

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

Part I : VEGETATIVE GROWTH CHARACTERISTICS.

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ABSTRACT

Intraspecific hybridization among four cultivars of snapdragon, i.e. P₁ = Sonnet wit (white), P₂ = Sonnet karmijn (red), P₃ = Sonnet rose (rose) and P₄ = Sonnet geel (yellow) was 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.

The main objective of this investigation 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 vegetative growth and also the type of gene action for the different traits.

Additive and dominance gene effects were significant in the F₁ and F₂ – generations with respect to plant height. The overdominance gene effects played an important role in the inheritance of plant height. Heritability in narrow sense was intermediate in both generations and no inbreeding depression was obtained for most crosses. Most of dominant genes have positive effects and increased plant height. All F₁ – crosses achieved positive heterosis.

Additive gene effect played the major role by the inheritance of the number of branches per plant. Heritability in narrow sense was intermediate in the F₁ and F₂ generations. Most of dominant genes have negative effects and decreased the number of branches. The overdominance gene effects played an important role for F₁ hybrids and partial dominance in the F₂ generations. The dominant genes were more frequent than recessive in the parents. Most crosses achieved positive heterosis.

Additive and dominance genes effects were involved in the inheritance of the number of leaves per plant. Heritability in narrow sense was moderate indicating that this trait could be advanced by selection. The degree of dominance $(H_1/D)^{1/2}$ was found to be overdominance in the F₁ hybrids confirmed with W_r, V_r graph. In the F₂ generations the results of W_r, V_r graph contradicted with the ratio $(H_1/D)^{1/2}$ indicated the presence of epistasis. Dominance genes seemed to be acted in negative direction in the F₁ hybrids and P₁ carried most recessive genes, while in the F₂ dominance genes acting in positive direction and P₂ and P₃ have most dominant genes.

In the F₁ hybrids, additive and dominance components were found to be not significant with respect to leaf area. Environmental effects were high and such large environmental role and also overdominance was involved in the inheritance of leaf area. The parent seemed to carry more dominant genes than recessive. Dominant genes seemed to be acting in positive direction and increased leaf area.

INTRODUCTION

Snapdragon (*Antirrhinum majus*) is widely cultivated in gardens and houses. It is used as a cut flower, pot plant and for cultivation in flowerbeds. The flowers of snapdragon have an unfamiliar and attractive shape and colours. The flowers are arranged in simple racemes or spikes. The plant

may be tall or short, upright or semi spherical according to varieties. (El-Gamassy and Nada, 1974).

The genetics and inheritance of plant height, the number of branches per plant, the number of leaves per plant as well as leaf area have been biometrically analyzed and studied in *Antirrhinum majus* (El-Torky, 1981 and Misiha, 1991) as well as in many other plants (Ahmed and Ismail, 1999; Deore *et. al.*, 1997 and Kumar *et al.*, 1998).

Estimation of genetic variances and its components are the first step to determine the most appropriate breeding scheme, the choice of an efficient breeding method on the magnitude and type of gene effect prevailing in the population under study. The diallel cross analysis of Hayman (1954 and 1957) is a useful method to divide the phenotypic variation into genotypic and environmental components and further subdivide the genotypic variation into additive and non-additive components. To improve any quantitative character which show a continuous range of variation, information about the gene action of the character has to be acquired. The different gene actions involved in the inheritance of such characters are additive (resulting from average effects of genes) and non - additive (resulting from dominance and epistasis effects among the genes). The relative importance of these two components provides the breeder with valuable information about the possibilities and methods of improving these characters. If the additive gene action appears to be more important contributor to the genetic variability of a character, a maximum improvement in this particular character must be expected by the breeder through a carefully designed selection programme. On the contrary, the presence of a relatively high non – additive gene suggests that a hybrid programme will perform good prospects for the characters under consideration, as a result of a direct relationship between the non – additive gene action and heterosis (Jinks, 1954).

MATERIALS AND METHODS

The effects of crossing different cultivars of snapdragon (*Antirrhinum majus*, L.) on the characteristics of vegetative growth were studied throughout three generations, i.e. parental, first and second generations. The experiments were carried out during three successive growing seasons of 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; P₁ = Sonnet wit (white), P₂ = Sonnet karmijn (red), P₃ = Sonnet rose (rose) and P₄ = Sonnet geel (yellow) were obtained from Hamer Bloemzaden b.v., Holland.

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 F₁ – seeds. The F₁ – seeds were sown on December 8, 1996. The F₁ – young plants were transplanted on February 25, 1997. As soon as the F₁ – plants started to bloom, selfings were carried out to obtain the F₂ – 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. Plant height (in cm.) measured from the soil surface to the top of the longest branch.
2. Number of branches per plant.
3. Number of leaves per plant.
4. The leaf area (in cm.²) expressed as the average mean weight of a leaf divided by the mean weight of one cm.².

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. Plant height

Statistical analyses proved that P₃ was the tallest among the parents and it differed significantly from all parents (Table 1). Crosses derived from the P₃ in either the parental or the maternal directions were taller than the parents in both the first and second seasons except the cross P₃ × P₂. All crosses exhibited significant positive heterosis estimates (Table 2). There were no differences between the F₁-crosses and their reciprocals except those of the P₁ × P₄ and P₄ × P₁. In the F₂ generations, most of the crosses and their reciprocals showed no differences with two exceptions, i.e. P₁ × P₄ and P₃ × P₄ and their reciprocals. The difference was due to the maternal effect. Most crosses gave no inbreeding depression as shown in Table 2 except for P₃ × P₂ and P₂ × P₄ indicating that additive gene effect was important for plant height and also dominance gene effect in some crosses as reported also by Mahdy *et al.* (1983) on cotton and Abdel- Sabour *et al.*, (1996) on wheat.

The assumptions of Jinks (1954) and Hayman (1954) of diploid segregation and homozygous parents were found valid and no reciprocal differences may be considered valid with some degrees of confidence. The method of testing the assumptions of no epistasis, no multiple alleles and uncorrelated gene distribution, was done through the regression coefficient (b) by calculating the regression of covariance on the variance; b was found to be significantly different from zero (b= 0.97 ± 0.09 in the F₁ and 0.92 ± 0.19 in the F₂) and is not significantly different than 1.0 (Fig. 1), therefore the assumptions were valid as reported by Misiha (1991) on *Antirrhinum majus*.

Genetic parameters presented in Table 3 indicated that the dominance gene effect "H₁" as well as the additive gene effect "D" were significant in both F₁ and F₂ indicating their importance in the inheritance of plant height. On the other side, "E" component estimating environmental

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1+2

Fig1+2

effect was significant only in the F_1 indicating minor effect of environment on plant height variation. These results agreed with the finding of Misiha (1991) on *Antirrhinum majus* and Madić (1996), on barley. The proportion ($H_2/4H_1$) was 0.25 in the F_1 and KD/KR preparation was found to be close to the unity indicating that the dominant and recessive genes were distributed in equal proportions among the parents, while in the F_2 , $H_2/4H_1$ was less than 0.25 indicating a symmetry of positive and negative gene proportions in the parents with KD/KR which was larger than the unity indicating that the parent carry more dominant than recessive genes.

$(H_1/D)^{1/2}$ estimate of the degree of dominance suggested over-dominance in both generations. This result is supported by the finding shown in W_r , V_r graph (Fig1), where the regression line intercepted the W_r axis in a negative position in both F_1 and F_2 generations which agreed with results of Bakheit and Ezzat (1987) on sesame. In the F_1 , "P₃" had most dominant genes and P₁ and P₄ had most recessive genes, while P₂ had equal frequency of dominant and recessive genes. In the F_2 , P₃ and P₂ had most dominant genes, while P₄ had most recessive genes and P₁ had equal frequency of dominant and recessive genes. Correlation coefficient of $W_r + V_r$ and V_r was negative suggesting that most of dominant genes had positive effect and increased plant height, which agreed with the results of Weber (1976) on peas and El-Torky (1981) on *Antirrhinum majus*.

The estimates of heritability in broad sense were high (Table 3) indicating that plant height was a genetically controlled character, while the narrow sense heritability estimates were moderate in both generations reflecting the moderate magnitude of additive gene effect in the inheritance of plant height.

2. Number of branches per plant

The mean values for the number of branches per plant are presented in Table 1. The data showed that P₁ and P₂ achieved the highest number of branches in the F_1 and F_2 and they were statistically different from P₃ and P₄, which had the lowest number of branches. By the F_1 -progenies, P₂×P₄ and P₃×P₄ and their reciprocals as well as P₃ × P₂ and P₂×P₁ produced more branches than their parents, they had also positive heterosis values expressing a clear hybrid vigour (Table 2), while P₃×P₁, P₁×P₄ and P₄×P₁ were similar to their parents producing comparatively low number of branches and had also negative heterosis values. The F_2 -progenies of all crosses were intermediate between their parents except those of P₁×P₂, P₃×P₄, P₃ ×P₄ and their reciprocals which had higher number of branches compared to their parents.

Inbreeding depression (I.D.) estimates (Table 2) were found to be positive for each of the crosses P₁×P₃, P₂×P₄, P₃×P₄ and their reciprocals as well as for the P₃×P₂ progeny. The other crosses achieved negative I.D. estimates indicating that additive gene effect had a major effect in the inheritance of the number of branches per plant and that the dominant gene effect was also involved.

Due to the presence of significant differences between crosses, the diallel analysis was employed to the data according to the method of Hayman

(1954) to test the validity of the assumption of analysis. It could be concluded that diploid segregation, homozygous parents and no reciprocal differences have been already proven to be valid. The assumptions, no epistasis, no multiple alleles and uncorrelated gene distribution could be tested by calculating (b) which was not found to differ significantly from 1.0 ($b = 0.96 + 0.36$), while in the F_2 $b = 0.81 + 0.02$ indicating that these assumptions were not fulfilled (Fig. 2). Estimates of genetic parameters and ratios were calculated and presented in Table 3. The “ H_1 ” component estimating dominance was found to be significant in the F_1 and non-significant in the F_2 , while “ D ” component was significant in the two seasons indicating that the additive gene effect played a major role in the inheritance of this trait, which agreed completely with the findings of Misiha (1991) on *Antirrhinum majus* and Cinsoy (1992) on soybean. The “ E ” component was not significant either in F_1 or in F_2 indicating that there was minor effect of environment in the variation of this trait. There was a symmetry of positive and negative gene proportion in the parents from ratio $H_2/4H_1$ supported by KD/KR , which was larger than 1.0 in the F_1 - generation indicating that parents carry more dominant genes than recessive, while in the F_2 , there was equal distribution in the parents according to $H_2/4H_1$ which was larger than 0.25 and confirmed also by KD/KR , which was equal to the unity. With regard to $(H_1/D)^{1/2}$, estimation was close to 1.0 in F_1 indicating the presence of overdominance, while in the F_2 , it was found to be lower than 1.0 suggesting a partial dominance. These results agreed with the (W_r, V_r) graph as shown in Fig 2. The regression line intercepted the W_r axis in a position near to the origin expressing a complete dominance case in F_1 , while in F_2 , the regression line intercepted W_r axis in positive position indicating a partial dominance. The W_r, V_r points corresponding to the parents P_3 and P_4 fall near to the point of origin suggesting that these parents carried most dominant genes, while P_1 carried most recessive genes and P_2 had nearly equal frequency of dominant and recessive genes in both F_1 and F_2 . Moreover, the $(W_r + V_r)$ values were positively correlated with the parental means indicating that most of dominant genes had negative effect and decreased the number of branches per plant. With regard to h^2/H_2 ratio, it indicated that one group of gene exhibiting dominance was found to control the number of branches.

Heritability in broad sense was high in the F_1 and F_2 generations (Table 3) indicating that this character was genetically controlled. In the same time heritability in narrow sense was moderate in F_1 and F_2 referring to the presence of additive gene effect, so this character could be advanced by selection as reported by Yadav and Chankar (1991) on okra and Misiha (1991) on *Antirrhinum majus*.

3. Number of leaves per plant

The mean values of the number of leaves per plant presented in Table 1 indicated that the parents differed greatly from each other. The parent (P_1) produced the highest values for F_1 and F_2 followed by P_2 .

The crosses which involved P_2 always gave high values in the F_1 -and F_2 – generations and achieved positive heterosis values (Table 2), with one

exception ($P_2 \times P_1$), whereas P_1 gave only one case of positive heterosis by its cross with P_2 , all other crosses achieved negative values.

There were no differences between the crosses and their reciprocals except those of $P_1 \times P_3$ and $P_3 \times P_4$ in the F_1 , $P_1 \times P_2$ and $P_1 \times P_4$ in the F_2 .

The importance of additive gene effects on the number of leaves per plant was obviously detected from Table 2 due to the negative values obtained for inbreeding depression (I.D) in most cases. Only two crosses gave positive values, i.e., $P_2 \times P_3$ and $P_3 \times P_4$, which gives an indication to the possible role of dominance genes as supported by Singh and Sudhir (1996) on *Papaver somniferum*.

As reviewed previously, diallel cross analysis suggested by Hayman (1954) was based on several assumptions. No epistasis, no multiple allele, and uncorrelated gene distribution are valid. These results confirmed with the regression coefficient of W_r upon V_r which did not differ significantly from 1.0 in F_1 and F_2 ($b=1.02 \pm 0.26$, 1.03 ± 0.14 respectively) and it differed significantly from Zero in F_2 (Fig. 3). The other assumptions of diploid segregation, homozygous parents were valid, no reciprocal differences assumption was valid with some degrees of confidence. The results presented in Table 3 showed that the additive genetic component "D" was significant in F_1 and F_2 and also dominance genetic component " H_1 " was significant indicating the importance of additive gene and dominance gene for this character. These results agreed with Shamsuddin *et al.* (1980) on tobacco. The "E" component estimating the environment effect was significant in F_2 only. The $H^2/4H_1$ ratio was less than 0.25 in both generations, indicating a symmetry of positive and negative genes in the parents and that the parents carry more dominant genes than recessive reflecting proportion KD/KR , which was larger than one in F_1 but the parents seemed to carry more recessive genes than dominant in F_2 , where KD/KR was found to be less than 1.0. The proportion $(H_1/D)^{1/2}$ in F_1 was larger than 1.0 indicating overdominance. This could be confirmed with the W_r , V_r graph as shown in Fig. 3 where the regression line intercepted W_r axis in negative position, while in F_2 $(H_1/D)^{1/2}$ was less than 1.0 indicating partial dominance which disagreed with W_r , V_r graph, where regression line intercepted W_r axis in negative position indicating overdominance, since epistasis can decrease or increase the average degree of dominance (Hayman, 1957). In addition, Mather and Jinks (1971) reported that the ratio H_1/D is not a measure of degree of dominance, so this estimate is not true and the graphic analysis may be reliable. The W_r , V_r points corresponding to the parents in the F_1 for P_4 and P_3 had most dominant genes, while P_1 had more recessive genes, but in F_2 , P_4 carried most recessive genes, while P_1 , P_3 , P_2 were found to be in intermediate position.

Correlation coefficient between parental means and $W_r + V_r$ was positive in F_1 indicating that most of the genes exhibiting dominance were associated with the lower number of leaves, while in F_2 , the position was reversed.

Heritability in broad sense was high (Table 3). This finding indicated that the number of leaves per plant is under the control of genes, while heritability in narrow sense was found to be moderate in the F_1 and F_2 , which

agreed with the results of Rastogi *et al.* (1995) on Chinese cabbage and Khar *et al.* (1997) on cauliflower.

4. Leaf area

Parents were not significantly different from each other, while in the F₂ generations, P₃ produced the highest value (Table 1). Progenies of all crosses achieved higher values for leaf area compared to their parents. They also obtained positive heterosis values indicating the presence of hybrid vigour for all crosses (Table 2). No significant differences were found between crosses and their reciprocals except in the case of P₁ x P₃ in the F₁ and P₁ x P₃, P₁ x P₄ and P₃ x P₄ in the F₂. Inbreeding depression values were positive in the crosses P₁ x P₂, P₂ x P₁, P₃ x P₁, P₄ x P₁, P₂ x P₃ and P₄ x P₃ indicating the importance of dominance genes controlling the inheritance of the character. These results agree with the findings of Deore *et al.* (1997) on and Zhao *et al.* (1997). On the other hand, the inbreeding depression values were negative in P₁ x P₃, P₁ x P₄, P₃ x P₂, P₂ x P₄, P₄ x P₂ and P₃ x P₄ indicating the control of additive gene effect in the inheritance of leaf area for these crosses (Table 2). Assumptions of no epistasis, no multiple allele and uncorrelated distribution were found valid by calculating regression coefficient (b) of covariance between all offspring of the parent and their non - recurrent parent on the variance of these offspring, b is not significantly different than 1.0 in both F₁ and F₂ (b=0.40±0.28, 0.84±0.42 respectively) indicating the validity of the three assumptions mentioned earlier. This result was also confirmed with W_r, V_r graph as shown in Fig. 4, where W_r was related to V_r by straight line. With regard to the other assumptions of diploid segregation, homozygous parents, they were found valid and no reciprocal differences assumption may be considered valid with some degrees of confidence. In the F₁, the "E" component estimating environmental effects was significant as shown in Table 3 indicating the important role of environment in the control of leaf area, which agreed with the conclusion of Faluyi (1986) on cashew. The "D" and "H₁" components were not significant. The large environmental role might be expected to mask any heritable variation (Randall and Ruth, 1993). Other ratios couldn't be calculated because the relevant components were not significant (Hayman, 1954). In the F₂, the "D" component, estimating additive gene effect, was not significant, while "H₁" component, estimating dominance gene effect, was significant indicating that the dominance gene effect played a major role in the inheritance of leaf area. This agreed with Yadav *et al.* (1981) on wheat. There is a symmetry of positive and negative genes in the parents from the H₂/4 H₁ ratio supported by KD/KR ratio, which was larger than unity indicating that the parents seemed to carry more dominant genes than recessives. The proportion (H₁/D)^{1/2} was larger than the unity indicating the presence of overdominance. This was confirmed with the W_r, V_r graph (Fig. 4), where the regression line intercepted W_r in negative position and the degree of dominance could be estimated from the graph in the F₁, where the regression line intercepted W_r in negative position indicating the presence of overdominance. It can be concluded from the graph that P₁ had the most recessive genes in F₁ and F₂, but P₄ had the most dominant genes followed by P₂ and P₃ in the F₁, while P₄ seemed to carry

Fig3+4

more recessive genes than dominant. The correlation coefficient between parental mean Y_r and W_r , V_r had a negative value in the F_1 and F_2 indicating that most of dominant genes had positive effect and increased leaf area.

Heritability in broad sense was moderate in F_1 (0.52) reflecting the environmental effect, while it was high in the F_2 (0.89) indicating that leaf area is a genetically controlled character (Table 3). Heritability in narrow sense was low (0.1 in the F_2) reflecting the weak effect of additive genes. The ratio h_2/H^2 was lower than the unity indicating that leaf area is under the control of one group of genes exhibiting dominance.

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تحليلات بيومترية لبعض الصفات الكمية الهامة في حنك السبع

١. مواصفات النمو الخضري.

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أجريت هذه الدراسة في معهد بحوث البساتين بحداثق انطونيداس بالإسكندرية في الأعوام ١٩٩٦/٩٥ ، ١٩٩٧/٩٦ و ١٩٩٨/٩٧ بغرض إنتاج أنماط مختلفة من حنك السبع وتحديد النظام الوراثي المتحكم في وراثة صفات النمو الخضري وكذلك الفعل الجيني المتحكم في الصفات الكمية المدروسة لتحديد إمكانية إنتاج الصفات الخضرية المرغوبة تبعاً لمتطلبات السوق.

وقد استخدمت في الدراسة أربعة أصناف من نبات حنك السبع وهم
(white),
 $P_1 = \text{Sonnet wit}$

$P_2 = \text{Sonnet karmijn (red)}$, $P_3 = \text{Sonnet rose (rose)}$ and $P_4 = \text{Sonnet geel (yellow)}$

حيث أجريت بينهم كل التهجينات الممكنة. وأظهرت النتائج وجود فروق معنوية بين الهجن في كل الصفات المدروسة وقد استخدمت طريقة هابمان لتحديد النظام الوراثي المتحكم في وراثة الصفات.

وبالنسبة لصفة طول النبات : ثبتت أهمية الفعل الجيني المضيف والسيادي في كلا الجيلين مع وجود سيادة متفوقة. درجة التوريث بالمعنى الضيق متوسطة ولم يظهر إنخفاض لطول النبات في الجيل الثاني عن الجيل الأول لأغلب الهجن ولذلك يمكن تحسين الصفة بالانتخاب. أظهر التحليل البياني أن الأب (P_3) يحتوي على معظم الجينات السائدة كما أن معظم الجينات السائدة تؤدي إلى زيادة طول النبات. ظهرت قوة الهجين في كل الهجن الناتجة.

وبالنسبة لصفة عدد الأفرع : ثبتت أهمية التأثير المضيف للجينات. درجة التوريث بالمعنى الضيق كانت متوسطة مما يعنى إمكانية تحسين الصفة بالانتخاب. معظم الجينات السائدة تقلل عدد الأفرع والأب (P_1) يحتوي على معظم الجينات المتنحية. وجود سيادة متفوقة في الجيل الأول وسيادة جزئية في الجيل الثاني. الجينات السائدة أكثر تكراراً من الجينات المتنحية وظهرت قوة الهجين في أغلب الهجن.

أما بالنسبة لصفة عدد الأوراق : فلقد ثبتت أهمية كل من التأثير المضيف للجينات والتأثير السيادي مع وجود سيادة متفوقة في كلا الجيلين ووجود التفوق في الجيل الثاني. درجة التوريث بالمعنى الضيق متوسطة. الجينات السائدة تقلل من عدد الأوراق في الجيل الأول الأب (P_1) يحتوي على أغلب الجينات المتنحية بينما الجينات المتنحية هي التي تقلل الصفة في الجيل الثاني. الأبوين (P) و (P_3) يحتويان على أغلب الجينات السائدة.

وعند دراسة المساحة الورقية : كانت التأثيرات البيئية معنوية بينما التأثيرات الوراثية غير معنوية في الجيل الأول. اتضحت أهمية الفعل الجيني المضيف في الجيل الثاني وكذلك وجود السيادة المتفوقة. احتوت الأباء على جينات سائدة بكمية أكبر من الجينات المتنحية وكانت الجينات السائدة تزيد من المساحة الورقية. احتوى الأب (P_2) على معظم الجينات السائدة.

Table1: Mean values of plant height, number of branches/ plant, number of leaves/ plant and leaf area of the F₁ and F₂ generations for the different selfings and crosses of *Antirrhinum majus*.

Genotypes ¹⁾	Mean ²⁾ plant height (cm)		Mean ²⁾ no. branches/plant		Mean ²⁾ no. leaves/ plant		Mean ¹⁾ leaf area (cm ²)									
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂								
P ₁ x P ₁	35.4	gh	48.9	gh	82.3	a	66.3	cd	1200.6	a	1123.3	bc	7.2	d	7.90	i
P ₂ x P ₂	33.7	hi	51.5	fgh	56.3	bc	71.3	bc	770.6	h	1003.3	cd	8.8	cd	10.7	ghi
P ₃ x P ₃	45.5	bcde	61.9	cd	33.3	d	20.3	h	701.0	fgh	766.0	fg	9.8	bcd	13.5	defg
P ₄ x P ₄	32.7	i	41.1	i	31.0	d	26.6	gh	606.6	gh	652.6	g	11.6	bcd	9.30	hi
P ₁ x P ₂	38.8	fgh	53.0	fg	81.6	a	90.2	a	1084.0	ab	1377.3	a	12.3	bcd	12.0	efgh
P ₂ x P ₁	40.7	defg	58.7	d	88.3	a	83.9	ab	985.0	abcd	1203.6	b	13.7	bc	14.1	cde
P ₁ x P ₃	49.3	ab	64.6	bc	56.0	bc	36.3	efgh	896.3	bcdef	991.0	cde	11.1	bcd	16.2	bcd
P ₃ x P ₁	51.6	a	69.0	a	49.0	cd	37.8	efg	575.0	h	839.0	ef	20.6	a	20.0	a
P ₁ x P ₄	41.1	g	58.5	de	32.6	d	45.0	ef	587.0	h	913.3	def	12.9	bc	16.8	bc
P ₄ x P ₁	44.5	f	62.8	bcd	48.3	cd	49.8	de	592.6	h	1112.0	bc	13.2	bc	13.7	def
P ₂ x P ₃	45.3	bcde	61.1	cd	47.3	cd	47.3	ef	1030.3	abc	1005.6	cd	12.4	bcd	12.7	efg
P ₃ x P ₂	46.8	abc	48.3	h	74.0	ab	50.5	de	974.6	bcde	1131.0	bc	9.5	bcd	10.9	fgh
P ₂ x P ₄	45.5	bcde	59.1	d	57.3	bc	48.5	e	806.3	defg	1018.0	cd	14.5	b	16.0	bcd
P ₄ x P ₂	39.8	efg	54.3	ef	62.0	bc	46.3	ef	766.0	efgh	1135.0	bc	10.6	bcd	13.6	defg
P ₃ x P ₄	48.8	ab	63.8	bc	56.6	bc	36.8	efgh	858.3	cdef	774.0	fg	11.5	bcd	17.8	ab
P ₄ x P ₃	46.2	abcd	67.1	ab	46.6	c	31.5	fgh	600.6	h	877.0	def	13.3	bc	13.6	defg
L.S.D. 0.05	6.0		4.4		18.9		17.2		216		164		5.3		3.0	

1) Seed parent is the first one, P₁= white, P₂- red- purple, P₃= red, P₄= 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.

Table 2 : Estimates of heterosis and inbreeding depression (I.D) for plant height, number of branches/ plant, number of leaves/ plant and leaf area for the different crosses of *Antirrhinum majus*.

Genotypes ¹⁾	plant height (cm.)		No. of branches/ plant		No. of leaves/ plant		leaf area (cm ²)	
	Heterosis	I.D.	Heterosis	I.D.	Heterosis	I.D.	Heterosis	I.D.
P ₁ x P ₂	4.20 ^{N.S}	-0.50 ^{N.S}	+12.3 ^{N.S}	-16.1 ^{N.S}	+98.4 ^{N.S}	-20.9 ^{N.S}	4.3 ^{N.S}	+0.5 ^{**}
P ₂ x P ₁	6.10*	-9.80**	+19.0*	-0.22 ^{N.S}	-0.6 ^{N.S}	-15.4 ^{N.S}	5.7*	+4.50*
P ₁ x P ₃	8.80**	-2.40 ^{N.S}	-1.8 ^{N.S}	+26.9**	-54.50 ^{N.S}	-3.1 ^{N.S}	2.6 ^{N.S}	-36.9**
P ₃ x P ₁	11.10**	-6.50*	-8.8 ^{N.S}	+13.4 ^{N.S}	-375.8**	-34.3 ^{N.S}	12.1**	+7.70**
P ₁ x P ₄	7.00**	-8.20**	-24.05**	-52.1**	-316.6**	-44.2 ^{N.S}	3.5 ^{N.S}	-22.4**
P ₄ x P ₁	10.4**	-9.60**	-8.3 ^{N.S}	-12.6 ^{N.S}	-311.0**	-76.4 ^{N.S}	3.8 ^{N.S}	+3.70 ^{N.S}
P ₂ x P ₃	5.70*	-3.90 ^{N.S}	+2.5 ^{N.S}	-9.7 ^{N.S}	+294.8**	+8.8 ^{N.S}	3.1 ^{N.S}	+5.60*
P ₃ x P ₂	7.20**	+26.7**	+29.2**	+25.5**	+238.8*	-9.2 ^{N.S}	0.2 ^{N.S}	-4.20*
P ₂ x P ₄	12.30**	+0.80 ^{N.S}	+13.6 ^{N.S}	+7.3 ^{N.S}	+117.7 ^{N.S}	-17.9 ^{N.S}	4.3 ^{N.S}	-3.40 ^{N.S}
P ₄ x P ₂	6.60*	-1.20 ^{N.S}	+18.3*	+17.9*	+77.4 ^{N.S}	-13.3 ^{N.S}	0.4 ^{N.S}	-18.80**
P ₃ x P ₄	9.70**	-2.00 ^{N.S}	+24.4**	+26.8**	+204.5*	+17.5 ^{N.S}	0.8 ^{N.S}	-46.0**
P ₄ x P ₃	7.10**	-14.90**	+14.4 ^{N.S}	+22.5*	-53.2 ^{N.S}	-34.9 ^{N.S}	2.6 ^{N.S}	+5.2*
L.S.D. 0.05	5.2		16.4		187.3		191.9	
L.S.D. 0.01	7.0		22.1		252.2		258.5	

1) Seed parent is the first one, P₁= white, P₂- red- purple, P₃= red, P₄= 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.

Table 3 : Estimates of genetic parameters and ratios with their respective standard errors in F₁ and F₂ for plant height, number of branches/ plant, number of leaves/ plant and the leaf area of *Antirrhinum majus*.

Estimate	Plant height (cm.)		No. of branches/ plant		No. of leaves/ plant		Leaf area (cm ²)	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
D	30.38±1.68*	71.85±10.47*	530.92± 67.06*	659.95±27.41*	63394.11±9207.80*	43077.74±1552.65*	00.05±3.15 ^{N.S}	4.61±2.86 ^{N.S}
H ₁	63.27±4.89*	728.15±125.01*	543.37±194.94*	499.89±318.71 ^{N.S}	105183.52±26766.05*	136704.67±18528.87*	18.03±9.18 ^{N.S}	150.28±33.26**
H ₂	64.15±4.52*	610.12±112.44*	440.44±179.94*	615.54±294.20 ^{N.S}	71716.33±24707.12*	118553.36±16664.84*	16.37±8.47 ^{N.S}	134.67±30.70*
h ²	140.95±3.06*	159.80±76.27*	97.06±122.05 ^{N.S}	-394.19±199.55 ^{N.S}	-415.08±16758.45 ^{N.S}	8560.72±11303.50 ^{N.S}	26.67±5.74*	36.50±20.82 ^{N.S}
F	-6.28±4.32 ^{N.S}	120.65±53.08*	231.35±172.28 ^{N.S}	-315.05±138.89 ^{N.S}	57148.04±23655.27*	-10887.18±7867.38 ^{N.S}	2.45±8.11 ^{N.S}	9.14±14.49 ^{N.S}
E	4.33±0.75*	2.4±4.6 ^{N.S}	43.1±29.99 ^{N.S}	35.93±12.25 ^{N.S}	5610.13±4117.85 ^{N.S}	3234.83±694.36*	3.4±1.41*	1.1±1.27 ^{N.S}
(H ₁ /D) ^{1/2}	1.44	1.59	1.01	0.43	1.2	0.89	1.95	2.85
H ₂ /4H ₁	0.25	0.20	0.20	0.30	0.17	0.21	0.24	0.22
KD/KR	0.86	3.23	1.54	1.00	2.07	0.75	2.11	2.06
r(y _r , W _r + V _r)	-0.93	-0.69	0.09	0.92	0.99	-0.51	-0.91	-0.81
h ² _{Ns}	0.46	0.35	0.56	0.60	0.45	0.45	0.12	0.10
h ² _{Bs}	0.88	0.95	0.87	0.86	0.87	0.86	0.52	0.89
h ² /H ₂	2.19	0.26	0.22	0.64	0.05	0.07	0.35	0.27

N.S., * : Non significant and significant respectively (The significance was defined in the F₁, when the value exceeded 1.96; while in the F₂, the significance was tested by t- test at P= 0.05 and 2 degrees of freedom).

