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Six Generations Mean Analysis Using Scaling and Joint Scaling Tests in Faba Bean (*Vicia faba* L.)

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ESTIMATE of the genetic parameters, gene effects through generation mean analysis in two faba bean crosses were carried out at the Fac. Agric. Experimental Farm, Minia University, Egypt during three successive seasons 2015/18. Heritability values in broad sense were higher than heritability in narrow sense for all traits in both crosses. Heterosis over better parent, mid parents and inbreeding depression were positive for all traits in the two crosses. Degree of dominance was higher than one for all traits in both crosses. The significant positive additive gene effect for days to 50% flowering DF and plant height PH in cross I and biological yield BY/P and 100 seed weight 100 SW in cross II, indicates effective selection for these traits. Values of dominance effects were greater the additive effects for all traits. Complementary epistasis type for traits like PH and no. seeds/plant NS/P in cross I and DF, PH and 100SW in cross II indicates that the two selected parents for crossing are different. For this reason, it is possible to achieve genetic advance in breeding program of these traits. Duplicate epistasis type was predominant than complementaryepistasis type in different traits in the two crosses. Hence, recurrent selection could be improved of these traits in advanced generations.

Keywords: heritability, heterosis, inbreeding, dominance,complementary,duplicate,epistasis.

Introduction

Faba bean (*Vicia faba* L.) is animportant legume crop in Egypt and the world.It is grown in Egypt as pulse seeds crop. It'sseed has high protein content with range from 20 to 40%, starch, cellulose and minerals. So it is used as food crop for human as well as fodder crop for animals. Besides the high protein content in faba bean seeds, it is an efficient crop in fixation of atmospheric nitrogen and improves soil fertility through biological N_2-fixation (Haridy and El-Said, 2016). Maximizing production of faba bean become necessary to fill the gap between consumption and production to meet demands of Egyptian people. This could be achieved by increasing productivity through developing new high yielding varieties and improving cultural practices (Yamani, 2012).

Knowledge about the mode of inheritance and nature of gene action is very importantto determine the efficient breeding procedure for achieve maximum genetic improvement to develop high yielding varieties in faba bean (Beyene, 2015). Determination of the gene effects controlling complex quantitative traits is very important. Various biometrical techniques are used for knowledge of the inheritance of quantitative traits which can predict the performance of the genetic material before startingselection. Moreover, joint scaling test is better than otherscaling tests as it provides estimates of geneticparameters along with the adequacy of the model if the number of generations is more than the number ofestimated genetic parameters. Generation mean analysis (Mather and Jinks, 1982) provides information on the relative importance of averageeffects of the genes (additive effects), dominance deviations and effects due to nonallelic genetic interactions or epistatic geneeffects (additive x additive, dominance x dominance and additive x dominance) in determining genotypic values of the individuals and consequently, mean genotypic values of families and generations. Bishnoi et al. (2018) concluded that the traits showing

preponderance of fixable component of variance should be more responsive to selection than the traits with non-fixable component of variance. Based on that, the suitable breeding method to improve faba bean has been reported. The present study was carried out to estimate the genetic parameters, main and interaction gene effects in two faba bean crosses through generation mean analysis method.

Materials and methods

The present study was carried out at the Fac. Agric. ExperimentalFarm, Minia University, Egypt during three successive winter growing seasons 2015/18. The experimental materials were six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) derived from two crosses: Cross I: Giza 40 (P_1) x Sakha 1 (P_2) and Cross II: Rena Mora (P_1) x Giza 40 (P_2). The origin and pedigree of the three of faba bean varieties are presented in Table 1.

TABLE 1. Origin and pedigree of the three parental varieties of the two crosses

Variety	Pedigree
Giza 40	Selected fromanearly variety Rebaya 40
Sakha 1	Giza 716 x 620/283/85
RenaMora	Introduced from Spain

In 1st season, 2015/16, the parents are crossed to produce the F_1 hybrids seed.In 2ndseason 2016/17, The plants of F_1 hybrids were selfed to produce F_2 seeds. In addition to F_1 plants used as female parent for backcrossed to their parents (P_1 and P_2) to produce first backcross (BC_1) and second backcross (BC_2). In 3rd season 2017/18, 20, 20, 20, 120, 80 and 80 plants from P_1, P_2, F_1, F_2, BC_1 and BC_2, respectively grown in a randomized complete blocks design with three replications. The replicate consisted of 2, 2, 2, 12, 8 and 8 ridges for each entry. Ridge length of 2 meters length, 60 cm apart and 20 cm between plants within ridge on one side. The following nine studied traits were recorded on plants: Days to 50% flowering (DF), Plant heightin cm (PH), Biological yield / plant in g(BY/P), Seed yield / plant in g (SY/P), Harvest index (HI) =[(GY/P)/(BY/P)]x100, Number on branches / plant (NB/P), Number of pods / plant (NP/P), Number of seeds / plant (NS/P) and 100 seed weight in g (100 SW).Analyses of variance were performed on the different studied traits using the two way analysis of variance as outlined by Steel and Torrie (1980).Mather (1949) found that scaling test may be estimated individually or

jointly according to Cavalli (1952) joint scaling test. Scaling test: Four scaling test A, B, C and D performed to predict that the studied traits were genetically controlled by only additive and dominance effects assuming absence of gene interaction (epistasis). For confirmation of adequacy of additive dominance model, and to realize presence of higher order interallelic interactions, joint scaling test as suggested by Cavalli (1952) was also applied. Significance of deviationof the four scales from zero was estimated by "t" test. When any scale from the four was found significantly deviated from zero, the additive – dominance model considered inadequate. In this case, six parameters (m, d, h, i, j and l) model as suggested by Hayman (1958) was applied to estimate main gene effects additive (d) and dominance (h) and epistatic components *i.e.,* additive x additive (i), additive x dominance (j) and dominance x dominance (l). The complementary epistasis type was found in case of (h) and (l) effects had the same sign,while duplicate epistasisexists in case of opposite signs of the two effects (Kearsey and Pooni, 1996).

Generation mean analysis was performed according to the method of Maher and Jinks (1982) in which mean of the trait (Y) determined as follows: $Y = m + \alpha [d] + \beta [h] + \alpha^2 [i] + 2 \alpha \beta [j] + \beta^2 [l]$ where; Y is the mean of one generation, m is the mean of all generations, d is the sum of additive effects, h is the sum of dominance effects, i is the sum of additive x additive interactions (complementary), l is the sum of dominance x dominance interaction (duplicate) and j is sum of additive x dominance interaction and α, β, α^2, $2\alpha\beta$ and β^2 are coefficients of genetic parameters. The genetic parameters m, d, h, i, j and l were tested for significance using t-test. The adequacy of the additive – dominance model was estimated by chi square test. Heterosis and inbreeding depression were calculated according to Singh and Chaudhary(1977) as follows: Heterosis from mid parents $Hm\% = [(\overline{F1}) - mp)] / (\overline{F1}) x100$, Variance of heterosis deviation=vF_1+1/4vP_1+1/4vP_2,Heterosis from better parent $Hbp\% = [(\overline{F1}) - (\overline{bp})] / (\overline{F1}) x100$, Variance of heterosis deviation = $vF_1 + v bp$

Inbreedingdepression $ID\% = [(\overline{F1}) - (\overline{F2})] / (\overline{F1}) x100$,Variance of inbreeding depression = $vF_1 + vF_2$

Significance of heterosis estimated by 't' test: t = deviation/√Variance of deviation.

Degree of dominance h/d was calculated according to Smith 1(952).

Heritability in broad sense (Hb) and in narrow sense (Hn) were calculated as follows: $Hb = [vF_2 - (vP_1 + vP_2 + vF_1)/3]/vF_2$, $Hn = [2vF_2 - (vBC_1 + vBC_2)]/vF_2$

Genetic advance Ga estimated with 5% selection intensity of i=2.063 for all traits where $Ga = i*Hb*\sqrt{v}$ F_2 (Johnson et al., 1955) where, v = variance

The components of variation in six populations were determined by F_2 variance according to Mather and Jinks 1982 as follows:

Environmental within family variance $Ew = (vP_1 + vP_2 + 2vF_1)/4$

Additive genetic variance $D = 4vF_2 - 2(vBC_1 + vBC_2)$

Dominance variance $H = 4(vBC_1 + vBC_2 - vF_2 - vEw)$

F correlation between D and H over all loci = $vBC_1 - vBC_2$

Results and Discussion

Mean squares of the studied traits of six populations (Table 2) revealed significant differences (p≤0.01) for all traits in the two crosses except for days to 50% flowering in first cross was significant difference (p≤0.05). This refers topresence genetic variation and possibility of selection for the different studied traits. Similar results were reported by Haridy and El-Said (2016) and Abd El-Zaher (2016).

Where DF, PH, BY/P, SY/P, HI, NB/P, NP/P NS/P and 100 SW denote; days to 50% flowering, plant height, biological yield/plant, seed yield/plant, harvest index, number of branches/plant, number of pods/plant,number of seeds/plant and 100 seed weight.*, ** significant at 0.05 and 0.01 level of probability, respectively.

Mean of the studied traits of six populations in the two crosses are presented in Table 3. Mean P_1 was higher than P_2 for days to 50% flowering and plant height in both crosses. By contrast, mean P_2 was surpassedP_1 for no. of pods/plant and no. of seeds/plant in the two crosses. Mean P_2 was higher than $P_1$for biological yield/plant, seed yield/plant, harvest index, number of branches/plant and 100 seed weight in cross I, also the contrast was found for the same traits in cross II.In addition, the mean of P_2 for no. of pods and seeds / plant higher than P_1 in both crosses. Mean F_1 hybrids was higher than the better parent for all the studied traits in both crosses, indicating presence of heterotic effects for all traits.BC_1 surpassed the best parent for DF and PH in the two crosses. Abd El-Zaher (2016) observed that F_1 mean surpassed the high parent in the two crosses for all the studied traits, indicating over dominance. Abo Mostafa*et al.* (2014) found that some crosses had trueheterosisabove mid-parents and better parent for seed yield, indicating to high role of non-additive gene action. Farshadfar*etal.* (2008) stated high heterosis in F_1 hybrid for seed yield, biological yield, harvest index, pods/plant and seeds/plant.

TABLE 2. Mean squares of the studied traits in cross I (Giza 40 x Sakha 1) and cross II (Rena Mora x Giza 40)

Cross	Cross I			Cross II		
S.V.	Rep	Populations	Error	Rep	Populations	Error
d.f.	2	5	10	2	5	10
DF	6.09	18.24*	3.94	0.09	13.47**	0.72
PH	16.51	203.91**	3.58	0.14	219.43**	1.87
BY/P	0.45	283.87**	1.88	8.72	243.96**	6.11
SY/P	3.95	148.30**	1.29	1.8	100.83**	5.15
HI	11.51	87.55**	3.97	7.45	39.59**	5.48
NB/P	0	1.74**	0.02	0.12	1.39**	0.03
NP/P	1.2	63.23**	1.38	0.32	60.45**	0.34
NS/P	0.34	148.97**	4.18	0.1	580.17**	1.06
100SW	2.98	41.39**	2.29	1.75	213.50**	0.7

Where DF, PH, BY/P, SY/P, HI, NB/P, NP/P NS/P and 100 SW denote; days to 50% flowering, plant height, biological yield/plant, seed yield/plant, harvest index, number of branches/plant, number of pods/plant,number of seeds/plant and 100 seed weight.*, ** significant at 0.05 and 0.01 level of probability, respectively.

TABLE 3. Mean and standard error of the studied traits of six generations in the two crosses

Trait	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
DF	Cross I	51.77±0.68	50.55±0.46	51.98±0.36	55.74±0.57	56.73±0.71	54.45±0.52
	Cross II	53.64±0.55	50.94±0.39	55.06±0.41	56.63±0.54	56.45±0.42	53.90±0.59
PH	Cross I	91.00±1.56	89.30±1.66	104.85±1.60	85.06±1.08	95.49±1.24	81.51±1.31
cm	Cross II	92.24±0.47	84.58±0.61	110.05±0.79	90.60±0.94	92.66±1.09	92.11±0.59
BY/P g	Cross I	58.09±1.01	78.18±0.88	88.07±1.10	51.91±0.63	57.31±0.66	78.42±0.68
	Cross II	93.44±0.68	85.66±0.82	107.23±1.24	81.50±1.51	94.55±1.07	89.28±1.70
SY/P g	Cross I	20.82±0.65	30.03±0.99	37.74±0.87	18.59±0.65	28.49±0.80	30.87±0.76
	Cross II	32.45±1.06	28.24±0.88	40.70±1.26	23.55±0.94	30.59±0.94	30.52±0.89
HI	Cross I	36.07±1.25	39.24±1.23	43.74±1.02	36.57±1.37	40.00±1.13	50.65±1.70
	Cross II	34.48±1.17	32.99±1.08	38.27±1.18	27.22±0.85	33.05±1.10	32.71±1.05
NB/P	Cross I	2.42±0.19	2.53±0.16	4.46±0.19	3.54±0.12	3.52±0.14	3.59±0.12
	Cross II	4.01±0.24	3.36±0.21	5.32±0.16	4.60±0.20	4.80±0.21	4.66±0.17
NP/P	Cross I	18.04±0.61	18.86±0.71	27.55±0.72	14.65±0.50	23.08±0.55	23.16±0.47
	Cross II	22.58±0.51	27.47±0.62	29.24±0.52	16.50±0.57	25.00±0.72	25.0±0.47
NS/P	Cross I	28.62±0.88	34.71±0.85	44.23±1.26	23.61±0.76	28.92±0.87	31.86±0.91
	Cross II	42.44±0.29	45.56±0.56	71.32±0.76	30.60±1.12	53.18±1.11	56.50±1.03
100SW g	Cross I	63.76±0.86	68.94±0.63	70.80±0.94	60.62±0.75	64.04±0.97	65.34±0.79
	Cross II	80.50±0.81	70.70±0.73	84.35±0.93	61.95±1.08	71.51±1.01	66.76±0.91

Genetic parameters and variation components of the studied traits in cross I and II are presented in Tables 4 and 5. Heritability values in broad sense (Hb) were higher than heritability in narrow sense (Hn) for all the studied traits in both crosses, indicating effective progress from selection for the studied traits. The high difference between Hb and Hn estimates for DF, PH, SY/P, HI, NS/P and 100SW in cross I, for HI and NP/P in cross II reflects the dominance effect in the genetic structure of these traits, which is in agreement with degree of dominance √H/D higher than unity and dominance variance (H) was higher than additive variance (D) for these traits. Therefore, narrow difference between Hb and Hn values for the rest studied traits in two crosses reflects the additive effect in the genetic structure of them, which is in agreement with degree of dominance √H/D lower than one and additive variance was higher than dominance variance for these traits (Table 4 and 5). Kumar et al. (2017) found that high heritability estimates indicated an additive gene action for the traits, and hence, possible trait improvement can be obtained through selection. Especially traits like seed yield, 100-seed weight, pods / plant, branches / plant and days to flowering should be given in consideration while performing selection for seed yield in segregating generations of faba bean.

Low heritability in narrow sense (<20%) was recorded for PH, SY/P, NS/P and 100SW in

cross I and for HI in cross II refer to major role of the environmental effects in the total phenotypic variation of these traits. Obiadalla et al. (2013) stated narrow sense heritability was 34.2 and 14.8% for earliness trait and ranged from 15.2 to 29.8% for branches / plant and plant height, respectively. Respecting to yield components, the estimates of narrow sense heritability ranged from 8.8 to 70.9% for pods/ plant and weight of 100 seed (g).

Moderate Hn (20-50%) was observed for DF, BY/P and NB/P in cross I, and NP/P in cross II. The rest studied traits showed high Hn values (>50%) in both crosses. Moderate genetic gain (14-40%) was found for PH in the two crosses, for HI (27.24%) in cross I and for BY/P (31.87), SY/P (16.53), NS/P (24.32) and 100SW (21.91%) in cross II. This indicated effective direct selection for these traits. While, the other traits showed low genetic gain less than 14%, indicating importance indirect selection for them. Abo Mostafa et al. (2009), Obiadalla et al. (2013), Akhshi et al. (2014), Kumar et al. (2017) and Mansour (2017) found that heritability values in broad-sense were higher than heritability values in narrow-sense for all traits, where the differences between broad and narrow-sense heritability were closest. The indirect selection would be fruitful due to the high values of narrow-sense heritability and the predicted genetic advance in these cases. Abd El-Zaher (2016) found that high

genetic gain was associatedwith rather high and moderate heritability estimate for most studied traits.Therefore selection for these traits in the two crosses under investigation shouldbe effective and satisfactory. Abdel Aziz and Mohamed (2015) found that the medium heritability and low genetic advance reported on the seed yield indicated that selection is ineffective in improving the seed yield.

Values of heterosis and inbreeding depression together refer to role of gene action in behavior of different quantitative characters. Heterosis based on better parent (Hbp), mid parents (Hmp) were significant positive for all the studied traits in the two crosses exceptfor DF and H bp for 100 seed weight in cross I was insignificant positive. Inbreeding depression (ID) was highly significant positive for all traits except for days to flowering were negative in both crosses (Tables 4 and 5) (Fig. 1 and 2). Positive sign for ID refer to value of F_2 progenies reduced compared to F_1 generation and vice versa. Obiadalla *et al.* (2013), Abdalla *et al.* (2015) and Haridy and El-Said (2016) observed high positive values of heterosis over mid parents, better parent and inbreeding depression for plant height, no. of branches/plant, no. of pods/plant and 100 seed weight.Inbreeding effects in F_2 (depression or gain) was significant for DF, PH, NB/P, NP/P, SY/P,100SWand seeds/plant. The seed yield components showed F_2 to be higher than F_1 due to remaining heterosis and transgressive segregation.

Degree of dominance (h/d) was higher than one for all the studied traits in both crosses, indicating over dominance effects in inheritance of traits. Abo Mostafa et al. (2009) found that

potence ratios were exceeded unity for most traits indicating over dominance effect. On the other hand, thevalues of this parameter were less than one for no. ofbranches/plant, seed yield/plant, and 100 seed weight, indicating partial dominance effect in control in the inheritance of these traits.The inbreeding depression estimates were positively significant (p≤0.01) for pods/plant, seeds/plant and seed yield/ plant.

Values of each of environmental variance within families Ew, additive D and dominance H component in the two crosses are presented in Tables 4 and 5. Correlation between D and H over all loci (F) indicated that dominance genes were in low performance parent for PH, BY/P, HI and NS/P in cross I and for DF, BY/P, HI and 100SW in cross II where negative F value for these traits were found. The ratio F/√HxD refers to magnitude and sign of dominance for all genes controlling the character. If this ratio equal or near the unity, indicating equal of importance and sign of dominance genes controlling the trait, hence ratio of √H/D is a good indicator of dominance. If this ratio F/√HxD was equal or near to zero, indicating not equalof importance and sign of dominance genes controlling the trait, hence ratio of √H/D is an indicator of average dominance. Therefore, based on mentioned before the ratio √H/D for all the studied traits in both crosses showed average dominance, where F/√HxD were equal or near to zero for all traits. Except for plant height in cross II in which F/√HxDnear one (0.99), hence ratio of √H/D is a good indicator of dominance. Similar results were obtained by Farshadfar et al. (2008) and Said (2014).

TABLE 4. Genetic parameters and variation components for the studied traits in cross I (Giza 40 x Sakha 1)

Trait	DF	PH	BY/P	SY/P	HI	NB/P	NP/P	NS/P	100-SW
Hb	86.13	62.88	57.86	71.78	87.83	62.31	68.55	69.97	80.06
Hn	39.52	13.82	49.59	9.16	52.79	47.16	55.99	14.78	13.97
GA	11.01	15.32	8.24	10.59	27.24	1.71	7.67	11.97	13.56
H mp	1.6	16.31**	29.25**	48.44**	16.16**	80.20**	49.32**	39.68**	6.71**
H bp	0.41	15.22**	51.60**	25.67**	11.47**	76.28**	46.08**	27.43**	2.7
ID	-7.23**	18.87**	41.06**	50.74**	16.39**	20.63**	46.82**	46.62**	14.38**
h/d	1.34	17.29	1.98	2.67	3.84	36.09	22.2	4.13	1.72
E_w	4.63	51.74	21.7	14.63	25.88	0.69	9.52	23.46	14.45
D	30.36	38.58	47.32	9.38	238.68	1.66	32.98	20.34	18.82
H	74.41	274.17	11.54	127.49	323.39	0.97	13.77	140.73	174.03
F	17.98	-14.43	-2.9	5.21	-127.76	0.43	6.67	-5.31	24.23
F/√HxD	0.39	-0.14	-0.12	0.15	-0.46	0.34	0.31	-0.1	0.42
√H/D	1.57	2.67	0.49	3.69	1.16	0.76	0.65	2.63	3.04

Where DF, PH, BY/P, SY/P, HI, NB/P, NP/P NS/P and 100 SW denote; days to 50% flowering, plant height, biological yield/plant, seed yield/plant, harvest index, number of branches/plant, number of pods/plant, number of seeds/plant and 100 seed weight. Hb, Hn, GA, Hmp, H bp, ID, h/d, Ew, D, H and F denote; heritability in broad, narrow sense, genetic advance, heterosis over mid parents, better parent, inbreeding depression, degree of dominance, environmental, additive, dominance variance and correlation between D and H overall luci, respectively.

TABLE 5. Genetic parameters and variation components for the studied traits in cross II (Renamora x Giza 40)

Trait	DF	PH	BY/P	SY/P	HI	NB/P	NP/P	NS/P	100-SW
Hb	88.12	92.41	93.47	77.96	69.46	82.9	84.76	95.68	90.14
Hn	77.66	85.57	82.3	73.14	12.87	81.44	49.32	79.51	63.63
GA	10.69	19.69	31.87	16.53	13.27	3.83	10.94	24.32	21.91
H mp	5.30**	24.48**	19.74**	34.12**	13.44**	44.37**	16.84**	62.09**	11.57**
H bp	2.65*	19.31**	14.76**	25.42**	10.99*	32.67**	6.44*	68.05**	4.78**
ID	-2.71*	17.67**	24.00**	42.14**	28.87**	13.53**	43.57**	57.09**	26.56**
h/d	2.05	5.65	4.54	4.92	6.09	5.03	1.72	17.51	1.79
E_w	3.91	9.2	21.13	25.43	26.63	0.78	5.71	7.81	14.62
D	53.74	182.62	449.68	154.48	22.06	8.16	38.64	241.32	176.7
H	15.28	24.79	108.87	11.77	192.16	0.61	56.56	93.11	143.54
F	-13.53	66.49	-138.34	6.7	-15.85	1.18	23.76	13.3	-26.89
F/√HxD	-0.47	0.99	-0.63	0.16	-0.24	0.53	0.51	0.09	-0.17
√H/D	0.53	0.37	0.49	0.28	2.95	0.27	1.21	0.62	0.90
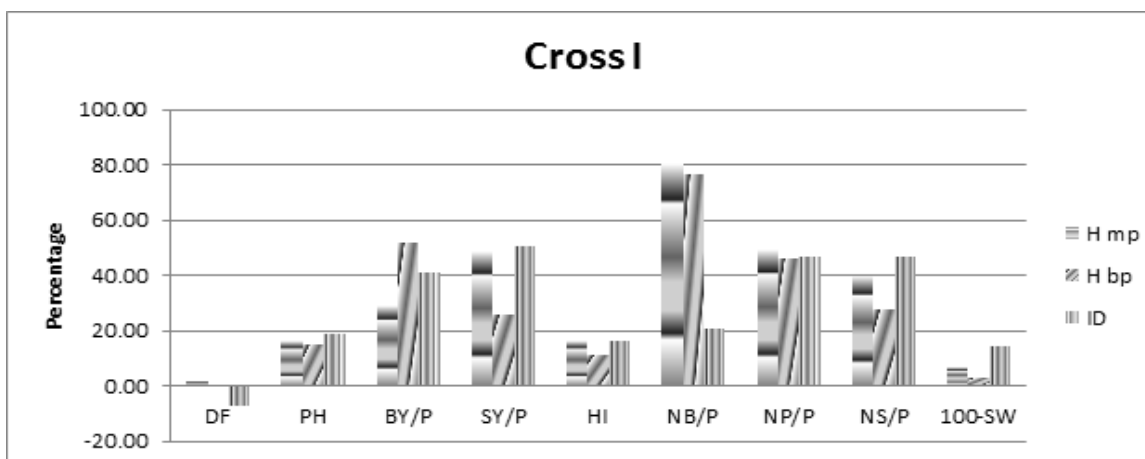
Fig. 1. Percentage of heterosis based on mid parent (Hmp), better parent (Hbp) and inbreeding depression (ID) forthe studied traits in cross I (Giza 40 x Sakha 1)
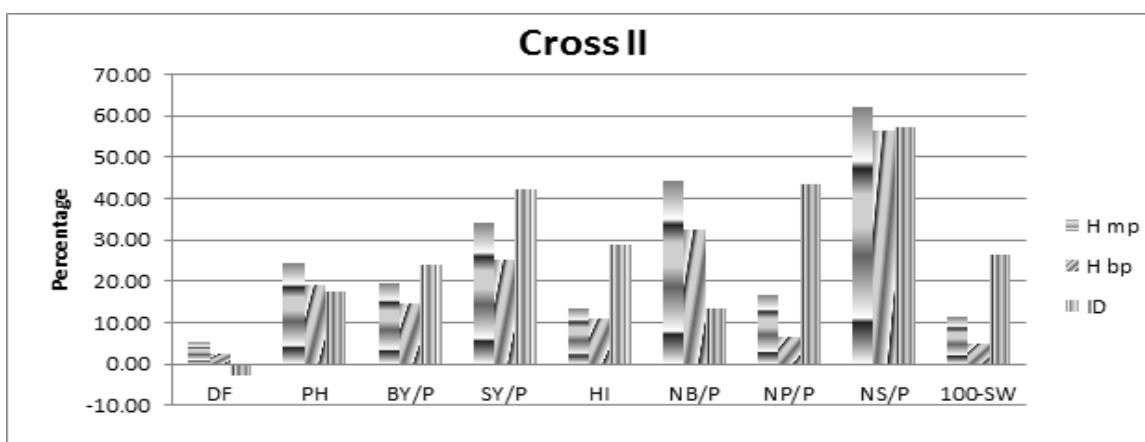
Fig. 2. Percentage of heterosis based on mid parent (Hmp), better parent (Hbp) and inbreeding depression (ID) for the studied traits in cross II (Renamora x Giza 40)

Generation mean analysis

The four individual scaling test A, B, C and D and χ² values of joint scaling test of all traits in the two crosses are shown in Table 6. The results of simple scaling revealed significant values of two or more of A, B, C and D scales and χ² values of joint scaling test for all the studied traits in both crosses except for number of branches per plant in the two crosses, indicating inadequacy of additive dominance model and presence of nonallelic gene interaction in inheritance of all traitsexcept NB/P. Therefore data was subjected to further analysis to estimate types of inter-allelic gene interaction (epistases) including additive x additive (i), additive x dominance (j) and dominance x dominance (l) in addition to the main effects.Non-significant values of individual scales and χ² were observed in number of branches per plant in two crosses, therefore additive–dominance model was adequacy in inheritance it and only main effects mean (m), additive (d) and dominance (h) were estimated. NB/P in both crosses might be used to develop pure lines in breeding programmes because the adequacy of the additive-dominance model.These results were in agreement with those reported by Kacharabhai (2015), Haridy and El-Said (2016)and Latha et al. (2018).Akhshi et al. (2014) generation

mean analysis with three-parameter genetic model showed inadequacy of additive-dominance simple model to illustrate the genetic mechanism of the evaluated traits. Significant differences for two or more individual scaling tests (A, B, C, and D) in both crosses were recorded.

Estimates of main and interaction gene effects of the studied traits in the two crosses are presented in Table 7. The mean effects (m) of all the studied traits were highly significant in both crosses, indicated that all the studied traits were quantitativelyinherited.The significant positive sign of additive gene effect refer to predominant additive effect for DF and PH in cross I and PH, BY/P and 100 SW in cross II, indicating simple selection for these traits could be effective. Similar results were revealed by Bishnoiet al. (2018). The significant negative sign of additive gene effect (d) for BY/P, SY/P, HI and NS/P in cross I and NS/P in cross II refer to these traits were not controlled by additive gene action in their inheritance.The rest traits showed not significant additive effect, indicating that early generation selection is not effective. While, dominance (h) effect was highly significant for all the studied traits in the two crosses except days to flowering,

TABLE 6. Scaling test and joint scaling test (χ²) for the studied traits in two crosses

Scales	A	B	C	D	χ²) ²d.f.)
Trait	Cross I (Giza 40 x Sakha 1)				
DF	9.71±13.08**	6.37±9.70**	16.68±25.27**	0.30±1.43	86.03**
PH	-4.87± 24.32	-31.13±25.59**	-49.76±50.43**	-6.88±2.81**	176.22**
BY/P	-31.54±13.51**	-9.40±13.75**	-104.77±29.94**	-31.91±1.56**	1023.61**
SY/P	-1.58±15.15	-6.03±14.63**	-51.97±30.13**	-22.18±1.71**	282.89**
HI	0.19±21.50	18.32±31.19**	-16.51±61.34*	-17.51±3.42**	37.48**
NB/P	0.16±2.77	0.19±2.41	0.29±5.69	-0.03±0.30	0.48
NP/P	0.57±10.77	-0.09±9.58	-33.4±23.02**	-16.94±1.23**	256.77**
NS/P	-15.01±17.08**	-15.22±17.66**	-57.35±35.47**	-13.56±1.97**	196.49**
100SW	-6.47±18.20**	-9.06±15.09**	-31.82±34.22**	-8.14±1.95**	81.21**
	Cross II (Renamora x Giza 40)				
DF	4.20±8.18**	1.80±10.86	11.82±24.00**	2.91±1.30*	37.45**
PH	-16.97±19.85**	-10.41±11.45**	-34.52±42.06**	-3.57±2.25	124.85**
BY/P	-11.57±20.16**	-14.33±31.05**	-67.56±67.21**	-20.83±3.62**	118.63**
SY/P	-11.97±18.32**	-7.90±17.38**	-47.89±43.07**	-14.01±2.28**	110.28**
HI	-6.65±21.00	-5.84±20.09*	-35.13±39.16**	-13.05±2.20**	71.03**
NB/P	0.27±3.99	0.64±3.31	0.39±9.18	-0.26±0.49	2.45
NP/P	-1.82±13.25**	-6.31±9.12**	-42.53±25.68**	-17.20±1.43**	295.53**
NS/P	-7.40±20.14**	-3.88±18.89	-108.24±49.82**	-48.48±2.71**	518.24**
100SW	-21.83±18.85**	-21.53±21.46**	-72.10±48.11**	-14.37±2.55**	296.03**

Where *, ** significant at 0.05 and 0.01 level of probability, respectively. DF, PH, BY/P, SY/P, HI, NB/P, NP/P NS/P and 100 SW denote; days to 50% flowering, plant height, biological yield/plant, seed yield/plant, harvest index, number of branches/plant, number of pods/plant, number of seeds/plant and 100 seed weight.

TABLE 7. Estimate of gene effects for the studied traits in the two faba bean crosses

Effect	Main effects			Interaction effects			Type of
	m	d	h	i	j	l	epistasis
Trait	Cross I (Giza 40 x Sakha 1)						
DF	55.74±0.57**	2.28±0.88*	0.22±2.92	-0.60±2.86	1.67±0.97	-15.48±4.32**	D
PH	85.06±1.08**	13.98±1.80**	28.46±5.96**	13.76±5.62**	13.13±2.13**	22.24±9.8**	C
BY/P	51.91±0.63**	-21.11±0.95**	83.76±3.41**	63.83±30.15**	-11.07±1.16**	-22.89±5.23**	D
SY/P	18.59±0.65**	-2.38±1.11*	56.68±3.58**	44.36±3.42**	2.23±1.25	-36.75±5.55**	D
HI	36.57±1.37**	-10.65±2.04**	41.11±6.97**	35.02±6.84**	-9.07±2.22**	-53.53±10.20**	D
NB/P	3.54±0.12**	-0.07±0.18	2.04±0.65**	-	-	-	-
NP/P	14.65±0.50**	-0.08±0.73	42.98±2.60**	33.88±2.46**	0.33±0.87	-34.36±3.92**	D
NS/P	23.61±0.76**	-2.94±1.26*	39.685±4.19**	27.12±3.94**	0.11±1.40	3.11±6.52	C
100SW	60.62±0.75**	-1.30±125	20.73±4.05**	16.28±3.91**	1.29±1.36	-0.74±6.22	D
	Cross II (Renamora x Giza 40)						
DF	56.63±0.54**	2.55±0.73**	-3.05±2.65	-5.82±2.59*	1.20±0.80	-0.18±3.77	C
PH	90.60±0.94**	0.55±1.24	28.78±4.59**	7.14±4.51	-3.28±1.29*	20.4±6.46**	C
BY/P	81.50±1.51**	5.27±2.00*	59.34±7.37**	41.66±7.25**	1.38±2.07	-15.76±10.42	D
SY/P	23.550.94**	0.07±1.29	38.38±4.78**	28.02±4.56**	-2.04±1.47	-8.15±7.01	D
HI	27.22±0.85**	2.07±1.42	30.65±4.63**	26.10±4.41**	1.33±1.62	-17.07±7.19*	D
NB/P	4.60±0.20**	0.14±0.27	2.16±1.01*	-	-	-	-
NP/P	16.50±0.57**	-0.20±0.86	38.62±2.93**	34.40±2.86**	2.25±0.95*	-26.27±4.32**	D
NS/P	30.60±1.12**	-3.32±1.51*	124.28±5.48**	96.96±5.42**	-1.76±1.54	-85.68±7.72**	D
100SW	61.95±1.08**	4.75±1.36**	37.49±5.20**	28.74±5.09**	-0.15±1.47	14.62±7.26*	C

Where *, ** significant at 0.05 and 0.01 level of probability, respectively. DF, PH, BY/P, SY/P, HI, NB/P, NP/P NS/P and 100 SW denote; days to 50% flowering, plant height, biological yield/plant, seed yield/plant, harvest index, number of branches/plant, number of pods/plant, number of seeds/plant and 100 seed weight. m, d, h, i, j and l denote; mean, additive effect, dominance effect, additive x additive, additive x dominance and dominance x dominance, respectively. D and C denote; duplicate epistasis and complementary epistasis.

indicating importance of dominance gene effects. Results of Abd El-Zaher (2016) agreed with these results. Values of dominance effect were greater the additive effect for all traits. The significant positive value of dominance gene effect (h) was more prevailed than additive gene effect (d) for PH, BY/P, SY/P, HI and NS/P in cross I and NS/P and 100SW in both crosses. This indicated that selection by pedigree or bulk or single seed descent methods should be delayed to later generations to reduce heterozygosity in the population.Similar results were reported by Abdel-Hafez eta.l (2016) and Abd El-Moghny (2016).

The similar significant sign of d and h for PH in cross I and BY/P and100SW in cross II indicatedprevailed role of additive and dominant effects for the inheritance of these traits. Therefore, it's possible use of Bi-parental mating or reciprocal recurrent selectionto improve these traits as stated by Latah et al. (2018).However, all genetic components were highly significant for plant height, biological yield/plant and harvest index in cross I.Obiadalla et al. (2013) indicated that additive genetic variance were positive and lower than those of non additive one for all the studied traits, indicating that non additive gene action played a major role in the inheritance of different traits under study. Bishnoiet al. (2018) observed dominance effect for days to 50% flowering (DF) and seed yield/plant (SY/P). By joint scaling test, additive effects was observed for DF, PH, NP/P and SY/P and of dominance and dominance x dominance interaction effect with respect to NB/P and 100SW. Duplicate epistasis was present in PH and 100 SW, DF, NP/P and SY/P and NB/P. Akhshi et al. (2014) suggested that both dominance and epistasis effects were important for most of the evaluated traits. Furthermore, expression of some traits in both crosses was affected by additive gene effects.

Respect to non-allelic interaction (epistases), significant additive x additive (i) effect was found for BY/P, SY/P, HI, NP/P, NS/P and 100SW in both crosses, in addition to PH in cross I and

DF in cross II.Additive x dominance effect (j) was significant for PH, BY/P and HI in cross I and for PH and NP/P in cross II. This means that these traits are not fixable by selection. Significant dominance x dominance effect (l) was observed for DF, PH, BY/P, SY/P, HI, NP/P in cross I, for PH, HI, NP/P, NS/P and 100SW in cross II. Significant effects for both of additive x dominance (j) and dominance x dominance (l) were observed for PH, BY/P and HI in cross I and forNP/P in cross II, this supporting presence of duplicate type of epitasis.Abo Mostafa*et al* (2009) found that highly significant positive of additive x dominance was observedfor no. of pods/plant.Type of epistasis was determined based sign effect of dominance (h) and dominance x dominance (l). Complementary epistatic type if h and l had same signs and duplicate type if they had opposite sings Kearsey and Pooni(1996) and Bishnoi et al. (2018). According to these reference, duplicate epistasis was found for DF, BY/P, SY/P, HI, NP/P and 100SW in cross I and for BY/P, SY/P, HI, NP/P and NS/P in cross II, where opposite signs for h and l. Complementary epistasis type for traits like PH and NS/P in cross I and DF, PH and 100SW in cross II indicates that the two selected parents for crossing are different. For this reason, it is possible to achieve genetic advance in breeding programme of these traits. Duplicate epistasis type was predominant than complementaryepistasis type in different traits in the two crosses. Hence, recurrent selection could be suggested for these traits as revealed by Samad*et al.* (2016).The additive x additive interaction (i) and duplicateepistasis types were found for BY/P, SY/P, HI and NB/P in both crosses in addition to 100SW in cross I and NS/P in cross II, indicating possible of obtainingtransgressivesegregants fromtheir two parents in later generations.

Conclusion

Heterosis based on better parent, mid parents were significant positive for most studied traits. NB/P in both crosses might be used to develop pure lines in breeding programmes because the adequacy of the additive-dominance model. Additive effect was predominant for DF and PH in cross I and PH, BY/P and 100SW in cross II, indicating effective simple selection for these traits.Additive and dominant effects play an important role in inheritance of PH in cross I and BY/P and 100SW in cross II. Therefore, it's possible use of Bi-parental mating or reciprocal recurrent selection to improve these traits.

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تحليل متوسط الاجيال الستة باستخدام اختبارات المقياس والمقياس المشترك فى الفول البلدى

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اجرى تقدير المقاييس الوراثية وتأثيرات الجين بطريقة تحليل متوسط الاجيال فى هجينين من الفول البلدى فى المزرعة التعليمية - كلية الزراعة - جامعة المنيا – مصر خلال ثلاث مواسم زراعية متتالية فى الفترة ٢٠١٥/١٨. وكانت قيم درجة التوريث بالمعنى الواسع أكبر من درجة التوريث بالمعنى الضيق لكل الصفات فى كلا الهجينين. كما قدرت قيم موجبة لقوة الهجين على اساس افضل الاباء ومتوسط الاباء وكذلك التدهور الناتج عن التربية الداخليةلكل الصفات فى الهجينين. كما كانت قيمة درجة السيادة اكبر من واحد لكل الصفات فى الهجينين. ووجدت قيم موجبة معنوية للتأثير الاضافى للجين لصفات عدد ايام تزهير ٥٠٪ وطول النبات فى الهجين الاول والمحصول البيولوجى/نبات ووزن ١٠٠ بذرة فى الهجين الثانى ما يدل على فعالية الانتخاب لهذه الصفات. وكانت قيم تأثيرات السيادة اعلى من تأثيرات الاضافة لكل الصفات. ووجد تأثير تفوقى مكمل لصفات طول النبات وعدد البذور/نبات فى الهجين الاول وعدد ايام تزهير٥٠٪ وطول النبات ووزن ١٠٠بذرة فى الهجين الثانى ما يدل على ان الاباء المنتخبة للتهجين كانت مختلفة وراثيا عن بعضها ولذلك فيمكن ان يتحقق تقدم وراثى فى برنامج التربية لهذه الصفات. وقد تغلب التفاعل التفوقى المتضاعف على التفاعل التفوقى المكمل فى الصفات المختلفة فى الهجينين وبالتالى يمكن استخدام الانتخاب الدورى العكسى لتحسين هذه الصفاتفى الاجيال المتقدمة.