Minufiya J. Agric. Res. Vol. 34 No. 4:1601-1612 (2009) "http://www.mujar.net"

GENETIC BEHAVIOUR OF SOME QUANTITATIVE PEA TRAITS UNDER SOUTHERN EGYPT CONDITIONS

A.A.A. El-Dakkak and A.H. Hussein
Horticulture Research Institute, Agric. Res. Center. Giza, Egypt

(Received: Jun. 15, 2009)

ABSTRACT: *This study was carried out during three successive winter seasons 2005/2006 to 2007/2008 at the Agricultural Research Station of Shandaweel, Sohag Governorate. Six populations of two pea crosses were studied to determine the gene actions and heterosis under southern Egypt conditions. The nature of gene action controlling most of the studied traits seems to be more cumulative (non-additive) than additive although the additive genetic variance was important. Potence ratio that measured the average of dominance confirmed the partial dominance for earliness (in both crosses) and over dominance for the remainder growth traits.*

The range of both types of F_1 heterosis for studied characters indicated that the expression of heterosis varied according to different crosses and characters investigated. It is worth mentioning that heterotic effect was generally more pronounced for pod yield/feddan than any components in the F_1 generation and it was more pronounced in the F_1 than F_2 generation in most traits.

The existence of both additive and non-additive effects in the inheritance of yield components demonstrated that a considerable amount of readily fixable variations present and available for the plant breeder to manipulate.

Key words: *Pea, Additive and non–additive gene action, Heterosis and Heritability*

INTRODUCTION

Pea (*Pisum sativum* L.) breeders have a great consent on the notion of existence of potential for enhanced productivity in this crop (Kumaran *et al.*. 1995). Enhancing yield of peas, indeed, is one of the major objectives (Simakov, 1989), regardless of the initial purpose of any breeding program.

So when there are no differences, the breeders should create this variability through various methods of breeding, using six parameters one of these methods, to study additive, dominance, inbreeding depression and heterosis of the economic traits in peas to improve the crop through breeding procedures depends on the presence of genetic variability.

Segregating and non-segregating population could be used for computing the genetic parameters and types of gene action for any quantitative traits to study the relative importance of the additive, non- additive of agronomic traits in peas population.

Breeding studies of peas under southern Egypt conditions were directed mainly to analysis of gene action based on crosses (Abdou *et al.*, 1999, El-Dakkak, 2005, Shalaby, 1974, Waly and Abd El-Aal, 1986, Zayed, 1998, Zayed *et al.*, 2005). The objective of the present study, therefore, was to investigate potential of the variation of some pea genotypes and study the mode of inheritance and gene action for some continuously traits under southern Egypt condition for breeding recombinant homozygous-genotype (s) with enhanced yield and earliness.

MATERIALS AND METHODS

The present study was conducted in the winter seasons of 2005/2006, 2006/2007 and 2007/2008 at the Agricultural Research Station of Shandaweel, Sohag Governorate. The soil in the experimental site was clay loam.

Six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for two pea crosses (Alaska x Dwarf Gray Sugar) and (Alaska x Early Perfection) were used in this study. In the first season (2005/2006), the parents were crossed to produce F_1 hybrids. In the next season of 2006/2007, part of the F_1seeds was planted and back-crossed to both parents to produce BC_1 (F_1 x P_1) and BC_2 (F_1 x P_2) generations. In addition, F_1 plants were selfed to produce F_2 seeds. In the winter season 2007/2008 dry seed of the six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for the two crosses were planted in November 2007 in pre-irrigated soil, which had about 50% of its available moisture. Mono-super phosphate (15% P_2O_5) was broadcasted during soil preparation at rate of 300 kg/feddan.

Seed planting was on the northern side of 3m length and 0.7m wide rows. In row space was 20cm. The experiment was randomized complete blocks (RCBs) with three replicates consisted of 4 rows of the first five populations (parents, F_1, BC_1 and BC_2) as well as 10 rows of F_2 plants. Where 80% to 90% of seeds emerged, a light watering was applied. No nitrogen fertilizer was used in raising plants. Otherwise, all cultural practices were followed as recommended for production of pea crop.

Data were recorded based on competitive plants from each population for number of days to 50% flowering, stem length (cm), number of branches per plant, pod length (cm), number of seeds per pod, total soluble solids and total green-pod yield (ton/feddan).

Statistical procedures:

Averages representing mean plot values were subjected to the analysis of variance (ANOVA) procedure of RCBs design (Gomes and Gomes, 1984) to test the differences between parental genotypes for studied traits in the two crosses.

Biometrical anaiyses:

Estimates of the arithmetic and geometric gene action were calculated according to Powers and Lyon (1941). Relative potence of gene set was used to determine the direction of dominance according to Smith (1952). Heterosis and inbreeding depression were calculated according to Mather and Jinks (1971).

RESULTS AND DISCUSSION

Growth traits:

Stem length (cm) was studied in the two pea crosses. The coefficient of variability for P_1, P_2, F_1, F_2, BC_1 and BC_2 generations in (Table 1) was 2.25. 2.86. 2.26. 16.66, 3.17 and 3.40%, respectively for the $cross_1$ (Alaska x Dwarf Gray Sugar) and was 2.25, 3.62, 2.20, 26.04, 4.87 and 3.76%, respectively for the $cross_2$ (Alaska x Early Perfection). It was clear that the segregating populations of both crosses, i.e., F_2, BC_1 and BC_2 had a higher coefficient of variability values comparing to the non-segregating ones (P_1, P_2 and F_1) indicating that variability was largely due to genetic constituents. On the other hand, transegressive segregation was observed in Both direction of the F_2 populations for stem length and tendency towards the high parent of number of branches/plant.

For studied crosses, the expected arithmetic and geometric means of segregating population i.e., F_2, BC_1 and BC_2 for the flowering date trait may ranged as equal (Table 2) and thus the actual corresponding means were lower or higher than each one. Hence the nature of gene action cannot be determined in this case, as both actions, i.e., additive and non-additive were presented in equal amounts. On the other hand, the difference between the observed F_1 mean ($cross_1$). and the calculated arithmetic and geometric means were significant, however, the observed F_1 mean of this cross (48.7 days) was more closer to the geometric mean (48.8 days). Under such conditions. the nature of gene action controlling the flowering trait seems to be more cumulative (non-additive) than additive. These results seemed generally to agree with those reported by Katiyar *et al.*. (1987). Kumar *et al.*, (1996) and Zayed (1998).

BC_1 population kept up its level of ranking and superiority in the earliness in both crosses (Table 2), while F_1 hybrid performed the same trend in both stem length and number of branches followed by BC_2 (stem length), BC_2 and F_2 (number of branches) and P_1 in the earliness of both crosses. Generally, the $cross_1$ have the best values rather than the $cross_2$ in each of the growth traits in all populations except number of branches (F_1, F_2 and BC_1) and stem length (BC_1 and BC_2), which exhibited reverse trend.

The comparison between the means of F_1 hybrid (in both crosses) and the two corresponding parents showed that the number of branches in F_1 (4.9 and 5.1 for $cross_1$ and $cross_2$, respectively) was significantly higher than the highest parent (4.0 and 3.3 for $cross_1$ and $cross_2$, respectively), this figure suggest over dominance for the branches numerous plant. The means of F_1 and F_2 exceeded that of high parent by 22.5 and 5%. respectively in the $cross_1$ and 54.5 and 30.3%, respectively in the $cross_2$.

Table 1. Range and coefficient of variability (C.V%) for parents, F_1, F_2, BC_1 and BC_2 of both pea crosses.

Item		Plant height (cm)		No. of braches/plant		Pod length (cm)		No. of seeds/pod		Yield (ton/fed)	
		Range	C.V%	Range	C.V%	Range	C.V%	Range	C.V%	Range	C.V%
Cross$_1$	P_1	79.2 - 89 8	2.25	1 7 – 2.6	5.98	5.5 – 7.5	6.31	5 - 8	11.95	1 478 – 1 822	3.19
	P_2	115 - 131	2.86	3 5 – 4 4	6 34	6 – 8.5	6 63	4 - 7	11.04	2.282 – 2 999	3 10
	F_1	126 – 138.2	2.26	4 5 – 5.9	6 11	6.3 – 8 1	5 17	5 - 8	11.86	3.506 – 4.595	2.08
	F_2	66 0 - 141.0	16.66	3.0 – 10.0	28.30	3.5 – 9.2	12.82	2 - 9	29.79	1.274 – 3 731	14.64
	BC_1	108 – 115.5	3.17	2.1 – 3 1	9.77	6 – 8.1	7.19	5 - 8	12 82	2.466 – 3.840	3.46
	BC_2	106 – 123 4	3 40	3 8 – 4.9	6.84	6 3 – 8.2	6 86	5 - 8	14 31	2.581 – 2.927	4 11
Cross$_2$	P_1	79 2 - 89 8	2 25	1.7 – 2.6	5.98	7 – 7.5	7.31	5 - 8	11 95	1.478 – 1.822	3.19
	P_2	88.3 101.4	2.62	2.8 – 3.0	8.56	5 3 – 8.5	8 16	4 - 8	12.43	2 965 – 3.953	3 13
	F_1	125 - 137	2.20	4.5 – 5.8	5 84	6.8 – 9.7	7 44	6 - 9	11.30	3.212 – 4.583	2.51
	F_2	54 - 150	26.04	2.0 – 12.0	43.48	6 – 9.2	18.89	2 - 9	23.59	1.607 – 4 510	18.04
	BC_1	116 - 134	4.87	3.0 – 4.0	7.47	6.1 - 8	8.29	4 - 8	18 03	3.046 – 4.454	3.77
	BC_2	126 – 141	3 76	3.4 – 4.6	7.20	7.6 – 10.4	8.93	5 - 9	15.41	3.941 – 5 318	4 12

Table 2. Actual mean for the six populations of both pea crosses for the studied growth traits.

Populations	Flowering date		Stem length		No. of branches	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
P_1	40.3	40.3	83.6	83.6	2.2	2.2
P_2	59.0	62.3	122.8	95.3	4.0	3.3
F_1	48.7	53.6	131.7	130.3	4.9	5.1
F_2	53.7	59.0	108.3	100.4	4.2	4.3
BC_1	37.7	41.0	115.6	120.3	2.7	3.5
BC_2	56.7	59.0	128.5	133.7	4.3	4.0
MS	230.1**	277.7**	933.4**	1248.9**	3.25**	2.94**
LSD:						
0.05	1.3	1.5	4.6	5.2	0.3	0.3
0.01	1.8	2.1	6.6	7.3	0.4	0.4

MS: Mean square for genotypes.
** Highly significant of F-test at 0.01% probability level.

Regarding stem length trait, the arithmetic and geometric means of the F_1, F_2, BC_1 and BC_2 of both studied crosses (Table 3) were close to each other revealing that the genes having additive and non-additive effects controlled this character. Also, F_2 actual means of stem length was found to lie between mid and high parent values with a high tendency towards the high parent in both crosses suggesting that the non-additive genetic variance was predominant and played the major part in the inheritance of stem length than other types of gene action. Singh *et al.*, (1987), Zayed (1988, 1998), and Sarawat *et al.*, (1994) reported similar results. Actual F_2 mean of branches number was slightly higher than both expected arithmetic and geometric means, and both expected means may be regarded as equal in the all segregated populations of both crosses. This indicates that the number of branches/ plant is controlled by additive and dominance genes.

Table 3. Expected arithmetic and geometric means for the populations of the pea crosses for the studied growth traits.

Expected Mean	Flowering date		Stem length		No. of branches	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
Arithmetic:						
F_1	49.67	51.33	103.22	89.47	3.08	2.73
F_2	49.17	52.50	117.48	109.87	4.01	3.92
BC	44.50	47.00	107.67	106.93	3.57	3.65
BC_2	53.83	58.00	127.28	112.80	4.45	4.18
Geometric:						
F_1	48.78	50.14	101.34	89.27	2.95	2.68
F_2	48.75	51.88	115.60	107.90	3.82	3.70
BC_1	44.30	46.52	104.94	104.36	3.29	3.35
BC_2	53.58	57.84	127.21	111.44	4.42	4.08

Yield component traits:

Regarding both the pod length and number of seeds/pod traits, for studied crosses, the expected arithmetic and geometric means of populations may be regarded as equal (Table 4) and thus the actual respective means were lower or higher than each one. This indicates that both additive and dominance are operated in the expression of both traits. On the other hand, actual F_1 (cross$_2$) mean for pod length was found to lie between mid and high parent values with a high tendency towards the high parent suggesting that the non-additive genetic variance was predominant and played the major part in the inheritance of pod length than other types. while BC_1 and BC_2 actual means of number of seeds were found to lie between mid and high of respective parent for both crosses with a high tendency towards the high parent (BC_1 of cross$_1$ and BC_2 of cross$_2$) or mid parents (BC_1 of cross$_2$ and BC_2 of cross$_1$) suggesting that the non-additive gene action played the major part in the controlling this traits.

Table 4. Actual mean of the six populations of both pea crosses for yield components traits.

Populations	Pod length (cm)		No. of seeds /pod		TSS		100-seeds weight (gm)		Yield/feddan	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
P_1	6.5	6.5	6.3	6.3	16.5	16.5	34.3	34.3	1.75	1.75
P_2	7.1	7.9	5.6	6.9	11.7	14.2	28.8	37.3	2.84	3.77
F_1	7.3	7.7	6.9	7.0	17.0	17.3	38.7	38.3	4.13	4.08
F_2	6.4	7.1	5.2	5.5	12.5	14.9	25.6	33.9	3.18	3.82
BC_1	6.8	6.9	6.2	6.5	17.1	17.0	37.3	40.3	3.18	3.91
BC_2	7.3	8.1	6.0	6.8	11.2	15.6	31.8	41.8	3.30	4.96
MS	0.45**	1.22**	1.01**	0.90**	23.8**	4.48**	75.9**	30.1**	1.80**	3.91**
LSD										
0.05	0.3	0.2	0.2	0.16	0.4	0.3	0.7	0.4	0.06	0.06
0.01	0.4	0.3	0.3	0.23	0.6	0.5	0.9	0.6	0.08	0.08

MS: Mean square for genotypes.

** Highly significant of F-test at 0.01% probability level.

The coefficient of variability for the six generations of both studied crosses in (Table 5) cleared that the coefficient of variability in F_1 was smaller than parents in pod length (cross$_1$), number of seeds/pod (cross$_2$) and yield (both crosses), and the greatest variation was thus evident in F_2 of both crosses in all studied traits suggesting that the variability was largely genetic. Moreover, transegressive segregation was observed in both direction of the F_2 populations for the most of the studied traits.

The observed F_2 means in TSS ($cross_1$& $cross_2$), 100-seeds weight ($cross_1$) was relatively close to the calculated geometric mean than to the arithmetic one, indicating that non-additive gene effects were mostly important than other types of gene action.

Also, F_2 mean of yield ($cross_1$&$cross_2$) was closer to the arithmetic mean rather than the geometric one indicating that additive gene effect was involved in the genetic behavior of yield. From above mentioned results, both additive and dominance effects controlled the yield components. Therefore, the existence of both additive and non-additive effects demonstrated that a considerable amount of readily fixable variations present and available for the plant breeder to manipulate.

Table 5. Expected arithmetic and geometric means for the populations of the pea crosses for yield components traits.

Expected Mean	Pod length (cm)		No. of seeds/pod		TSS		100-seeds weight(gm)		Yield/feddan(km)	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
Arithmetic.										
F_1	6.78	7.18	5.95	6.60	14.07	15.33	31.55	35.78	2.30	2.76
F_2	7.03	7.46	6.43	6.82	15.54	16.32	35.14	37.07	3.21	3.42
BC_1	6.87	7.10	6.60	6.67	16.73	16.88	36.50	36.27	2.94	2.92
BC_2	7.18	7.82	6.25	6.97	14.33	15.75	33.78	37.78	3.49	3.93
Geometric										
F_1	6.78	7.16	5.94	6.59	13.86	15.20	31.43	35.75	2.23	2.57
F_2	7.01	7.43	6.40	6.81	15.35	16.26	34.91	36.98	3.03	3.24
BC_1	6.86	7.07	6.59	6.66	16.73	16.88	36.43	36.21	2.69	2.67
BC_2	7.18	7.82	6.27	6.97	14.08	15.67	33.42	37.78	3.43	3.92

The range of both types of F_1 heterosis for studied characters are given in Table 6. The results indicated that the expression of heterosis varied with crosses and characters investigated. Heterosis for pod length varied from 7.4 to -2.5% when both types of heterosis are considered. Desirable positive MP heterosis was observed in both crosses, but the $cross_2$ showed negative HP heterosis for this trait. For number of seeds/pod, estimates of the two types of F_1 heterosis varied between 15.0% to 1.4%. Both $cross_1$ and $cross_2$ showed positive MP heterosis, whereas only $cross_1$ exhibited HP heterosis.

The heterosis expression for TSS varied from 20.6% to 3.0%for the two types of F_1 heterosis (Table 6). Both $cross_1$ and $cross_2$ showed positive heterosis (over mid and high parent) Regarding 100 seeds weight. the magnitude of significant positive heterosis was up to 22.5% over MP and 12.8% over HP. Concerning yield/fed., significant heterosis up to 79.6% over MP and 45.4%over HP was recorded.

Table 6. Potence ratio, F_1 and F_2 heterosis over mid (MP) and high (HP) parent and inbreeding depression (I.D) for studied traits of both crosses.

Traits	Cross	Potence ratio	Heterosis %				I.D
			F_1 over		F_2 over		
			MP	HP	MP	HP	
Flowering date	$Cross_1$	-0.1	-2.0	20.7	8 05	33.08	10 4
	$Cross_2$	0.21	4 7	33 3	14 94	46.29	9.9
Stem length	$Cross_1$	1 45	27.6	7.3	4 92	-11 83	-17 8
	$Cross_2$	6.96	45.6	36.7	12.25	5 35	-22.9
No. of branches	$Cross_1$	2.1	58.1	22.5	35.92	5.8	-14.9
	$Cross_2$	4.4	8 9	54 5	56.93	31 5	-15.7
Pod length	$Cross_1$	1 5	7.4	2.8	-5 74	-9.86	-11.9
	$Cross_2$	0 8	6 9	-2.5	-1 60	-10.51	-8.6
No of seeds	$Cross_1$	2.7	15.0	9.5	-12.10	-16.98	-24 2
	$Cross_2$	1.4	6.1	1.43	-16.21	-19.86	-21.3
TSS	$Cross_1$	1.2	20.6	3.0	-11 37	-24.29	-26.7
	$Cross_2$	1.7	13.1	4.8	-2 87	-9.53	-13.9
100-seeds weight	$Cross_1$	2.6	22.5	12.8	-18.86	-25 3	-33 9
	$Cross_2$	1 6	7.0	2 7	-5 20	-9.04	-11.3
Yield /feddan	$Cross_1$	3.4	79.6	45.4	38.26	11.97	-23.0
	$Cross_2$	1.3	47.8	8.2	38.41	1.33	-0 26

As shown in Table (6), the maximum significant MP and HP heterosis in desirable direction (79.6% &45.4% respectively) were recorded for seed yield/fed.. Prakash *et al.*. 1993 recorded high magnitude of positive heterosis over the mid-parental value for yield.

Both crosses in all the traits of yield component showed significantly negative heterotic effect in the F_2 except seed yield, which exhibited significantly positive effects in both crosses. It is worth mentioning that heterotic effect was generally more pronounced for yield/fed., than any components in the F_1 generation and it was more pronounced in the F_1 than F_2 generation in most traits.

Potence ratio (Table 6) that measured the average of dominance confirmed the partial dominance for flowering dates (in both crosses). Over-dominance was detected for remainder growth traits (stem length and number of branches) in both studied crosses. These results agree with Zayed 1998 and Zayed *et al.*, 2005 for flowering date and stem length.

Heterosis effects of the F_1 and F_2 populations for the three studied growth traits in both crosses are presented in Table 6. Negative value of heterosis for flowering date is the desirable value, since earliness is an important objective for the pea breeder. It was found that heterosis effects in terms of deviation from both mid and high parent recorded desirable significant values for F_1 stem length and number of branches traits in the two crosses and flowering date in $cross_1$ only over mid-parent. Mishra *et al.*, 1993 observed heterosis for earliness in pea. On the other hand, significant positive heterotic effects were obtained in the F_2 generation of both crosses relative to both mid and high parent in all the three studied growth traits except the stem length ($cross_1$) over high parent.

The heterotic effects were generally, more pronounced for all growth traits of both crosses in the F_1 than F_2 generation, except stem length and number of branches in the $cross_2$ (relative to mid-parent), which exhibited reverse trend. Very striking inbreeding depression values were observed in the F_2 generation for stem length followed by number of branches and flowering date resulted in reducing of the non-additive variance and increases the additive one.

Potence ratio values indicate the existence of over dominance in both crosses in all characters except pod length ($cross_2$), which exhibited partial dominance. These results were in agreement with those obtained by Zayed (1998) and Zayed and Faris (1998).

In the F_1 data, the $cross_1$ was the earliest for flowering date and it had the highest values for stem length, 100-seeds weight and yield /fed., while the other cross was later in flowering and had the highest values for stem length, number of branches and pod length.

In the F_2 data, $cross_2$ had the highest values for all yield and its components than the $cross_1$. Better information could be obtained when both

F_2 and F1generations are compared in the same year. However, the performance of the F_2 crosses was less in values than the corresponding F_1crosses for all traits, indicating very striking inbreeding depression in the F_2 generation.

Inbreeding depression value was ranging from -33.9% to -0.26% for both crosses in all characters. $Cross_1$ exhibited inbreeding depression value more than $cross_2$ in all quality traits.

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السلوك الوراثى لبعض الصفات الكمية فى البسلة تحت ظروف جنوب مصر

أبو بكر عبد العظيم الدقاق ، أحمد حلمى حسين
معهد بحوث البساتين - مركز البحوث الزراعية – الجيزة .

الملخص العربى

أجريت هذه الدراسة بمحطة البحوث الزراعية- شندويل- سوهاج خلال الموسم الشتوى للأعوام ٢٠٠٥ الى ٢٠٠٨ . حيث تم استخدام ٦ عشائر من كلا الهجينين والتى قيمت فى الموسم الشتوى ٢٠٠٧/٢٠٠٨ وهذه الهجن هى (الاسكا × دوارف جراى شوجر) . (الاسكا × ايرلى بيرفكشن) وقد تم اختيار الصنف الاسكا لتميزه بالتبكير فى الازهار بينما الصنفين الآخرين لتميزهما فى المحصول ومكوناته .

زرعت بذور العشائر فى تجربة قطاعات كاملة عشوائية ذات ثلاث مكررات . وتم تسجيل بيانات على عدد الأيام لازهار ٥٠% من النباتات. طول الساق . عدد الفروع بالنبات وطول القرن، عدد البذور بالقرن . المواد الصلبة الذائبة الكلية بالبذور الخضراء . وزن ١٠٠ بذرة خضراء والمحصول الكلى من القرون الخضراء.

وقد أظهرت النتائج ما يلى:

١- وجود اختلافات وراثية بين التراكيب الوراثية المختلفة لكل الصفات.

٢- رغم وجود فعل الجين الاضافى الا أن فعل الجين السيادى كان له الأثر فى التحكم فى معظم الصفات تحت الدراسة

٣- ظهرت انواعا مختلفة من السيادة الجينية ذات التأثير على الصفات حيث السيادة الجزئية كانت هى المؤثرة فى الإزهار . بينما السيادة الفائقة فى صفات النمو الاخرى.

٤- من دراسة قوة الهجين فى الصفات المختلفة تبين انها اختلفت بين الهجن والصفات تحت الدراسة وقد ظهر عامة أن محصول القرون أظهر قوة هجين اعلى من اى من مكونات المحصول الأخرى فى الجيل الأول والذى كان واضحا أنه أكبر كذلك من الجيل الثانى فى معظم الصفات.