقیهای دی آلیل شامل چهار رقم لوبیا (دو رقم لوبیا چیتی و دو رقم لوبیا قرمز) و نسلهای اول و دوم آنها مورد تجزیه واریانس قرار گرفت و تخمین ضعف ناشی از خودگشنی وقابلیت توارث برای عملکرد بذر، تعداد غلاف در گیاه، تعداد بذر در گیاه، تعداد بذر در غلاف و وزن یکصد بذر محاسبه گردید. نسل دوم بطور معنی داری از نظر عملکرد بذر و تعداد بذر و غلاف در گیاه برتر از والدین و ضعیف تر از نسل اول بود. متوسط ضعف خودگشنی برای سه صفت فوق و برای تعداد بذر در غلاف و وزن بذر بسیار معنی دار بود. بطور کلی، قسمت اعظم هتروزیس نسل اول برای عملکرد بذر، تعداد غلاف و بذر در گیاه و تعداد بذر در غلاف پس از یک نسل خودگشنی از بین رفت. در تلاقیهای بین ارقام لوبیا چیتی و لوبیا قرمز، تخمین های ضعف خودگشنی و هتروزیس بسیار قابل ملاحظه بود. تخمینهای قابلیت توارث برای کلیه صفات اندازه گیری شده نشان دادند که قسمت اعظم تغییرات ایجاد شده مبنای ژنتیکی داشته که دال بر امکان اصلاح نبات از راه انتخاب میباشد. بعلاوه تعداد بذر در گیاه بهترین شاخص تخمین میزان عملکرد بود.

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heterosis and I.D. were associated with the between-group (Pinto and Kidney) crosses. Estimates of h^2 for all traits evaluated indicated that a fairly large portion of the observed variation for these traits was genetic, suggesting the feasibility of improvement by selection. Seeds per plant was found to be the best indicator of seed yield.

INTRODUCTION

Quantitative characters of primary importance in crop improvement are polygenic in nature and are greatly influenced by environmental factors. Each of the many genes controlling a quantitative trait contributes very little to the total expression of the character. The expression of a certain metric measure depends on the magnitude of the effect of individual genes interacting with environmental factors to produce the final phenotype.

Inbreeding depression (I.D.) is the converse of heterosis and is an expression of the same phenomenon. During inbreeding, genes segregate and go towards fixation brought about by homozygosity. Thus, lines with great differences in genes or gene complexes may be produced. Some lines receive more favorable genes than others, accounting for differences observed in the degree of I.D. in different lines.

Kheradnam *et al.* (5), crossing two pure line cowpea (*Vigna sinensis* L.) cultivars, found that the mean values of F_2 for most characters studied approached the values of midparent, thus exhibiting I.D. as a result of one generation of natural selfing. They also found that values of heterosis were generally greater than those for I.D. Gritton (4), using eight pea (*Pisum sativum* L.) cultivars in a diallel cross, reported significant heterosis and I.D. in all traits studied except days to bloom. Yield heterosis of F_1's based on midparent and on high parents were found to be 55 and 28%, respectively, when averaged over two locations and two years. In a cross involving two common bean cultivars (U.I. 111 and Torbat), Sarafi *et al.* (8) found heritability (h^2) estimates of 46.7, 47.8, 63.4, and

70.6% for pods per plant, seed yield, 100-seed weight, and seeds per pod, respectively. In the F_2 and F_3 populations originating from the same cross, h^2 estimates were 29% for pods per plant, 33 to 37% for 100-seed weight, and 38 to 42% for seeds per pod (7).

Estimates of combining ability, reciprocal effects, and heterosis for a four-parent diallel cross in common beans have been reported earlier (3). This paper reports on the I.D. and h^2 estimates from the F_2 generation of the same diallel cross.

MATERIALS AND METHODS

Two Pinto (U.I. 111 and U.I. 114), two Kidney (California Red 1104 and Montcalm), and two Tropical Black (Black Turtle Soup and San Fernando) cultivars of common beans (*Phaseolus vulgaris* L.) were selected as parents and crosses were made among them in all possible combinations in the greenhouse. The F_1 seeds were grown to obtain F_2 seed. The Tropical Blacks flowered much later than those of the Pintoes and Kidneys and did not set enough F_1 seeds for field planting. Thus the experiment was confined to only four parental cultivars.

In summer of 1979, a single plot of each of the parents and their corresponding 12 F_1's and three plots of each of the 12 F_2's were planted in a randomized complete block design with three replications at the Bajgah Agricultural Experiment Station of the College of Agriculture. Characteristics of the parents, the crossing technique, the relationships between parents and F_1's, several genetic parameters based on the parental and F_1 data, the field plot arrangements, and the characters measured have been reported previously (3).

The data obtained in the field for each character were subjected to the analysis of variance and the sums of squares among genotypes were partitioned into four

comparisons; i.e., parents vs. F_1's, parents vs. F_2's, F_1's vs. F_2's, and among F_2's. Inbreeding depression (I.D.) was measured using the following formula:

$$I.D. = (\bar{F}_1 - \bar{F}_2)/\bar{F}_1$$

where $\bar{F}_1$ and $\bar{F}_2$ are the means of the F_1 and F_2 populations, respectively. Heritability (h^2) was calculated using the formula given by Mahmud and Kramer (6).

RESULTS

Average performances of the F_2's together with the overall means of parents, F_1's and F_2's for the characters evaluated are presented in Table 1. The overall F_1 mean was significantly higher than that of the parents for all characters except the 100-seed weight for which F_1's showed a significantly smaller value. The F_2's on the average, showed a significant decrease in all characters as compared to the F_1 generation. The mean of all characters in the F_2 generation approached those of the parents, but the seed yield, pods per plant, and seeds per plant were still significantly greater than the parents. The relationships between parents and F_1's have previously been discussed in detail (3); it is our aim here to describe characteristics of the F_2 generation in terms of I.D. and h^2 based on the relationships between F_2 and earlier generations.

Estimates of I.D. for different characters and in crosses are reported in Table 2. Very few I.D. values were significant when the cross involved parents belonging to the same commercial group (i.e., $P_1 \times P_2$, $K_1 \times K_2$, or their reciprocals). In fact the crosses U.I. 111 x U.I. 114 and California Red x Montcalm did not exhibit any significant I.D. in any of the characters. The crosses which showed significant I.D. in all traits studied were U.I. 111 x California Red, U.I. 114 x California Red, and Montcalm x U.I. 114. In between-group crosses, when California Red

Table 1. Mean values of different characters for the F_2 progeny and some relative comparisons.

Source of F_2 generation† (male/female)	Seed yield/ plant (g)	Pods/ plant	Seeds/ plant	Seeds/ pod	100-seed wt. (g)
$P_1 \times P_2$	75.7	64.8	190.0	3.16	35.5
$P_2 \times P_1$	59.5	54.2	161.8	3.09	34.4
$P_1 \times K_1$	56.1	61.2	163.7	2.81	32.8
$K_1 \times P_1$	51.6	56.3	157.6	2.87	32.2
$P_1 \times K_2$	57.4	56.4	164.4	2.89	32.7
$K_2 \times P_1$	61.2	59.2	174.8	3.01	33.6
$P_2 \times K_1$	60.4	63.2	179.4	2.82	34.0
$K_1 \times P_2$	64.7	68.8	182.8	3.00	33.2
$P_2 \times K_2$	58.1	62.3	175.4	2.79	34.5
$K_2 \times P_2$	57.2	55.2	164.0	3.18	32.2
$K_1 \times K_2$	49.5	41.2	118.8	2.96	39.0
$K_2 \times K_1$	49.0	42.9	113.7	2.68	39.6
Parental mean	51.7	48.5	136.8	2.81	38.4
F_1 mean	80.1	66.8	216.4	3.25	37.0
F_2 mean	58.4	57.1	161.9	2.94	34.5
Parents vs. F_1's	**	**	**	**	*
Parents vs. F_2's	*	**	**	ns	**
F_1's vs. F_2's	**	**	**	**	**
Among F_2's	**	**	**	**	**

†P_1 = U.I. 111, P_2 = U.I. 114, K_1 = California Red, K_2 = Montcalm.

*,** Significant at the 5 and 1% probability levels, respectively.

Table 2. Estimates of inbreeding depression (I.D.) percentage for different characters and crosses.

Cross† (male/female)	Seed yield/ plant	Pods/ plant	Seeds/ plant	Seeds/ pod	100-seed wt.
$P_1 \times P_2$	-22.73	-19.57	-12.46	-1.28	2.61
$P_2 \times P_1$	20.54*	14.66	20.70*	1.28	5.24
$P_1 \times K_1$	45.24**	31.12**	40.48**	12.46*	11.63**
$K_1 \times P_1$	39.92**	26.27**	32.40**	7.12	11.33**
$P_1 \times K_2$	17.62	4.96	18.60	14.50**	10.73**
$K_2 \times P_1$	28.55**	17.50*	23.82**	4.14	9.24**
$P_2 \times K_1$	40.17**	24.48**	34.23**	14.54**	7.62*
$K_1 \times P_2$	23.18**	4.07	19.47*	6.25	10.52**
$P_2 \times K_2$	28.14**	6.10	19.52*	14.68**	4.96
$K_2 \times P_2$	40.90**	25.26**	38.56**	12.88**	9.75*
$K_1 \times K_2$	14.59	10.66	19.61	6.92	-0.85
$K_2 \times K_1$	18.38	6.02	25.18	20.24**	-0.25
Mean I.D.±S.E., %	24.54±5.25	12.63±4.00	23.34±3.97	9.48±1.84	6.88±1.29

†P_1= U.I. 111, P_2= U.I. 114, K_1= California Red, K_2= Montcalm.

*,**Significant at the 5 and 1% probability levels, respectively.

was used as the female parent, all characters showed I.D. in the F_2 generation. Reciprocal differences, in many cases, affected the magnitude of the I.D. estimates. Values of h^2 percentage based on variances of the parents and their respective F_2 progeny are reported in Table 3. Number of seeds per plant was the most and seed yield the least heritable characters. The within-Pinto crosses, in all cases, and the within-Kidney crosses, in almost half the cases, had h^2 values lower than the mean of all crosses involved. Whereas, in half of the between-group crosses (U.I. 111 x California Red, U.I. 111 x Montcalm, California Red x U.I. 114 and U.I. 114 x Montcalm), the h^2 values were greater than the mean value for all traits measured.

DISCUSSION

Following one generation of natural self fertilization (F_1 to F_2), yield and yield components were significantly decreased (Table 1). The characters previously found (3) to exhibit the highest heterosis (i.e., seed yield and seeds per plant), had also the highest overall I.D. (Table 2). Most of the heterosis obtained from crossing was thus negated by selfing the F_1 generation. This conclusion is in agreement with the results of Kheradnam *et al.* (5) on cowpeas and of Bassiri and Smith (1) on red clover (*Trifolium pratense* L.).

A great part of the superiority of the F_1 crosses for seed yield, pods per plant, seeds per plant, and seeds per pod was due to nonadditive (dominance and epistasis) gene effects (3) and this in turn was the reason for the high I.D. observed for the characters in the F_2 generation. Furthermore, estimates of heterosis and I.D. were similar but in different directions. However, the values obtained for I.D. were generally lower than those for heterosis. This was anticipated, since the estimates of I.D. theoretically account for only 50% of the expected change. The

Table 3. Estimates of heritability (h^2) percentage for different characters and crosses.

Cross† (male/ female)	Seed yield/ plant	Pods/ plant	Seeds/ plant	Seeds/ pod	100-seed wt.
$P_1 \times P_2$	-51.5	27.3	25.9	3.7	-34.5
$P_2 \times P_1$	-11.1	24.8	19.4	30.9	-64.4
$P_1 \times K_1$	40.0	75.6	64.4	67.1	39.1
$K_1 \times P_1$	-35.7	19.4	34.2	36.1	31.3
$P_1 \times K_2$	55.2	66.1	71.5	67.7	61.0
$K_2 \times P_1$	44.4	45.2	57.0	38.5	72.6
$P_2 \times K_1$	61.4	49.9	61.2	35.6	51.2
$K_1 \times P_2$	58.6	74.0	66.6	56.5	51.8
$P_2 \times K_2$	66.8	63.3	74.8	70.4	68.9
$K_2 \times P_2$	69.3	32.8	67.0	55.7	62.4
$K_1 \times K_2$	11.8	6.5	45.8	49.0	39.2
$K_2 \times K_1$	2.4	-3.2	12.0	58.9	45.5
Mean h^2 ±S.E., %	26.0±12.1	40.1±7.6	50.0±6.3	47.5±5.6	35.3±12.1

†P_1= U.I. 111, P_2=U.I. 114, K_1= California Red, K_2=Montcalm.

mean values obtained for heterosis and I.D. in this study are, in general, greater than those obtained by Gritton (4) for the same characters in peas.

Estimates of h^2 for all characters evaluated (Table 3) indicate that a fairly large portion of the observed variation in F_2 generation was due to the genetic make-up of the parental cultivars. Seed yield, with a relatively low h^2 estimate, seems to be highly sensitive to environmental effects. The wide range of h^2 estimates, reflected in the standard error value for yield, further supports the high influence of environmental effects on the yielding ability of the parental lines.

The magnitudes of h^2 estimates reported for yield and yield components of the common beans are contradictory in the literature; whereas Coyne (2) found very low values, Sarafi *et al.* (8) and Sarafi (7) reported very high h^2 estimates for these traits. Although the magnitudes of h^2 obtained in the present work are in agreement with those of the latter investigators, it seems that the discrepancies are due to the method of calculating h^2 and to the generations used.

The relatively low mean h^2 value obtained for yield suggests that in breeding high yielding cultivars, progress would be expected to be rather slow if mass selection was practiced. However, selection on the basis of some specific family means would result in a more rapid progress. Furthermore, seeds per plant which had the highest mean h^2 and a low standard error of h^2 in different crosses, could be regarded as a good indicator of seed yield since it also had a very high association (r=0.98**) with seed yield (3).

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