

## IMPACT OF SCALING AND JOINT SCALING TESTS IN DECIDING THE SUITABLE BREEDING APPROACH FOR IMPROVING SOME PEA TRAITS

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### ABSTRACT

*Significance one or more of the three individual scaling tests A, B and C as well as the joint of scaling test ( $X^2$ ) revealed the presence of epistasis in all studied traits of two pea crosses, except number of ovules/pod (Cross1).*

*Estimates of the type of gene action for these traits revealed that the dominance gene action (h) was the main type of gene effects for both crosses in all characters, except number of ovules/pod (Cross1). Additive gene effects are of minor importance in the explanation of traits variation. Generally, both additive and non-additive gene effects as well as one or more of the three types of epistasis i.e., additive x additive (i), additive x dominance (j) and dominance x dominance (l) were important in the genetic system controlling all studied characters.*

*Due to the major role of the non-additive effects recurrent selection for specific combining ability can be suggested as a good breeding procedure, but with certain limitations. Duplicate type of epistasis was recorded for all studied traits, except for pod width (Cross1). On the other hand, the complementary type of epistasis was recorded for number of ovules/pod. Over-dominance was detected for pod length, number of ovules/pod, pod width (Cross2) and number of seeds/pod (both crosses). Meanwhile, partial dominance was exhibited for number of ovules/pod, pod width, number of pods/plant (Cross1), plant height and yield (both crosses). Heritability, in narrow sense, was low for number of seeds/pod, pod length and yield (Cross1) and moderate to high for remainder traits.*

**Key words:** *Pea, Additive and non-additive gene action, Scaling test, Joint scaling test, Heritability*

### INTRODUCTION

To carry out a successful breeding program for the improvement of desired traits in pea, (*Pisum sativum*) the breeder should have enough knowledge about various types of gene effects. However, the improvement of both quantitative and qualitative traits of pea depends on the presence of genetic variability that permits effective selection. It is assumed in most analysis that non-allelic interaction are absent although these analysis rarely provide a valid test of this assumption. Also, the tests of epistatic gene effects are very important for plant breeder along with the other two types of gene effects i.e., additive and dominance (Gamble 1962).

Comstock (1955) has shown how the presence of epistatic gene effects will cause an upward bias in the estimates of both the additive and dominance genetic variance. Perhaps, inclusion of epistasis in the analysis model would decrease the amount of additive genetic variance, but this does

not appear to be the complete explanation. Hayman (1958) described parameters related to those of Anderson and Kempthorne(1954) which permit estimation of the additive, dominance, additive x additive, additive x dominance and dominance x dominance gene effects with less difficulty in their interpretation. Many authors directed studies of pea breeding mainly to analysis of gene effects for understanding the mode of inheritance of the yield and its attributes under upper Egypt conditions as Zayed (1998), Zayed *et al* (1999), Kandeel *et al* (2005), Zayed *et al* (2005) and El-Dakkak *et al* (2009). They reported the importance of both additive and dominance in expression of most pea traits.

The estimates of epistatic interaction (s) along with additive and dominance gene effects were applied by Singh and Sharma (2001), Sharma and Rastogi (2001), Singh *et al* (2003) and Singh and Sharma (2004). They stated that the additive (d), dominance (h) and all the three interacting gene effects played a major role in the inheritance of most studied quantitative traits. They added that, majority of the crosses in each studied trait exhibited the duplicate type of epistasis. Singh and Singh (1990) suggested that reciprocal recurrent selection would be useful to develop elite populations in such cases.

The aim of the present investigation was to study the type of gene action, type of epistasis and components of the genetic variation and their derived ratios for some traits of two pea crosses to obtain additional information about some genetic parameters to help the breeder to handle the segregating generations.

## MATERIALS AND METHODS

### Description of the parental genotypes and experimental procedures

The present study was carried out at Shandaweel Research Station, Sohag Governorate during three winter successive seasons i.e., 2005/2006, 2006/2007 and 2007/2008. In the first season (2005/2006), 3 elite parental genotypes were grown and two pea crosses were made by hand, i.e., Alaska x Dwarf Gray Sugar and Alaska x Early Perfection. In the second season, 2006/2007, seeds of two F<sub>1</sub>'s were planted to produce F<sub>2</sub> and it were back-crossed to both parents to produce BC<sub>1</sub> (F<sub>1</sub> x P<sub>1</sub>) and BC<sub>2</sub> (F<sub>1</sub> x P<sub>2</sub>). In the third season, 2007/2008, the obtained seeds of the six populations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>) of both crosses were sown on 5<sup>th</sup> November 2007 and evaluated using a randomized complete block design with three replications. Each plot consisted of 30 ridges, the ridge was 3 m length and the distance between plants was 20 cm on each side of the ridge and 70 cm was left between ridges. The experimental plot consisted of four ridges for each parent, F<sub>1</sub> and back-crosses as well as 10 ridges for F<sub>2</sub> generation. The

recommended agricultural practices of pea production were applied at the proper time.

#### Recorded data

Data were collected on competitive plants of each population for plant height, number of branches/plant, pod length, pod width, number of seeds/pod, number of ovules/pod, number of pods/plant and green pod yield (g/plant).

#### Biometrical analyses

- a- The scaling test A, B and C were applied as outlined by Mather and Jinks (1971) to test the presence of non-allelic interactions using the following equations:

$$A = 2 \overline{BC_1} - \overline{P_1} - \overline{F_1}$$

$$B = 2 \overline{BC_2} - \overline{P_2} - \overline{F_1}$$

$$C = 4 \overline{F_2} - 2 \overline{F_1} - \overline{P_1} - \overline{P_2}$$

The significance of any of these scales is taken to indicate the presence of non-allelic interaction. The standard error of A, B and C was done by taking the square root of respective variances of A, B or C.

- b- Joint scaling test was proposed by Cavalli (1952) as indicated  $X^2$  (qui square) was applied to test the adequacy of the genetic studied model controlling the characters. However, non-significant  $X^2$  and/or scaling test means that the simple additive-dominance model is adequate. In this case, the genetic model of Jinks and Jones (1958) would be applied.
- c- Digenic interaction model analysis: In the case of significant  $X^2$  and/or scaling tests i.e., the simple additive-dominance model is inadequate, six parameter models were used according to Hayman (1958) to separate out the components of genetic variance to its main effects. The estimated gene effects included the mean effect parameter (m), additive (d), dominance (h), additive X additive (i), additive X dominance (j) and dominance X dominance (l) types of gene action. Estimation of scaling tests and gene effects were tested for significance from zero using t-tests.
- d. The genetic components of variance for each character in the studied crosses were partitioned into additive (D), dominance (H) genetic variance and environmental variance (E) using Mather (1949) and Mather and Jinks (1971) formula as follows:

$$E = \frac{1}{4} (VP_1 + VP_2 + 2 VF_1)$$

$$D = 4 VF_2 - 2 VBC_1 - 2 VBC_2$$

$$H = VBC_1 + VBC_2 - VF_2 - E$$

$$F = VBC_2 - VBC_1$$

$$(H/D)^{\frac{1}{2}} = \text{Average degree of dominance.}$$

Heritability in narrow sense was computed according to Mather and Jinks (1971).

## RESULTS AND DISCUSSION

### Adequacy of the genetic model

Data presented in Table (1) provide evidence for insignificant A, B and C non-allelic interaction tests and joint scaling test ( $\chi^2$ ) for ovules/pod (Cross1), indicating that the simple genetic model was adequate to explain the genetic variation controlling the inheritance of this character in this cross. On the other hand, significance of one or more of the three individual scaling tests A, B and C for the remaining traits and crosses revealed the presence of epistasis in these traits and crosses. Therefore, there is a clear evidence of the inadequacy of the simple additive-dominance model for these characters. Generally, 11 out of 16 cases of the traits and crosses gave similar trends of significantly positive non-allelic interaction for one or more of the scaling tests. Furthermore, six parameters were used to estimate the type of gene effects for these traits. These results are in agreement with those reported by Sharma and Rastogi (2001).

**Table 1. Testing for non-allelic interaction (scaling test A, B and C) and joint scaling test ( $\chi^2$ ) for the studied traits of two pea crosses.**

Trait	Cross	A $\pm$ S.E	B $\pm$ S.E	C $\pm$ S.E	$\chi^2$	No. of crosses showing significantly positive non-allelic interaction
Pod length	1	-0.06 $\pm$ 0.22	0.17 $\pm$ 0.19	-2.51** $\pm$ 0.38	**	Zero
	2	-0.41 $\pm$ 0.26	0.36 $\pm$ 0.31	-1.57** $\pm$ 0.36	**	
Seeds/pod	1	-0.80** $\pm$ 0.36	-0.42 $\pm$ 0.38	-5.00** $\pm$ 0.70	**	Zero
	2	-0.40 $\pm$ 0.46	-0.40 $\pm$ 0.44	-5.16** $\pm$ 0.61	**	
Ovules/pod	1	-0.234 $\pm$ 0.27	-0.166 $\pm$ 0.25	0.534 $\pm$ 0.46	NS	1 cross
	2	-0.633** $\pm$ 0.25	1.266** $\pm$ 0.33	-0.467 $\pm$ 0.44	**	
Pod width	1	0.034 $\pm$ 0.03	-0.282** $\pm$ 0.03	0.296** $\pm$ 0.05	**	2 crosses
	2	0.064 $\pm$ 0.04	0.084* $\pm$ 0.04	-0.246** $\pm$ 0.06	**	
Pods /plant	1	8.268** $\pm$ 0.74	-1.197 $\pm$ 1.40	156.2** $\pm$ 4.82	**	2 crosses
	2	20.43** $\pm$ 0.67	13.134** $\pm$ 1.20	40.336** $\pm$ 4.18	**	
Plant height	1	15.64** $\pm$ 1.49	-23.89** $\pm$ 2.22	-45.99** $\pm$ 6.59	**	2 crosses
	2	31.37** $\pm$ 2.30	42.113** $\pm$ 2.96	5.886 $\pm$ 10.38	**	
Branches /plant	1	-1.727** $\pm$ 0.12	-0.384 $\pm$ 0.20	7.675** $\pm$ 0.63	**	2 crosses
	2	-0.293* $\pm$ 0.12	-0.334 $\pm$ 0.25	6.639** $\pm$ 0.90	**	
Green yield /plant	1	41.16** $\pm$ 3.70	-33.37** $\pm$ 4.89	-16.87 $\pm$ 14.54	**	2 crosses
	2	167.25** $\pm$ 3.75	169.45** $\pm$ 6.34	133.03** $\pm$ 21.3	**	
Total	1				5	11
	2				6	

\*, \*\* significantly at 0.05 and 0.01 levels of probability, respectively.

### **Gene action and epistasis effects**

Different types of gene effects were presented in Table (2). Results revealed that mean effect of  $F_2$  performance (m) was highly significant for all studied traits in the two crosses. Initially, it was noted that these characters were quantitatively inherited. Moreover, the additive gene effects (d) were highly significant positive for number of ovules/pod and pod width in the Cross 1, however, (d) estimates were significantly negative or not significantly positive or negative for the remainder traits and crosses. Meanwhile, dominance effects (h) were significant or highly significant positive for all studied traits except both number of ovules/pod and number of pods/plant in the Cross 1 as well as number of branches/plant in the two crosses. Hence, improvement of these traits could be achieved through recurrent selection procedure (Singh and Narayanan 2000). Dominance gene action (h) was the main type of gene effects in both crosses for all characters, except number of ovules/pod (Cross1). The type of epistatic interaction (i) (additive x additive) was significant for all characters in both crosses, except number of ovules/pod, pod width and yield in Cross 1 and number of pods/plant in Cross 2. Additive x dominance type of epistasis (j) was involved in controlling all traits in both crosses. Meanwhile, the (l) type of epistasis (dominance x dominance) was significant in all traits for both crosses, except pod length (Cross2) and yield in Cross1. These results showed that both additive and dominance as well as one or more of the three types of epistasis i.e., additive x additive (i), additive x dominance (j) and dominance x dominance (l) were important in the genetic system controlling in most studied traits.

Again, additive gene effects were exhibited by 12 of the 16 cases (8 traits x 2 crosses), however, the relative magnitude of these effects to the mean effects (m) suggests that they are of minor importance in the explanation of traits variation (Table 1). Therefore, more rapid advance must be made in a breeding program for the improvement of pea traits, by using a breeding procedure which emphasis the dominance and epistatic gene effects. Singh and Sharma (2004) stated that the additive (d), dominance (h) and all the three interacting gene effects played a major role in the inheritance of quantitative characters, such as seeds/pod, pod/plant and green pod yield.

The magnitude of the epistatic parameters relative to the mean effects (m) is small in all studied traits, except plant height and yield (Cross2), in which the absolute magnitude of the epistatic gene effects are larger than the mean effects and approach that of the dominance effects. However, in all traits and crosses, except both pod width and number of branches/plant in Cross1, the magnitude of the total epistatic effects relative to the mean effects is larger than the magnitude of the additive effects relative to the

**Table 2. Six parameter genetic model and type of epistasis for studied traits of two pea crosses.**

Trait	Cross	Mean [m]	Additive [d]	Dominance [h]	Add.xAdd. [i]	Add.xDom. [j]	Dom.xDom. [l]	Type of epistasis
Pod length	1	6.20** ± 0.08	-0.43** ± 0.12	3.11** ± 0.41	2.62** ± 0.39	-3.67** ± 0.14	-2.73** ± 0.59	Dupl.
	2	6.89** ± 0.06	-1.10** ± 0.18	2.08** ± 0.45	1.52** ± 0.43	-4.34** ± 0.19	-1.47 ± 0.78	Dupl.
Seeds /pod	1	4.98** ± 0.15	0.16 ± 0.21	4.73** ± 0.75	3.78** ± 0.72	-2.99** ± 0.24	-2.56 ± 1.07	Dupl.
	2	5.35** ± 0.12	-0.30 ± 0.28	4.80** ± 0.76	4.36** ± 0.74	-3.45** ± 0.31	-3.56** ± 1.26	Dupl.
Ovules /pod	1	7.93** ± 0.47	7.00** ± 0.07	-1.84 ± 0.16	-	-	-	-
	2	7.83** ± 0.09	-1.47** ± 0.18	1.62** ± 0.51	1.10** ± 0.49	-4.9** ± 0.19	-1.73 ± 0.81	Dupl.
Pod width	1	1.11** ± 0.01	0.21** ± 0.01	0.13 ± 0.05	0.05 ± 0.05	-0.39** ± 0.02	0.20** ± 0.07	Comp.
	2	1.21** ± 0.01	-0.05 ± 0.03	0.45** ± 0.07	0.39** ± 0.07	-0.65** ± 0.03	-0.54** ± 0.12	Dupl.
Pods /plant	1	94.46** ± 1.20	-9.03** ± 0.49	-146.1** ± 4.89	-159.9** ± 4.89	-23.70** ± 0.51	163.6** ± 5.18	Dupl.
	2	60.87** ± 1.03	-9.50** ± 0.38	10.43 ± 4.21	-6.47 ± 4.19	-24.17** ± 0.42	-27.4** ± 4.18	Dupl.
Plant height	1	105.97** ± 1.61	0.15 ± 0.97	66.28** ± 6.77	37.75** ± 6.73	-41.64** ± 1.05	-29.5** ± 7.58	Dupl.
	2	101.7** ± 2.58	11.18** ± 1.28	120.26** ± 10.64	79.37** ± 10.62	-52.97** ± 1.33	-152.9** ± 11.54	Dupl.
Branches /plant	1	5.93** ± 0.15	-1.57** ± 0.07	-7.88** ± 0.63	-9.79** ± 0.63	-2.65** ± 0.08	11.90** ± 0.68	Dupl.
	2	5.58** ± 0.22	-0.53** ± 0.07	-4.85** ± 0.90	-7.27** ± 0.90	-1.61** ± 0.08	7.89** ± 0.94	Dupl.
Green yield /plant	1	263.69** ± 3.53	-9.93** ± 2.29	177.03** ± 14.93	24.65 ± 14.83	-82.19** ± 2.58	-32.44 ± 17.04	Dupl.
	2	318.50** ± 5.24	86.50** ± 2.30	314.31** ± 21.55	203.67** ± 21.47	-158.8** ± 2.51	-540.4** ± 23.04	Dupl.

\*, \*\* significantly at 0.05 and 0.01 levels of probability, respectively.

Dupl. = Duplicate type of epistasis.

Comp. = Complementary type of epistasis.

mean effects. Regarding to the individual epistatic gene effects, additive x additive and additive x dominance effects appear to contribute more to the performance of most traits and crosses than do the dominance x dominance gene effects. Such a relative importance could be expected since the F<sub>1</sub> means indicate considerable heterosis (Gamble 1962).

As suggested in the previous discussion, the reciprocal recurrent selection breeding procedure proposed by Comstock *et al* (1949) appears to be the best available to meet the requirements. This procedure was designed to be equally effective for both additive and non-additive gene effects. Because of results reported in this paper indicate non-additive effects to be of major importance, recurrent selection for specific combining ability as proposed by Hull (1945) can be suggested as a good breeding procedure,

considering some limitations as accurate selection of the tester variety to be used in the top cross. Although, the recurrent selection procedure is not usually used for improvement of self-fertilized crops, it was applied by Lyon *et al* (1987) for *Phaseolus* improvement. Generally, theoretical considerations indicate that the reciprocal recurrent selection procedure would be superior to recurrent selection for general combining ability if non-additive gene effects or over-dominance effects were important. Also, it would be more effective than recurrent selection for specific combining ability if additive gene effects are important.

Finally, all types of gene action effects (d, h and epistasis) were highly significant or significant, while, dominance x dominance component (l) epistatic effect was higher in magnitude and played a major role in the inheritance of these traits. Similar results were reported by Sharma and Rastogi (2001), Singh *et al* (2003) and Singh and Sharma (2004).

The signs of (h) and (l) genetic parameters were considered for all the traits. In general, (h) showed positive significance while dominance x dominance (l) gene effects exhibited negative significance. This might be due to cancellation effects of positive and negative genes.

Duplicate epistasis was observed, as revealed by differences in signs of h and l in crosses, which exhibited significant epistasis, for all studied traits, except pod width (Cross1) in which the complementary type of epistasis was recorded. In duplicate type of epistasis (the ratio 15:1) identical substance of substances interchangeable in effect are presumably produced by the dominant alleles at both loci. It showed complementary epistasis for pod width in Cross1 where similar signs were obtained for both h and l. In complementary type of epistasis (the ratio 9:7) genes probably produce different substances both of which were needed for the phenotypic manifestations of some property. Duplicate type of epistasis for the most studied traits further confirms the prevalence of dominance effects (Singh and Sharma 2001).

The components of genetic variance (Table 3) revealed that additive genetic variance (D) was fairly consistent in magnitude for dominance effects (H) for pod length (Cross1), number of pods/plant (Cross2) and number of branches/plant (both crosses), resulting in  $(H/D)^{1/2} = 1$ . On the other hand, the additive genetic variance (D) was the main type controlling each of number of ovules/pod, pod width, number of pods/plant (Cross1), plant height (both crosses) and yield (both crosses), resulting in  $(H/D)^{1/2} < 1$ , indicating that phenotypic selection may be useful for improving these characters. But the non-fixable type was more important for pod length (Cross2), number of seeds/pod (both crosses), number of ovules/pod (Cross2) and pod width (Cross2), resulting in  $(H/D)^{1/2} > 1$ .

**Table 3. Components of the genetic variation and their derived ratios and narrow sense heritability for the studied traits of two pea crosses.**

Trait	Cross	D	H	E	F	(H/D) <sup>2</sup>	h <sup>2</sup> <sub>n</sub>
Pod length	1	0.012	0.012	0.009	-0.002	1.00	33.3
	2	0.050	0.068	0.012	0.009	1.17	46.0
Seeds/pod	1	0.056	0.120	0.025	0.006	1.464	33.7
	2	0.106	0.160	0.027	-0.001	1.233	44.3
Ovules/pod	1	0.060	0.048	0.030	-0.0002	0.900	36.1
	2	0.034	0.092	0.013	0.013	1.171	41.4
Pod width	1	0.006	0.00104	0.0002	-0.0001	0.417	39.5
	2	0.0008	0.0012	0.00023	-0.00001	1.189	44.6
Pods /plant	1	5.262	4.972	0.046	0.0035	0.972	67.1
	2	3.953	4.005	0.085	-0.0109	1.007	64.5
Plant height	1	8.53	7.916	0.312	0.094	0.963	65.1
	2	23.248	21.053	0.273	-0.730	0.952	67.7
Branches /plant	1	0.084	0.084	0.0030	0.0005	0.999	64.1
	2	0.1862	0.1865	0.0026	0.0005	1.001	65.4
Green yield /plant	1	39.206	37.824	2.280	-0.366	0.982	30.3
	2	99.444	97.772	2.2204	-0.16	0.992	65.1

The "F" value which refers to the frequency distribution of increasing and decreasing alleles in the genetic constitution of the parental genotypes, was positive for pod length (2<sup>nd</sup> cross), seeds/pod (1<sup>st</sup> cross), ovules/pod (2<sup>nd</sup> cross), pods/plant (1<sup>st</sup> cross), plant height (1<sup>st</sup> cross) and number of branches/plant (both crosses), indicating that increasing alleles were more frequent in the genetic make up of the parental genotypes, while the negative values obtained for the remaining crosses suggest that dominant decreasing alleles were more frequent (Table 3).

The ratio of additive genetic portion to the phenotypic genetic variance as indicated by heritability in narrow sense was high and amounted to 65.1 and 67.7% for plant height (Cross1 and Cross2, respectively), 64.1 and 65.4% for number of branches/plant (Cross1 and Cross2, respectively), 67.1 and 64.5% for (Cross1 and Cross2, respectively) for number of pods/plant and 65.1% for Cross1 of green yield/plant. Similar findings have been reported by Zayed *et al* (1999), Singh and Dhillon (2004) and Zayed *et al* (2005).

The estimates of narrow sense heritability (h<sup>2</sup><sub>n</sub>) were moderate and valued 36.1 and 40.5% for ovules/pod (Cross1 and Cross2, respectively), 39.5 and 44.6% for pod width (Cross1 and Cross2, respectively), 44.3 and 46.0% for Cross2 of seeds/pod and pod length, respectively. On the other hand, h<sup>2</sup><sub>n</sub> values were low for yield, Cross1 (30.3%), pod length, Cross1 (33.3%) and seeds/pod, Cross1 (33.7%), hereby selection will be difficult and should be delayed to later segregating generations.



## REFERENCES

- Andrson, V.L. and O. Kempthorne, (1954). A model for study of quantitative. *Genetics*. 39: 881-898.
- Cavalli, L.L., (1952). An Analysis of linkage in quantitative inheritance. *Quantitative Inheritance* (Ed. E.C.R. Reeve and C.H. Waddington) pp. 135-144.
- Comstock, R.E. (1955). *Theory of quantitative genetics*. Cold Spring Harbor Symposia on Quant. Biol. 20: 92-102.
- Comstock, R.E., H.F. Robinson and P.H. Harvey, (1949). A breeding procedure designed to make maximum use of both general and specific combining ability. *Agron. J.*, 41: 360-367.
- El-Dakkak, A.A.A., M.A. Abd El-Hady and A.H. Hussein (2009). Gene action expression of some pea (*Pisum sativum* L.) traits as effected by seasonal variation of Southern Egypt conditions. *Egypt J. Appl. Sci.*, 24(4A): 241-256.
- Gamble, E.E., (1962). Gene effects in corn (*Zea mays* L.) 1- Selection and relative importance of gene effects for yield. *Canad. J. Pl. Sci.*, 42 (4): 339-34.
- Hayman, B.I. (1958). The separation of epistatis from additive and dominance variation in generation means. *Heredity*. 12: 371-390.
- Hull, F.H. (1945). Recurrent selection and specific combining ability in corn. *J. Amer. Sci. Agron.*, 37: 134-145.
- Jinks. J.J. and R.M. Jones, (1958). Estimates of the components of heterosis. *Genetics*. 43: 223. 234.
- Kandeel, N.M., G.A. Zayed, A.M. Damarany and A.A. Abdou (2005). Gene action and epistasis using triple test cross procedure in pea. *Egypt J. Appl. Sci.*, 20.(9): 262-281.
- Lyon, M.E., M.H. Dickson and J.E. Hunter, (1987). Recurrent selection for resistance to white mold in *Phaseoulus* sp. *J. Amer. Soc. Hort. Sci.*, 112: 149-152.
- Mather, K., (1949). *Biometrical Genetics*. Dover Pub., Inc., London. 158 p.
- Mather, K. and J.L. Jinks, (1971). *Biometrical Genetics*. Chapman and Hall Ltd., London, 382 p.
- Sharma, M.K. and K.B. Rastogi, (2001). Analysis of gene effects for agronomic and maturity characters in pea (*Pisum sativum* L.). *Legume Res.*, 24 (1): 32-35.
- Singh, N., G.S. Dhillon, G.S. Chahal and M. Singh, (2003). Genetic analysis for pod yield and earliness in garden pea (*Pisum sativum* L. var. Hortense). *Crop Improv.*, 30 (1): 45-49.
- Singh, N. and G.S. Dhillon, (2004). Genetic variability for pod yield and its contributing traits in garden pea (*Pisum sativum* L. var. Hortense). *Haryan. J. Hort. Sci.*, 33 (3/4): 300-301.

- Singh, L.P. and S.S. Narayanan, (2000). Biometrical Techniques in Plant Breeding. Klyani Publishers, New Delhi, 2<sup>nd</sup> ed.
- Singh, T.H. and R.R. Sharma, (2001). Gene action for yield and its components in three crosses of pea (*Pisum sativum* L.). Indian J. Genetic & Pl. Breed., 61 (2): 174-175.
- Singh, T.H. and R.R. Sharma, (2004). Inheritance of quantitative characters in garden pea (*Pisum sativum* L. Subsp. Hortense Asch and Greabn). Legume Res., 27 (4): 255-259.
- Singh, M.N. and R.B. Singh, (1990). Estimation of additive, dominance and genetic epstatic effects for certain yield characters in pea .India J. Genet 50 (4): 348 -353.
- Zayed, G.A., (1998). Inheritance of some quantitative characters in peas. Egypt. J. Appl. Sci., 13 (3): 242-253.
- Zayed, G.A., A.H. Amer and Horeya M. Hassan, (1999). Combining ability and path coefficient analysis in pea under Southern Egypt conditions. Zagazig J. Agric. Res., 26 (3A): 611-621.
- Zayed, G.A., F.A. Helal and S.T. Farag, (2005). The genetic performance of some continuously variable characteristics of pea under different locations. Annals Agric. Sci., Moshtohor, 43: 337-346.

### أهمية تداخل القياسات الوراثية المختلفة في تحديد طريقة التربية المناسبة لتحسين بعض صفات البسلة

أحمد حلمي حسين و أبو بكر عبد العظيم الدقاق وجمال ابوستة زايد

معهد بحوث البساتين - مركز البحوث الزراعية - الجيزة- مصر

أجري هذا البحث بمحطة البحوث الزراعية بشندويل خلال ثلاثة مواسم شتوية من ٢٠٠٦/٢٠٠٥ الى ٢٠٠٧/٢٠٠٦ لدراسة تأثير الفعل الجيني ومدى تأثيره بوجود التفاعل غير الأثلي للإستفادة به فسي إمكانية تحسين صفات المحصول ومكوناته وبعض صفات النمو في هجينين من البسلة هما (الاسكا × دوارف جرای شوجر) ، (الاسكا × ايرلى بيرفكشن) .

وكانت أهم النتائج المتحصل عليها كما يلي:

أظهرت نتائج إختبار الـ Scaling وكذلك الـ Joint scaling وجود تفاعل غير الأثلي (أى تفوق) لجميع الصفات المدروسة في كلا الهجينين ما عدا صفة عدد البويضات/قرن بالهجين (الاسكا × دوارف جرای شوجر) مما يدل على أهمية الفعل الوراثي التفوقى في وراثه هذه الصفات والإستفادة منها فسي برامج التربية .

كان التأثير المضيف معنوياً موجباً لصفتي عدد البويضات/قرن وعرض القرن في الهجين الأول ولم يظهر أى تأثير موجب في الهجن الثانى ، بينما كانت السيادة ذات تأثير موجب معنوى أو عالى المعنوية

فى كل الصفات المدروسة بالهجينين ما عدا صفة عدد البويضات/قرن وعدد القرون/نبات فى الهجين الأول وكذلك صفة عدد الفروع/نبات فى الهجينين. لوحظ أن جميع الصفات المدروسة كانت تحت تأثير فعل الجين التفوقى من نوع ال Duplicate type of epistasis ما عدا عرض القرن (هجين ١) مما يؤكد النتائج المتحصل عليها عن تأثير السيادة ، وفى نفس الوقت وجد أن تأثير فعل الجين التفوقى من نوع ال Complementary type of epistasis كان واضحا فى صفة عدد البويضات/قرن. كانت السيادة فاتقة فى صفات طول القرن وعدد البويضات/قرن وعرض القرن (هجين ٢) وعدد البذور/قرن (الهجينين) ، فى حين كانت السيادة الجزئية فى عدد البويضات/قرن وعرض القرن وعدد القرون (هجين ١) وارتفاع النبات وكذلك المحصول (الهجينين) . كانت درجة التوريث فى النطاق الضيق منخفضة فى صفات عدد البذور/قرن وطول القرن والمحصول (هجين ١) بينما كانت متوسطة الى عالية فى باقى الصفات. كما توضح الدراسة قيم كفاءة توريث فى المفهوم الضيق تتراوح من ٣٣ - ٦٨% تقريبا للصفات المختلفة .

وتوضح هذه الدراسة أهمية الانتخاب التكرارى للقدرة الخاصة على الالتلاف والتي تعتبر من أهم الطرق التى ينصح باستخدامها فى برنامج تحسين البسلة تحت ظروف هذه الدراسة مع بعض الاعتبارات الخاصة عند اختيار الأب الاختيارى المناسب للتهجين القمى.

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