

# **Diallel Analysis for Some Quantitative Characters in** *Petunia hybrida* **Hort**

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Summary. Flowering time, plant height and flower size in *Petunia hybrida* Hort. (multiflora type) have been genetically analysed by means of a  $5 \times 5$  diallel cross. The results indicated that: (1) the three characters are controlled by additive-dominance polygenic systems. The contribution of the additive gene actions to the genetic variance of flowering time was relatively higher than that of dominance. The reverse situation was found for plant height and flower size. (2) Dominance is ambi-directional for the three characters. Ratios of average dominance were in the range of partial for flowering-time, complete for plant height and overdominance for flower size. (3) Number of genes (or gene groups) controlling the characters are about 3, 3 and 5 for flowering time, plant height and flower size; respectively, (4) Heritability estimates are 0.84, 0.88 and 0.89 in the broad-sense and 0.40, 0.49 and 0.37 in the narrow-sense, for flowering time, plant height and flower size; respectively. (5) Heterosis as percent increase of the mean  $F_1$ -hybrid above the higher parent, or decrease below the lower parent, was observed for flowering time (+ 9.7% to  $+$  13.3%), for plant height (-13.6% to  $-$  20.3%) and for flower size  $(+ 2.5\% \text{ to } + 16.0\%).$ 

Key words: Diallel  $-$  Quantitative  $-$  Characters  $-$  Heterosis - *Petunia* 

#### **Introduction**

*Petunia hybrida* Hort.  $(2n = 14)$  is one of the more popular ornamental plants. Knowledge of the genetic architecture of the present natural variation in *Petunia* is fundamental before breeding new types with economic interest.

During the past few years, a remarkable depression in many quantitative characters, especially in flower size of *Petunia,* was noticed in Egyptian gardens. This may be due to the fact that selfed seeds of many hybrid types introduced from abroad have been used for several succes-

sive years. This phenomenon interested us enough to genetically analyse some of the important quantitative characters in the multiflora plants of the local types. A  $5 \times 5$ diallel cross was carried out for studying the genetics of flowering time, plant height and flower size in *Petunia hybrida* Hort. This is pre-requisite for constructing some local hybrid types.

### **Material and Methods**

Five different inbred lines of *Petunia hybrida* Hort. (all belonging to multiflora types) were used as parents in a diallel cross. These lines were:

- Line 1: A white flower local inbred line; flowering about 150 days from sowing; plant height about 45 cm; flower diameter about 65-70 mm.

- Line 2: A red flower inbred line selected from 'Red Joy' which was introduced to Egypt in 1968; flowering about 175-180 days from sowing; plant height about 13-15 cm; flower diameter about 65-70 mm.

Line 3: A violet flower local inbred line; flowering about 220-225 days from sowing; plant height about 30 cm.: flower diameter about 65-70 mm.

- Line 4: A purple flower local inbred line; flowering about 140-150 days from sowing; plant height about 25 cm; flower diameter about 50-55 mm

- Line 5: A pink flower local inbred line; flowering about 190 days from sowing; plant height about 20 cm; flower diameter about 55-60 mm.

Seeds from each line (selfed for several generations) were sown under greenhouse conditions in the Orman Botanical Gardens at Giza, in the season 1971/1972. At the 4- leaf stage, seedlings (about 30 days old) were transplanted to the field. Successive sowings, each of a two week interval, especially for the earlier parents, were made to allow overlapping in flowering times of the different lines. The 5 *Petunia* lines were crossed in all possible combinations of a complete diallel, including reciprocals, giving a total of 20 crosses. In  $1972/1973$  all F, -hybrids and their respective parents were grown (as mentioned above) and selfed seeds for growing the  $F<sub>2</sub>$  were obtained. In this season, a second cycle of crosses between the parental lines was made to obtain additional  $F_1$ -hybrid seed. In the season 1973/1974, the parents, the  $F_1$ 's

and  $F<sub>2</sub>$ 's, were grown simultaneously in the Experimental Field of the Orman Botanical Gardens. A randomized complete block design with two replications was used. Data were recorded on an individual plant basis for the following characters:

a) *Flowering time:* measured as number of days from sowing to the opening of the first flower.

b) *Plant height: The* main stem height (in cm) of each plant from soil surface up to the apex was recorded,

c) *Flower size:* Measured as the mean diameter (in mm) of the first 5 flowers on the main stem of each plant.

Statistical analyses were carried out according to the model proposed by Hayman (1954a, b). The variance/covariance (Vr/Wr) graphical analyses were based on the method of Jinks (1954). The narrow-and broad-sense heritability values were estimated by the method described by Mather and Jinks (1971).

It should be noted that the genetic analysis of flower colour and variegation of the present diallel cross was a part of the present investigations and the results are presented elsewhere (Hussein and Misiha 1978).

## **Results**

## *Analysis of Variance and Estimates of the Components of Genetic Variance*

Data of the parents,  $F_1$  and  $F_2$  (totalled over two replications) for the 5-parent diallel with regard to the characters

Table 1. Mean flowering time in days (FT) and mean flower size in mm (FS) of parents (diagonal), F<sub>1</sub> hybrids (upper right) and F<sub>2</sub> populations (lower left) for a 5 X 5 diallel in *P. hybrida.* (values are totalled over 2 replications).

Parents	Purple	White	Red	Pink	Violet	Mean $F_1$ arrays
	(1)	(2)	(3)	(4)	(5)	
Purple $(1)$	FT 287.3	331.6	328.6	236.6	377.5	332.5
	FS 103.9	142.3	140.0	114.5	143.2	128.8
White	FT 350.7	302.2	307.6	307.1	329.5	315.6
(2)	FS 129.8	137.3	138.9	146.4	137.1	140.4
(3)	FT 362.0	323.0	354.8	310.2	221.5	324.5
Red	FS 140.3	138.8	135.4	157.1	148.1	143.9
(4)	FT 329.4	321.7	328.1	377.9	327.5	327.8
Pink	FS 127.7	134.6	146.1	116.7	138.5	134.6
Violet $(5)$	FT 387.9	348.6	360.4	351.0	447.9	360.8
	FS 144.7	135.2	145.8	136.5	135.0	140.4
Mean $F_2$ -	FT 343.4	531.2	345.6	343.6	379.2	
arrays	FS 129.3	135.1	141.3	132.3	139.4	
Parent means (days)	FT 143.7	151.1	177.4	189.0	224.0	
(mm)	FS 52.0	68.7	67.7	58.4	67.5	

Table 2. Mean plant height (cm) of parents (diagonal),  $F_1$  hybrids (upper right) and  $F_2$  populations (lower left), for a 5  $\times$  5 diallel cross in *Perunia hybrida.* (values are totalled over 2 replications)



(flowering time, plant height and flower size (diameter)) are presented in Tables 1 and 2, where the parental means are given at the bottom. Analysis of variances of the data (totalled over the 2 replications) are given in Table 3. According to Aksel and Johnson (1963), a common environmental component of variation,  $\hat{E}$ , was measured by block  $\times$  treatment interaction, using the ordinary method for analysis of variance in a randomized block design. It was found that this component of variation was highly significant for flowering time, significant for plant height and insignificant for flower size. The word treatment refers here to the parents,  $F_1$ 's and  $F_2$ 's separately.

In flowering time (Table 1), the values of the  $F_1$  and  $F<sub>2</sub>$  generations differ significantly from each other. Similarly, the parental values differ significantly from each other. In plant height and in flower size, the values of the  $F_1$  and  $F_2$  generations do not differ significantly from each other, however; the parental values show significant differences.

The estimates of the genetic and environmental components of variance and covariance, the various genetic ratios computed by Hayman's method (1954a, b), and narrow as well as broad-sense hertitabilies estimated according to Mather and Jinks (1971) for the three characters under study are given in Table 4. The  $\hat{D}$  component measuring the additive variation was highly significant for the 3 traits. The  $\hat{H}_1$  component measuring dominance variation was also highly significant. However it was slightly smaller in magnitude than the  $\hat{D}$  component for flowering time and slightly higher in magnitude for plant height and flower size.

On the basis of the additive-dominance model, additive genetic variance is about 1.1, 0.7 and 0.4 that of the dominance components for flowering time, plant height and flower size, respectively. The component of variation due to dominance effects correlated for gene distribution  $(\hat{H}_2)$  was highly significant for the three characters. This indicates asymmetrical distribution of the dominant genes controlling these characters in the genetic background of the parental lines. The over-all dominance effects of heterozygous loci  $(h_2)$  were also highly significant, which indicate that the effect of dominance is due to heterozygosi-

Table 3. Analyses of variances for flowering time, plant height and flower size in a 5 X 5 diallel cross in *P. hybrida* 

Sources of variation	d.f.		Flowering time			Plant height			Flower size		
		S.S.	M.S.	F.	S.S.	M.S.	F.	S.S.	M.S.	F.	
<b>Blocks</b>		588.48	588.48	11.667 <sup>b</sup>	4.69	4.69	0.750	0.08	0.08	0.498	
Treatments	24	23001.45	958.39	19.001 <sup>b</sup>	2180.50	90.85	14.536 <sup>b</sup>	1953.14	81.38	506.094	
Blocks X treat.	24	1210.52	50.44		149.92	6.25		3.86	0.16		
Total	49	24800.45			2345.11			1957.08			

b highly significant ( $P < 0.01$ )





Significant

Highly significant

ty. This result is equally applicable for the three traits.

The (F) value measuring the covariance of additive and dominance effects was highly significant in the case of flowering time and flower size, but insignificant for plant height. This suggests that dominant and recessive alleles for flowering time and flower size are not equally distributed among the parents, while they are about equal in distribution for plant height. The F value, being of a positive sign, in case of flowering time and flower size, leads to the conclusion that there was an excess of dominant alleles in the background of the parents affecting both characters. The situation is reversed with regard to plant height, since the  $\hat{F}$  value has a negative sign.

The quantity  $(\hat{H}_1/\hat{D})/2$ , which is a weighted measure of the average degree of dominance at each locus, was 0.87, 1.16 and 1.52 for flowering time, plant height and flower size, respectively (Table 4). These values indicate partial dominance for flowering time, almost complete dominance for plant height and moderate over-dominance for flower size.

The proportion of the genes with positive and negative effects in the parental lines is  $\hat{H}_2/4 \hat{H}_1 = \overline{u} \ \overline{v} \ 0.16$  for flowering time,  $= 0.25$  for plant height and  $= 0.23$  for flower size (Table 4).

In case of flowering time, these results suggest an unequal distribution of the negative and positive alleles among the parents, while they suggest an equal distribution of  $\pm$  alleles for plant height and flower size. Moreover, since  $\hat{H}_2$  was significantly different from  $\hat{H}_1$  for flowering time, this again suggests that the parents contain positive and negative genes in an unequal proportion. On the contrary,  $\hat{H}_2$  was found not to be significantly different from  $\hat{H}_1$  for plant height and flower size. These results suggest that positive and negative alleles of the latter characters may have an isodirectional distribution among the parents.

On the other hand, the ratio  $(4 \hat{D} \hat{H}_1)/\frac{1}{2}$  + F /  $(4 \hat{D} \hat{H}_1)/\frac{1}{2}$  $-\hat{F}$ , measuring the proportion of dominant and recessive genes in the parents, was found to be 3.4 for flowering time. This value being much more than unity suggests that dominant genes are in excess. This ratio was found to be close to unity for plant height. This suggests that dominant and recessive genes for plant height are distributed in equal proportions among the parents. The same fraction was found to be about 1.31 for flower size. This result being more than unity suggests that dominant genes for flower size are in excess.

The results reported for flowering time and flower size concerning the excess of dominant genes are in accordance with the results detected from the  $\hat{F}$ -values of both characters (Table 4).

The fraction  $\hat{h}_2/\hat{H}_2$ , which estimates the number of genes (or groups of genes), indicated that in *P. hybride*  flowering time is under the control of at least three groups of genes; plant height is under the control of a similar number; while flower size is under the control of about five groups of genes (Table 4).

Broad-sense heritabilities were found to be 0.85, 0.89 and 0.90, while narrow-sense heritabilities were found to be as low as 0.44, 0.39 and 0.38 for flowering time, plant height and flower size; respectively (Table 4).

The coefficients of correlation between the parental order of dominance (i.e.  $Wr + Vr$ ) and parental measurements  $Y_r$  (i.e. the corresponding values of the main diagonal are given in Table 5. The r-values were found to be insignificant for the three characters, suggesting that dominance was ambidirectional (fluctuating in direction).

The values of  $r^2$  were found to be about 0.32, 0.15 and 0.30 for flowering time, plant height and flower size, respectively. None of them is close to unity. Therefore, estimation of the measurements of the completely dominant and completely recessive parents, and consequently

Table 5. Estimates of the array variances  $(V_r)$ , array parent offspring covariances  $(W_r)$  and correlation coefficients between parental order of dominance  $(W_r + V_r)$  and parental measurements  $y_r$ , estimated from the totalled measurements over blocks; for the three characters under study

Array		Flowering time				Plant height				Flower size			
	Wт	Vr	$Wr + Vr$	VI.	Wr	Vr	$Wr + Vr$	Vr	Wг	Vr	$Wr + Vr - vr$		
1	446.6	256.2	702.8	287.3	82.8	69.5	152.3	25.6	66.8	83.7	150.5	103.9	
2	45.5	48.4	93.9	302.2	34.9	18.3	53.2	40.4	$-11.0$	3.9	$-7.1$	137.3	
3	58.9	89.5	148.4	354.8	19.0	11.8	30.8	49.0	$-8.4$	17.7	9.3	135.4	
4	194.1	204.2	398.3	377.9	$-18.4$	34.2	15.8	60.1	61.8	86.4	148.2	116.7	
5.	496.6	594.1	1090.7	447.9	70.8	83.0	153.8	89.6	$-3.6$	6.9	3.3	135.2	
Total	1241.7	1192.4	2434.1	1770.1	189.1	216.8	408.9	264.7	105.6	198.6	304.2	628.5	
		0.57 not significant			0.12 not significant			$-0.55$ not dignificant					
$r^2$	0.32				0.15			0.30					

the prediction of the possible limits of selection amongst the genes showing dominance, seems to be meaningless.

#### *The Wr/Vr Regression Analysis*

The  $F_1$  and  $F_2$ -diallel regression analyses for the three characters were made according to the method of Jinks (1954).

a) Flowering time: The graphical analysis for both  $F_1$ and  $F_2$  (Fig. 1 A, B) shows that the regression coefficients (b) of  $W_r$  on  $V_r$  do not differ significantly from unity. The positions of both regression lines are slightly to be left of the origin, indicating the presence of partial dominance in both generations. Variety 5 (Violet) behaved as the most recessive parent, as indicated from its position at the end of the regression lines. On the contrary, parent 2 (white) behaved in the  $F_1$  and  $F_2$  as having the most dominant alleles, while parent 3 (red) showed this behaviour in  $F_2$  only. Moreover, parents 1 (purple) and 4 (pink) possessed balanced amounts of recessive and dominant alleles in the  $F_1$  generation. In addition, in  $F_2$  it was found that parent 4 has nearly equal amounts of dominant and recessive alleles. The scatter of array points along the regression lines suggests great genetical diversity for flowering time among the parents.

b) Plant height: The graphical analysis for both  $F_1$  and  $F<sub>2</sub>$  (Fig. 2 A, B) shows that the regression coefficients (b) of  $W_r$  on  $V_r$  do not differ significantly from unity. The regression line in the  $F_1$ -graph passes through the origin, indicating almost complete dominance and absence of epistasis. On the other hand, the regression line of the  $F_2$ graph cuts the  $W_r$ -axis slightly above the origin and lies close to the limiting parabola (Fig. 2 B), indicating some deviation towards partial dominance. The lines 5 (white) and 1 (red) behaved as the most recessive parents, as indicated from their positions at the end of the regression line. On the contrary, parent 4 (violet) behaved in the  $F_1$ and  $F_2$  as having the most dominant alleles; parent 2 (pink) seems to behave as having balanced amounts of recessive and dominant alleles in  $F_1$  and in  $F_2$  generations. Only parent 3 (purple) showed contradiction in its behaviour from  $F_1$  to  $F_2$ . In  $F_1$ , it behaved as possessing balanced amounts of recessive and dominant alleles while in  $F<sub>2</sub>$  it behaved as having the most dominant alleles. The reason behind this contradiction in behaviour is not known.

c) Flower size: The graphical analysis of  $F_1$  (Fig. 3 A)



Fig. 1.  $V_r/W_r$  regression of flowering time in F<sub>1</sub>(A) and in F<sub>2</sub>(B) Fig. 2.  $V_r/W_r$  regression of plant height in F<sub>1</sub>(A) and in F<sub>2</sub>(B)



shows that the regression coefficient (b) of  $W_r$  on  $V_r$  does not differ significantly from unity. The position of the regression line was to the right of the origin. This indicates the presence of overdominance, which is in accordance with the result detected from the parameter  $(\hat{H}_1/\hat{D})/2$  reported in Table 4. On the other hand, the graphical analysis of  $F_2$ -data (Fig. 3 B) shows that the regression coefficient (b) is deviating significantly from unity, suggesting the prevalence of non-allelic interaction (epistasis) in some arrays. The position of the  $F_2$  regression line is slightly to the left of the origin, indicating partial dominance in this generation. The varieties 1 (purple) and 4 (pink) behaved as the most recessive parents, as indicated from their positions at the right-hand end of the  $F_1$ -regression line (Fig. 3 A), while both are converted to have positions nearly at the middle of the  $F_2$ -regression line (Fig. 3 B). The latter situation indicates that both parents have about equal amounts of dominant and recessive alleles. The parents 3 (red) and 5 (violet) behave similarly in both  $F_1$  and  $F<sub>2</sub>$  regression analyses. They fall in position at the extreme left-hand ends of the regression-lines. This suggests that lines 3 and 5 have the most dominant alleles. Among the 5 varieties genetically analysed for flower size, par-



**Fig. 3**  $V_f/W_f$  regression of flower size in  $F_i$  (A) and in  $F_2$  (B)

ent 2 (white) shows a clear-cut contradiction between the  $F_1$  and  $F_2$ -regression results. In  $F_1$  (Fig. 3 B), it falls at the extreme left-hand and of the regression line, behaving as having the most dominant alleles like parents 3 and 5. In  $F<sub>2</sub>$  (Fig. 3 B) it falls at the extreme right-hand end of the regression line, behaving as having the most recessive alleles among other parents.

#### *Heterosis*

Any significant increase of the  $F_1$  hybrid plants above the higher parent, or any significant decrease below the lower parent was considered to be heterosis.

Heterosis relative to the higher parent (HP) was calculated as:  $\frac{F_1 - HP}{HP} \times 100$ ; while heterosis relative to the lower parent (LP) was calculated as:  $\frac{F_1 - LP}{IP} \times 100$ 

a) Flowering time: The mean values of mid-parent  $(\overline{P})$ , early parent (EP), late parent (LP) and the  $F_1$ 's of all crosses are given in Table 6. Deviations of  $F_1$ 's from  $\overline{P}$ , EP and LP are given as percentages in the right-hand part of the same table. In only one cross (viz.  $P_1 \times P_2$ ) did the  $F_1$ hybrid plants show heterosis towards the late flowering direction, surpassing significantly the late parent. On the contrary, three  $F_1$ 's (viz.  $P_3 \times P_4$ ,  $P_3 \times P_5$  and  $P_4 \times P_5$ ) showed heterosis towards the early flowering direction. Deviations of the  $F_1$  hybrids from the relatively earlier parents were mostly significant or sometimes highly significant. In other crosses, the  $F_1$ 's are either almost equal to mid-parents or close to any of the corresponding parents.

b) Plant height: The mean values of mid-parent  $(\overline{P})$ short parent (SP), tall parent (TP) and  $F_1$ 's of all crosses are presented in Table 7. Deviations of  $F_1$ 's from  $\overline{P}$ , SP and TP are given as percentages in the right-hand part of the same table. In only two crosses (viz.  $P_2 \times P_4$  and  $P_3 \times$  $P_5$ ) did the  $F_1$  hybrid plants negatively surpass the magnitude of the corresponding short parents, showing mostly highly significant heterosis towards the short direction. In other crosses, the  $F_1$  hybrids are either about equal to mid-parent or close to any of the corresponding parents.

c) Flower size: The mean values of mid-parent  $(\overline{P})$ , small flower parent (SF), large flower parent (LF) and the  $F'_1$ 's of all crosses are given in Table 8. Deviations of  $F_1$ 's from  $\overline{P}$ , SF and LP are given as percentages in the righthand part of the same table. In 7 out of the 10 crosses (see Table 8), the  $F_1$  hybrid showed heterosis towards the large flower direction, surpassing the corresponding larger flower parents. The extent of heterosis varied from 2.57% to 16.02%. On the contrary, no crosses showed heterosis towards the small flower direction. In other crosses, the  $F_1$ 's were either about equal to mid-parent or close to any of the corresponding parents of each cross.

Table 6. Mean performance of earlier parent (EP), later parent (LP), mid parent  $(\overline{P})$ ,  $F_1$ 's and expression of heterosis percentage for flowering time. The underlined values represent real heterotic  $F_1$ 's

	Flowering time (days)			Heterosis as $%$ F, -deviation from				
Croses	EP	LP	P	$F_{1}$	EP	$\overline{\mathbf{p}}$	LP	
$P_1 \times P_2$	143.63	151.08	147.36	165.82	15.44 <sup>a</sup>	12.53 <sup>a</sup>		
$P_1 \times P_3$	143.63	177.38	160.51	164.28	14.37 <sup>a</sup>	2.35	$\frac{9.74}{-1.38}$	
$P_1 \times P_4$	143.63	188.93	166.28	163.30	$-13.69^{\rm a}$	$-1.79$	$-13.56$	
$P_1 \times P_s$	143.63	223.95	183.79	188.75	$31.41^a$	$-2.69$	$-15.71b$	
$P_2 \times P_3$	151.08	177.38	164.29	153.80	1.79	$-6.35$	$-13.29b$	
$P_2 \times P_4$	151.08	188.93	170.01	153.54	1.62	$-9.68$	$-18,73^{b}$	
$P_2 \times P_3$	151.08	223.95	187.51	164.74	9.03	$-12.14a$	$-26.44b$	
$P_3 \times P_4$	177.38	188.93	183.16	155.08	$-12.57^a$	$-15.32b$	$-17.92b$	
$P_3$ X $P_5$	177.38	223.95	200.67	160.75	$\overline{29.38}$	$-19.89b$	$-28.22^{\rm b}$	
$P_{a} \times P_{5}$	188.93	223.95	201.44	163.74	$-13.33^{b}$	$-18.71^{b}$	$-49.23b$	

 $P_1$  = purple,  $P_2$  = white,  $P_3$  = red,  $P_4$  = pink,  $P_5$  = violet - = early direction

 $a =$  significant

 $<sup>b</sup>$  = highly significant</sup>

Table 7. Mean performance of short parent (SP), tall parent (TP), mid-parent  $(\overline{P})$ ,  $F_1$ 's and expression of heterosis percentage for plant height. The underlined values represent real heterotic  $F_1$ 's

Croses	Plant height (cm)			Heterosis as $% F_1$ -deviation from						
	<b>SP</b>	TP	P	$F_1$	<b>SP</b>	TP	$\overline{P}$			
$P_1 \times P_2$	12.78	20.22	16.50	19.24	50.31 <sup>b</sup>	4.87	16.57 <sup>b</sup>			
$P_1 \times P_3$	12.78	24.51	18.65	22.77	78.20 <sup>b</sup>	$-7.08$	$22.15^{b}$			
$P_1 \times P_2$	12.78	30.07	21.43	23.66	85.17 <sup>b</sup>	$21.30^{b}$	$10.45^{b}$			
$P_1 \times P_5$	12.78	44.79	28.78	32.00	150.39 <sup>b</sup>	$-28.55^{b}$	11.16 <sup>b</sup>			
$P_2 \times P_3$	20.22	24.51	22.36	23.34	$15.43^{b}$	$-4.77$	4.36 <sup>b</sup>			
$P_2 \times P_4$	20.22	30.07	22.36	17.47	$-13.60b$	$-41.90b$	$-21.88^{b}$			
$P_2 \times P_5$	20.22	44.79	32.50	27.98	$38.40^{b}$	$-37.51b$	$-31.90b$			
$P_2 \times P_4$	24.51	30.07	27.29	29.02	18.42 <sup>b</sup>	$-3.97b$	$6.35^{b}$			
$P_3 \times P_5$	24.51	44.79	34.65	19.54		$-56.36^{b}$	$-43.59b$			
$P_{4} \times P_{5}$	30.07	44.79	37.43	31.82	$\frac{-20.25^{b}}{5.81^{b}}$	$-28.96^{b}$	$-15.01b$			

 $P_1$  = red,  $P_2$  = pink,  $P_3$  = purple,  $P_4$  = violet,  $P_5$  = white, - = short direction <sup>b</sup> highly significant

Table 8. Mean performance of small flower parent (SF), large flower parent (LF), mid-parent  $(\overline{P})$ ,  $F_1$ 's and expression of heterosis percentage for flower size. The underlined values represent real heterotic  $F_i$ 's

Croses		Flower diameter (mm)		Heterosis as $%F$ , -deviation from			
	SF	LF	$\mathbf{P}$	$F_{1}$	SF	LF	p
$P_1 \times P_2$	51.95	58.37	55.16	57.23	10.17	$-1.94$	3.67
$P_1 \times P_3$	51.95	67.51	59.73	71.58	37.79 <sup>b</sup>	6.03	19.84 <sup>b</sup>
$P_1 \times P_4$	51.95	67.68	59.81	70.02	34.78 <sup>b</sup>	3.45	17.06 <sup>b</sup>
$P_1 \times P_5$	51.95	68.51	60.29	71.13	36.91 <sup>b</sup>	3.63	17.97 <sup>b</sup>
$P_2 \times P_3$	58.37	67.51	62.94	69.25	18.63 <sup>b</sup>	2.57	10.02 <sup>b</sup>
$P_2 \times P_4$	58.37	67.68	63.02	78.53	34.52 <sup>b</sup>	$-6.02$	24.59 <sup>b</sup>
$P_2 \times P_3$	58.37	68.51	63.50	73.15	25.32 <sup>b</sup>	6.58	15.19 <sup>b</sup>
$P_{a} \times P_{a}$	67.51	67.68	67.54	74.05	9.69 $b$	9.41	9.55 $b$
$P_3 \times P_5$	67.51	68.51	68.07	68.54	1.53	0.12	$-0.12$
$P_{4} \times P_{6}$	67.68	68.51	68.15	69.44	2.46	1.18	1.89

 $P_1$  = purple,  $P_2$  = pink,  $P_3$  = violet,  $P_4$  = red,  $P_5$  = white

<sup>b</sup> highly significant

## **Discussion**

The results obtained from the present diallel analysis will be discussed for each character alone.

#### *Flowering Time*

Results of the present investigation clearly indicate that flowering time in *Petunia hybrida* is governed by additive and dominant gene actions. Since the contribution of the additive gene actions to the genetic variance was relatively higher than the contribution of dominance, this may indicate the possibility to select for new flowering time lines. This is because the additive genetic variance is fixable, as in the sense of Mather (1971). These results are in agreement with Lawrence (1963), Watts et al. (1970), and E1-Haddad (1975) working with other plants. The average degree of dominance was less than unity, indicating partial dominance which agrees with Singh et al. (1971) and E1- Haddad (1975). Furthermore, the fraction  $\hat{H}_2/4\hat{H}_1$  suggests asymmetry at loci showing dominance, but the significance of the value  $[(4 \hat{D}\hat{H}_1)\frac{1}{2} + F(4 \hat{D}\hat{H}_1)\frac{1}{2} - \hat{F}]$  than unity suggests that dominant genes are in excess. The significant positive  $\hat{F}$ -value and the correlation coefficient  $(r)$ provide the same information, which agrees well with Johnson and Eunus (1964) in barley and Phull et al. (1970) in *Pearl millet*. The ratio  $h_2/H_2$  which reflects the number of genes or gene groups controlling the character and exhibiting dominance to some degree, was about 3. The broad-sense heritability estimate was 0.84. This value was reduced, however; in the narrow-sense to a value of 0.44. On the other hand, the graphical analysis (Jinks 1954) showed that the regression (b) did not differ significantly from unity, which indicates the presences of partial dominance. The same result was provided by the term  $(\hat{H}_1/\hat{D})$ <sup>1</sup>/<sub>2</sub> having the value of 0.87. Heterosis estimates showed that only one cross was significantly heterotic towards the late direction and three crosses towards the early direction. This heterosis was observed in crosses involving parents belonging to the group having the most dominant alleles with the parents having the most recessive alleles, which agrees with that reported in tomato by Khanna and Chaudhary (1974).

# **Plant Height**

Results of the present investigations indicated that plant height is governed by additive and dominant gene actions. Additive genetic variance was about 0.73 of that of the dominance variance. These results are in accordance with those reported in barley (Kumar 1976). The value of the average degree of dominance was 1.1 ; indicating complete dominance, which agrees with Khanna and Chaudhary (1974) in tomato and with Halloran (1975) in wheat. The faction  $\hat{H}_2/4\hat{H}_1$  being close to 0.25 suggests symmetrical distribution at loci showing dominance, which is in accordance with Kumar (1976) in garden pea. Moreover, the value  $[(4 \hat{D}\hat{H}_1)\frac{1}{2} + \hat{F}/(4 \hat{D}\hat{H}_1)\frac{1}{2} - \hat{F}]$  was about equal to unity, indicating almost equal proportions of dominant and recessive genes in the parents. This is supported by the negative non-significant  $\hat{F}$ -value found in the present study.

The present results indicate that plant height in *Petunia hybrida* is possibly under the control of three genes or gene groups. Moreover, heritability estimates in broadsense were about 0.88, but these estimates were reduced to a value of about 0.39 in the narrow-sense.

The graphical analysis of the character (Jinks 1954) showed that the  $F_1$  regression line (not significantly different from unity) is passing through the origin, indicating complete dominance. The same conclusion was provided by the result predicted from the term  $(\hat{H}_1/\hat{D})\frac{1}{2}$ . On the other hand, the  $F_2$  regression analysis indicated partial dominance. This contradiction between the results obtained from  $F_1$  and  $F_2$  generations is similar to that reported in garden pea (Kumar 1976). No interpretation could be made in this respect.

Heterosis estimates showed that only two cases out of the ten crosses were significantly heterotic towards the short direction. This heterosis was observed in crosses involving parents belonging to the group having the most dominant alleles with the parents having the most recessive alleles. This conclusion agrees well with the results reported in tomato (Khanna and Chaudhary 1974).

### *Flower Size*

Flower diameter was used as an indicator for studying the inheritance of flower size in the present investigations. The results clearly indicated that the character is inherited under the control of a polygenic system with additive and dominant gene actions. The biometrical estimates showed that at least five minor genes (or gene groups) are governing flower size in the present multiflora material *of Petunia hybrida.* 

In this respect, Ewart (1965) found a single major gene and some polygenes accounting for the differences in flower size between multiflora and grandiflora petunia types. A similar polygenic system was reported in chick peas, however with a smaller number of genes (Khosh-Khui and Nikneja 1971). The results showed that the variance due to dominance effects was about 2.4 times that of the variance due to additive effects. The average degree of dominance reached about 1.5, indicating over-dominance. This result is supported by the  $F_1$  regression analysis.

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Moreover, the results suggest asymmetrical distribution at loci showing dominance and present in excess of recessives in the parents. Heritability estimates of the character were about 0.89 for the broad-sense and about 0.37 for the narrow-sense. The latter value may indicate that the fixable genetic variation (as in the sense of Mather and Jinks 1971) is probably less than the non-fixable genetic variation due to dominance. This can be a ground to explain the observed deterioration in flower size *of Petunia* grown in the Egyptian gardens.

Heterosis estimates showed that seven cases out of the ten crosses were heterotic towards the large direction and surpassing the corresponding larger parents in magnitude. The high values of heterosis were observed in crosses involving parents carrying the most dominant alleles with the parents having the most recessive ones. This is in accordance with the results found in plant height studied in the present investigations, which again agrees with Khanna and Chaudary (1974) in the tomato.

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Accepted August 28, 1978 Communicated by H.F. Linskens

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