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Inheritance of Flower Size in *Petunia Hybrida* L.

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ABSTRACT

The present investigation was carried out to study the genetic system controlling flower size in *Petunia hybrida*. Five different pure lines of *Petunia hybrida* were entered in a 5 × 5 daillel cross. Methods of analysis proposed by Hayman (3) and Mather and Jinks (5) were used. The results obtained are summarized as follows:

1. This character is controlled by an additive-dominance polygenic system. The contributions of additive gene actions to the genetic variance were sulatively lower than the contribution of dominance.
2. The dominance was ambidirectional.
3. The number of genes (or gene groups) controlling the character was about 5. Heritability estimates was 0.89 in the broad sense and 0.37 in the narrow sense.
4. Heterosis expressed as percent increase of the mean of F_1 above the higher parent was observed and ranged between +2.6 to +16%.

INTRODUCTION

Among winter annuals, *Petunia hybrida* L. ($2n = 14$), is considered one of the most popular ornamental plants. A remarkable depression in most characters and specially in flower size of this plant was noticed in Egyptian gardens.

Diallel design was used to study the mode of inheritance of this character. Ewart (2) studied the inheritance of flower size in *Petunia grandiflora* and *Petunia multiflora*. He found that large flower size is possibly inherited as a single dominant gene, but lethal or sub-lethal genes may be closely linked to it.

El-Gamassy *et al.* (1) found in *Petunia hybrida* that large flower diameter was dominant over the small one and one to three pairs of genes governed the inheritance of this character.

MATERIALS AND METHODS

This experiment was carried out in Orman Botanical Garden, Giza, Egypt during 1971–1974. Five different inbred lines of *Petunia hybrida* L. were used as parents in a diallel cross. These lines were white (Local cultivar), red (Dutch cultivar introduced in

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1968 under the name "Red Joy", Violet (Local cultivar), Purple (Local cultivar), Pink (American cultivar introduced in 1965).

Selfed seeds of each variety were sown. At the time of antheses, buds of a suitable size were chosen for emasculation. The whole process of hybridization was usually made between 8 to 12 a.m. daily. In the third season the parents, the F_1's the F_2's and the backcrosses were grown in a randomized complete block design replications. Flower size was measured as the mean diameter of the first 5 flowers on each plant (in mm). Statistical analysis of this quantitative character was carried out according to the model proposed by Hayman (3). The narrow and broad sense of heritability values were estimated by the method described by Mather and Jinks (5).

RESULTS AND DISCUSSION

Components of genetic variance

The mean flower diameter of the parents, the F_1 and F_2 populations are given in Table 1.

The common environmental component of variation (E) was measured by block ×

Table 1 The total means over blocks for a 5 × 5 diallel cross in *Petunia hybrida* for flower diameter. Parents, diagonal, F_1 hybrids, (upper right), F_2 populations (lower left).

		F_1 generation					
	Parents	Purple (1)	White (2)	Red (3)	Pink (4)	Violet (5)	Mean F_1 arrays ± S.E. = 2.0980
F_2 generation	Purple (1)	103.90	142.25	140.04	114.47	143.17	128.76
	White (2)	129.75	137.26	138.89	146.36	137.09	140.37
	Red (3)	140.31	138.79	135.36	157.05	148.11	143.89
	Pink (4)	127.70	134.61	146.08	116.74	138.50	134.62
	Violet (5)	144.70	135.16	145.84	136.47	135.02	140.37
	Mean F_2 Arrays ± S.E. = 2.0539	129.27	135.11	141.27	132.32	139.43	

Table 2 Estimates of the components of variation and their standard errors for flower diameter in a 5 × 5 diallel cross in *Petunia hybrida*.

	Contents of variation		
Notation	Estimated values	Proportional values	
D	54.18 ± 0.3007**	$(H_1/D)^{1/2}$	1.5166
F	22.26 ± 1.7520**	$(H_2/4H_1)$	0.239
H_1	128.26 ± 13.8200**	$(4DH_1)^{1/2} + F^1/(4DH_1)^{1/2} - F$	1.308
H_2	123.04 ± 7.2388**	h_2/H_2	4.63
h_2	570.14 ± 12.8840**	Heritability broad	89.7%
E	0.1608 ± 0.1732$^{n.s.}$	Narrow	37.8%

**highly significant.

treatment interaction using the ordinary method for analysis of variance in a randomized complete block design.

The mean values of the F_1 and F_2 generations did not differ significantly from each other, but the parental values showed significant differences. The estimates of the components of variation of the present character are given in Table 2. The (D) component measuring the additive variation was highly significant. The (H) component measuring dominance variation was also highly significant, however it is higher in magnitude than the (D) component. The component of variation due to dominance effects correlated with gene distribution (H_2) was highly significant, which indicated asymmetrical distribution of the dominant genes in the parental lines. The over-all dominance effects of heterozygous loci (h_2) were also highly significant, which indicates that the effect of dominance is due to heterozygosity. The (H) value which measures the covariance of additive and dominance effects was also highly significant. This suggests that dominant and recessive alleles are not equally distributed among the parents. This is in accordance with the above mentioned result detected by the (H_2) parameter. Since (F) value has the positive sign, it can be concluded that there is an excess of dominant alleles in the parents.

The quantity $(\hat{H}_1/\hat{D})^{1/2}$ which is a weighted measure of the average of dominance at each locus $= 1.52$, which is much more than unity. This would indicate moderate over-dominance. The quantity $\hat{H}_2/4H_1$ which is a measure of the proportion of genes with positive and negative effects in the parents was 0.23, suggesting some asymmetry at loci showing dominance. Since the values of $\hat{H}_2$ were not significantly different from those of $\hat{H}_1$, it may be assumed that the parents contain positive and negative genes in similar proportions. On the other hand, the ratio $(4\hat{D}\hat{H}_1)^{1/2}+F/(4\hat{D}\hat{H}_1)^{1/2}-F$ measuring the proportion of dominant and recessive genes in the parents was 1.308 which is more than unity. This suggests that dominant genes are in excess, which is in accordance with the result detected from the F-value. The fraction $\hat{h}_2/\hat{H}_2$ which estimates the number of genes or gene groups controlling this character was 4.63. These genes controlled flower diameter of petunia (Table 2).

Heterosis

In Table 3, the mean value of flower diameter of small flower parent (SF), grand flower parent (GF) mid-parent ($\bar{P}$) and F_1's of all crosses are presented. Deviations of F_1's from (SF), (GF), and ($\bar{P}$) are given as percentages (Table 3). In seven crosses, the F_1 hybrid showed heterosis towards the grand flower direction, exceeding the grand flower parent values. The extent of heterosis varied from 2.57% (P_2 pink × P_3 violet), to 16.02% (P_2 pink × P_4 red). On the contrary, no crosses showed heterosis towards the small flower direction. In other crosses, the F_1 hybrids were either almost equal to the mid-parent or lied near any of the corresponding parents of each cross.

Flower diameter was used as an indicator for studying the inheritance of flower size in the present investigation. 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 genes or gene groups are governing flower size in *Petunia hybrida*, which clearly contradicts the single gene-system reported by Ewart (2). 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. Moreover, the results suggest symmetrical distribution at loci showing dominance and present in excess over recessives in the

Table 3 Mean performance for flower diameter of parents, F_1's, and expression of heterosis percentage in a 5 × 5 diallel cross in *Petunia hybrida*. The underlined values represent heterotic F_1's.

Grosses	Flower diameter				Deviation of F_1 as % of		
	SF	GF	$\bar{P}$	F_1	SF	GF	$\bar{P}$
$P_1 \times P_2$	103.90	116.74	110.32	114.47	10.47	−1.94	3.76
$P_1 \times P_3$	103.90	135.02	119.46	143.17	37.79**	6.03	19.84**
$P_1 \times P_4$	103.90	135.36	119.65	140.04	34.78**	3.45	17.06**
$P_1 \times P_5$	103.90	137.02	120.58	142.25	36.91**	3.63	17.97**
$P_2 \times P_3$	116.74	135.36	125.88	138.50	18.63**	2.57	10.02**
$P_2 \times P_4$	116.74	135.26	126.05	157.05	34.52**	16.02**	24.59**
$P_2 \times P_5$	116.74	137.36	127.00	146.30	25.32**	6.32	15.19**
$P_3 \times P_4$	135.02	135.36	135.19	148.11	9.69*	9.41*	9.55*
$P_3 \times P_5$	135.02	137.26	136.14	137.09	1.53	0.12	−0.12
$P_4 \times P_5$	135.36	137.26	136.31	138.89	2.46	1.18	1.89

Sf: small flower   Gf: grand flower $\bar{P}$: mid-parent P_1: purple
P_2:pink P_3: violet P_4: red P_5: white

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 (according to Mather and Jinks, 5) 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 parent in magnitude. The high values of heterosis were observed in crosses involving parents carrying the most dominant alleles with the parent having the most recessive ones.

The Wr/Vr regression analysis

The F_1 and F_2 diallel regression analysis was made according to the method of Mather and Jinks (5) and Jinks (4). These are presented in Figures 1 and 2. The graphical analysis of F_1 showed that the regression coefficient (b) of Wr on Vr did not differ significantly from unity. The position of the regression line was to the right of the origin Figure 1. This indicates the presence of over-dominance, which is in accordance with the result detected from the parameter $(\hat{H}_1/\hat{D})^{1/2}$. On the other hand, the graphical analysis of F_2 data showed that the regression coefficient (b) deviated significantly from unity, suggesting the prevalence of non-allelic interaction (epistasis) of some arrays. The position of the regression line is slightly of the left of the origin (Fig. 2) indicating partial dominance in this generation due to segregation. The varieties 1 (purple) and 4 (pink) behaved as the most ressessive parents, as indicated from their position at the right-hands end of the F_1 regression line (Fig. 1), while both varieties are converted to have positions nearly at the middle of the F_2 regression line (Fig. 2). The latter situation indicates that both parents have nearly equal amounts of dominant and recessive allels. The parents 3 (red) and 5 (violet) behave similarly in both F_1 and F_2 regression analysis. These two varieties fall in positions at the extreme left-hand ends of the F_1 and F_2-regression lines (Figs. 1 and 2). It can be concluded that parents 3 and 5 behave as having the most dominant alleles. Among the five varieties studied in this diallel analysis for flower size, parent 2 shows a clear-cut

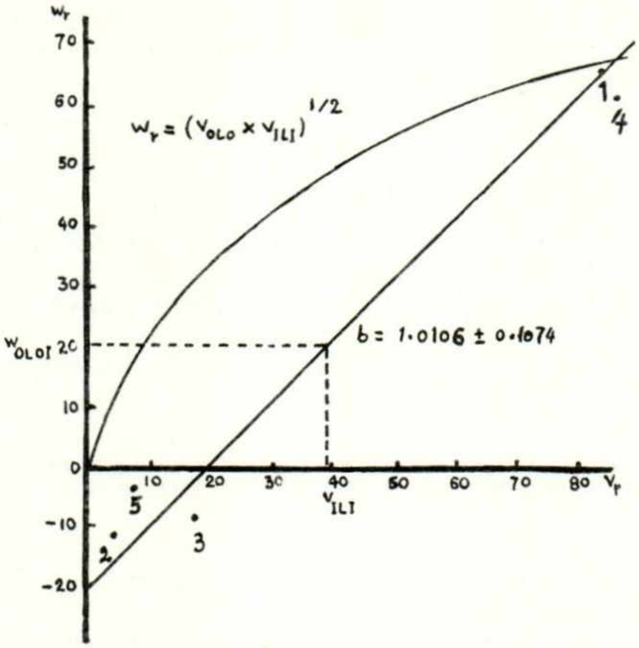

Fig. 1. V_r/W_r regression of flower size in the F_1.

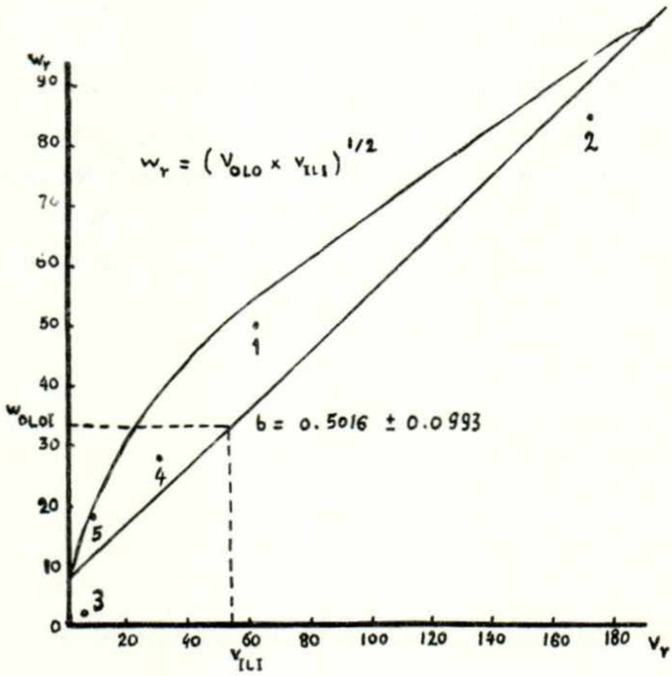

Fig. 2. V_r/W_r regression of flower size in the F_2.

contradiction between the F_1 and F_2-regression analysis; In the F_1 (Fig. 1), it falls at the extreme left-hand end of the regression line, behaving like parent 3 and 5 as having the most dominant alleles. In the F_2 (Fig. 2), it falls at the extreme right-hand end of the regression line, behaving as having the most recessive alleles among other parents.

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وراثة قطر الزهرة في نبات البتونا .Petunia hybrida L

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المستخلص

أجريت هذه التجربة لدراسة النظم الوراثية التي تحكم صفة قطر الزهرة في نبات البتونيا .Petunia hybridaLوقد استخدمت خمس سلالات نقية وهجنت بعمل كل التوافيق الممكنة وتتلخص النتائج في الآتي :—

١ — يتحكم في توريث هذه الصفة أنظمة وراثية عديدة الجينات من النوع ذات الأثر الوراثي المتجمع السيادة (Additive) .

٢ — أظهرت النتائج أن السيادة في هذه الصفة كانت من نوع السيادة الفائقة (Over dominance) .

٣ — وجد أن عدد الجينات (أو المجموعات الجينية) التي تحكم توريث هذه الصفة هى خمسة .

٤ — كان المكافىء الوراثي بمعناه الواسع (broad-sense) ٠,٨٩ وبمعناه الضيق (narrow sense) ٠,٣٧ .

٥ — درست قوة الهجين(heterosis) معبرا عنها بالنسبة المئوية لزيادة متوسط الهجين عن الأب الأكبر أو بقلته عن الأب الأصغر فكانت ما بين ٢,٦-١٦٪ .