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HETEROSIS, INBREEDING DEPRESSION AND GENE ACTION OF SOME QUANTITATIVE CHARACTERS IN A DIALLEL CROSS AMONG FIVE WHITE LUPIN GENOTYPES

[42]

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ABSTRACT

The present investigation was carried out at Giza Research Station during 1999/2000, 2000/2001 and at Shandaweel Research Station in 2001/2002 growing seasons. All F_1' and F_2' Hybrids (including reciprocals) in a diallel mating design between five white lupin genotypes differing in origin (Giza-1, Dijon-2, Line 20, Line 37/3 and Kiev Mutant) were studied. Significant differences among genotypes and some crosses were detected for all studied characters, indicating genetic variability for all variables. Significant differences between some hybrids and their reciprocals were observed for all studied charcters, suggesting that earliness, seed yield and its components appeared to be influenced by the female parent. Negative heterosis percentage relative to mid parent was significant in seventeen crosses for days to maturity. Heterosis percentage was significantly positive in twelve, seven, eleven, thirteen, five and twelve crosses for plant height, number of branches, pods, seeds, 100-seed weight and seed yield per plant, respectively. Moreover, heterosis over the better parent was significant in some crosses for all studied characters except number of branches per plant. Eight, eleven, three, six, seven, five and eight crosses expressed significant inbreeding depression in F_2 for days to maturity, plant height, number of branches, pods, seeds, 100-seed weight and seed yield per plant. respectively. Additive component of genetic variability "D" was consistently significant or highly significant over generations for all studied characters. Dominance effects played an important role in the inheritance of all traits. The additive gene action was more important than the non-additive one and selection would be effective in early generations for improving these traits. Narrow sense heritability ranged from 29.0 % for 100-seed weight to 89.7 %for days to maturity. In general, position of array members on the Wr, Vr graph varied widely among generations. For P_1 (Giza-1) and P_4 (Line 37/3) had most recessive alleles for days to maturity. Moreover, P_5 (Kiev Mutant) contained most recessive genes for plant height, number of branches, pods, seeds, 100-seed weight and seed yield per plant.

Key words: White lupin, Diallel cross, Heterosis, Inbreeding depression, Heritability.

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INTRODUCTION

White lupin, *Lupinus albus* L. is an annual grain legume traditionally cultivated around the Mediterranean and along Nile Valley where it is used for human consumption, green manuring and as forage (**Huyghe, 1997**). The species (*L. albus* L) is diploid with 2 n= 50 and a generally self-pollinated crop with an average of 3.7 % outcrossing (**Barbacki and Kapsa, 1960**). The Egyptian genotypes have good productivity, but the high level of alkaloid in the seeds and their late maturity are considered the main problems of the genotypes. Cross breeding and selection in the segregating generations could improve these traits (**Hoballah, 1991**).

Diallel cross technique (**El-Hady *et al* 1998; Abdalla *et al* 1999 and others**) have been used to obtain considerable information on the magnitude of heterosis and to gain a better understanding of the nature of gene action involved in controlling quantitative characters. The exploitation of heterosis through synthetics and ultimately hybrids could pay off in improved yield potential. Several authors reported that the manifestations of heterotic effects in lupins ranged from significantly negative to significantly positive estimates for number of days to maturity, plant height and number of branches per plant as well as for seed yield and its components (**Polkanova and Nagorskaya, 1976; Lukashevich, 1981; Strautina, 1979; Okaz *et al* 1986; Agarkova *et al* 1991 and Sech & Huyghe, 1991**). The studies of Savvicheva (1979) and Lukashevich (1981 & 1983) indicated that early maturity, plant height, number of pods and seeds per

plant as well as 1000 seed weight expressed intermediate inheritance or showed dominance or overdominance depending on the cross of F_1 intervarietal hybrids of *L. luteus*. On the other hand, **Agarkova *et al* (1991)** reported that heterosis for yield and stem length due to the additive effect of recessive genes could be greater than that resulting from heterozygosity in intraspecific hybrids of *L. angustifolius*. **Debelyi and Derbenskii (1988)** found that depression of lateral branching on the central raceme was predominant in hybrids of *L. angustifolius* when a determinate habit variety was the maternal parent.

The estimation of additive and dominance components of genetic variance is very important in evaluating the potential of any heterotic response. Narrow-sense heritability is the ratio of additive genetic variation to phenotypic variation and expresses the extent of resemblance between relatives and allows the determination of the response to selection. **Yassen (1988)** reported that genetic variances were due to dominance or additive effects of genes for flowering time, plant height, yield and some of its components and heritability estimates in narrow sense for 100-seed weight recorded 23.81, 24.61 or not calculated, depending on the cross in F_2 hybrids of *L. albus*. **Sech and Huyghe (1991)** stated that flowering time and reproductive characters showed high heritability and a mainly additive effects in F_1 hybrids of *L. albus*. Moreover, many of the yield characters were controlled by genes with additive effects, indicating that selection for these characters would be likely to be effective as reported by **Klochko *et al* (1996)** in *L. angustifolius*, and **Khotyljova *et al* (1996)** in *L. luteus*.

The present study was undertaken to estimate the magnitude of heterosis and inbreeding depression as well as understanding the nature of gene action and estimating heritability of different characteristics in white lupin hybrids.

MATERIAL AND METHODS

The present investigation was carried out during 1999/2000, 2000/2001 and 2001/2002 using the diallel mating design including reciprocals among five widely diverse white lupin genotypes. Three varieties: Giza-1 (P_1), Dijon-2 (P_2) and Kiev Mutant (P_5) along with the two promising M_6 mutant lines: Line 20 (P_3) and Line 37/3 (P_4), which were assessed and selected from a previous study (**El-Sayad, 1997**), were used as parents in the current investigation. Origin, pedigree and some characteristics of these genotypes are presented in Table (1).

Table 1. Origin, pedigree and some characteristics of the five white lupin genotypes.

Genotype	Origin	Pedigree	Date of maturity	Growth habit	Alkaloid content
P_1 (Giza 1)	Egypt	Land race (local variety)	Late	Indeterminate	High alkaloid (bitter lupin)
P_2 (Dijon 2)	France	French variety	Late	Indeterminate	High alkaloid (bitter lupin)
P_3 (Line 20)	Egypt	M6-induced mutant line derived from the Hungarian cv. Kereskedelmi by 20 KR*	Late	Indeterminate	Moderate alkaloid (bitter lupin)
P_4 (Line 37/3)	Egypt	M6- induced mutant line derived from cv. Giza 2 by 40 KR.	Early	Indeterminate ·	Moderate alkaloid (bitter lupin)
P_5 (Kiev Mutant)	Ukraine	Ukrainian variety derived from cv. White 70 by gamma-ray	Early	Determinate	Free alkaloid (sweet lupin)

* KR of gamma-rays.

In 1999/2000 growing season, all possible cross combinations among the five white lupin parents were made. In the second season (2000 / 2001) rehybridization were made to increase F_1 seeds as well as F_2 seeds were raised from the F_1 plants at Giza Research Station. During 2001/2002 growing season, all the diallel mating progenies were evaluated in a randomized complete block design with three replications at Shandaweel Research Station. Seeds were sown 20 cm within rows, 60 cm apart. Sowing dates took place at early Novem-

ber. Number of plants sampled per plot varied from 10 plants in parents and F_1's to 50 plants in F_2's. The following characters were recorded: number of days from sowing to 90 % maturity of plants per plot, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight (g) and seed yield per plant (g). Differences among genotypes were tested by conducting a regular analysis of variance of complete block design on plot mean basis. Heterosis and inbreeding depression determination were conducted as outlined by **Foolad and Bassiri (1983)**. Appropriate "t" test were made for the significance of the F_1 crosses means from the mid and better parental values (**Wynne et al 1970**) and for the F_2 crosses means from F_1 values (**Al-Rawi and Kohel, 1969**). Values of Vr, Wr genetic components and ratios were estimated according to **Hayman (1954 a & b)**.

RESULTS AND DISCUSSION

Statistical analysis presented in Table (2) revealed highly significant differences among tested genotypes, parents, crosses and parent vs. crosses for most studied characters, indicating wide genetic variability for studied variables.

The mean performance of parents, F_1's and F_2's including reciprocals for different characters are presented in Table (3). Kiev Mutant behaved as the earliest parent in maturity and recorded the lowest value of plant height, number of branches, pods, seeds and seed yield per plant as well as 100-seed weight. Giza-1 was the latest genotype and gave the highest number of branches per plant. Moreover, Dijon-2 had the highest value

of plant height, 100-seed weight and seed yield per plant. Line 20 recorded the highest number of pods and seeds per plant followed by Line 37/3. Regarding the test crosses in F_1 and F_2 generations, four crosses: Line 20 x Kiev Mutant, Line 37/3 x Kiev Mutant and reciprocal and Kiev Mutant x Giza-1 exhibited fewer number of days to maturity. None of the crosses exceeded significantly the tallest parent. The cross Dijon-2 x Giza-1 recorded the highest value of plant height, while crosses Dijon-2 x Kiev Mutant, Line 20 x Kiev Mutant and Line 37/3 x Kiev Mutant had shortest plant heights. Two crosses: Giza-1 x Line 37/3 and Kiev Mutant x Line 37/3 gave higher number of branches per plant. Concerning number of pods/plant, five crosses: Giza-1 x Dijon-2, Dijon-2 x Line 20, Kiev Mutant x Giza-1, Kiev Mutant x Dijon-2 and Kiev Mutant x Line 37/3 exhibited the highest number of pods/plant. Four crosses: Giza-1 x Dijon-2 and reciprocal, Dijon-2 x Line 37/3 and Kiev Mutant x Line 37/3 recorded the highest number of seeds/plant. None of the crosses exceeded the heaviest 100-seed weight parent. Five crosses: Giza-1 x Dijon-2, Dijon-2 x Line 37/3, Line 20 x Dijon-2, Line 37/3 x Giza-1 and Line 37/3 x Line 20 showed higher estimates for 100-seed weight. With regard to seed yield/plant, five crosses: Giza-1 x Dijon-2, Dijon-2 x Line 37/3, Line 20 x Dijon-2, Line 37/3 x Giza-1 and Kiev Mutant x Line 37/3 exhibited highest values for this trait. The previously mentioned crosses would prospect in white lupin breeding for improving the maturity date and productivity.

Regarding to reciprocal effects (Table 3), results revealed significant differences between some hybrids and their

Table 2. Mean squares of variance for number of days to maturity, plant height, number of branches, pods, seeds, 100-seed weight and seed yield per plant in F_1 and F_2 of 5 parental diallel cross.

Source of variance	Df	Days to maturity		Plant height		No. of branches/plant		No. of pods/plant	
		F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Replicates	2	0.50	0.63	34.06	4.69	0.38	1.15*	38.02**	2.70
Genotypes	24	208.65**	104.08**	1408.59**	2333.91**	2.30**	2.47**	94.95**	84.17**
Parents	4	217.27**	217.27**	6031.60**	6031.60**	6.66**	6.66**	249.35**	250.01**
Crosses	19	206.59**	84.30**	322.53**	1653.38**	1.29**	1.52**	55.59**	46.97**
P. vs. C	1	213.31**	26.44*	3551.72**	473.09**	4.01**	3.75**	225.19**	127.66**
Error	48	4.47	4.07	22.28	27.33	0.93	0.32	5.13	3.81

* and ** significant at 5 % and 1 % level of probability, respectively.

Table 2. Cont'd

Source of variance	df	No. of seeds/plant		100-seed weight		Seed yield / plant	
		F_1	F_2	F_1	F_2	F_1	F_2
Replicates	2	15.13	38.56	2.77	2.48	32.22	1.73
Genotypes	24	1305.59**	1408.58**	29.83**	31.54**	259.22**	211.64**
Parents	4	2946.57**	2946.57**	52.23**	52.23**	546.73**	546.73**
Crosses	19	803.90**	967.92**	25.83**	28.76**	169.10**	136.84**
P. vs. C	1	4273.92**	3629.17**	16.04	1.49	821.54**	292.46**
Error	48	78.85	42.23	7.18	3.05	21.17	9.44

* and ** significant at 5% and 1% level of probability, respectively.

Table 3. Mean performance of parents, F_1 and F_2 generations for the studied characters.

Genotype	Days to maturity		Plant height (cm)		No. of branches/plant		No. of pods/plant	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
P_1 (Giza-1)	177.5		160.4		6.8		33.0	
P_2 (Dijon -2)	172.5		177.1		6.1		28.7	
P_3 (Line 20)	171.0		154.3		6.0		35.3	
P_4 (Line 37/3)	161.8		166.5		6.4		30.9	
P_5 (Kiev Mutant)	157.6		66.0		3.1		12.9	
P_1 x P_2	171.3	170.6	163.3	162.6	5.9	6.9	38.1	35.2
P_1 x P_3	175.0	175.0	164.6	175.3	6.2	7.1	34.1	29.0
P_1 x P_4	186.3	170.0	163.7	147.2	7.6	6.1	29.3	26.5
P_1 x P_5	164.0	161.3	154.3	96.4	5.7	5.2	27.6	25.8
P_2 xP_1	169.6	171.0	172.4	178.4	6.8	6.8	40.4	29.8
P_2 x P_3	166.0	168.6	166.9	151.3	6.6	7.3	30.2	41.1
P_2 x P_4	163.6	168.0	147.3	167.2	6.1	7.0	35.0	28.8
P_2 x P_5	160.6	160.6	147.9	107.5	6.0	5.2	33.8	27.3
P_3 x P_1	169.6	167.0	174.8	165.1	6.9	6.2	35.3	32.3
P_3 x P_2	166.0	176.3	161.5	171.7	6.1	6.2	36.8	32.8
P_3 x P_4	162.0	169.3	155.3	142.3	5.7	6.6	32.3	35.3
P_3 x P_5	159.0	161.0	138.9	125.4	6.0	5.7	19.8	31.5
P_4 xP_1	164.6	170.6	170.6	166.4	6.6	6.3	30.9	36.3
P_4 x P_2	164.3	165.3	170.9	171.5	6.8	5.6	31.7	31.4
P_4 x P_3	166.6	166.0	168.8	153.1	5.8	6.3	32.2	31.5
P_4 x P_5	154.6	158.3	153.4	114.7	4.5	5.2	33.7	27.7
P_5 x P_1	153.3	163.0	168.2	158.7	6.7	5.7	35.4	28.0
P_5 x P_2	154.3	164.6	170.8	166.6	5.7	7.2	34.1	33.9
P_5 x P_3	153.3	168.0	156.5	160.4	6.4	6.7	32.1	34.4
P_5 x P_4	153.6	157.0	160.2	139.4	6.8	7.1	32.4	35.3
LSD 0.05	3.54	3.31	7.75	8.58	1.03	0.93	3.72	4.58
0.01	4.72	4.41	10.33	11.44	1.37	1.24	4.95	6.11

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Table 3. Cont'd.

Genotype	No. of seeds/plant		100-seed weight (g)		Seed yield/plant (g)	
	F_1	F_2	F_1	F_2	F_1	F_2
P_1 (Giza-1)	117.0		37.0		42.1	
P_2 (Dijon -2)	115.3		44.3		49.0	
P_3 (Line 20)	125.5		38.6		47.3	
P_4 (Line 37/3)	123.3		37.5		46.2	
P_5 (Kiev Mutant)	50.6		32.5		16.7	
P_1 x P_2	152.0	133.6	38.2	40.4	55.1	51.4
P_1 x P_3	115.0	108.9	38.5	36.3	44.0	39.4
P_1 x P_4	111.1	108.2	39.2	38.4	43.4	41.6
P_1 x P_5	100.8	99.7	40.6	36.3	40.5	36.2
P_2 xP_1	149.7	134.0	40.8	32.9	60.6	38.3
P_2 x P_3	100.6	167.8	41.0	34.2	41.2	57.1
P_2 x P_4	130.8	131.9	41.8	39.5	55.2	52.6
P_2 x P_5	130.2	106.3	36.7	33.9	43.8	34.7
P_3 x P_1	134.8	131.9	33.4	36.8	45.8	48.2
P_3 x P_2	137.0	126.6	44.6	35.5	61.9	44.5
P_3 x P_4	132.3	125.4	37.4	34.7	49.5	42.1
P_3 x P_5	91.3	108.2	35.5	40.4	30.0	42.2
P_4 xP_1	119.0	149.8	41.4	38.2	49.4	56.9
P_4 x P_2	136.0	115.5	39.6	39.9	53.9	43.6
P_4 x P_3	107.4	120.7	42.5	40.4	45.7	48.2
P_4 x P_5	134.1	90.6	39.2	40.4	51.7	36.2
P_5 x P_1	143.0	113.1	36.0	37.3	52.5	43.1
P_5 x P_2	114.0	137.8	35.9	39.2	40.7	54.0
P_5 x P_3	139.2	125.9	35.8	34.6	49.4	42.7
P_5 x P_4	129.7	132.9	42.8	36.2	51.8	46.7
LSD $_{0.05}$	14.57	10.66	4.40	2.86	7.55	5.04
$_{0.01}$	19.43	14.22	5.86	3.82	10.07	6.72

reciprocals. One cross (Line 20 x Giza-1) for days to maturity , two crosses (Dijon-2 x Giza-1 and Kiev Mutant x Line 37/3) for plant height, one cross (Kiev Mutant x Line 37/3) for number of branches/plant, two crosses (Line 20 x Giza-1 and Kiev Mutant x Giza-1) for number of seeds/plant, one cross (Line 37/3 x Line 20) for seed index and one cross (Kiev Mutant x Giza-1) for seed yield/plant in both of F_1 and F_2 as well as two crosses (Kiev Mutant x Dijon-2 and Kiev Mutant x Line 73/3) in F_2 expressed significant reciprocal effects. Results suggested that earliness, seed yield and its components appeared to be influenced by the female parent. Reciprocal differences may result from plasmon differences or plasmon gene interactions. Also, maternal effects showed possibility to pass from F_1 to F_2. The fact that such effects were detected in F_2 indicated the importance of maternal and plasmon effects in inheritance of these characters.

Heterosis percentages relative to mid $\overline{(MP)}$ and better $\overline{(BP)}$ parent are presented in Table (4). Regarding number of days to maturity, data showed that seventeen crosses were significantly earlier than the means of mid-parents with heterosis percentage ranging from –1.7 to –8.5. Additionally, heterosis percentages relative to mid parent were significantly positive in twelve, seven, eleven, thirteen, five and twelve crosses with a range of 4.3–48.6; 15.2-42.2; 15.0-63.9; 9.6-70.6; 11.0-22.3 and 13.2-78.6 % for plant height, number of branches, pods, seeds, 100-seed weight and seed yield/plant, respectively. However heterosis percentages relative to better parent were significant in five, two, five, four, one and three crosses with a range of –2.5 to –2.9; 4.9-9.0; 13.3-22.4; 12.9-29.9; 14.1 and 23.7-26.3% for days

to maturity, plant height, number of pods, seeds, 100-seed weight and seed yield per plant, respectively. The high magnitudes of heterotic values found in these materials were expected due to the diversity of the parents. Therefore, improvement would be expected from selection in the advanced segregating generations. **Yassen (1984)** found significant heterosis over mid parent for days to flowering, plant height, pods/ plant, seeds / pod, 100-seed weight and seed yield/plant. These findings are in accordance with those reported by **Lukashevich (1981); Strautina (1979) and Agarkova et al (1991).**

Results of inbreeding depression in F_2 generation for studied traits are given in Table (4). Concerning number of days to maturity, eight crosses exhibited significant inbreeding depression ranging from –2.4 to –9.5 %. Moreover, eleven, three, six, seven, five and eight crosses expressed significant inbreeding depression in F_2 for plant height, number of branches, pods, 100-seed weight and seed yield per plant with a range of 5.6-37.5; 14.9-19.7; 14.9-20.9; 9.6-32.4; 10.6-20.4 and 13.6-36.8 %, respectively. On the other hand, significant inbreeding gain was observed in some F_2 crosses for some studied characters. These results are in general agreement with those reported by **Abdalla et al (1999)** in faba beans.

Estimates of the genetic and environmental components of variance and other statistics derived from these estimates are presented in Table (5). Additive components of genetic variability (D) were significant or highly significant for all traits, indicating that the additive gene action was more important than the non- additive in controlling the inheritance of the

Table 4. Percentage of heterosis over mid parent (MP) and better parent (BP) as well as percentage of inbreeding depression (ID) for various studied characters.

Cross	Days to maturity			Plant height			No. of branches/plant			No. of pods/plant		
	Heterosis over MP	Heterosis over BP	Inbreeding depression ID	Heterosis over MP	Heterosis over BP	Inbreeding depression ID	Heterosis over MP	Heterosis over BP	Inbreeding depression ID	Heterosis over MP	Heterosis over BP	Inbreeding depression ID
P₁ x P₂	-2.1**	-0.7	0.4	-3.3	-7.8*	0.4	-9.2	-13.2	-16.9*	23.3**	15.5**	7.6
P₁ x P₃	0.3	2.3*	0.0	4.6*	2.6	-6.5**	-3.1	-8.8	-14.5	-0.3	-3.4	14.9*
P₁ x P₄	9.8**	15.1**	8.8**	0.1	-1.7	10.1**	15.2*	11.8	19.7**	-8.4	-11.2	9.6
P₁ x P₅	-2.2**	4.1**	1.7	36.3**	-3.8	37.5**	14.0	-16.2*	8.8	20.0**	-16.4**	6.5
P₂ xP₁	-3.1**	-1.7	-0.8	2.1	-2.7	-3.5	4.6	0.0	0.0	30.7**	22.4**	26.2**
P₂ x P₃	-3.4**	-2.9**	-1.6	0.7	-5.8*	9.4**	10.0	8.2	-10.6	-5.6	-14.4**	-36.1**
P₂ x P₄	-2.2**	1.1	-2.7*	-14.3**	-16.8**	-13.5**	-3.1	-4.7	-14.8	17.5**	13.3*	17.7**
P₂ x P₅	-2.7**	1.9	0.0	21.6**	-16.5**	27.3**	30.4**	-1.6	13.3	62.5**	17.8**	19.2**
P₃ x P₁	-2.8**	-0.8	-1.5	11.1**	9.00**	5.6*	7.8	1.5	10.1	3.2	0.0	8.5
P₃ x P₂	-3.4**	-2.9**	-6.2**	-2.5	-8.8**	-6.3*	1.7	0.0	-1.6	15.0**	4.2	10.9
P₃ x P₄	-2.6**	1.2	-4.5**	9.0*	-6.7**	8.4**	-8.1	-10.9	-15.8	-2.4	-8.5	-9.3
P₃ x P₅	-3.2**	0.9	-1.3	26.0**	-10.0**	9.7**	33.3**	0.0	5.0	-17.8**	-43.9**	-59.1**
P₄ xP₁	-3.0**	1.7	-3.7**	4.3*	2.5	2.5	0.0	-2.9	4.6	-3.4	-6.4	-17.5*
P₄ x P₂	-1.7*	1.5	-0.6	-0.5	-3.5	-0.4	7.9	6.3	17.7*	6.4	2.6	0.9
P₄ x P₃	-0.1	3.0**	0.4	5.3*	1.4	9.3**	-6.5	-9.4	-8.6	-2.7	-8.8	2.2
P₄ x P₅	-3.1**	-1.9	-2.4*	31.9**	-7.9**	25.2**	-6.3	-29.7**	-15.6	53.9**	9.1	17.8**
P₅ x P₁	-8.5**	-2.7*	-6.3**	48.6**	4.9*	5.7*	34.0**	-1.5	14.9*	53.9**	7.3	20.9**
P₅ x P₂	-6.5**	-2.1	-6.7**	40.5**	-3.4	2.5	23.9**	-.6.6	-26.3**	63.9**	18.8**	0.6
P₅ x P₃	-6.7**	-2.7*	-9.5**	42.0**	1.4	-2.5	42.2**	6.7	-4.7	33.2**	-9.1	-7.2
P₅ x P₄	-3.8**	-2.5*	-2.2	37.8**	-3.8	12.9**	41.7**	6.3	-4.4	47.9**	4.9	-8.9

* and ** significant at 5 % and 1 % level of probability, respectively.

Table 4. Cont'd

Cross	No. of seeds / plant			100-seed weight			Seed yield / plant		
	Heterosis over MP	Heterosis over BP	Inbreeding depression ID	Heterosis over MP	Heterosis over BP	Inbreeding depression ID	Heterosis over MP	Heterosis over BP	Inbreeding depression ID
$P_1 \times P_2$	30.8**	29.9**	12.1**	-6.1	-13.8**	-5.8	20.8**	12.4	6.7
$P_1 \times P_3$	-5.2	-8.4	5.3	1.9	-0.3	5.7	-1.6	-7.0	10.5
$P_1 \times P_4$	-7.6	-9.9	2.6	5.1	4.5	2.0	-1.8	-6.1	4.2
$P_1 \times P_5$	20.3**	-13.8*	1.1	16.7**	9.7	10.6*	37.8**	-3.8	10.6
$P_2 \times P_1$	28.8**	27.9**	10.5*	0.2	-7.9	19.4**	32.9**	23.7**	36.8**
$P_2 \times P_3$	-16.5**	-19.8**	-66.8**	-0.7	-7.5	16.6**	-14.5*	-15.9*	-38.6**
$P_2 \times P_4$	9.6*	6.1	-0.8	2.2	-5.6	5.5	16.0**	12.7	4.7
$P_2 \times P_5$	56.9**	12.9*	18.4**	-4.4	-17.2**	7.6	33.1**	-10.6	20.8**
$P_3 \times P_1$	11.1*	7.4	2.2	-11.6*	-13.5*	-10.2	2.5	-3.2	-5.2
$P_3 \times P_2$	13.8**	9.2	7.6	8.0	0.7	20.4**	28.4**	26.3**	28.1**
$P_3 \times P_4$	6.4	5.4	5.2	-1.8	-3.1	7.2	5.8	4.7	14.9*
$P_3 \times P_5$	3.6	-27.3**	-18.5**	-0.3	-8.0	-13.8*	-6.3	-36.6**	-40.7**
$P_4 \times P_1$	-1.0	-3.5	-25.9**	11.0*	10.4	7.7	11.8	6.9	-15.2*
$P_4 \times P_2$	14.0**	10.3	15.1**	-3.2	-10.6*	-0.8	13.2*	10.0	19.1**
$P_4 \times P_3$	-13.7**	-14.4*	-12.4*	11.6*	10.1	4.9	-2.4	-3.4	-5.5
$P_4 \times P_5$	54.1**	8.8	32.4**	12.0*	4.5	-3.1	64.1**	11.9	29.9**
$P_5 \times P_1$	70.6**	22.2**	20.9**	3.5	-2.7	-3.6	78.6**	24.7**	17.8**
$P_5 \times P_2$	37.4**	-1.1	-20.9**	-6.5	-19.0**	-8.4	23.7**	-16.9	-32.7**
$P_5 \times P_3$	58.0**	10.9	9.6*	-4.0	-7.3	3.4	54.4**	4.4	13.6*
$P_5 \times P_4$	49.1**	5.2	-2.5	22.3**	14.1*	15.4**	64.4**	12.1	9.9

* and ** significant at 5 % and 1 % level of probability, respectively.

Table 5. Estimates of genetic and environmental components with mean of genetic estimates and heritability values for various studed characters in F_1's and F_2's diallel cross.

Genetic	Days to maturity		Plant height	
components	F_1	F_2	F_1	F_2
D	7093** ±6.64	71.11** ± 1.61	2002.95** ± 45.84	2001.73** ± 45.84
H_1	59.07* ± 17.50	13.06± 4.36	1449.31** ± 123.82	512.19 ± 218.17
H_2	44.99± 15.84	9.81± 3.95	944.73** ± 112.31	363.19 ± 197.88
F	-21.84 ± 16.15	9.07 ± 4.04	1978.04** ± 114.53	1002.17* ± 201.8
h^2	44.56* ± 10.69	4.79 ± 2.67	752.79** ± 75.82	95.27 ± 133.60
E	1.49± 2.64	1.31± 0.66	7.58 ± 18.71	8.81 ± 32.98
$(H_1/D)^{1/2}$	0.913	0.429	0.851	0.506
$H_2/4H_1$	0.190	0.188	0.163	0.177
K_D/K_R	0.823	1.188	2.008	1.800
h^2/H_2	0.990	0.489	0.797	0.262
Heritability	0.807	0.897	0.521	0.852
t^2	0.175	0.001	0.002	0.088

* and ** significant at 5 % and 1 % level of probability, respectively.

Table 5. Cont.

Genetic components	No. of branches/plant		No. of pods/plant		No. of seeds/plant	
	F_1	F_1	F_1	F_1	F_1	F_1
D	2.09** ± 0.11	2.10** ± 0.13	81.21** ± 10.38	80.82** ± 3.76	956.75** ± 82.33	968.16** ± 57.61
H_1	1.20* ± 0.29	1.23* ± 0.36	92.76* ± 28.05	49.15 ± 10.15	1253.04* ± 222.36	723.83* ± 155.59
H_2	0.87* ± 0.26	0.81 ± 0.33	67.09 ± 25.43	33.14* ± 9.20	910.13* ± 201.68	560.08* ± 141.13
F	1.68 ** ± 0.27	1.75** ± 0.33	81.38* ± 25.94	67.15** ± 9.38	1088.36* ± 205.67	681.11*± 14392
h^2	0.77* ± 0.17	0.72* ± 0.22	45.56 ± 17.17	25.06 ± 6.21	895.44** ± 136.16	765.20**± 95.28
E	0.13 ± 4.38	0.12 ± 5.42	2.15 ± 4.23	2.53 ± 1.53	25.43 ± 33.61	14.03 ± 23.52
$(H_1/D)^{1/2}$	0.759	0.765	1.069	0.779	1.144	0.865
$H_2/4H_1$	0.181	0.164	0.181	0.169	0.182	0.193
K_D/K_R	1.879	1.914	1.742	1.888	1.805	1.614
h^2/H_2	0.888	0.897	0.679	0.756	0.984	1.366
Heritability	0.517	0.549	0.403	0.578	0.295	0.594
t^2	0.008	0.023	0.008	0.008	0.003	0.015

* and ** significant at 5 % and 1 % level of probability, respectively.

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Table 5. Cont.

Genetic components	100-seed weight (g)		Seed yield / plant (g)	
	F_1	F_2	F_1	F_1
D	15.08* ± 2.65	16.40* ± 2.84	175.04** ± 22.16	179.20** ± 0.86
H_1	14.51 ± 7.18	22.76 ± 7.69	177.15 ± 59.86	89.43** ± 2.33
H_2	12.09 ± 6.51	13.66 ± 6.98	142.45 ± 54.29	63.19** ± 2.11
F	8.71 ± 6.46	21.90 ± 7.11	133.81 ± 55.36	136.47** ± 2.16
h^2	1.92 ± 4.39	-0.33 ± 4.71	170.70* ± 36.65	60.44** ± 1.43
E	2.34 ± 1.08	1.01 ± 1.16	7.20 ± 9.04	3.04** ± 0.35
$(H_1/D)^{1/2}$	0.981	1.178	1.006	0.706
$H_2/4H_1$	0.208	0.150	0.201	0.177
K_D/K_R	1.410	1.972	1.562	1.903
h^2/H_2	0.159	-0.024	1.198	0.956
Heritability	0.450	0.290	0.470	0.647
t^2	0.755	0.117	0.045	0.004

* and ** significant at 5 % and 1 % level of probability, respectively.

characters and that selection would be effective for these traits in segregating generations. In each case H_1 and H_2 (dominance components of genetic variance) were highly significantly different from zero and H_1 was greater than H_2 in all cases, indicating that the positive and negative alleles at the loci for these traits were not equal in proportion in the parents. Theoretically, H_2 should be equal to or less than H_1 **(Hayman, 1954 b)**. H_1 vales were greater than D for 100-seed weight, suggesting that non-additive genetic variance is more important than the additive variance. These results are in general agreement with those obtained by **Sech & Huyghe (1991) and Khotyljova et al (1996)**. The covariance of additive and dominance effects (F) was insignificantly negative in one case (number of days to maturity in F_1) and significantly positive in other traits. Negative estimates of F indicate excess of recessive alleles, while the positive estimates of F indicate excess of dominant ones. Overall dominance effects of heterozygous loci (h^2) was insignificantly negative in one case (100-seed weight in F_2), while these effects were positive and significant in other traits, indicating that the effect of dominance was due to heterozygosity and that direction of dominant was positive. `All estimates of the environmental variance (E) were insignificant for all traits studied except seed yield per plant, indicating that this trait has been affected by environmental factors. **Yassen (1988) and Sech & Huyghe (1991)** found high estimates of environmental variance (E) in white lupin seed yield. Overall degree of dominance estimated by $(H_1/D)^{1/2}$ ranged from complete to over dominance in number of pods, seeds, seed yield/plant and 100-seed weight which suggested

that the over dominance or espistasis are important in the inheritance of these traits. However, for number of days to maturity, plant height and number of branches/plant, the dominance relationship was suggested to be partial. Results reported by **Yassen (1988); Sech and Huyghe (1991) and Klochko et al (1996)** supported the evidence that both additive and dominance gene action are the most important components controlling variation in number of days to maturity, seed yield and its components. In general, the values of $H_2/4 H_1$ were slightly below the maximum value of 0.25, which arises when u=v=0.5 over all loci, indicating that positive and negative alleles were not equally distributed among the parents. The estimates of K_D/K_R were greater than one for all traits, indicating excess of dominant genes in the parents. The number of effective factors h^2/H_2 ranged from –0.024 to 1.366. It may be noted that this value is underestimated either when the dominance effects of all genes concerned are not equal in size and direction or when the distribution of the genes is correlated or when both conditions are fulfilled **(Jinks, 1954)**. Narrow sense heritability estimates ranged from 0.290 for 100-seed weight to 0.897 for number of days to maturity. These results indicated that dominant genetic variance was more important for number of seeds/plant and 100-seed weight. However, days to maturity, plant height, number of branches, pods and seed yield/plant are mostly controlled by additive gene action and it is possible to breed for improving these traits. These results are in accordance with those reported by **Yassen (1988); Sech and Huyghe (1991) and Klochko et al (1996)** in lupins. Significance of t^2

indicated the failure of the hypotheses postulated by **Hayman (1954 b).**

The Vr and Wr graphs are presented in Figs (1 to 14). The slope of the regression line in the Vr, Wr graph did not differ from unity for all traits except number of days to maturity in F_2 but was significantly different from zero for all characters except 100-seed weight in F_1 and F_2 generations. These results revealed the absence of genic interaction for all traits. However, days to maturity had complementary type of epistasis. The insignificant difference of the regression coefficient from zero indicated no real relationship among Vr and Wr and no further reliable interaction could be made.

The intercepts of the regression lines on the Wr axis deviated below the origin and showed over dominance for number of seeds / plant in F_1. For the remaining traits partial dominance was observed as the regression lines deviated above the origin. The distribution of the parental arrays along the regression line for all the characters suggested wide distribution of dominant and recessive alleles among the parents. The scattering of parental arrays provided the information about the presence of different types of alleles in different parents for different characters

which is useful in practicing selection of parents for improving specific characters. However, the Vr, Wr graph varied among generations. This may be attributed to the large environmental variance. In the present study visual inspection of array points on the regression line of Vr, Wr graph will be restricted to all characters in F_1 and F_2. For number of days to maturity array points for P_1 (Giza-1) and P_4 (Line 37/3) were farthest from the origin and had recessive alleles, while P_5 (Kiev Mutant) appeared to possess most dominant alleles in this respect. On the other hand, P_5 (Kiev Mutant) was the farthest from the origin and had recessive alleles for plant height, number of branches, pods, seeds and seed yield per plant. With respect to 100-seed weight P_2 (Dijon-2) and P_5 (Kiev Mutant) were farthest from the origin and contained most recessive genes. In general, the graphic analysis indicated the inconsistency of array points over generations and that neither of the parents had the possible complete dominance or recessive alleles for any of the characters. It is, therefore, possible to accumulate the favourable genes in the parents by using appropriate breeding procedures, i.e. recurrent selection.

Dialled analysis in white lupin
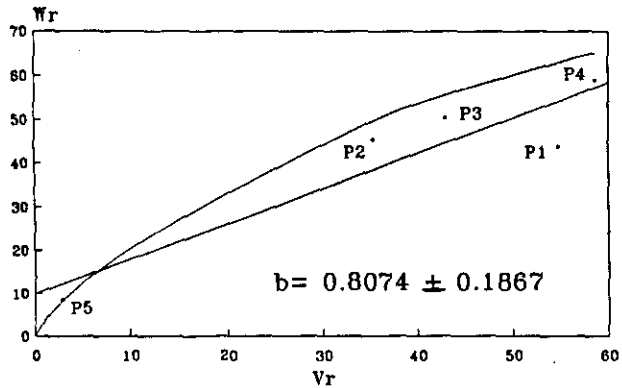
Fig.(1):Wr/Vr relationship for
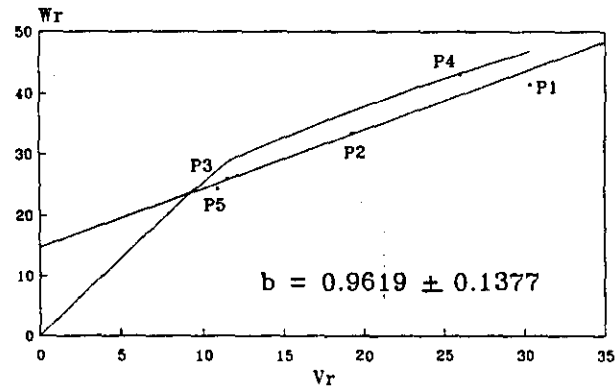No. of days to maturity in F1 generation

Fig.(2):Wr/Vr relationship for
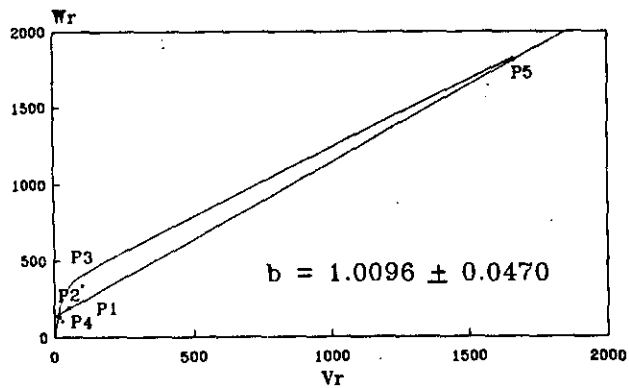No. of days to maturity in F2 generation

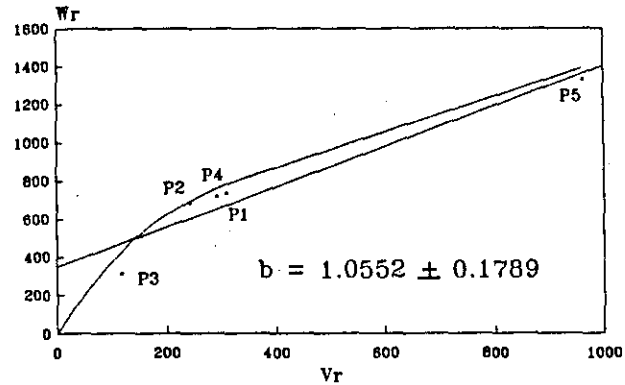Fig.(3):Wr/Vr relationship for
Plant height in F1 generation

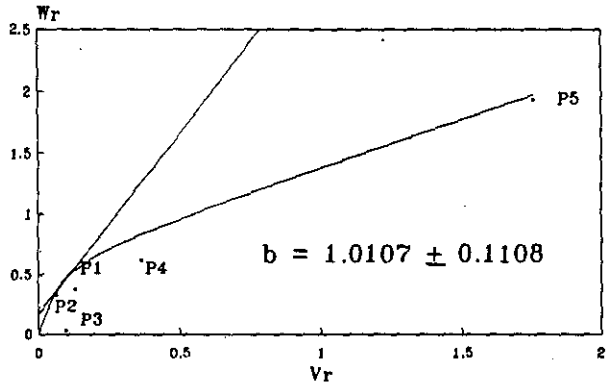Fig.(4):Wr/Vr relationship for
Plant height in F2 generation

Fig.(5):Wr/Vr relationship for
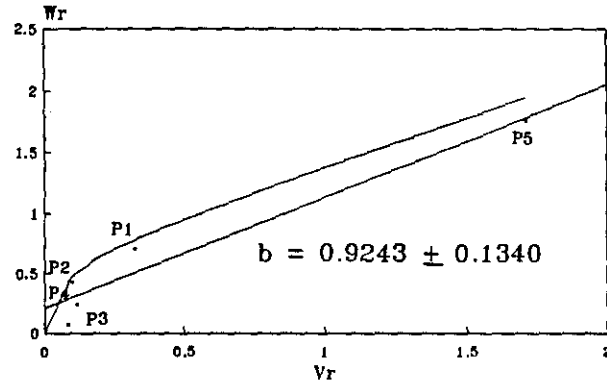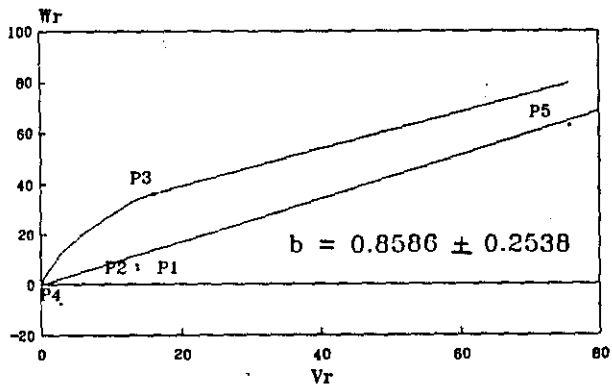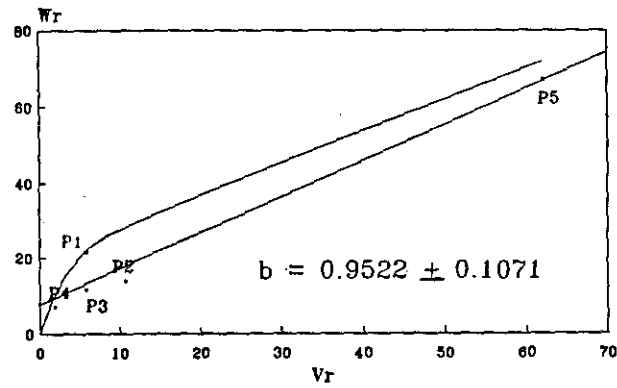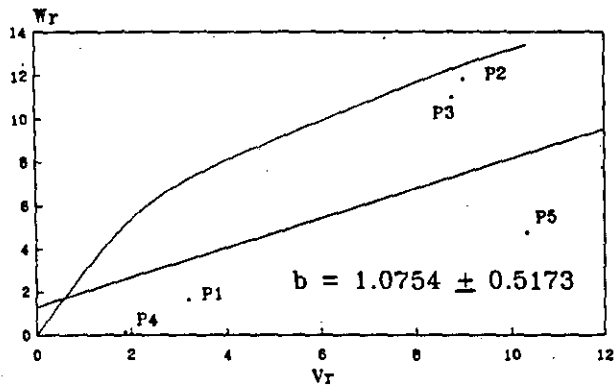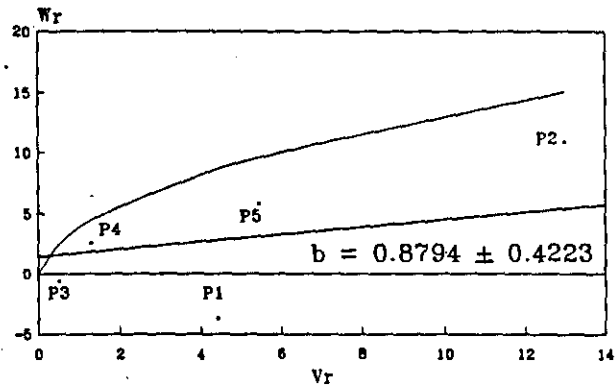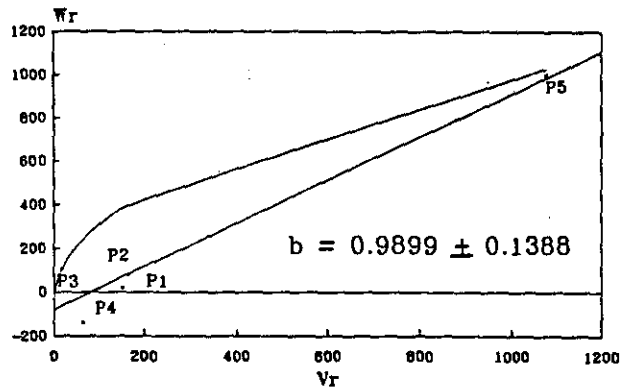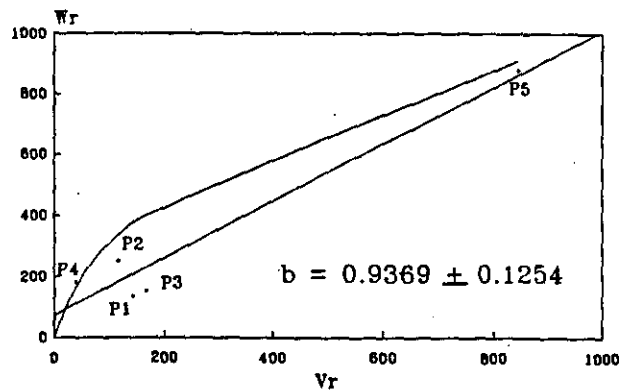No. of branches/plant in F1 generation

$$b = 1.0107 \pm 0.1108$$

Fig.(6):Wr/Vr relationship for
No. of branches/plant in F2 generation

$$b = 0.9243 \pm 0.1340$$

Fig.(7):Wr/Vr relationship for
No. of pods/plant in F1 generation

$$b = 0.8586 \pm 0.2538$$

Fig.(8):Wr/Vr relationship for
No. of pods/plant in F2 generation

$$b = 0.9522 \pm 0.1071$$

Fig.(9):Wr/Vr relationship for
100-Seed weight in F1 generation

$b = 1.0754 \pm 0.5173$

Fig.(10):Wr/Vr relationship for
100-Seed weight in F1 generation

$b = 0.8794 \pm 0.4223$

Fig.(11):Wr/Vr relationship for
No. of seed/plant in F1 generation

$b = 0.9899 \pm 0.1388$

Fig.(12):Wr/Vr relationship for
No. of seed/plant in F2 generation

$b = 0.9369 \pm 0.1254$
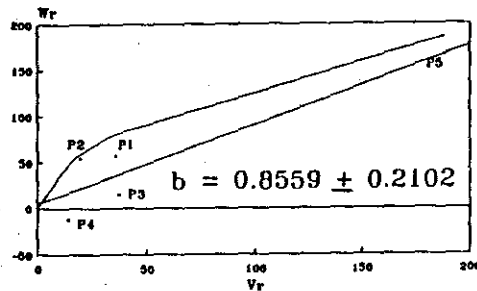
Fig.(13):Wr/Vr relationship for
seed yield/plant in F1 generation

$$b = 0.8559 \pm 0.2102$$
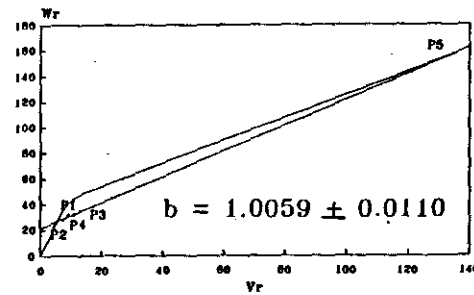
Fig.(14):Wr/Vr relationship for
seed yield/plant in F2 generation

$$b = 1.0059 \pm 0.0110$$

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قوة الهجين والتدهور نتيجة للتربية الذاتية والفعل الجينى لبعض الصفات الكمية للهجن التبادلية بين خمسة تراكيب وراثية من الترمس

[٤٢]

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١- قسم بحوث المحاصيل البقولية-معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية- الجيزة-مصر

أجريت هذه الدراسة على خمسة آبـاء (جيزة-١ ، ديجون-٢، السلالة ٢٠، السلالة ٣٧/٣، طفرة كييف) من الـترمس وجميـع الهجن التبادلية بينها متضمنة الهجن العكسية فى الجيل الأول والثـاني خـلال المواسـم ١٩٩٩ / ٢٠٠٠ ، ٢٠٠٠ / ٢٠٠١ ، ٢٠٠١ / ٢٠٠٢ بهدف تقدير قـوة الـهجين والتدهور نتيجة للتربية الذاتية وكذلك لدراسة

فعل الجين وتقدير نسبة التوريـث والتوقـع
بإمكانية تحسين صفات عـدد الأيـام حتـى
النضج- طول النبات- عدد الفروع للنبـات-
عــدد القرون للنبات-عدد البذور للنبــات-
وزن ١٠٠ بــذرة – وزن محصول النبات.

أظهرت النتائج تفوق بعض هجن الجيـل
الأول تفوقاً معنوياً مقارنة بمتوسط الأبويـن
والأب الأحسن، كذلك حدث تدهور معنـوى
فى نباتات الجيل الثانى لبعض الهجن نتيجـة
للتربية الذاتية لجميع الصفات المدروسة.

كان هناك تأثيرات معنوية وثابتة خـلال
الجيلين لبعض الـهجن العكسـية لجميـع
الصفات المدروسة ممـا يوضـح أهميـة
التأثيرات الأمية فى وراثة هـذه الصفات.

أظهر تحليل النتـائج أن العوامـل ذات
الأثر التجميعى كــانت معنويـة أو عاليـة
المعنوية وثابتة باختلاف الأجيـال لجميـع
الصفات المدروسة وكان هناك أيضــاً دوراً
لتأثير السيادة لجميع الصفات. وكان تــأثير
العوامل ذات الأثر التجميعى أكثر أهمية مـن

دور العوامل ذات الأثر غير التجميعى فـى
وراثة الصفات المدروسة مما يؤكد جـدوى
الإنتخاب لـهذه الصفـات خـلال الأجيـال
الإنعزالية المبكرة.

تراوحت كفاءة التوريث بالمعنى الخـلص
مـن ٢٩ % لصفـة وزن ١٠٠ بذرة إلـى
٨٩,٧ % لصفة عدد الأيام مـن الزراعـة
حتى النضج.

أظهرت الأشكــال البيانية لتوزيع الآبـاء
حـول خط الانحدار انه كان مختلفا مـن
جيل إلى آخر ولكن بوجه عـام كان الأب
الأول (جيزة-١) والأب الرابــع (السـلالة
٣/٣٧) يحتوى كل منـها علـى معظـم
العوامل المتنحية لصفة عـدد الأيـام حتـى
النضج بينما كـان الأب الخـامس (طفـرة
كييف) محتويا على معظم العوامل المتنحيـة
لصفة طـول النبــات وعـدد الفـروع
للنبات وعـدد القرون للنبات وعدد البذور
للنبات ووزن ١٠٠ بـذرة ووزن محصـول
النبات.