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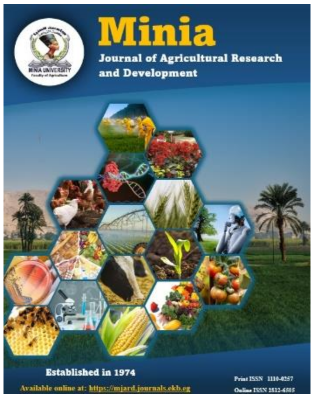

Studying the Genetic Behavior to Improve some Quantitative Traits of Peas under Sohag Conditions

Hala Sedky Abd-Ellah Mousa

Horticulture Research Institute, Agriculture Research Center, Egypt

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ABSTRACT

To determine the nature and degree of gene action for yield and its component traits in two pea crosses, the current study used the generation mean analysis and the chi-square test. With the exception of the shellout % in the Boogie x Balmoral cross, practically all of the traits showed one or more types of epistatic effects, according to scaling and joint scaling tests. For the other traits, significant Chi-square values and the results of all three scaling tests, or any of the individual tests A, B, or C demonstrated that the digenic interaction plays a role in inheritance of the traits studied. Duplicative epistasis was observed in all studied traits of the two crosses, except for number of branches per plants, pod width and weight of 100-seeds in cross 1, as well as shellout percentage in cross 2, where complementary epistasis prevailed. For most of the quality traits in this study, the dominance gene effects were stronger than the additive ones. In early segregating generations, it is advised to select for traits controlled by the dominating additive component. It could be concluded that in most of the studied traits, selection should be postponed to later generations of selection. Moreover, the findings obtained in this study suggested that reciprocal recurrent selection should be adopted to obtain higher yield.

Keywords: Scaling test, Gene action, I.D. and Heterosis.

INTRODUCTION

Thorough understanding many kinds of gene effects is necessary for breeders to implement a successful breeding program aiming to improve desired qualities in peas. However, the presence of genetic variety that allows for efficient selection is necessary for the enhancement of pea metrics as well as quality. Non-allelic interactions are absent in most of the analyses, although these analyses hardly ever offer a reliable test of this assumption. In addition to the other two categories of

*** Corresponding author: Hala Sedky Abd-Ellah Mousa**
E-mail address: : halasedky028@gmail.com

gene effects dominance and additive tests of epistasis gene effects are crucial for plant breeders (**Gamble, 1962 and Hussien et al. 2009**). **Comstock et al. (1949)** demonstrated how the estimations of both dominance and additive genetic variance will be upwardly biased when epistatic gene effects are present. Although it doesn't seem to be the only answer, adding epistasis to the analytical model might reduce the amount of additive genetic variance. The parameters that **Hayman (1958)** described are similar to those of Anderson and Kempthorn's and allow for the estimation of the dominance, additive, additive x dominance, additive x additive, and dominance x dominance gene effects with less interpretation difficulties. Many authors, including **Zayed (1998), Zayed et al. (1999a), Kandeel et al. (2005), Zayed et al. (2005), and El-Dakkak et al. (2009)**, focused their studies on pea breeding primarily on gene effects analysis to comprehend the mode of inheritance of the yield and its attributes under Upper Egypt conditions. They also noted that the significance of both additive and dominance in expression of the most of pea traits. To effectively utilize the genetic variability present in pea breeding material for seed production, the breeder would require a fundamental understanding of yield inheritance and its closely linked components in order to design an effective selection program. In the current study, generation mean analysis was used to discover epistasis and assess the additive and dominant components of variance for yield components in two sets of pea crosses. **Singh and Sharma (2001), Sharma and Restogi (2001), Singh et al. (2003), and Singh and Sharma (2004)** applied estimates of epistatic interaction (s) in addition to additive and dominance gene effects. They concluded that the inheritance of most quantitative traits under their studies was significantly influenced by the additive (d), dominance (h), and all three interacting gene effects. Additionally, the duplicate form of epistasis was present in the majority of crossings in each characteristic. According to **Singh et al. (1997)**, elite populations could be developed by reciprocal recurrent selection.

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. Also to obtain additional information about some genetic parameters to help pea breeders in the future studies in the segregating generations of selection.

MATERIALS AND METHODS

This study was conducted in Shandaweel Research Station, Sohag Governorate, Egypt during three winter seasons of 2021/2022, 2022/2023 and 2023/2024.

In the first season (2021/2022), 4 parental genotypes (obtained from the Horticulture Research Institute, Giza, Egypt) were crossed to generate F_1 progenies, i.e., Boogie x Balmoral and Progress 9 x On Ward.

In the second season (2022/2023), some seeds from the F_1’s and the two corresponding parents were planted to advance to F_2 progenies and backcrosses were generated. Backcrosses to P_1 and P_2 were done using F_1 (F_1 was crossed with P_1 and P_2 respectively).

Using a randomized full block design with three replications, the obtained seeds of the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of both crosses were seeded on November 20, 2023, to be evaluated **in the third season**; 2023/2024.

The designed plots were prepared as each ridge was 3 m in length and the distance between plants was 20 cm on side of the ridge and 60 cm between every two ridges.

Each experimental plot had ten ridges for the F_2 generation and three ridges for each parent, F_1, and back-crosses, respectively. At the right moment, the suggested agricultural methods for pea production were carried out according to the good agricultural practices for pea production recommended by the Egyptian Ministry of Agriculture and Soil reclamation.

The traits assessed were NB/P; number of branches/plant, SL: stem length (cm), PL: pod length (cm), NS/P: number of seeds/pod, PW: pod width (cm), SP: shellout percentage (%), 100-SW: 100-seeds weight (g) and PY/P: pod yield/plant (g).

Pollination procedure: The emasculation and pollination of pea were done as follow:

- Assess if the bud is prepared to anthesis in a day and the maturity of the flower.
- The petals and stamen were carefully removed with a sterilized forceps. To prevent the flower from falling from the peduncle, the second hand should be used to hold the flowers firmly and gently while using the sterilized forceps to remove the stamen and petals. The anthers and floral filaments were carefully removed. The flowers had been successfully emasculated at this point.
- For pollination, the emasculated flowers were prepared. An established plant's mature flower was taken from its peduncle, teased, and was used as a source of pollen.
- The dehisced anther was rubbed on the emasculated flower. Care was taken to prevent contamination of any kind of pollen.
- The emasculated and re-pollinated flowers were promptly covered with the pollinated bags.
- For ease of identification, the pollinated flowers were appropriately tagged and labeled.
- One day following pollination, the bags were removed.
- Successful pollination was indicated by the formation of pods from the hand-pollinated flowers.

Genetic studies were conducted on the six generations generated: P_1, P_2, F_1, F_2, backcross to P_1 (BC_1) and backcross to P_2 (BC_2).

Biometrical analyses:

a- As described by **Mather and Jinks (1982)**, the scaling tests A, B, C, and D were used to determine whether non-allelic interactions were present using the following equations:

$A = 2\overline{BC}_1 - P_1 - F_1$

$B = 2BC_2 - P_2 - F_1$

$C = 4F_2 - 2F_1 - P_1 - P_2$

$D = 2F_2 - BC_1 - BC_2$

$V(A) = 4V(\overline{BC}_1) + V(\overline{P}_1) + V(F_1)$

$V(B) = 4V(BC_2) + V(P_2) + V(F_1)$

$V(C) = 16V(F_2) + 4V(F_1) + V(P_1) + V(P_2)$

$V(D) = 4V\overline{F}_2 + V\overline{BC}_1 + V\overline{BC}_2$

Any of these scales' significance is seen as a hint that non-allelic interaction is present.

b- **Cavalli (1952)** created the joint scaling test, which used $\mathbf{X^2}$ (qui square) to assess how well the genetic model under study controlled the characteristics. However, non-significant X^2 and/or scaling test means that the simple additive-dominance model is adequate. The **Jinks**

and Jones (1958) genetic model would be used in this situation.

c- Digenic interaction model analysis: In the case of significant of both X^2 and/or scaling tests i.e., the simple additive-dominance model is inadequate, six parameters model were used according to **Hayman (1958)** to separate out the components of genetic variance to its main effects. The mean effect parameter (m), additive (d), dominance (h), dominance x dominance (l), additive x additive (i) and additive x dominance (j) forms of gene action were among the estimated gene effects.

$\bar{m} = \bar{F}_2$

$\bar{d} = \bar{BC}_1 - \bar{BC}_2$

$\bar{h} = \bar{F}_1 - 4\bar{F}_2 - 0.5\bar{P}_1 - 0.5\bar{P}_2 + 2\bar{BC}_1 + 2\bar{BC}_2$

$\bar{i} = 2\bar{BC}_1 + 2\bar{BC}_2 - 4\bar{F}_2$

$\bar{j} = \bar{BC}_1 - 0.5\bar{P}_1 - \bar{BC}_2 + 0.5\bar{P}_2$

$\bar{l} = \bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\bar{F}_2 - 4\bar{BC}_1 - 4\bar{BC}_2$

The levels of heterosis over the mid-parent or parental average (Hmp), heterosis over the best parent (Hbp) and inbreeding depression from F_1 to F_2 were calculated:

Heterosis over mid-parent (Hmp) = $[(F_1\text{-MP})/\text{MP}] \times 100$

Heterosis over best parent (Hbp) = $[(F_1\text{-BP})/\text{BP}] \times 100$

Inbreeding depression (ID) = $[(F_1\text{-}F_2)/F_1] \times 100$

where F_1, F_2, mp and bp were the means for F_1 hybrid, F_2 population, mid-parent and best parent of each, respectively.

RESULTS AND DISCUSSION

Mean performance:

Table 1 displays the mean of the six populations (P_1, P_2, F_1, F_2, BC_1, and BC_2) for the characteristics under study in the two pea crosses. All characteristics under study showed significant variations among the six generations, suggesting the presence of genetic variation. For each character under study in the two crosses, the F_1 mean values exceeded the mid values of the two parental means except 100-green seeds weight in the two crosses and both of number of seeds/pod and shellout percentage in cross 2 indicating the prevalence of heterotic effects and dominance effects controlling these characteristics. The F_1 means were higher than the superior parent for No. of branches and pod yield/ plant in the two crosses, stem length in cross 2 and each of pod length, pod width, No. of seeds/pod and shellout percentage in cross 1, indicating the over dominance effect. The mean performance levels of the F_2 population exceeded those of the highest parents for No. of branches and shellout percentage in the two crosses, stem length in cross 2 and each of pod length, No. of seeds/pod, 100-green seeds weight and pod yield/ plant in cross 1, suggesting that the transgressive segregation for these characteristics can be used to discover superior parental lines. The same findings were documented by **Zayed *et al*. (1999b); Zayed *et al*. (2005); Hussien *et al*. (2009); Mousa and El-Solimany (2025).**

Table 1. Mean performance ± standard error of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of two pea crosses for the studied traits.

Trait	**Cross**	**Generations**					
		P_1	P_2	F_1	F_2	BC_1	BC_2
NB/P	C_1	3.57±0.15	3.67±0.09	4.4±0.11	3.97±0.32	3.87±0.11	3.77±0.19
	C_2	4.07±0.14	4.13±0.16	5.07±0.14	4.51±0.16	4.95±0.15	4.25±0.16
SL	C_1	74.07±1.20	99.93±1.10	94.53±1.04	91.68±1.81	90.00±1.58	95.80±1.83
	C_2	104.93±1.64	105.77±1.43	107.27±2.81	108.89±2.50	116.10±2.65	102.27±3.29
PL	C_1	9.18±0.12	8.99±0.18	9.52±0.18	10.54±0.21	10.97±0.20	10.11±0.21
	C_2	11.91±0.39	8.49±0.34	9.78±0.18	9.03±0.55	9.95±0.21	9.31±0.17
PW	C_1	1.38±0.03	1.34±0.03	1.49±0.04	1.25±0.06	1.23±0.04	1.28±0.05
	C_2	1.69±0.03	1.46±0.04	1.60±0.04	1.38±0.08	1.57±0.07	1.42±0.04
SP	C_1	48.92±1.24	49.39±1.93	54.27±1.46	53.13±2.86	53.00±0.98	53.68±1.16
	C_2	41.31±0.79	40.04±0.98	33.20±1.06	44.45±2.78	38.27±1.05	43.45±1.56
NS/P	C_1	7.10±0.14	7.0±0.18	8.20±0.21	8.13±0.23	8.60±0.18	8.37±0.15
	C_2	6.60±0.11	6.40±0.21	6.30±0.11	6.59±0.17	6.65±0.14	6.90±0.14
100-SW	C_1	45.80±1.60	41.70±0.94	41.70±0.95	49.20±2.82	50.17±1.02	49.03±1.37
	C_2	64.20±1.78	35.20±1.31	31.20±1.45	41.23±2.31	40.60±1.81	36.75±3.01
PY/P	C_1	219.37±3.47	202.30±3.13	292.53±2.80	239.15±4.69	264.63±4.14	271.17±4.22
	C_2	235.20±3.43	269.10±4.54	376.48±4.50	231.15±7.12	351.54±5.00	302.83±4.48

C_1: Boogie x Balmoral and C_2: Progress 9 x On Ward.

Gene effects:

Data presented in table 2 provide evidence for insignificant A, B, C and D non-allelic interaction tests and the joint scaling test (X^2) for shellout percentage in cross 1, shows that the additive-dominance model is sufficient to explain the type of gen action for this trait in this cross and that non-allelic interactions are absent. Meanwhile, significant one or more of the four individual scaling tests A, B, C and D for the remaining traits and crosses revealed the presence of epistasis in these characteristics and crosses, therefore, there is a clear evidence of the inadequacy of the simple additive-dominance model for explaining the inheritance of these characteristics.

Generally, 10 out of 16 cases of the traits and crosses gave for one or more of the scaling tests, similar features of a significant non-allelic interaction. Additionally, the type of gene effects for these traits was estimated using six parameters. These results agree with those reported by **Sharma and Rastogi (2001) and Hussien *et. al.*, (2009).**

Table 2. Scaling test parameters A, B, C and D for all studied traits of two pea crosses.

Trait	Cross	Scaling test				χ^2	No. of crosses showing significantly positive non-allelic interaction
		A	B	C	D		
NB/P	C_1	0.24±0.17	0.53**±0.23	0.16±0.76	0.30±0.39	**	Two crosses
	C_2	-0.77**±0.21	0.69**±0.22	0.27±0.42	-0.18±0.22	**	
SL	C_1	-11.4**±2.08	2.87±2.33	-3.66±4.53	-2.44±2.51	**	One cross
	C_2	-20.00**±3.59	8.50*±4.21	-10.31±6.74	-0.59±3.78	**	
PL	C_1	-3.24**±0.26	-1.70**±0.28	-4.96**±0.54	0.007±0.30	**	One cross
	C_2	1.80**±0.35	-0.35±0.30	3.86*±1.33	-1.21±0.66	**	
PW	C_1	0.42**±0.05	0.28**±0.06	0.69**±0.15	0.003±0.08	**	Two crosses
	C_2	0.16*±0.08	0.23**±0.06	0.85**±0.19	-0.23*±0.10	**	
SP	C_1	-2.82±1.58	-3.71±1.93	-5.69±6.94	-0.42±3.41	NS	One cross
	C_2	-2.02±1.43	-13.66**±1.98	-30.06**±6.57	7.19*±3.38	**	
NS/P	C_1	-1.89**±0.26	-1.54**±0.24	-2.03**±0.59	-0.70*±0.30	**	Zero
	C_2	-0.40*±0.18	-1.09**±0.21	-0.75±0.44	-0.37±0.23	**	
100-SW	C_1	-12.84**±1.59	-14.65**±1.76	-25.90**±6.69	-0.80±3.40	**	One cross
	C_2	14.20**±2.48	-7.09±3.65	-3.12±5.74	5.12±3.35	**	
PY/P	C_1	-17.37**±5.42	-47.51**±5.44	50.12**±11.62	-57.50**±6.40	**	Two crosses
	C_2	-91.41**±6.63	39.92**±6.35	332.67**±17.55	-192.08**±9.09	**	

*, ** Significant at $P < 0.05$ and $P < 0.01$ level of probability respectively, C_1: Boogi x Balmoral and C_2: Progress 9 x On Ward.

Table 3 presents the findings from the analysis of the six parameters. For all examined traits of the two crosses, the mean affect (m), which represents the contribution from the overall mean plus the locus effects and interactions of the fixed loci, was highly significant, suggesting that these traits are quantitatively inherited. Similar results were presented by **Hussien et al. (2009) and Latha et al. (2018).**

Additive gen effects (d) were high positive significant for, no. of branches in cross 2, stem length in the cross 2, pod length in crosses 1 and 2, pod width in cross 2 and pod yield/plant in cross 2, Similar findings suggest that additive gene effects play a major role in the inheritance of these characteristics and that using various selection techniques may help further improve them. However, pedigree methods are advantageous for this.

While the negative significant value found for no. of seeds/pod in cross 2 and negative highly significant values for both of stem length in cross 1 and shellout percentage in cross 2 were caused by the decision to identify one parent as P_1 or P_2. These findings accord with those achieved by **Singh and Naryanana (2000)**.

The estimated mean (m) displays the contribution from the overall mean plus locus effects and fixed locus interaction. The quantitative inheritance of the traits is shown by the degree of significance in mean (m) values for yield and other variables under study.

Table (3) showed that the dominance gene effects were positive significant or highly positive significant for stem length and no. of seeds/pod in cross 1, no. of branches and pod width in cross 2 and pod yield/plant in the two crosses. These findings demonstrate how crucial dominance gene effects are to the inheritance of these characteristics. Regarding the dominance effects negative sign, in shellout percentage and 100-seeds weight in cross 2, showed that the alleles causing these characteristics' lower values were over dominant than those causing their high values. However, the inheritance of the number of branches, pod width, shellout percentage and pod yield/plant in cross 2, were influenced by major additive and dominance gene effects, additionally, cross 1's stem length showed both additive and dominant gene effects that are essential to the inheritance of these traits, with dominance gene effects being greater than additive ones. Selecting favorable characters may also be used in the early generations, but it would work best in the later ones after the dominant impact subsided.

The additive × additive gene effects (i) were either highly positive significant or positive significant (Table 3) for pod width in cross 2, no. of seed/pod in cross 1 and pod yield/plant in the two crosses, shown that there are more genes for these traits and that selection could be useful to improve them. Similar results were obtained by **Mousa (2010), Zayed et al., (2010) and Hussien et al., (2009)**. However, negative significant value of additive × additive gene effects was obtained for shellout percentage in cross 2. These findings demonstrated the parents' alleles dispersion. Because there is no additive genetic influence to fix this characteristic, selection is useless in early segregating generations. Positive highly significant additive × dominance gen effects (j) were obtained for no. of branches and pod yield/plant in cross 2, pod length in cross 1 and stem length in both pea crosses. Delaying selection to later generations with more homozygosity, where additive and additive × additive variances are prevalent, would be preferable because additive × dominance epistasis tends to segregate in latter generations. Negative and significant or highly significant additive × dominance gen effects were reported for pod length, shellout percentage, no. of seeds/pod and 100-seeds weight in the cross 2, also for pod yield/plant in the cross 1, proving that the low-performing parent carries the dominant genes.

The dominance × dominance gene effects (l) were positive highly significant only in cross 1, for pod width. According to these findings, the dominance x dominant gene action plays an essential role in the genetic system controlling this trait in this cross, and selection ought to be successful in later generations. Negative highly significant and dominance × dominance gene interactions (l) were found in the two peas crosses for number of seeds/pod and pod yield/plant as well as in the cross 1 for pod length and 100-seeds weight, showing that they have a decreasing effect on the expression of these characteristics and that breeding is not important for future generations.

When the sign of the dominance and dominance × dominant gene effects is the same, the epistasis type is considered complimentary (**Said 2014, Mistry et al. 2016**) and duplicate epistasis in cases where the sign differed. Table 3 presented that duplicate epistasis was controlling for all characteristics under study in the cross 1 and 2, except for no. of branches, pod width and 100-seeds weight in cross 1, as well as shellout percentage in cross 2, When complimentary epistasis predominated, suggesting that for the majority of characteristics, duplicate epistasis was more important than complementary epistasis.

High magnitude dominance [h] and dominance x dominance [l] gene interaction effects would not be expected because a duplicative kind of epistasis prevents trait improvement through selection (**Mistry et al. 2016**). For duplicate kinds of epistasis, biparental mating is advised. Similarly, selection in F_3 and later can ameliorate the situation when complimentary type epistasis is present (**Thakare et al. 2017**).

In order to improve the majority of the traits under study, extensive selection across subsequent generations was required because non-additive effects outweighed additive effects. Additionally, in early segregations, inter-mating may yield desired segregates by breaking unfavorable linkages; alternatively, recurrent selection may be used to handle the aforementioned crosses for quick improvement. Further evidence of the ubiquity of dominant effects is provided by duplicate epistasis for the most traits under study (**Singh and Sharma, 2001**). The additive x additive interaction (i) and duplicate epistasis types were discovered for pod yield/plant (both crosses), No. seeds/ pod (cross 1) and pod width (cross 2), suggesting the potential for acquiring transgressive segregants from their two parents in subsequent generations.

Table 3. Estimates of components of generation means based on perfect fit solution (Joint Scaling Test)

Trait	Cross	Gene effects						Epistasis
		Mean (m)	Additive (d)	Dominance (h)	Additive x Additive (i)	Additive x Dominance (j)	Dominance x Dominance (l)	
NB/P	C_1	3.97**±0.19	0.10±0.13	0.17±0.79	-0.61±0.79	0.29±0.27	1.37±0.92	Complementary
	C_2	4.51**±0.09	0.70**±0.13	1.33**±0.46	0.36±0.45	1.46**±0.28	-0.45±0.66	Duplicate
SL	C_1	91.68**±1.04	-5.80**±1.39	12.41*±5.09	4.87±5.02	14.27**±2.94	-13.41±7.18	Duplicate
	C_2	108.9**±1.45	13.8**±2.44	3.10±7.76	1.20±7.56	28.5**±5.03	-12.70±11.85	Duplicate
PL	C_1	10.54**±0.12	0.87**±0.17	0.43±0.60	-0.01±0.59	1.54**±0.35	-4.93**±0.86	Duplicate
	C_2	9.03**±0.32	0.63**±0.16	2.00±1.33	2.41±1.32	-2.15**±0.43	-0.97±1.47	Duplicate
PW	C_1	1.25**±0.04	-0.05±0.04	0.12±0.16	-0.01±0.16	-0.14±0.07	0.70**±0.21	Complementary
	C_2	1.38**±0.05	0.15**±0.05	0.49*±0.21	0.46*±0.21	0.07±0.09	-0.07±0.26	Duplicate
SP	C_1	53.13**±1.65	-0.68±0.87	5.96±6.91	0.84±6.82	-0.89±2.19	-7.37±7.77	Duplicate
	C_2	44.45**±1.60	-5.19**±1.08	-21.85**±6.81	-14.37*±6.77	-11.64**±2.28	-1.31±7.87	Complementary
NS/P	C_1	8.13**±0.13	0.23±0.14	2.54**±0.61	1.40**±0.59	0.35±0.31	-4.83**±0.81	Duplicate
	C_2	6.59**±0.10	-0.25*±0.12	0.55±0.47	0.75±0.46	-0.69*±0.27	-2.24**±0.64	Duplicate
100-SW	C_1	49.20**±1.63	1.14±0.98	-0.45±6.84	1.59±6.80	-1.81±2.24	-29.09**±7.76	Complementary
	C_2	41.23**±1.34	3.86±2.03	-28.73**±6.79	-10.23±6.70	-21.28**±4.25	17.34±9.93	Duplicate
PY/P	C_1	239.15**±2.71	-6.54±3.41	196.70**±12.98	115.00**±12.80	-30.15**±7.34	-179.88**±17.93	Duplicate
	C_2	231.15**±4.11	48.72**±3.88	508.49**±18.43	384.15**±18.17	131.33**±8.42	-435.64**±23.41	Duplicate

*$p < 0.05$, **$p < 0.01$, C_1: cross 1, C_2: cross 2.

Heterosis in F_1 hybrids

The F_1 hybrids yielded more NB and PY/P in two crosses as well as PW, SP and NS in cross-1 than the F_2 populations and the corresponding best parent (Table 4 and Fig. 1). Estimating the values of heterosis and deterioration associated with inbreeding provides important information about the pattern of dominant genetic influence, which is expressed through various quantitative traits. Table 4 and figure 1 show inbreeding depression, which is defined as a decrease in F_2 generation performance compared to F_1.

Heterosis was evident in most traits. The average level of heterosis over the mid-parent (Hmp) and best parent was positive for NB, PL, PW, NS and PY/P in cross-1. Average superiority over the best parent (Hbp) was negative for PL, PW and NS of cross-2. No cross showed high heterosis in all traits. Heterosis for yield over the mid-parent or the better parent (Hbp) could always be attributed to a significant level of heterosis in at least one of the yield components. The lowest values of most measures of heterosis were found for hundred seed weight in both crosses.

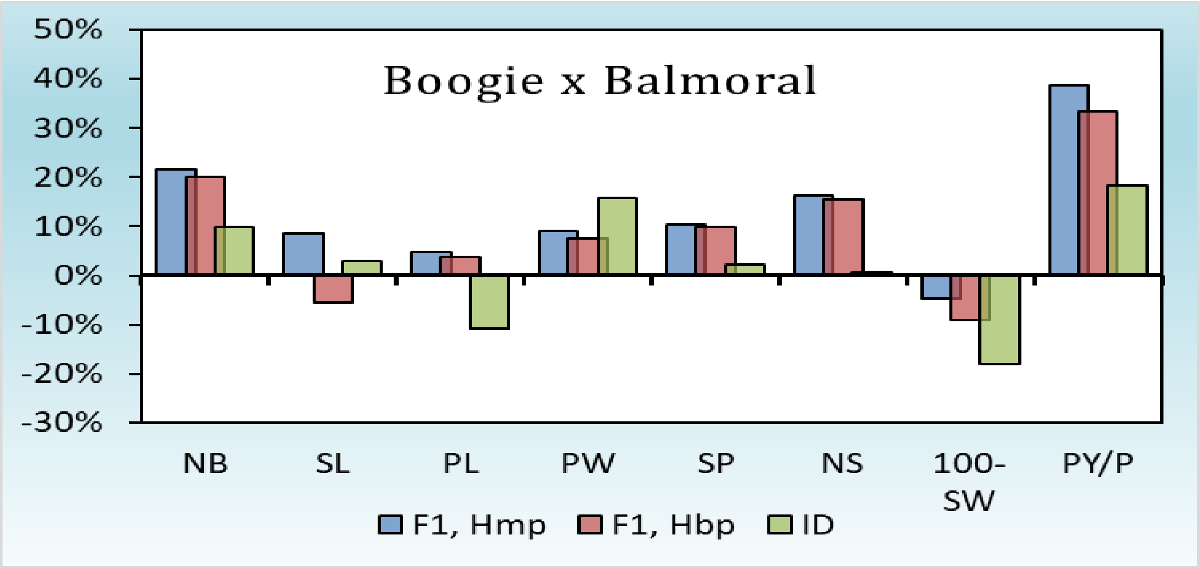


Fig. 1: F_1 heterosis over mid-parent (Hmp) and best parent (Hbp) as well as F_2 inbreeding depression (ID) of pea cross-1

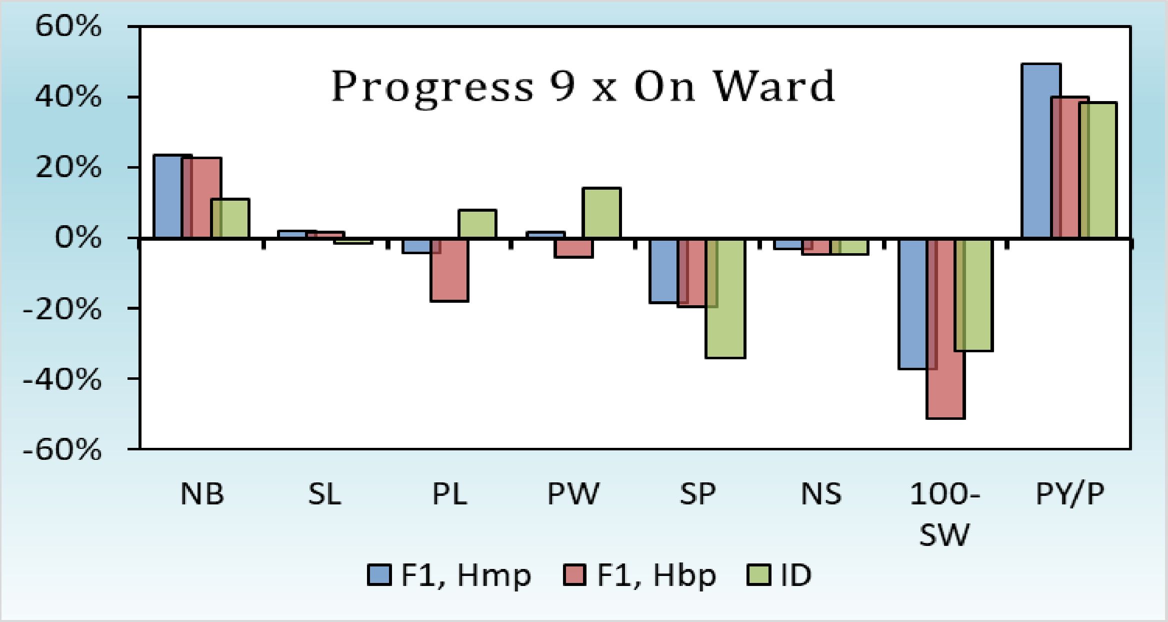


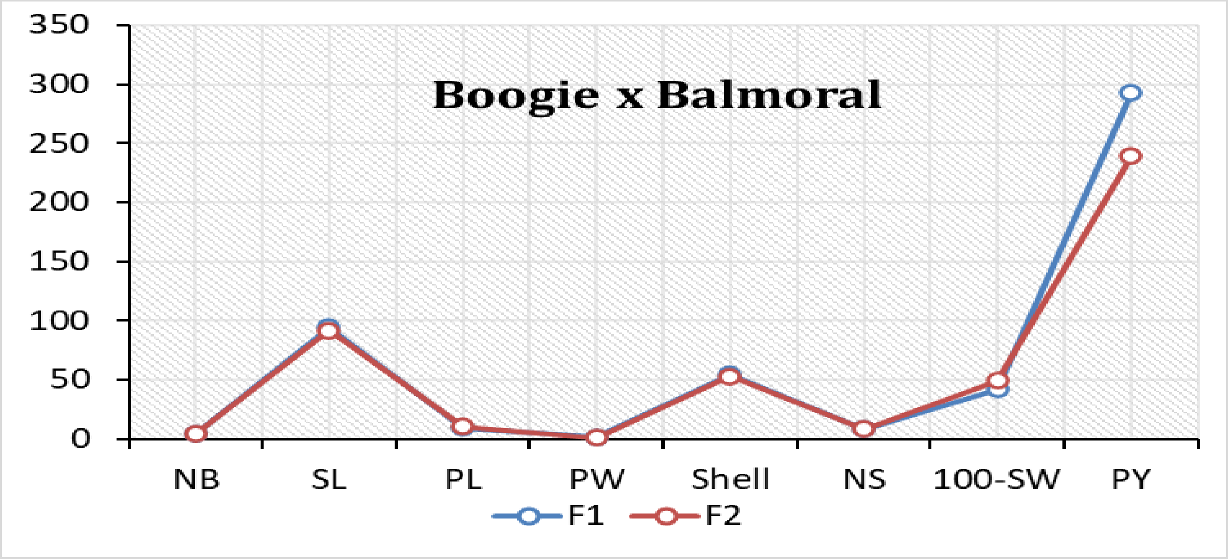
Fig. 2: F_1 heterosis over mid-parent (Hmp) and best parent (Hbp) as well as F_2 inbreeding depression (ID) of pea cross-2.

Table 4. Heterosis of F_1 and inbreeding depression (ID) for two pea crosses for all studied traits.

	Cross	NB	SL	PL	PW	SP	NS	100-SW	PY/P
Hmp (F_1)	C_1	21.55%	8.66%	4.84%	9.10%	10.41%	16.22%	-4.67%	38.75%
Hbp (F_1)	C_1	19.99%	-5.40%	3.74%	7.52%	9.89%	15.40%	-8.94%	33.35%
ID	C_1	9.77%	3.01%	-10.71%	15.74%	2.10%	0.78%	-17.98%	18.25%
Hmp (F_1)	C_2	23.68%	1.82%	-4.09%	1.68%	-18.38%	-3.05%	-37.22%	49.31%
Hbp (F_1)	C_2	22.78%	1.42%	-17.84%	-5.32%	-19.63%	-4.50%	-51.40%	39.90%
ID	C_2	10.93%	-1.51%	7.73%	14.10%	-33.89%	-4.56%	-32.14%	38.60%

Performance of the F_2 generation

Heterosis of the F_2 generation was more than half that of the F_1 for SL, PL, PW, Shell (SP), NS and 100-SW. F_2 values was more than that of the F_1 for SL, Sell (SP), NS and 100-SW of cross-2 as well as PL and 100-SW in cross-1 in which most traits had F_1 comparable to F_2 (fig. 3). These corresponded to values of inbreeding depression of these traits. Negative inbreeding depression signifies a slight improvement in F_2 generation (**Aher et al., 2006 and Abd-Elmonem et al. 2010**).



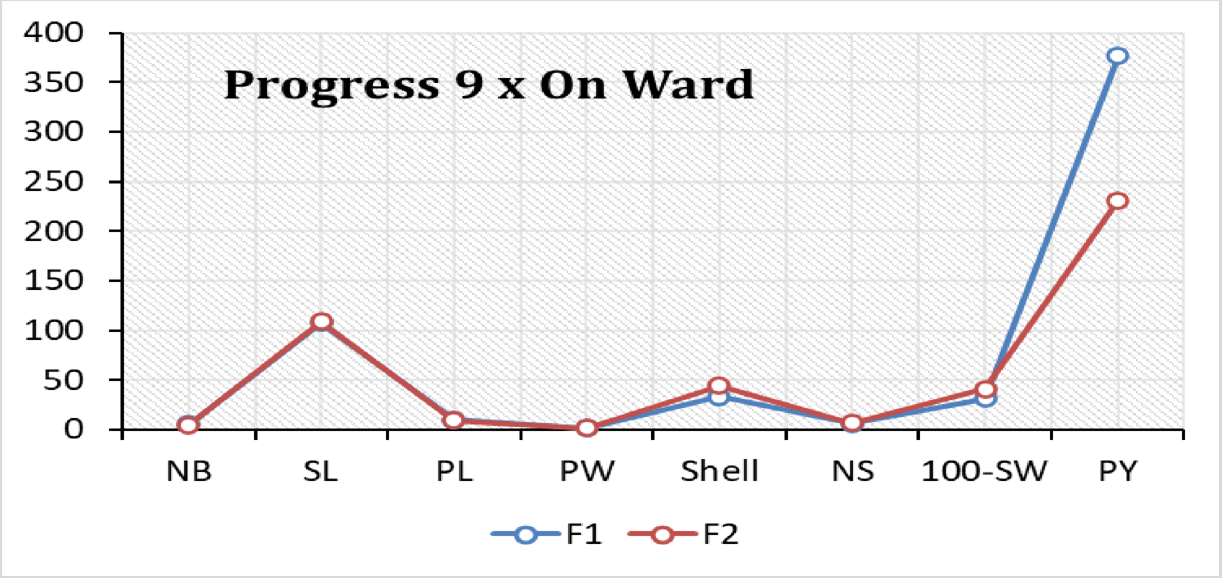


Fig. 3: Comparative traits between F_1 and F_2 of cross 1 (Up) and cross 2 (Down)

CONCLUSION

Each attribute that was focused on in this study has complex genetic behavior. It's possible that the early segregating generation's simplistic selection process didn't make a significant impact in improving these characteristics of pea. Later generations may successfully take advantage of the complicated genetic behavior, especially the dominance and additive components. Therefore, it is recommended that the later generation of the segregated population in peas could be the target of selection for the enhancement of any of these characteristics, especially seed yield. It is advised to use the bulk method of selection, which selects after achieving homozygosity for the greatest number of heterozygous loci. In the early segregating generation (F_2), biparental hybridization among recombinants would result in superior genetic combinations that might accumulate favorable genes for a high yield potential in a single line.

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الملخص العربي

دراسة السلوك الوراثي لتحسين بعض الصفات الكمية في البسلة تحت ظروف سوهاج

هاله صدقي عبداللاه موسى

معهد بحوث البساتين - مركز البحوث الزراعية - الجيزة - مصر

أجري هذا البحث بمحطة البحوث الزراعية بشندويل خلال ثلاثة مواسم شتوية (2022/2021 و 2023/2022 و 2024/2023) لتقدير طبيعة وتأثير الفعل الجيني للمحصول ومكوناته في هجينين من البسلة وهما (بوجي × بالمورال) و (بروجرس × اون ورد) عن طريق تحليل متوسط الأجيال واختبار مربع كاي. باستخدام موديل الست عشائر (P_1 و P_2 و F_1 و F_2 و BC_1 و BC_2) وقد كشف اختبار Scaling و Joint scaling وجود نوع واحد أو أكثر من التفاعلات الغير أليلية لجميع الصفات باستثناء نسبة التصافي في الهجين (بوجي × بالمورال). أما بالنسبة لباقي الصفات فقد أكدت معنوية أحد أو كل اختبارات A Scaling أو B أو C بالاضافة الي قيم مربع كاي المعنوية وجود تفاعلات غير أليلية (أي التفوق) في توريث هذه الصفات. كما لوحظ وجود تفاعل التفوق المضاعف Duplicate في جميع الصفات محل الدراسة في كلا الهجينين باستثناء عدد الفروع وعرض القرن ووزن 100 بذرة في الهجين الأول، وكذلك نسبة التصافي في الهجين الثاني حيث وجد تفاعل التفوق التكاملي Complementary. وكان تأثير السيادة أكثر وضوحًا من التأثير الإضافي للجينات لمعظم الصفات محل الدراسة. لذلك يُنصح بانتخاب الصفات التي يتحكم بها الفعل الإضافي في الجيل الانعزالي المبكر، بينما يُؤجل الانتخاب للصفات التي يتحكم بها الفعل السيادي إلى الأجيال المتأخرة. كما أشارت نتائج الدراسة إلى ضرورة إجراء الانتخاب المتكرر المتبادل للحصول على محصول عالي من البسلة

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