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BIOMETRICAL ANALYSIS OF SOME IMPORTANT QUANTITATIVE CHARACTERS IN SNAPDRAGON (*Antirrhinum majus*, L.).

Part II : Flowering Characteristics.

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ABSTRACT

Intraspecific hybridization among four cultivars of snapdragon, i.e. P_1 = Sonnet wit (white), P_2 = Sonnet karmijn (red), P_3 = Sonnet rose (rose) and P_4 = Sonnet geel (yellow) was carried out during three successive seasons: 95/1996, 96/1997 and 97/1998 at Antoniadis Botanical Garden, Horticulture Research Institute, Agriculture Research Center, Alexandria, Egypt.

The main objective of this work was to produce new patterns of snapdragon, especially with reference to flower characteristics. Diallel cross analysis was used to study and determine the genetic system controlling flower traits and also the type of gene action for the different traits.

The results showed that the additive and dominance gene effects were important in the inheritance of days to: first flower bud, showing colour and opening of the first floret. In the F_1, dominance gene effect was significant. The degree of dominance and Wr, Vr graph indicated overdominance in the F_1, but partial dominant in the F_2. Most of dominant genes acted toward earliness. The parents P_1 and P_2 have most dominant genes. All F_1 – progenies achieved negative heterosis towards the earliness.

As for the number of spikes, the additive gene effects were important in the inheritance of that trait and overdominance was involved in the F_1 and F_2 generations. Dominance genes seemed to be acting in negative direction in the F_1, while in the F_2, dominance seemed to be acting in positive direction. Heritability in narrow sense was moderate in the F_1 hybrids but low in the F_2 generations, which indicated that environment effect had minor effect on this trait. Most of the F_1 – progenies obtained hybrid vigour.

With respect to spike length, the additive and dominance gene effects were important in the inheritance of this trait and overdominance was involved. Dominance genes seemed to be acting in positive direction and increasing spike length. Narrow sense heritability was moderate in the F_1 but low in the F_2. Environmental component was significant in both generations. F_1 – progenies achieved hybrid vigour.

As for the number of florets per spike, the dominance gene effect played the major role in the inheritance of this trait and overdominance was involved. In addition, additive gene variance was significant in the F_2 generations only indicating that it was possible to accumulate the favorable genes. Heritability in narrow sense was moderate to low in the F_1 hybrids and F_2 generations. Dominant genes seemed to be acting in positive direction and increased the number of florets. The two parents P_3 and P_4 seemed to carry most dominant genes. The F_1 – crosses obtained positive heterosis.

INTRODUCTION

The snapdragon (*Antirrhinum majus*) attracted the attention of plant breeders to produce and introduce new types and colours in breeding programmes in order to improve the quality of flowers and vegetative growth.

The genetics and inheritance of the different flower characteristics such as the number of days to the first flower bud, to showing colour and the opening of the first floret have been biometrically analyzed and studied in *Antirrhinum majus* by many authors (Rabinowitch *et al.*, 1977; El-Torky, 1981 and Misiha, 1991). On the other hand, the number of florets per spike, spike length and the number of spikes per plant have been also studied by many researchers because of their economic and commercial impact (El-Torky, 1981; Misiha, 1991 and Mann and Sharma, 1995).

The diallel cross analysis of Hayman (1954 and 1957) is an important tool for dividing the phenotypic variation into genotypic and environmental components and further subdivide the genotypic component into additive and dominance components. The additive component results from the average effects of genes, while the non – additive results from dominance and epistasis effects among the genes. If the additive gene action proved to be more important contributor to the genetic variability of a specific trait, a maximum improvement in this trait must be expected by the breeder through selection programmes, while the presence of a high non – additive gene action suggests that hybridization programme will perform good prospects for the character as a result of a direct relationship between the non – additive gene action and heterosis (Jinks, 1954).

MATERIALS AND METHODS

The effects of crossing between different cultivars of snapdragon (*Antirrhinum majus*, L.) on the flowering characteristics were studied throughout three generations, i.e. parental, first and second generations. The experiments were carried out during three successive growing seasons, 95/1996, 96/1997 and 97/1998 at Antoniadis Botanical Garden, Horticulture Research Institute, Agriculture Research Center, Alexandria, Egypt.

Certified seeds of four snapdragon cultivars; P_1 = Sonnet wit (white), P_2 = Sonnet karmijn (red), P_3 = Sonnet rose (rose) and P_4 = Sonnet geel (yellow) were obtained from Hamer Bloemzaden b.v., Holland.

The seeds of parental cultivars (first season) were sown on December 10, 1995. Seedlings were transplanted on March 5, 1996. As soon as the plants started to flower, all possible crossing combinations were made to obtain the F_1 – seeds. The F_1 – seeds were sown on December 8,1996. The F_1 – young plants were transplanted on February 25, 1997. As soon as the F_1 – plants started to bloom, selfings were carried out to obtain the F_2 – seeds which were sown on October 18, 1997 and transplanted on December 10, 1997.

The layout of the experiments was a randomized complete block design with three replications (Steel and Torrie, 1986). Each replication

contained 16 selfings and crosses (16 genotypes) and every selfing and cross consisted of 36 plants.

The collected data included :

1. Flowering characteristics which included the number of days to the appearance of the first flower bud; the number of days to showing colour and the number of days to the opening of the first floret on the spike, these characters were all measured from seed sowing.
2. Number of spikes per plant.
3. Spike length (in cm.) measured as the distance between the first floret and the apex of the spike.
4. Number of florets per spike.

The nature and the amount of genetic parameters were performed by Hayman's approach (Hyman, 1954 and 1957), which was used to divide phenotypic variation into genotypic and environmental components. The detailed description of the various genetic properties and parameters were calculated after Singh and Chaudri (1977).

RESULTS AND DISCUSSION

1. Flowering characters

Mean values of the flowering characters are shown in Table 1. Data showed that both of the white cultivar (P_1) and the red/purple cultivar (P_2), in F_1 or F_2 generations proved to be early flowering cultivars, since they needed relatively shorter time to produce their flower buds, to start the showing colour stage, to begin to open their florets compared to the red cultiver (P_3) and the yellow (P_4) one, which needed longer time to flower. The crosses of the two early parents, P_1 and P_2 gave also early flowering plants. These results supported the negative heterosis values, which were found for all crosses indicating the presence of hybrid vigour for all the flowering characters as shown in Table 2. Positive inbreeding depression estimates were recorded for most crosses (Table 2). Indicating the importance of additive genes controlling the inheritance of flowering earliness expressed as the number of days to flower bud, number of days to showing colour and number of days to the opening of the first floret on the spike. Very few crosses have achieved negative inbreeding depression estimates indicating the importance of dominance gene effects in such cases, as reported by Watts *et al.* (1970), Yiran *et al.* (1991) on *Gerbera* and Lohithaswa *et al*. (1996) on grain amaranth.

Assumptions of no epistasis, no multiple alleles and uncorrelated gene distribution were found to be valid. These assumptions were tested by calculating regression coefficient (b) of covariance on the variance. Regression coefficient (b) was significant from zero in the F_2 (0.70 ± 0.13, 0.76 ± 0.1 and 0.79 ± 0.12) for days to the first flower bud, days to showing colour and days to opening of the first floret, indicating that the genetic hypothesis was valid for all studied traits, but (b) was not significant (b=0.91 ± 0.29, 0.78 ± 0.28, and 0.79 ± 0.29) for days to the first flower bud, days to

showing colour and days to opening of the first floret respectively. At the same time, (b) was not significantly different from 1.0 in both F_1 and F_2 for all studied traits indicating the validity of the three assumptions mentioned before. Also, the diploid segregation, homozygous parents was valid and no reciprocal differences may be considered valid with some degrees of confidence. So, genetic parameters calculated and presented in Table 3 indicated that "D" value estimating the additive component was significant and also "H_1" value estimating the dominance component was significant in both F_1 and F_2 for all studied traits suggesting that both additive and dominance genes were important in the inheritance of the number of days to the first flower bud, days to showing colour, and days to opening of the first floret. This result agreed with Yiran *et al.* (1991), on *Gerbera*. At the same time, environment have effect in the variation of the number of days to showing colour in F_1 due to the significant value of the "E" component. The $H_2/4H_1$ values was less than 0.25 in the F_1 and F_2 for all characters indicating a symmetry of positive and negative gene proportion in the parents.

This result was confirmed with KD/KR ratio, which was larger than 1.0 suggesting that parents seemed to carry more dominant genes than recessive for all traits in F_1 and F_2 generations except for the number of days to showing colour in F_1, where KD/KR was less than 1.0 indicating that parents carried more recessive genes than dominants.

Figures 1,2 and 3 illustrated the Wr, Vr graphs for the flowering traits. The regression line intercepted the Wr axis in a negative position suggesting the presence of overdominance in F_1. This confirmed with proportion $(H_1 / D)^{1/2}$, which was larger than 1.0, while regression line intercepted Wr axis in a positive position in the F_2 suggesting a partial dominance. This agreed with the proportion $(H_1/D)^{1/2}$ as shown in table(3), where the value was less than one in F_2 indicating partial dominance for all traits. This result agreed with Chuni *et al.* (1996) on *Eleusine caracana*. Theoritically this was expected, since the inbreeding decreases the effect of intra allelic interaction, since the heterozygosity decreased (Sallam *et al.,*1985). The Wr, Vr points corresponding to the parent P_1 near to the point of origin followed by P_2 in F_1 and F_2 indicating that P_1, P_2 carry most dominant genes while P_3 and P_4 fall far from origin in F_2 indicating that they carry most recessive gene, while P_3 in F_1 fall in intermediate position for all traits. Correlation Wr + Vr and Yr was positive indicating that most of the dominance genes acted towards earliness, this agreed with El-Torky (1981) on *Antirrhinum majus*, and Horn (1994) on *Pelargonium.*

Heritability in broad-sense was high in the F_1 and F2 indicating that these characters are genetically controlled, (Table 3), while narrow sense heritability was moderate in F_1 but high in F_2 reflecting high additive gene effect. So this character could be easily advanced by carefully designed selection program (Lohithaswa *et al.*,1996).The proportion h^2 / H_2 in F_1 was larger than the unity indicating that there are two groups of genes controlling flowering time. This result agreed with that of Ryder (1988) on lettuce. On the other hand , one group was involved in the F_2. It may be noted that this value is underestimated when the dominance effects of all the equal genes concerned are not equal in size and direction (El-Hady *et al.,* 1998).

Table 1: Mean values of the number of days to first flower bud, showing colour and the opening of the first floret of F_1 and F_2 generations of the different selfings and crosses of *Antirrhinum majus*.

Genotypes[1)]	Days to 1st. flower Bud [2)]		Days to showing colour [2)]		Days to opening of 1st. floret [2)]	
	F_1	F_2	F_1	F_2	F_1	F_2
P1 x P1	147.3 cde	131 gh	154.6 cd	146 ij	161.3 bc	156.2 h
P2 x P2	146.6 de	135.8 efg	156 c	152.7 fghi	162 bc	161.5 fgh
P3 x P3	156 a	180.1 a	164.6 a	191.5 a	171 a	198.8 a
P4 x P4	154.3 ab	166 b	163 ab	177 b	170 a	185 b
P1 x P2	145.6 de	136.6 efg	152.6 cd	151.7 ghi	160.3 bc	161.6 fgh
P2 x P1	147 de	138.9 defg	153.6 cd	154.7 efgh	160.6 bc	163.9 efg
P1 x P3	148 cd	145.4 d	156.6 c	161.3 de	163.6 b	172.1 d
P3 x P1	145 de	141.5 def	154.6 cd	157.4 efg	160.3 bc	163.2 efgh
P1 x P4	141.3 ef	123.4 h	149 de	139.7 j	156.6 cd	148.7 I
P4 x P1	144.3 de	134 fg	153 cd	151.7 jh	159.3 bc	161.2 gh
P2 x P3	146 de	150.6 c	155.3 cd	166 cd	163.6 b	175 cd
P3 x P2	149 bcd	155.7 c	158.3 bc	172.3 bc	165 ab	180.3 bc
P2 x P4	136.3 f	133.3 g	145.6 ed	148.6 hi	151.6 d	157.8 gh
P4 x P2	144.3 de	137.9 defg	152.6 cd	153.6 fghi	159.3 bc	162.8 fgh
P3 x P4	147.3 de	143.6 de	157 c	160.6 de	163.3 b	170 de
P4 x P3	153.6 abc	142.1 def	163 ab	159.4 def	170 a	168.5 def
L.S.D.$_{0.05}$	6.2	8.1	5.9	6.8	6.3	7.2

1) Seed parent is the first one, P_1 = white, P_2 = red – purple, P_3 = red and P_4 = yellow.

2) Values in the same column not followed by the same letter are significantly different at the 0.05 probability level.

Table 2 : Estimates of heterosis and inbreeding depression (I.D.) for the number of days to the first flower bud, showing colour and the opening of the first floret for the different crosses of *Antirrhinum majus.*

Genotype[1)]	Days to 1st. flower bud		Days to showing colour		Days to opening of 1st. floret	
	Heterosis	I.D	Heterosis	I.D	Heterosis	I.D
P_1 x P_2	-1.3 N.S	7.6*	-2.7 N.S	5.3 N.S	-1.3 N.S	4.9 N.S
P_2 x P_1	-0.05 N.S	6.9 N.S	-1.7 N.S	3.9 N.S	-1.0 N.S	3.7 N.S
P_1 x P_3	-3.6 N.S	3.1 N.S	-3.0 N.S	1.5 N.S	-2.5 N.S	0.4 N.S
P_3 x P_1	-6.6*	3.8 N.S	-5.0 N.S	2.8 N.S	-5.8 N.S	3.9 N.S
P_1 x P_4	-9.5**	14.1**	-9.2**	11.0**	-9.0**	10.9**
P_4 x P_1	-6.5*	8.5*	-5.8*	5.5 N.S	-6.3*	4.6 N.S
P_2 x P_3	-5.3*	-1.7 N.S	-5.0 N.S	-2.2 N.S	-2.9 N.S	-1.2 N.S
P_3 x P_2	-2.3 N.S	-3.0 N.S	-2.0 N.S	-4.2 N.S	-1.5 N.S	-3.6 N.S
P_2 x P_4	-14.1**	3.7 N.S	-13.9**	2.8 N.S	-14.4**	2.0 N.S
P_4 x P_2	-6.1*	5.8 N.S	-6.9*	4.0 N.S	-6.7*	3.6 N.S
P_3 x P_4	-7.8**	3.9 N.S	-6.8*	2.2 N.S	-7.2*	1.5 N.S
P_4 x P_3	-1.5 N.S	8.8*	-0.8 N.S	6.6*	-0.5 N.S	6.3 N.S
L.S.D. $_{0.05}$	5.3	7.2	5.1	6.4	5.4	6.7
L.S.D. $_{0.01}$	7.2	9.7	6.9	8.6	7.4	9.0

N.S.,*,: Not significant, significant at p = $_{0.05}$ and $_{0.01}$ respectively.**
Seed parent is the first one, P_1 = white, P_2 = red – purple, P_3 = red and P_4 = yellow.

Table 3:Estimates of genetic parameters and ratios with their respective standard errors in F_1 and F_2 for the number of days to the first flower bud, showing colour and the opening of the first floret for the different crosses of *Antirrhinum majus.*

Estimates	Generation	Days to 1st. Flower bud.	Days to showing colour.	Days to opening of 1st. floret.
D	F_1	18.16 ± 5.67*	20.60 ± 6.36*	21.41 ± 6.92*
	F_2	547.84 ± 36.3*	435.91 ±19.08*	396.31 ± 16.72*
H_1	F_1	49.59 ± 16.5*	43.14 ±18.49*	47.0 ± 20.12*
	F_2	1948.78 ±433.62*	1328.09 ± 227.71*	1192.72 ± 199.52*
H_2	F_1	47.01± 15.23*	40.35 ± 17.07*	42.90 ± 18.57*
	F_2	1514.12 ± 390*	1027.79 ± 204.81*	920.22 ± 179.46*
h^2	F_1	62.56 ± 10.33*	58.18 ± 11.57*	51.38 ± 12.59*
	F_2	280.6 ± 248.05 N.S	176.89 ± 96.69 N.S	140.27 ± 121.72 N.S
F	F_1	3.64 ± 14.58 N.S	-1.86 ± 16.34 N.S	1.62 ± 17.7 N.S
	F_2	782.86 ± 184.1*	529.36 ±138.92*	479.30 ± 84.72*
E	F_1	4.6 ± 2.53 N.S	4.23 ± 2.84*	4.83 ± 3.09 N.S
	F_2	8.03 ± 16.2 N.S	5.60 ± 8.53*	6.23 ± 7.47 N.S
$(H_1/D)^{1/2}$	F_1	1.65	1.44	1.48
	F_2	0.94	0.87	0.86
$H_2/_4H_1$	F_1	0.23	0.23	0.22
	F_2	0.19	0.19	0.19
KD/KR	F_1	1.12	0.93	1.05
	F_2	7.25	5.5	5.60
r(yr, Wr+Vr)	F_1	0.82	0.78	0.77
	F_2	0.98	0.98	0.97
$h^2_{(ns)}$	F_1	0.81	0.84	0.82
	F_2	0.95	0.95	0.94
$h^2_{(bs)}$	F_1	0.34	0.46	0.43
	F_2	0.81	0.82	0.82
h^2/H_2	F_1	1.33	1.44	1.19
	F_2	0.18	0.17	0.15

N.S.,*,: Not significant, significant at p= $_{0.05}$ and $_{0.01}$ respectively (The significance was defined in the F1, when the values exceeded 1.96; while in the F2, the significance was tested by t- test at (P= 0.05 and 2 degrees of freedom).**

2. Number of spikes per plant

The mean number of spikes are presented in Table 4 showed that, the two parental cultivars P_1 and P_2 had the higher number of spikes and they were significantly different from P_3 and P_4 in the two seasons. In the F_1, the crossing between P_1 and P_2 in both directions gave the highest number of spikes compared to other crosses. It was found that P_2 was able to transmit this trait to its progeny in most crosses, while P_1 failed to do that completely except when crossed of course, to P_2 as mentioned earlier. More or less, similar results were obtained in the F_2 -population. All crosses achieved positive heterosis except for P_1 X P_3, P_1 X P_4 and their reciprocals showing that the small number of spikes of P_3 and P_4 had transmitted to their crosses with P_1 only. Most of crosses achieved no inbreeding depression (I.D), due to

the negative values presented in Table 5 except for P_2 X P_1 , P_3 X P_2 , P_4 X P_2 and P_3 X P_4 .

Table 4 : Mean values of the number of spikes/ plant , spike length and number of florets / spike for selfings and different crosses of *Antirrhinum majus*.

Genotypes[1)]	Mean [2)] no. of flortes/spike				Mean [2)] spike length (cm.)				Mean [2)] number of spike			
	F_1		F_2		F_1		F_2		F_1		F_2	
$P_1 \times P_1$	15.0	f	17.0	i	15.2	ef	18.5	gh	25.0	ab	16.0	cde
$P_2 \times P_2$	16.3	ef	21.0	h	11.9	g	14.6	i	19.0	bcde	15.3	cde
$P_3 \times P_3$	18.6	cde	26.0	efg	16.7	de	20.7	efg	12.6	fg	5.3	g
$P_4 \times P_4$	18.6	cde	25.6	ef	12.9	fg	15.5	hi	8.0	g	9.3	fg
$P_1 \times P_2$	18.0	Cde	21.0	h	17.2	cde	20.2	fg	27.3	a	31.1	a
$P_2 \times P_1$	17.0	def	27.3	def	15.7	ef	24.7	bcd	27.3	a	21.9	b
$P_1 \times P_3$	20.0	bc	26.6	fg	21.1	a	26.6	bc	13.6	defg	15.6	cde
$P_3 \times P_1$	20.0	bc	36.0	a	19.9	abc	32.4	a	18.6	cdef	16.2	cde
$P_1 \times P_4$	19.6	bcd	29.3	cde	17.8	bcde	25.8	bcd	13.0	efg	20.5	bc
$P_4 \times P_1$	23.3	a	33.3	ab	20.5	ab	26.8	bc	15.0	def	17.6	bcd
$P_2 \times P_3$	19.6	bcd	26.6	ef	16.2	e	23.3	def	19.0	bcde	15.8	cde
$P_3 \times P_2$	19.0	bcd	23.0	gh	16.1	e	16.7	hi	23.3	abc	14.0	def
$P_2 \times P_4$	18.3	cde	31.0	bc	16.0	e	23.9	cde	19.0	bcde	17.5	bcd
$P_4 \times P_2$	19.0	bcd	30.3	bcd	17.2	cde	27.0	bc	23.0	abc	16.1	cde
$P_3 \times P_4$	20.6	bc	24.6	fg	19.4	abcd	23.9	cde	19.3	bcd	10.0	fg
$P_4 \times P_3$	21.6	ab	31.6	bc	19.6	abcd	27.5	b	13.0	efg	11.5	ef
L.S.D. $_{0.05}$	2.7		3.5		3.1		3.3		6.2		5.3	

1) Seed parent is the first one, P_1= white, P_2- red- purple, P_3= red, P_4= yellow.
2) values in the same column not followed by the same letter are significantly different at the 5% probability level.

Table 5 : Estimates of heterosis and inbreeding depression (I. D.) for the number of florets / spike, spike length and number of spike / plant for selfings and different crosses of *Antirrhinum majus*.

Genotypes[1)]	No. of floret/ spike		Spike length (cm.)		No. of spike/ plant	
	Heterosis	I.D.	Heterosis	I.D.	Heterosis	I.D.
$P_1 \times P_2$	2.3 $^{N.S}$	+12.2**	3.6**	+0.5 $^{N.S}$	+5.3 $^{N.S}$	-30.7**
$P_2 \times P_1$	1.3 $^{N.S}$	-30.0**	2.1 $^{N.S}$	-77.0**	+5.3 $^{N.S}$	+2.9 $^{N.S}$
$P_1 \times P_3$	3.2**	-7.0**	5.1**	-11.3**	-5.2 $^{N.S}$	-48.5**
$P_3 \times P_1$	3.2**	-54.0**	3.9**	-47.2**	-0.2 $^{N.S}$	-11.8**
$P_1 \times P_4$	2.8*	-22.9**	3.7**	-27.5**	-3.5 $^{N.S}$	-93.0**
$P_4 \times P_1$	6.5**	-20.6**	6.4**	-15.6**	-1.5 $^{N.S}$	-48.0**
$P_2 \times P_3$	2.1 $^{N.S}$	-9.1**	1.9 $^{N.S}$	-24.6**	+3.2 $^{N.S}$	-7.3*
$P_3 \times P_2$	1.5 $^{N.S}$	+6.3**	1.8 $^{N.S}$	+15.5**	+7.5**	+20.1**
$P_2 \times P_4$	0.8 $^{N.S}$	-40.9**	3.6**	-30.0**	+5.5**	-16.3**
$P_4 \times P_2$	1.5 $^{N.S}$	-32.1**	4.8**	-38.9**	+9.5**	+10.0**
$P_3 \times P_4$	2.0 $^{N.S}$	+5.8**	4.6**	-7.2**	+9.0**	+24.3**
$P_4 \times P_3$	3.0*	-22.2**	4.8**	-24.4**	+2.7	-23.8**
L.S.D. $_{0.05}$	2.4	3.0	2.7	3.2	5.4	5.7
L.S.D. $_{0.01}$	3.2	4.1	3.6	4.3	7.3	7.7

1) Seed parent is the first one, P_1= white, P_2- red- purple, P_3= red, P_4= yellow.
N.S; *, Not significant, significant at 0.05 and 0.01 respectively.**
2) Values in the same column not followed by the same letter are significantly different at the 5% probability level.

The assumptions of diploid segregation, homozygous parents are considered valid. The assumption of no reciprocal difference was also valid with some degrees of confidence. The assumptions of no epistasis, no multiple allele and uncorrelated gene distribution in the F_1 and F_2, was

supported with the regression coefficient (b), which was not significant than the unity in F_1 and F_2, since the regression coefficient differed significantly from zero (Fig. 6).

It could be noticed from Table 6 that the "D" component estimating additive gene effect and "H_1" component estimating dominance gene effect were significant and relatively equal indicating that both of them are involved in the inheritance of the number of spikes per plant which agreed with the findings of Hassaballa *et al.,* (1984) on wheat. "E" component was significant in the F_1 but was not significant in the F_2 indicating that environment had minor effect in the variation of this trait. There was a symmetry of positive and negative genes proportion in the parents which appeared from the H_2 / $4H_1$ ratio which was larger than 0.25 in F_1 and F_2 supported by the KD/KR proportion which was larger than the unity in the F_1 only indicating that parents seemed to carry more dominant genes than recessive as found by Ahmed *et al.* (1998) on barley. The $(H_1 /D)^{1/2}$ proportion was found larger than 1.0 indicating overdominance which could be confirmed by the Wr,Vr graph (Fig.6), where the regression line intercepted Wr axis in negative position in F_1, while in the F_2, regression line intercepted Wr axis in positive position indicating partial dominance which disagree with the proportion $(H_1 /D)^{1/2}$ reflecting epistasis (Hayman, 1957). P_3, as shown in (Fig.6) was near to the origin indicating that P_3 carried most dominant genes but P_1 carried most recessive genes, while P_2 and P_4 occupied an intermediate position in F_1 while in the F_2, all parents were in intermediate position. Parental mean was positively correlated with Wr + Vr indicating that the low number of spike was dominant over the high number in the F_1, while the contrast happened in the F_2.

Heritability in broad sense was high in the F_1 and F_2, indicating that the number of spikes per plant is genetically controlled. Heritability in narrow sense was moderate in F_1 expressing the high presence of high additive gene effect in the inheritance of this trait. The proportion of h^2 / H_2 showed that there was only one gene exhibiting dominance controlling this trait.

3. Spike length

The results in Table 4 revealed that the parent P_3 had the highest value of spike length followed by P_1, P_4 and P_2 either in F_1 or F_2. Most crosses exceeded the parental averages indicating the presence of hybrid vigour in both F_1 and F_2 generations, which was confirmed by the positive heterosis estimates (Table 5). No differences between crosses and reciprocals were found in the F_1, but in the F_2, there were some differences between P_1 X P_2 , P_1 X P_3 , P_2 X P_3 and P_3 X P_4 and their reciprocals. All crosses had negative inbreeding depression values except for P_1 X P_2, P_3 X P_2 indicating that the additive gene effect was found to be important in the inheritance of spike length and that the dominance gene effect was also involved

Table 6 : Estimates of genetic parameters and ratios as well as their respective standard errors in the F_1 and F_2 for the number of florets / spike, spike length and number of spike / plant for selfings and different crosses of *Antirrhinum majus*.

Estimate	No. of florets / spike		Spike length (cm.)		No. of spike / plant	
	F_1	F_2	F_1	F_2	F_1	F_2
D	2.36 ± 1.27 N.S	16.71 ± 3.57*	3.59 ± 0.86*	6.52 ± 0.55*	49.69 ± 4.07*	22.48 ± 6.51*
H_1	8.21 ± 3.69*	259.15 ± 40.86*	15.94 ± 2.50*	314.10 ± 6.51*	53.97 ± 11.84*	159.28 ± 77.68*
H_2	7.64 ± 3.40*	236.24 ± 38.38*	15.35 ± 2.31*	302.19 ± 6.01*	42.08 ± 10.93*	151.83 ± 69.87*
h^2	13.67 ± 2.31*	60.36 ± 26.03 N.S	32.49 ± 1.56*	112.49 ± 8.13*	19.83 ± 7.4*	35.03 ± 47.39 N.S
F	-0.52 ± 3.26 N.S	24.80 ± 18.12 N.S	-2.04 ± 2.21 N.S	0.15 ± 2.83 N.S	17.74 ± 10.47 N.S	-51.13 ± 32.98 N.S
E	0.93 ± 0.56 N.S	1.53 ±1.59 N.S	1.2 ± 0.38*	1.31 ± 0.25*	4.7±1.82*	3.4 ± 2.9 N.S
$(H_1/D)^{1/2}$	1.86	1.96	2.1	3.4	1.04	1.3
$H_2/4H_1$	0.23	0.22	0.24	0.24	0.19	0.23
KD/KR	0.88	2.2	0.76	1.0	1.41	0.07
$R(y_r, W_r+ V_r)$	-0.9	-0.97	-0.66	-0.56	0.58	-0.49
H^2_{Ns}	0.37	0.22	0.38	0.07	0.59	0.22
H^2_{Bs}	0.79	0.91	0.85	0.94	0.87	0.86
H^2/H_2	1.78	0.25	2.1	0.37	0.47	0.23

N.S.,* Non significant and significant respectively (The significance was defined in the F_1, when the value exceeded 1.96; while in the F_2, the significance was tested by t-test at P= 0.05 and 2 degrees of freedom).

The assumptions of diploid segregation, homozygous parents were valid, while that of no reciprocal differences was valid with some degrees of confidence. The genetic parameters presented in Table 6 indicated that the "D" component estimating additive gene effect was significant in the F_1 and F2. The "H_1" component estimating dominance gene effect was larger than D indicating that dominance gene effect played a major role in the inheritance of spike length which agreed with Lavi *et al.* (1991) on avocado and Misiha (1991) on *Antirrhinum majus* The environment had also an important effect in the variation of spike length. Proportion H_2 /4H_1 was less than 0.25 indicating a symmetry of positive and negative genes proportion in the parents in F_1 and F_2 which was confirmed by KD/KR proportion in the F_1 which was less than 1.0 indicating that the recessive gene was larger than the dominant one in the parents. In the F_2, KD/KR was equal to the unity indicating symmetry distribution of positive and negative genes. The observed contradiction between $H_2/4H_1$ and KD/KR in the F_2, may be due to that some genes of overdominance are playing an outstanding role in controlling this trait (Ahmed and Ismail 1999). Fig. 5 presented Wr,Vr graph which showed that regression coefficient (b=0.74$\pm$ 0.3 in the F_1) was not significantly different from 1.0. Therefore, the genetic hypothesis was found valid confirming the absence of non-allelic interaction. The same result was found in the F_2 where b=0.79$\pm$0.09 which was significantly different from zero and not significantly different from 1.0. The regression line have intercepted the Wr axis in a negative position indicating the presence of overdominance in the F_1 and F_2 which was confirmed by the proportion of $(H_1/D)^{1/2}$ which was larger than 1.0. These results agreed with that of Mann and Sharma (1995) on wheat. P_4 carried most recessive genes while P_3, P_2 and P_1 fall in an intermediate position from origin in the F_1 and F_2 generations. The correlation coefficient of Yr on Wr+Vr was negative indicating that dominance genes acted towards

taller spike (tall spike is dominant over short one), which agreed with the findings of El-Torky (1981) on *Antirrhinum majus.*

Heritability in broad sense was high in the F_1 and F_2, indicating that spike length is a genetically controlled character as previously found by El-Torky (1981). Heritability in narrow sense was moderate in F_1 and low in F_2 reflecting the limited role of additive gene, which agreed with Abdel-Sabour *et al.* (1996) on wheat. Two groups of genes had controlled spike length in F_1, while one group was involved in the F_2. It could be noticed that this value is underestimated when the dominance effects of all the genes concerned are not equal in size and direction (El-Hady *et al.,* 1998).

4. Number of florets per spike

Mean values of the number of florets per spike presented in Table 4 indicated that the parents greatly differed from each other; P_3 and P_4 produced the highest values in the F_1 or F_2 as well followed by P_2 then P_1. All F_1 and F_2 crosses achieved comparatively higher number of florets per spike compared to their parents. These results have been strongly supported by the positive heterosis values obtained for all crosses(Table 5). This result agreed with the finding of Dalal and Gill (1965) on flax.

On the other hand, the importance of additive gene effects on the number of florets per spike was obviously detected from Table 5 due to the negative values obtained for inbreeding depression (I.D.) for the majority of the crosses. Only three crosses gave positive values; P_1XP_2, P_3 X P_2, and P_3 X P_4 which gives an indication to the possible role of dominance genes as found by El-Torky (1981) on *Antirrhinum majus* and Byregowda *et al.* (1997) on *Vigna radiata*.

The assumptions of no epistasis, no multiple alleles and uncorrelated gene distribution were found to be valid, where the regression coefficient (b), (Fig. 4) was not found to differ significantly from the unity (b= 0.69 $\pm$ 0.27, 0.92 $\pm$0.16 in the F_1 and F_2 ; respectively) . Also, the assumptions of diploid segregation and homozygous parents were valid but the assumption concerning no reciprocal differences was not fulfilled. Hayman (1957) reported that the estimates of the genetic parameters for traits which exhibited a partial failure of the assumptions are still possible. The “D” component estimating the additive gene effect was not significant in the F_1 , while it was significant in the F_2 as shown in Table 6.The “H_1” component estimating dominance was significant in the F_1 and F_2 indicating its importance in the inheritance of the number of florets per spike, while there was minor effect for the environment in the variation of this trait.

The proportion $H_2/4H_1$, was less than 0.25 suggesting a symmetry of positive and negative genes proportions in the parents in F_1 and F_2 confirmed by KD / KR proportion which was less than the unity indicating that the parents seemed to carry more dominant genes than recessive in the F_1 , while the situation was reversed in the F_2 . As shown in Fig. 4, the regression line has intercepted the Wr axis in a negative position in F_1 and F_2 indicating the presence of overdominance. This result was confirmed by the ratio $(H_1 / D)^{1/2}$ which was larger than the unity. The Wr,Vr points corresponding to the parents P_3 and P_4 were near to the origin indicating that they carried most

dominant genes, while P_1 carried most recessive genes and P_2 was in an intermediate position in both F_1 and F_2 generations. The (Wr+Vr) value was negatively correlated with the parental means, so it appears that the high number of florets per spike is dominant over the low number, which agreed completely with the findings of El-Torky (1981) on *Antirrhinum majus*.

Heritability in broad sense was high in the F_1 and F_2 indicating that the number of florets per spike is under the control of genes as reported by Sharma *et al.* (1990) on soybean and Byregowda *et al.* (1997) on *Vigna radiata* .Heritability in narrow sense was moderate in F_1 but low in F_2. The ratio h^2 /H_2 indicated that, two groups of genes exhibiting dominance controlled this trait in the F_1.

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تحليلات بيومترية لبعض الصفات الكمية الهامة في حنك السبع
٢. مواصفات التزهير.

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أجريت هذه الدراسة فى معهد بحوث البساتين بحدائق انطونيادس بالإسكندرية فى الأعوام ١٩٩٥/٩٦ ، ١٩٩٦/٩٧ و ١٩٩٧/٩٨ بغرض إنتاج أنماط زهرية مختلفة من حنك السبع وتحديد النظام الوراثي المتحكم فى وراثة لون الأزهار وكذلك الفعل الجينى المتحكم فى عديد من الصفات الكمية المدروسة لتحديد إمكانية الجمع بين ألوان الأزهار المرغوبة مع الصفات الكمية المثلى لتوفير متطلبات السوق.

وقد استخدمت فى الدراسة أربعه أصناف من نبات حنك السبع وهم

P_1 = Sonnet wit (white), P_2 = Sonnet karmijn (red), P_3 = Sonnet rose (rose) and P_4 = Sonnet geel (yellow).

حيث أجريت بينهم كل التهجينات الممكنة.

وأظهرت النتائج وجود فروق معنوية بين الهجن فى كل الصفات المدروسة وقد استخدمت طريقة هايمان لتحديد النظام الوراثي المتحكم في وراثة الصفات.

أثبتت الدراسة أهمية التأثير المضيف للجينات وكذلك التأثير السيادى للجينات لصفات عدد الأيام إلى كل من صفات: ظهور البرعم، ظهور اللون لأول زهرة و تفتحها و كذلك جود سيادة متفوقة فى الجيل الأول لكل الصفات بينما وجدت سيادة جزئية فى الجيل الثاني. و الجينات السائدة تؤدى إلى التبكير فى الإزهار . الآباء (P_1) و (P_2) تحتوى على معظم الجينات السائدة. وجود قوه الهجين تجاه التبكير فى الأزهار درجة التوريث بالمعني الضيق متوسطة مما يؤكد إمكانية إنتاج نباتات أكثر تبكيراً في الإزهار عن طريق الانتخاب .

بالنسبة لعدد الزهيرات على الشمراخ الزهري: فلقد أثبتت الدراسة أهمية الفعل الجينى السيادى مع وجود سيادة متفوقة كما أن التأثير المضيف للجينات كان معنويا فى الجيل الثاني. درجة التوريث بالمعنى الضيق متوسطة فى الجيل الأول بينما منخفضة فى الجيل الثاني. الجينات السائدة تزيد من عدد الزهيرات. الآباء (P_3) و (P_4) تحتوى على معظم الجينات السائدة. ظهرت قوة الهجين فى الهجن الناتجة .

أما صفة طول الشمراخ الزهرى : فأثبتت الدراسة أهمية كل من الفعل الجينى السيادى والمضيف على الصفة مع وجود سيادة متفوقة. الجينات السائدة تزيد من طول الشمراخ .درجة التوريث بالمعنى الضيق متوسطة فى الجيل الأول ومنخفضة فى الجيل الثاني. وجود تأثير معنوي للبيئة فى كلا الجيلين. ظهرت قوة الهجين فى الهجن الناتجة. تبين من التحليل البياني أن الآباء (P_1)و (P_2) و (P_3) تحتوى على تكرارات متساوية من الجينات السائدة والمتنحية.

وقد أثبتت الدراسة بالنسبة لصفة عدد الشماريخ الزهرية أهمية كل من الفعل الجينى المضيف والسيادي فى وراثة هذه الصفة مع وجود سيادة متفوقة فى كلا الجيلين. وجود التفوق فى الجيل الثاني. الجينات السائدة تقلل من عدد الشماريخ فى الجيل الأول. الأب (P_1) يحتوى على معظم الجينات المتنحية أدت الجينات السائدة فى الجيل الثاني إلى زيادة عدد الشماريخ واتجهت درجة التوريث بالمعنى الضيق إلى النقص من الجيل الأول إلى الثاني. البيئة لها تأثير بسيط على الإختلافات المظهرية للصفة. أغلب الهجن تفوقت على متوسط آباءها.