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Heterosis and gene action of economic traits in pea under Sohag government condition

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Abstract

Nine genotypes of pea (Pisum sativum L.) were crossed in half diallel design to study heterosis, nature of gene action and heritability for earliness and yield components traits. Mean squares of genotypes were found to be highly significant for all studied traits, providing evidence for presence of considerable amount of genetic variation among studied genotypes. The results showed that the majority of crosses exhibited significant heterosis estimates over mid and best parents for all studied traits. The results indicated that the magnitude of additive genetic variance ($\sigma^2 A$) were positive and higher than those of non-additive ($\sigma^2 D$) one for all of studied traits, indicating that additive gene action played a major role in the inheritance of pea. The broad sense heritability values were 98.89 and 97.84% for days to flowering and number of branches per plant, respectively. While, the narrow sense estimates were 83.10 and 85.27%, for the same traits, respectively. For yield and its component traits the results showed that the estimated values of broad sense heritability were ranged from 96.30% for 100 seeds weight to 99.89% for fresh pods weight per plant. In the same time, the estimates of narrow sense heritability ranged from 64.90% to 91.83% for 100- seeds weight and number of pods per plant, respectively.

Keywords:
Pea, Heterosis, Gene action, Heritability

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INTRODUCTION

Pea (*Pisum sativum* L.) is a self-pollinated crop (2x=2n=14). It is considered one of the most important legume crops in Egypt. It is grown for local and export markets, as a vegetable crop for the green pod stage and/or for dry seeds, which contained between 22-25% protein. The total cultivated area of fresh pods pea crop in Egypt was 42142 feddan, yielded 183732 ton, with an average of 4.38ton per feddan (MALR, 2016). Several breeders interested in pea breeding, such as El-Dakkak *et al*. 2014 and 2015) indicated that there are great cropping potentials that have not been fully exploited so far. Thus, this study can help in benefiting from the varieties scattered throughout Egypt to raise efficiency in choosing the best of these. When choosing the ideal parental combination for crosses, it is important to consider the heterotic response and heterotic patterns. Half diallel mating is a common method for learning about the inheritance of quantitative traits (Griffing, 1956). For direct phenotypic selection, it is preferable to have genetic variation with a high heritability. Many breeders of peas, such as Dar *et al.* (2013)**,** Sureja and Sharma (2000) and Rashwan and El- Shaieny (2016) they found that the estimates of broad-sense heritability were very high. Enhancing the yield of peas is indeed one of the major objectives (Nayak and Baisakh, 1990) whatever the original intent behind any breeding program. To carry out a successful breeding program, the breeder should have enough knowledge about the type and relative amount of genetic variance components and their interaction with the environment for the attribute in question. Zayed *et al*. (2005) documented the importance of both additive and non-additive gene action for the expression of most pea traits, noting that the predominance of additive and additive x additive types of gene action was not influenced by internal population selection and that external changes would only be useful for enhancing the earliness. Investigation of heterosis could help in selecting some superior parents, which used in cross combinations for further exploitation in a breeding program for choosing desirable segregates. The percentage rise in the F_1 hybrid's mean value over its mid or better-performing parents is known as heterosis. It's possible that heterosis is a genetic expression of hybridization's advantages. To describe its manifestation effect as hybrid vigor, the term heterosis was created. Many studies have been done on pea to determine the amounts of heterosis for the different traits. Different heterotic values for pea were reported by several authors, i.e., Borah (2009), Pandey *et al*. (2006), Zayed and Faris (1998) and Patel *et al.* (2017). They suggested that the estimate and study of heterosis will have a direct effect on the breeding methodology to be used for pea improvement. Therefore, the objective of this investigation was to study heterosis and the types of gene action controlling the inheritance of economical traits of pea.

MATERIALS AND METHODS

The present investigation was carried out at Shandweel Agricultural Research Station, Sohag, during the two winter seasons of 2019/2020 and 2020/2021. Where, the soil of experiment area was clay loam in texture. Nine different pea genotypes (Pisum sativum L.) represented a wide range of variability in their economic traits, were used in this study. These genotypes were: Sweet-1 (P_1), Sweet-2 (P_2), Master B (P_3), Super-1 (P_4), Victory freezer (P_5), Super-2 (P_6), Gaara (P_7), Balmoral (P_8) and Progress (P_9). The Description of the nine parental genotypes are presented in table 1.

Table 1: Description of the nine parental genotypes; H.R.I: Horticultural Research Institute.

Cultivar	Source	Plant height (cm)	Dry seed colour	Dry seed texture	Flower colour
Sweet-1 (P_1)	H.R.I	Short	Green	Wrinkle	White
Sweet-2 (P_2)	H.R.I	Medium	Green	Wrinkle	White
Master B (P_3)	H.R.I	Short	Green	Wrinkle	White
Super-1 (P_4)	H.R.I	Medium	Green	Wrinkle	White
Victory freezer (P_5)	H.R.I	Medium	Green	Wrinkle	White
Super-2 (P_6)	H.R.I	Medium	Green	Wrinkle	White
Gaara (P_7)	H.R.I	Medium	Green	Wrinkle	White
Balmoral (P_8)	H.R.I	Medium	Green	Wrinkle	White
Progress (P_9)	H.R.I	Medium	Green	Wrinkle	White

In the winter season of 2019, the seeds of nine parental genotypes were planted and the selfing was undertaken to produce more seeds from each parental genotype. In the same winter season (2019), nine parental genotypes were crossed according to a half diallel mating design to produce 36 F_1 hybrids. In the winter season of 2020, parents (nine genotypes seeds) and their 36 F_1 hybrids were sown on October, 3 in a randomized complete block design with three replications. Each replicate contains 45 plots. Each plot consisted of one row with 3.5 m. long and 70 cm. apart between rows. Plants were spaced by 30 cm. within row. All agricultural practices were applied as recommended for pea production.

Data were recorded for the following traits: earliness trait [Number of days to 50% flowering "FD"; Number of Branches per Plant "No. B/P"; Number of Pods per Plant "No. P/P"; Fresh Pod Weight per plant"(FPW/P" (g); Fresh seed weight per plant "FSW/P" (g) and 100-Fresh Seed Weight "100-SW" (g). Data were subjected to the analysis of variance in order to test the significance of the differences among the 45 genotypes including the 9 parental genotypes and their 36 F_1 hybrids according to Cochran and Cox (1957).

Additive (σ^2A) and non-additive (σ^2D) genetic variances were estimated according to Matzinger and Kempthorne (1956) as follow:

$$\sigma^2 A = 2 \sigma^2 g$$
$$\sigma^2 D = \sigma^2 s$$

Estimates of heterosis % were calculated according to Singh and Khanna (1975) as following equations:

$$\text{Mid-parent heterosis } (\%) = (\bar{F}_1 \text{-M.P./M.P.}) \times 100$$

$$\text{M.P.} = (\bar{P}_i - \bar{P}_j)/2$$

$$\text{Best-parent heterosis } (\%) = (\bar{F}_1 \text{- B.P./B.P.}) \times 100$$

Estimates of heritability in both broad and narrow sense were calculated according to the following equations:

$$h^2 b\% = [(\sigma^2 A + \sigma^2 D) / (\sigma^2 A + \sigma^2 D + \sigma^2 e)] \times 100$$
$$h^2 n\% = [(\sigma^2 A) / (\sigma^2 A + \sigma^2 D + \sigma^2 e)] \times 100$$

RESULTS AND DISCUSSION

Genotypic variations

The analyses of variance for all studied traits for all genotypes (parents and F_1 hybrids) are presented in Table 2. There were highly significant differences among the studies genotypes for all studied traits.

Mean squares of genotypes (Table 2) were found to be highly significant for all studied traits. This provides evidence for presence of considerable amount of genetic variation among studied genotypes. These results are in harmony with those previously obtained by El-Dakkak (2005), Baghdady (2015), El-Dakkak *et al*. (2015) and Jaiswal *et al*. (2013).

Table 2: Analysis of variances of 9 parents and their 36 F1 hybrids for the studied traits.

S.V	D.F	Mean squares					
		FD	No. B /P	No. P/P	FPW/P	FSW/P	100-SW
REP.	2	2.05	0.0099	0.26	0.26	26.27	4.29
G.	44	137.39**	2.04**	283.28**	283.28**	3432.11**	21.34**
Erorr	88	1.53	0.044	0.58	0.58	6.21	0.79

*, ** Significant at 5 and 1% levels of probability, respectively**.**

Estimates of heterosis

Estimates of heterosis over mid parents for all studied traits are shown in Table 3. Earliness is an important aim in pea, thus, the negative heterosis value for number of days to 50% flowering is desirable in breeding program. In this direction, most of crosses flowered highly significant earlier than their mid parents with negative heterosis values ranging from –5.45% to –19.13%.

Respecting to vegetative traits, most crosses exhibited significant positive heterosis values relative to mid parents and ranged from (1.09% to 43.82%) for Number of branches per plant. Regarding to yield components significant positive heterosis values were also obtained from most crosses and ranged from (4.77% to 40.49%), (13.45% to 51.96%), for number of pods per plant and fresh pod weight per plant, respectively. Concerning total seed yield most crosses were also significantly better yielding than their mid parents and ranged from (11.03% to 56.70%) and (4.17% to 12.67%) for fresh seed weight per plant and 100

seed weight, respectively. Estimates of heterosis over best parents for all studied traits are presented in Table 4. In this direction, most crosses were significant flowered earlier than their best parents with negative heterosis values ranging from –10.08% to –13.64%. Respecting to vegetative traits, most crosses exhibited significant positive heterosis values relative to best parents for number of branches per plant (2.00% to 33.33%). Regarding to yield traits, significant positive heterosis values were also obtained from most crosses for number of pods per plant (6.56% to 16.86%) and fresh pod weight per plant (15.66% to 38.82%).

Concerning total seed yield most crosses were also significantly better yielding than their best parents and ranged from (16.07% to 48.58%) and (5.73% to 9.67%) for fresh seed weight per plant and 100 seed weight, respectively. In general, these results indicate that most crosses were significantly earlier and high yielding than their mid or better parents, suggesting the important role of non-additive gene action in the inheritance of studied traits. These results are in agreement with those reported by Pandey, *et al*. (2006); Shah and Zamin (2005); Baghdady (2015) and El-Dakkak (2015).

Table 3: Estimates of heterosis(%) over mid-parents for 36 F1 hybrids:

	FD	No. B /P	No. P/P	FPW/P	FSW/P	100-SW
P_1XP_2	-1.44	-6.76**	0.85	-7.40*	-7.68*	-9.59**
P_1XP_3	-4.61*	43.82**	3.11*	-8.74*	-6.70*	-8.43**
P_1XP_4	2.16	12.36**	13.23**	13.45**	6.20*	-8.32**
P_1XP_5	6.56**	21.62**	40.49**	27.95**	44.87**	-7.79**
P_1XP_6	-0.04	24.05**	17.65**	18.62**	22.81**	3.34*
P_1XP_7	4.81*	25.15**	35.12**	32.88**	24.84**	-4.37**
P_1XP_8	-0.64	-2.62**	11.32**	14.21**	39.27**	-5.42**
P_1XP_9	-4.89*	25.33**	-7.33**	-5.81	12.94**	-1.88
P_2XP_3	-2.48	-2.13**	5.86**	11.03*	7.18*	-0.14
P_2XP_4	-12.45**	-6.09**	10.33**	11.08*	13.14**	2.90*
P_2XP_5	-19.13**	2.00**	12.07**	12.63**	35.27**	5.57**
P_2XP_6	-15.94**	4.76**	11.74**	12.49*	23.39**	7.38**
P_2XP_7	-5.46**	-11.21**	21.49**	40.41**	35.60**	11.93**
P_2XP_8	-11.72**	-9.47**	4.77**	6.23	29.72**	8.44**
P_2XP_9	-16.71**	-7.92**	-3.66**	-11.09*	12.30**	4.17**
P_3XP_4	1.94	-6.43**	-8.30**	-6.65	-7.36*	-0.10
P_3XP_5	9.81**	27.66**	12.94**	21.33**	32.54**	1.36
P_3XP_6	-3.64*	32.45**	5.59**	7.56*	17.71**	4.43**
P_3XP_7	-1.50	21.95**	21.04**	51.96**	28.99**	-2.70*
P_3XP_8	4.46*	1.09**	10.64**	9.73*	33.66**	-4.01*
P_3XP_9	8.15**	27.27**	0.44	-7.53*	10.63*	-2.33*
P_4XP_5	-9.79**	6.96**	12.01**	7.71*	11.52**	2.77*
P_4XP_6	-7.64**	15.00**	12.97**	15.91**	21.85**	5.23**
P_4XP_7	-6.71**	10.67**	13.55**	3.38	15.22**	3.21*
P_4XP_8	-2.21	-4.76**	7.07**	2.98	14.62**	-4.24*
P_4XP_9	0.28	23.28**	0.38	-2.20	-2.50	-3.15*
P_5XP_6	-5.45**	22.86**	0.27	1.02	11.03**	12.67**
P_5XP_7	-3.78*	10.31**	22.11**	40.01**	48.89**	10.07**
P_5XP_8	-10.62**	7.00**	22.12**	23.46**	44.70**	0.11
P_5XP_9	-5.92**	17.82**	19.76**	5.53	39.77**	-0.90
P_6XP_7	-7.37**	13.30**	25.71**	29.90**	39.25**	3.09*
P_6XP_8	-3.68*	-2.77**	5.88**	-0.52	17.34**	5.26**
P_6XP_9	-10.09**	31.13**	6.97**	6.47	14.24**	-2.41*
P_7XP_8	-7.33**	-1.50**	29.61**	27.32**	56.70**	4.87**
P_7XP_9	-7.59**	13.78**	7.42**	-8.06	17.05**	-2.14*
P_8XP_9	-3.23*	12.65**	13.16**	0.11	27.81**	-4.22**
LSD $_{5\%}$	1.73	0.29	1.07	4.06	3.49	1.24
LSD $_{1\%}$	2.29	0.39	1.41	5.36	4.61	1.65

Table4: Estimates of heterosis (%) over best parent for 36 F1 hybrids.

	FD	No. B /P	No. P/P	FPW/P	FSW/P	100-SW
P_1XP_2	32.52**	-31.00**	-22.50**	-17.26**	-21.99**	-19.19**
P_1XP_3	-1.83	33.33**	2.97*	-19.40**	-11.67*	-14.01**
P_1XP_4	18.25**	-23.08**	-27.92**	-23.29**	-30.88**	-16.11**
P_1XP_5	32.52**	-10.00**	0.47	6.02	33.36**	-21.45**
P_1XP_6	24.36**	-10.91**	-24.81**	-19.71**	-18.63**	-6.86**
P_1XP_7	24.36**	-13.01**	-0.64	17.55**	3.30	-16.05**
P_1XP_8	35.58**	-34.97**	-27.46**	-17.00**	10.50*	-18.88**
P_1XP_9	40.67**	-7.84**	-36.64**	-34.56**	-11.75*	-6.78**
P_2XP_3	35.92**	-31.00**	-18.72**	-11.00*	-13.37**	-5.29**
P_2XP_4	0.00	-16.92**	-16.77**	-19.60**	-18.69**	0.25
P_2XP_5	-13.64**	2.00**	0.93	3.34	23.12**	-0.04
P_2XP_6	-10.27**	0.00	-15.19**	-18.47**	-9.23*	6.37**
P_2XP_7	5.42*	-19.51**	13.99**	38.82**	32.15**	9.67**
P_2XP_8	-10.68**	-23.08**	-18.03**	-16.29**	20.04**	3.47*
P_2XP_9	-10.08**	-8.82**	-18.87**	-33.54**	1.96	-2.35*
P_3XP_4	21.90**	-38.46**	-41.65**	-40.72**	-41.19**	-2.83*
P_3XP_5	41.32**	-10.00**	-19.30**	-8.78*	16.07**	-8.71**
P_3XP_6	24.06**	-9.09**	-32.56**	-31.64**	-24.05**	-0.06
P_3XP_7	20.82**	-18.70**	-11.07**	20.78**	2.23	-9.48**
P_3XP_8	47.79**	-34.97**	-27.95**	-26.07**	1.87	-12.91**
P_3XP_9	66.13**	-10.78**	-31.38**	-39.96**	-16.87**	-3.53*
P_4XP_5	-3.88*	-5.38**	-8.42**	-17.27**	-24.23**	-5.06**
P_4XP_6	-1.55	6.15**	11.96**	15.66**	17.48**	3.48*
P_4XP_7	-4.65*	7.69**	-10.27**	-24.64**	-15.84**	-1.41*
P_4XP_8	13.18**	-9.09**	1.77	-8.50*	-13.22**	-10.86**
P_4XP_9	24.81**	10.00**	-12.48**	-6.86	-25.11**	-6.91**
P_5XP_6	-5.41*	17.27**	-17.44**	-22.30**	-23.03**	5.73**
P_5XP_7	0.22	0.00	16.86**	29.81**	32.40**	6.28**
P_5XP_8	-3.36*	-9.09**	4.10**	4.32	22.84**	-0.70
P_5XP_9	8.98**	16.67**	11.02**	-15.96**	16.65**	-11.71**
P_6XP_7	-3.49*	7.32**	0.00	-5.17	4.20	0.08
P_6XP_8	4.11*	-13.99**	1.50	-11.45*	-8.83*	-0.46
P_6XP_9	4.11*	26.36**	-6.02**	1.60	-9.88*	-7.70**
P_7XP_8	4.68*	-8.39**	6.56**	1.19	48.58**	2.07*
P_7XP_9	12.10**	4.07**	-4.37**	-30.76**	8.83*	-9.99**
P_8XP_9	3.18	-3.50**	3.28*	-6.95	25.18**	-14.05**
LSD $_{5\%}$	**2.00**	**0.34**	**1.23**	**4.68**	**4.03**	**0.45**
LSD $_{1\%}$	**2.64**	**0.45**	**1.63**	**6.19**	**5.32**	**1.90**

Gene action

Estimates of all types of gene action for all studied traits are presented in Table 5. The results indicated that the magnitude of additive genetic variance ($\sigma 2A$) were positive and higher than those of non-additive ($\sigma 2D$) one for all of studied traits. This finding, indicating that additive gene action played a major role in the inheritance of these studied traits. Similar results were obtained by Dhaval et al. (2016), Jaiswal et al. (2013) El-Dakkak (2009) and Patel et al. (2017).

Table 5: Genetic components for all the studied traits.

Genetic components	FD	No. B /P	No. P/P	FPW/P	FSW/P	100-SW
$\sigma^2 A$	114.17	1.74	260.13	6853.45	2975.68	13.85
$\sigma^2 D$	21.69	0.26	22.57	845.97	450.22	6.7
$\sigma^2 e$	1.53	0.04	0.58	8.39	6.21	0.79
$h^2_{b.s}\%$	**98.89**	**97.84**	**99.8**	**99.89**	**99.82**	**96.3**
$h^2_{n.s}\%$	**83.1**	**85.27**	**91.83**	**88.92**	**86.7**	**64.9**

Estimates of heritability

The results in Table 5 showed that broad sense heritability estimates (H2 b %) were more than 96% and larger than their corresponding of narrow sense heritability (H2 n %). The estimates of narrow sense heritability were 83.1% for earliness. For vegetative traits, the estimates of narrow sense heritability are 85.27% for number of branches per plant. Respecting to yield components, the estimates of narrow sense heritability ranged from 88.92% to 91.83 for Fresh pod weight per plant and Number of pods per plant, respectively. Regarding to total seed yield, the estimates of narrow sense heritability ranged from 64.90% to 86.70% for 100 seed weight and Fresh seed weight per plant, respectively.

These results were in agreement with those obtained by Dhaval et al. (2016), Jaiswal et al. (2013) El-Dakkak (2009) and Patel et al. (2017). The estimate of narrow sense heritability presented additional evidence about the important of additive gene action for earliness and yield components.

CONCLUSION

From the data presented in this study it could be concluded that the cross combinations (P4xP6) and (P5xP7) showed desirable significant heterosis values for all studied traits. This finding reflects the presence of considerable heterosis values and suggested that additive gene effects played the major role in the inheritance of these traits. These promising crosses could be used for developing pea hybrids. As well as the obtained results reflected the importance role of additive gene action in the inheritance of these traits. Our findings suggested that selection program could be used for improvement of pea traits under Sohag governorate conditions. However, direct selection for pod yield was also successful. Then, early and high yielding elite homozygous genotypes with prospective arrays of yield and their component features can be extracted using pedigree selection or one of its derivative techniques.

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الملخص العربى

قوة الهجين وفعل الجين لبعض الصفات الأقتصادية في البسلة تحت ظروف محافظة سوهاج

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تم اجراء هذا البحث لدراسة طبيعة الفعل الجيني وقوة الهجين لبعض الصفات الإقتصادية في البسلة وذلك بإستخدام نظام التهجين النصف دائري بين تسعة تراكيب وراثية من البسلة. ويمكن تلخيص أهم النتائج كما يلي: أوضحت نتائج تحليل التباين وجود فروق معنوية بين التراكيب الوراثية (الآباء والهجن) لكل الصفات المدروسة. أظهرت معظم الهجن قوة هجين أعلي من متوسط الآباء وكذلك بالنسبة لأحسن الآباء في معظم الصفات المدروسة. كانت قيم التباين الوراثي المضيف (A σ^2) أعلي من قيم التباين الوراثي غير المضيف (D σ^2) لكل الصفات المدروسة. قدرت قيمة معامل التوريث في المدي الواسع وكانت أعلي قيمة هي 99.80% وذلك لصفة عدد القرون علي النبات الواحد بينما كانت أقل قيمة هي 97.84% وذلك لصفة عدد الأفرع لكل نبات. قدرت قيمة معامل التوريث في المدي الضيق وكانت تتراوح فيما بين 64.90% إلي 91.83% وذلك لصفتي وزن الـ 100 بذرة وعدد القرون علي النبات الواحد علي الترتيب. وهذه النتائج المتحصل عليها تبرهن علي الدور الكبير الذي يلعبه التباين الوراثي غير الإضافي كطبيعة للفعل الجيني في توريث هذه الصفات. توضح نتائج هذه الدراسة أن هناك عدد من الهجن الواعدة ذات قوة هجين عالية يمكن أستغلالها في إنتاج هجن متفوقة من البسلة.