GENE EFFECTS FOR YIELD AND YIELD COMPONENTS IN TWO SOYBEAN CROSSES UNDER NORMAL AND DEFFICIT IRRIGATIONS

F.E. Waly, S.M. Tarek and A.A. Abou Zied

Food Legume Research Section, Field Crops Research Institute, ARC.

ABSTRACT

The present study was conducted at the experimental farm of Itay EL-Baroud Agricultural Research Station, ARC during the summer season of 2017 and 2018 to determine the gene effects, heritability in broad and narrow sense and genetic advance % by using the five populations (P_1, P_2, F_1, F_2 and F_3) of the two crosses namely; Giza 21 x Line 164 and DR101-937 x Line 164. For this purpose the two crosses were grown in two experiments under normal irrigation (full number of irrigations) and reduced irrigation (half number of irrigations); each experiment was arranged in randomized complete block design with three replicates. The results showed that, mean squares due to of the two segregating generations F_2 and F_3 were higher than mean squares of non-segregating generations (P_1, P_2 and F_1) under normal and reduced irrigation for both crosses. Reduced irrigation had negative effects on seed yield and its components in the five populations of the cross Giza 21 x Line 164 where the reduced irrigation led to increasing number of empty pods/plant and decreasing number of pods/plant. Also, seed yield of P_1, P_2, F_1, F_2 and F_3 were sharply decreased under reduced irrigation. While, yield and its components of the cross DR101-937 x Giza 21 were not affected by reduced irrigation in all populations, except number of pods and seed yield of P_2; these traits sharply decreased under reduced irrigation. The C and D scaling test for all traits in the two crosses Giza 21 x Line 164 and DR101-937 x Giza 21 showed that at least one or both of C or D were found significant in normal and reduced irrigation, indicating the presence of non-allelic interaction in the inheritance of all studied traits. In both crosses, the additive gene action (d) and epistasis gene action from the type additive x additive (i) were significant for most yield traits under normal and reduced irrigations. Finally, the significance of dominance gene (h) was absent in all traits under both irrigation treatments. The desirable shape of epistasis (complementary) was presented in most traits in both crosses. The genetic advance (Δ G) of Giza 21 x Line 164 ranged from 1.66% in plant height to 12.99% in main root length under normal irrigation and ranged from 1.42% in 100-seed weight to 12.71% in seed yield/plant under reduced irrigation. The cross DR101-937 x Line 164 exceeded the cross Giza 21 x Line 164 in genetic advance% in most trait, where ΔG % of DR101-937 x Line 164 ranged from 3.32% for 100-seed weight to 17.03% for seed yield/plant under normal irrigation and ranged from 1.39% for 100-seed weight to 21.85% for seed yield/plant under reduced irrigation. From the previous results it could be clear that pedigree selection in the early segregation generations could be an excellent method of these crosses for the breeder view to select line of high genetic stability for most studied traits especially seed yield.

Key words: *Soybean, Gene action, Heritability, Genetic advance, Generation means analysis, Deficit irrigation*

INTRODUCTION

Soybean (*Glycine max L.*) is among the top ten of the most widely grown crops, with a world total production in 2017 over 352.6 million tons from dry seeds produced from harvested area of about 123.55 million hectares, while in Egypt, the harvested area in the same year was about 15000 ha produced approximately 45000 from dry seeds (FAOSTAT.

2017). Among the legumes, soybean is valued for its high (38–45%) protein content (Soy Facts 2017) also, soybean seed contains 18–19% oil (Livestock's Long Shadow 2016). Soybean is also viewed as an attractive crop for the production of biodiesel (Pimentel and Patzek 2008). It also has the ability to fix atmospheric nitrogen (Burris and Roberts 1993) and therefore requires minimal input of nitrogen fertilizer which often accounts for the single largest energy input in agriculture.

Plants are subjected to a range of abiotic and biotic stresses that affect their growth and development. In particular, it is predicted that water deficit will continue to be a major abiotic factor affecting global crop yields (Sharma and Lavanya 2002). Drought stress has led to a reduction of seed yield mainly due to the reduction of seed number. Nevertheless, there were only slight reductions in standard germination percentage and seedling axis dry weight of the harvested seeds. The authors suggested that drought stress affects the seed yield to a larger extend than seed quality. In soybean, drought reduces yield by about 40% (Specht *et al* 1999). Depending on hybrid characteristics, soybeans use about 450–700mm of water during the growing season (Dogan *et al* 2007). Plants use various mechanisms to cope with drought stress. These may be classified into three groups: drought escape, drought avoidance and drought tolerance. Drought escape allows the plant to complete its life cycle during the period of sufficient water supply before the onset of drought (Heatherly and Elmore 2004). The second mechanism, drought avoidance, involves strategies which help the plant maintain high water status during periods of stress, either by efficient water absorption from roots or by reducing evapotranspiration from aerial parts. The third mechanism, drought tolerance, allows the plant to maintain turgor and continue metabolism even at low water potential, e.g. by protoplasmic tolerance or synthesis of osmoprotectants, osmolytes or compatible solutes (Nguyen *et al* 1997). Significant progress in breeding for drought resistance cannot be made unless the stress is imposed year after year to allow direct selection for yield. For this reason, a field with poor moisture-holding capacity, soil uniformity and a reasonable drought each year is important, but is unfortunately very difficult to achieve (Pathan *et al* 2007).

The classical breeding design indicated that additive genetic variance will be more important than dominance variance in improving the seed yield. To exploit the existing genetic variability present in breeding material

1526

for seed yield as efficiently as possible, the breeder would need the basic information regarding the inheritance of grain yield and its closely related components for devising an efficient selection program. Breeder need detailed information about the nature of gene action, heritability and predicated genetic gain from yield and its components. These targets could be realized by breeding new high yielding, early maturing and drought tolerant genotypes in soybean. For genetic improvement of the crop, the breeding method to be adopted depends mainly on the nature of gene action involved in the expression of quantitative traits. The presence or absence of epistasis can be detected by the analysis of generation means using the scaling test, which measures epistasis accurately, whether it is complimentary or duplicate at the genic level (Bhor *et al* 2014). Two genetic models viz; Cavalli (1952) and Hayman (1958) were simultaneously used for determining the nature of gene action involved in the inheritance of yield and yield contributing characters. The information regarding gene action involved in control of inheritance for yield and yield contributing characters through generation mean analysis is of immense use to the plant breeder to decide suitable breeding strategy for improvement of these characters.

Therefore, the objectives of this study were to: Determining the heritability nature of gene action involved in the inheritance of yield and yield components and the appropriate breeding method that will be used to select the best genotypes under both normal and reduced irrigations.

MATERIALS AND METHODS

The two individual crosses (Giza 21 x line 164) and (DR101-937 x Line 164) were selected on the basis of their combining ability for seed yield and yield components traits from 15 individual crosses derived by half diallel mating design in 2016. In 2017 the parental genotypes, F_1 and F_2 were sown to obtain F_2 and F_3 seeds in addition to the hybridization among parents were make once again to obtain sufficient F_1 seeds. In 2018, the three generations, F_1, F_2 and F_3 in addition to their parents were evaluated under normal irrigation and reduced irrigation. Seed of all above generations were divided into two divisions and evaluated in two irrigation treatments (two experiments), every experiment was arranged in a randomized complete block design (RCBD) with three replicates. In the first experiment, all generations of the two crosses were evaluated under the normal irrigation

1527

with a full irrigation (Irrigate every 15 days). Meanwhile the same generations were evaluated under reduced irrigation with 50% irrigation (irrigate every 30 days).The plot size was three ridges in the parents, and F_1 and five ridges in F_2 and F_3. Each ridge was 3m long and 70 cm apart. Seeds were planted on both sides of the ridge at 20 cm hill spacing with one seed per hill. The wet planting method called (Herati) was used and all the other cultural practices were followed as recommended. Each experiment was surrounded by a wide border (10 m) to minimize effect of water permeability. Ten competitive plants from P_1, P_2, and F_1, 30 plants in F_2 and 50 plants in F_3 were randomly selected from each plot to record observations on traits viz., maturity date (days), number of empty pods/plant , plant height (cm), number of pods/plant, main root length (cm), 100- seed weight (g) and seed yield /plant (g).

Analysis of components of mean

I) Mather's Scaling Test: For testing the presence or absence of epistasis, scaling test was done following Mather (1949) and Hayman and Mather (1955). In the present investigation, only two scales (C and D) were used. The two different scales and the formulae for the computation of its standard error are given below:

I. Scales:

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

and $D = 4\overline{F_3} - 2\overline{F_2} - \overline{P_1} - P_2$

Standard error of scales:

S.E. of C $= [16V(\overline{F_2}) + 4V(\overline{F_1}) + V(\overline{P_1}) + \overline{V}$ $(P_2)]^{1/2}$ and **S.E. of D** $= [16V(\overline{F_3}) + 4V(\overline{F_1}) + V$ $(P_1) + V(P_2)]^{1/2}$

Where: VP_1, VP_2, VF_1, VF_2 and VF_3 are the variances of P_1, P_2, F_1, F_2 and F_3 populations, respectively.

The gene effects were estimated by the five parameter model as proposed by Hayman (1958).

The generation mean constitutes different combinations of components.

$P_1 = [m] + [d] + [l]$, $P2 = [m] + [d] + [i]$, $F1 = [m] + [h] + [l]$,

$F_2 = m + 1/2[h] + 1/4[l]$, $F3 = m - 1/4[h] + 1/16[l]$

Five parameters are involved in these expressions and five means are available for their estimation and the gene effects are estimated as follows m = F$_2$, d = 1/2P$_1$-1/2P$_2$, h = 1/16(4F$_1$-12F$_2$-16F$_3$), i = P$_1$-F$_2$+1/2(P$_1$-P$_2$+h)-1/4l and l = 1/3(16F$_3$-24F$_2$+8F$_1$)

The variances of these estimates are calculated as below
Vm =VF$_2$, Vd = 1/4(VP$_1$+VP$_2$), Vh = 1/36(16VF$_1$+144VF$_2$+256VF$_3$), Vi = VP$_1$+VP$_2$+1/4 (VP$_1$+P$_2$+Vh) +1/6Vl and Vl=1/9 (256VF$_3$+576VF$_2$+64VF$_1$)

The standards of these estimates can be found out in the usual way. Thus for example

$V (d)$ = 1/4VP$_1$+VP$_2$ and $S(d) = \sqrt{V(d)}$

The significance of (d) can be tested by calculating t= (d)/S(d)

Heritability in broad and narrow sense was calculated according to Mather (1949). Furthermore the predicated genetic advance (Δg) from selection was computed according to Johanson et al (1955) using 5% selection intensity.

The genetic gain as percentage of the F$_2$ mean performance (Δg %) was computed using the method of Miller et al (1958).

RESULTS AND DISCUSSION
Mean squares and mean performance
Mean squares of the two crosses

Mean squares and mean performance of the two crosses (Giza 21 x Line 164) and (DR101-937 x Line 164) of the five populations under normal and reduced irrigations are presented in Table 1. It is clear from data that mean squares of the two segregation generations F$_2$ and F$_3$ were higher than mean squares of non-segregation generations P$_1$, P$_2$ and F$_1$ under normal and reduced irrigations for both crosses. Where F$_2$ gave the largest values of mean squares and this finding indicated that F$_2$ had the highest number of genetic segregates compared with all other populations. A similar result was obtained by Zhu (1992). Also, the presented data showed that F$_2$ mean squares for number of pods/plant and seed yield /plant in reduced irrigation were greater than normal irrigation and this is considered an indicator of the high differences among all F$_2$ genetic segregates in their tolerance to reduced irrigation.

Mean performance of the two crosses
1. Cross Giza 21 x Line 164 mean performance

Data in Table 1 showed that P_2 was the earliest among all populations, it gave the lowest mean values for maturity date it reaches to full maturity after 103.60 and 99.94 in normal and reduced irrigations respectively. While, P_1 was the latest one among all populations with averages of 118.23 and 111.80 due to maturity under normal and reduced irrigations, respectively. Reduced irrigation had negative effects on seed yield and its components in the five populations of (Giza 21 x Line 164) it led to increase in number of empty pods/plant from 3.22, 5.61, 4.43, 3.22 and 3.64 under normal irrigation to 7.42, 10.74, 9.00, 8.95 and 9.32 under reduced irrigation for P_1, P_2, F_1, F_2 and F_3, respectively. While, the reduced irrigation led to decrease in number of pods/plant from 79.60, 63.00, 82.43, 62.11 and 59.17 of P_1, P_2, F_1, F_2 and F_3 in normal irrigation to 63.44, 48.26, 76.28, 55.00 and 55.79 in reduced irrigation for the same populations respectively. Also, seed yield of P_1, P_2, F_1, F_2 and F_3 were sharply decreased from 36.05, 25.75, 32.52, 26.01 and 24.99 g under normal irrigation to 24.34, 17.03, 26.95, 20.35 and 20.12 g under reduced irrigation respectively. The lowest effect of reduced irrigation was shown in the weight of 100-seed, while the large effect of reduced irrigation was shown in plant height and main root length. The plant heights of P_1, P_2, F1, F_2 and F_3 were sharply decreased from 106.63, 92.00, 116.63, 104.65 and 106.90 cm in normal irrigation to 95.56, 87.38, 107.46, 99.81 and 99.21 cm in reduced irrigation, while the main root length of P_1, P_2, F_1, F_2 and F_3 was increased from 11.97, 10.18, 16.01, 17.43 and 16.58 cm under normal irrigation to 25.91, 16.93, 27.29, 22.35 and 21.63 cm under reduced irrigation respectively.

2. Cross DR101-937 x Line 164 mean performance

The presented data in table 1 indicate that the average maturity date of Cross (DR101-937 x Line 164) five populations were not largely affected by reduced irrigation, except in P2 where, the average maturity date was 104.43 days under normal irrigation and decreased to 99.86 days under reduced irrigation. The number of empty pods/plant of P_1, P_2, F_1, F_2 and F_3 ranged from 4.36 in P_1 to 13.75 in F_2 under normal irrigation, while the same trait ranged between 4.28 in P_1 to 16.16 in F_1 under reduced irrigation. The average plant height of all populations did not differ largely in the two treatments, where it ranged from 89.79 cm in P_2 to 124.57 cm in F_1 under normal irrigation and the same trait ranged from 86.42 cm in P_2 to 122.08 cm in F_1 under reduced irrigation.

1530

Table 1. Means (x) and variance (S^2) for all studied traits in the five populations of the two crosses (Giza 21 x Line 164) and (DR101-937 x Line 164) under normal (N) and reduced (R) irrigation.

Trait		Populations									
		P1		P2		F1		F2		F3	
		Giza 21 x Line 164									
		N	R	N	R	N	R	N	R	N	R
Maturity date (days)	X	118.23	111.80	103.60	99.94	113.00	110.32	113.30	107.60	114.70	106.49
	S^2	5.70	1.33	29.80	0.55	4.51	0.24	33.38	23.99	13.57	9.83
No. of empty pods/plant	X	3.22	7.42	5.61	10.74	4.43	9.00	3.22	8.95	3.64	9.32
	S^2	5.70	0.83	1.33	0.24	2.31	0.63	4.59	1.84	5.82	0.78
Plant height (cm)	X	106.63	95.56	92.00	87.38	116.63	107.46	104.65	99.81	106.90	99.21
	S^2	15.85	7.67	9.50	5.04	5.82	2.68	86.97	85.67	82.77	3.99
No. of pods/plant	X	79.60	63.44	63.00	48.26	82.43	76.28	62.11	55.00	59.17	55.79
	S^2	7.32	84.30	6.50	15.20	42.33	27.70	180.51	203.47	246.77	137.60
Main root length (cm)	X	13.22	20.84	11.29	16.93	10.22	16.58	12.35	18.39	11.10	17.89
	S^2	9.26	0.83	6.74	0.04	5.70	0.26	4.66	4.11	7.21	3.46
100- seed weight (g)	X	17.66	16.25	16.88	17.03	15.64	15.03	16.46	16.56	16.80	16.18
	S^2	0.23	2.82	0.74	0.06	0.30	0.01	1.94	1.37	1.73	0.61
Seed yield/ plant (g)	X	36.05	24.34	25.75	17.03	32.52	26.95	26.01	20.35	24.99	20.12
	S^2	6.47	24.83	2.59	2.93	9.58	4.42	16.50	45.28	55.43	27.01
		DR101-937 x Line 164									
Maturity date (days)	X	138.91	137.76	104.43	99.86	115.80	111.68	122.76	119.93	121.68	117.98
	S^2	0.55	1.33	0.84	0.55	0.72	0.27	208.85	236.22	256.57	303.84
No. of empty pods/plant	X	4.36	4.28	6.00	10.67	13.50	16.16	11.75	13.77	9.28	8.89
	S^2	0.15	0.18	0.49	0.19	1.25	0.58	6.30	5.69	5.34	16.12
Plant height (cm)	X	94.58	94..18	89.79	86.42	124.57	122.08	101.45	97.05	97.00	96.01
	S^2	1.26	1.99	2.18	1.44	0.93	0.56	194.15	240.99	122.67	52.14
No. of pods/plant	X	67.68	62.21	61.55	47.03	90.37	86.78	99.67	98.95	96.03	97.01
	S^2	4.66	11.78	1.29	4.99	3.28	3.66	798.33	827.53	254.89	101.11
Main root length (cm)	X	11.97	25.91	10.18	16.93	16.01	27.29	17.43	22.35	16.58	21.63
	S^2	2.49	0.20	2.19	0.04	1.51	0.38	12.99	22.29	14.04	6.74
100- seed weight (g)	X	14.18	14.10	16.79	17.03	16.23	16.08	15.76	15.72	15.62	15.29
	S^2	0.09	0.03	0.68	0.06	0.21	0.01	2.72	1.22	2.93	2.09
Seed yield /plant (g)	X	23.79	21.79	24.54	16.69	33.34	30.32	37.16	35.97	36.49	35.99
	S^2	0.49	1.18	0.42	0.56	2.92	0.47	154.12	154.74	95.09	26.48

N = Normal irrigation   R = Reduced irrigation

The length of main root increased sharply in P_1, P_2, F_1, F_2 and F_3 from 11.97, 10.18, 16.01, 17.43 and 16.58 cm in normal irrigation to 25.91, 16.93, 27.29, 22.35 and 21.63 cm in reduced irrigation, respectively. For yield and its components, all populations did not affect by reduced irrigation, except P_2 where the average number of pods of this parent was decreased from 61.55 to 47.03 and seed yield decreased from 24.54 to 16.69 g in normal and reduced irrigation, respectively. Similar results were obtained by Malik et al., (2006).

A- Scaling test I:

F-test for non-segregation generations (P_1, P_2 and F_1) are presented in Table 2.

Table 2. Scaling test 1 of the non-segregation generations (P_1, P_2 and F_1) for all studied traits of the two crosses Giza 21 x Line 164 and DR101-937 x Line 164 under normal (N) and reduced (R) irrigation.

Trait	Cross	Populations					
		S^2P1/S^2P2		S^2P1/S^2F1		S^2P2/S^2F1	
		N	R	N	R	N	R
Maturity date (days)	**Giza 21 x Line 164**	NS	NS	NS	*	*	NS
	DR 101-937 x Line 164	NS	NS	NS	NS	NS	NS
No. of empty pods/plant	**Giza 21 x Line 164**	NS	NS	NS	NS	NS	NS
	DR 101-937 x Line 164	NS	NS	NS	NS	NS	NS
Plant height (cm)	**Giza 21 x Line 164**	NS	NS	NS	NS	NS	NS
	DR 101-937 x Line 164	NS	NS	NS	NS	NS	NS
No. of pods/plant	**Giza 21 x Line 164**	NS	*	NS	NS	NS	NS
	DR 101-937 x Line 164	NS	NS	NS	NS	NS	NS
Main root length (cm)	**Giza 21 x Line 164**	NS	**	NS	NS	NS	NS
	DR 101-937 x Line 164	NS	NS	NS	NS	NS	NS
100- seed weight (g)	**Giza 21 x Line 164**	NS	**	NS	**	NS	*
	DR 101-937 x Line 164	NS	NS	NS	NS	NS	*
Seed yield /plant (g)	**Giza 21 x Line 164**	NS	*	NS	*	NS	NS
	DR 101-937 x Line 164	NS	NS	NS	NS	NS	NS

NS = Not significant. * and ** = Significant at 5% and 1% level of probability respectively. N= Normal irrigation R= Reduced irrigation

Scaling test II and genetic parameters
Cross Giza 21 x Line 164
1. Scaling test II

The C and D scaling test (Table 3) due to the cross Giza 21 x Line 164 showed that at least one or both of C or D were found significant for maturity date, number of empty pods, number of pods/plant and seed yield/plant under normal irrigation and for plant height, number of pods/plant, 100-seed weight and seed yield/plant under reduced irrigation. In the same line the scale C was highly significant in the cross DR101-937 x Line 164 for all studied traits under both irrigation treatments, except for maturity date and 100-seed weight, while the scale D was significant for number of pods and seed yield per plant under both irrigation treatments in addition to main root length under the normal irrigation, indicating the presence of non-allelic interaction in the inheritance of all significant traits while, The scale (C) refers to the type of genetic interaction dominance x dominance, where the scale (D) refers to the type of genetic interaction additive x additive. However, some traits in the two crosses showed non-significant values for both C and D scales in both treatments, indicating the absence of non-allelic interacting mode of inheritance of these traits while the significant values in other traits in one of C or D or both of them refer to the presented non-allelic interacting mode of inheritance of the insignificant traits.

Our results indicated that the significant values in one of C or D or both of them refer to the presence of non-allelic interacting mode of inheritance of these significant traits. In the same way, Maloo and Nair (2005) also found significant at least one or two scales for days to 50 % flowering, days to full maturity, yield per plant, number of pods per plant, and plant height.

2. Genetic parameters

Scaling test II for cross Giza 21 x Line 164 is presented in Table 3. The results indicated that the C measure was significant and /or highly significant for number of empty pods/plant, number of pods/plant and seed yield/plant under normal irrigation and for number of pods/plant and 100-seed weight under reduced irrigation. These findings refer to the importance of epistasis gene action (dominance x dominance) in the inheritance of these traits.

1533

Table 3. Scaling test II and five parameters for all studied traits of the two crosses (Giza 21 x Line 164) and (DR101-937 x Line 164) under normal (N) and reduced (R) irrigations.

Traits	Treatment	Scaling test		Genetic parameters					Epistasis type
		C	D	M	D	H	I	l	
				Giza 21 x Line 164					
Maturity date (days)	N	5.47	10.43*	113.30**± 1.29	7.33**± 1.33	-3.94± 4.08	8.57*±4.27	6.67±12.32	Duplicate
	R	-1.95	-0.90	107.60**± 1.09	5.95**± 0.31	4.73± 3.44	12.19**±3.33	1.33±10.25	Comp.
No. of empty pods/plant	N	-4.83*	-0.87	3.22**± 0.48	-1.24*± 0.59	-0.27± 2.29	-2.67± 2.28	5.33± 5.88	Duplicate
	R	-0.36	1.25	8.95**± 0.30	-1.65**± 0.22	-0.96± 0.99	-4.15**± 1.05	2.00± 2.99	Duplicate
Plant height (cm)	N	-13.29	19.72	104.65**± 2.08	7.34**± 1.12	1.97± 8.76	-0.73± 7.78	43.87*± 22.84	Comp.
	R	1.55	14.28 **	99.81**± 2.07	4.09**± 0.79	6.66± 4.49	-1.09± 5.44	17.04± 17.01	Comp.
No. of pods/plant	N	-56.42 **	-31.74	62.11**± 3.00	8.33**± 0.83	22.83± 14.67	28.33*± 12.19	32.93±36.60	Comp.
	R	-44.09 **	1.29	55.00**± 3.19	7.61**± 2.23	12.27± 11.87	7.06± 11.61	60.26*± 32.88	Comp.
Main root length (cm)	N	4.60	-4.78	12.35**± 0.48	1.07± 0.89	1.93± 2.56	5.97*± 2.69	-12.40*± 6.59	Duplicate
	R	2.66	-2.97	18.39**± 0.45	1.96**± 0.21	0.12± 1.81	6.34**± 1.64	-7.51± 4.83	Duplicate
100- seed weight (g)	N	-0.06	-0.06	16.46**± 0.31	0.43*± 0.22	-1.64± 1.28	0.89± 1.15	0.002± 3.39	Duplicate
	R	2.92 *	-1.69	16.56**± 0.26	-0.39± 0.38	-0.001± 0.84	0.84± 1.16	-6.14**± 2.48	Comp.
Seed yield /plant (g)	N	-22.81 **	-13.84	26.01**± 1.35	5.15**± 0.67	7.04± 6.89	15.72**± 5.78	11.96± 16.97	Comp.
	R	-13.88 *	-1.61	20.35**± 1.51	3.65**± 1.18	5.02± 5.35	6.06±5.48	16.36± 15.09	Comp.

1534

Table 3. Cont.

Traits	Treatment	Scaling test		Genetic parameters					Epistasis type
		C	D	M	D	H	I	l	
				DR101-937 x Line 164					
Maturity date (days)	N	15.87	-1.93	122.67**±3.23	17.25**±0.26	-1.93±15.19	38.42**±12.54	-23.73±37.74	Comp.
	R	18.59	-5.65	119.93**±3.44	18.95**±0.31	-0.28±16.23	44.77**±13.39	-32.33±40.25	Comp.
No. of empty pods/plant	N	9.64**	3.34	11.75**±0.65	-0.82**±0.18	7.69**±2.27	-2.26±1.99	-8.38±6.09	Duplicate
	R	7.82**	-7.02	13.80**±0.53	-3.18**±0.14	14.68**±3.56	-0.42±2.75	-19.76*±8.05	Duplicate
Plant height (cm)	N	-27.80*	0.68	101.45**±3.12	2.42**±0.42	27.28±11.23	-0.31±10.12	38.04±31.17	Comp.
	R	-36.61**	9.31	97.05**±3.47	3.89**±0.41	19.49±9.24	-4.53±9.56	61.22*±30.34	Comp.
No. of pods/plant	N	89.21**	55.76*	99.69**±6.32	2.81**±0.55	3.67±18.47	-16.73±18.21	-44.53±57.31	Duplicate
	R	113.01**	80.92**	99.95**±6.43	7.61**±0.84	-2.92±15.42	-19.90±16.97	-42.78±54.23	Comp.
Main root length (cm)	N	15.42**	9.39*	17.38**±0.81	0.91±0.48	1.19±3.57	-1.92±3.13	-7.97±9.15	Duplicate
	R	-8.04*	-1.03	33.35**±1.05	4.49**±0.11	5.23*±3.05	8.33**±3.03	9.34±9.54	Comp.
100- seed weight (g)	N	-0.45	-0.08	15.75**±0.37	-1.31**±0.19	0.72±1.63	-2.64*±1.39	0.49±4.17	Comp.
	R	-0.42	-1.43	15.72**±0.25	-1.46**±0.07	1.40±1.32	-2.05*±1.06	-1.35±3.14	Duplicate
Seed yield /plant (g)	N	33.65**	23.29*	37.16**±2.78	-0.37*±0.21	-0.74±9.93	-10.66±8.97	-13.82±27.71	Comp.
	R	44.75**	33.54**	35.97**±2.78	2.55**±0.29	-3.83±7.06	-9.80±7.49	-14.95±23.89	Comp.

* and ** = Significant at 5% and 1% level of probability respectively, Comp. = complementary

On the other side, the scale measure D was significant and/or highly significant for maturity date under normal irrigation and plant height under reduced irrigation and this may refer to the importance of the gene action additive x additive in the inheritance of these two traits. The F_2 mean values (m) of the cross Giza 21 x Line 164 were highly significant for all studied traits under normal and reduced irrigations (Table 4).

1535

Table 4. Components of variation (D, H and E), broad-sense heritability (h^2 (b)), narrow-sense heritability (h^2 (ns)) and genetic advance% (ΔG %) for all studied traits of the two crosses (Giza 21 x Line 164) and (DR101-937 x Line 164) under normal (N) and reduced (R) irrigations.

Trait		D	H	E	h^2 (b)	h^2 (ns)	ΔG %
				Giza 21 x Line 164			
Maturity date (days)	N	3.41	29.63	-1.62	0.66	0.08	3.52
	R	4.63	552.53	-41.95	0.96	0.17	4.95
No. of empty pods/plant	N	0.03	2.19	-0.09	0.94	0.29	6.70
	R	5.06	1313.56	-154.12	0.98	0.30	8.16
Plant height (cm)	N	0.17	3.24	-0.23	0.80	0.13	1.66
	R	4.52	430.68	-53.04	0.95	0.31	5.91
No. of pods/plant	N	24.60	699.89	-38.13	0.86	0.11	4.66
	R	38.73	805.41	-73.22	0.81	0.18	9.61
Main root length (cm)	N	6.83	-15.39	3.36	0.46	0.36	12.99
	R	0.35	18.25	-1.58	0.92	0.19	4.36
100- seed weight (g)	N	0.38	7.40	-0.59	0.80	0.15	2.64
	R	0.72	3.12	-0.27	0.47	0.10	1.42
Seed yield /plant (g)	N	7.06	20.81	8.48	0.57	0.26	8.27
	R	9.15	178.31	-16.89	0.80	0.19	12.71
				DR101-937 x Line 164			
Maturity date (days)	N	0.69	968.55	-67.95	0.98	0.16	3.79
	R	0.57	1094.77	-76.09	0.99	0.16	4.25
No. of empty pods/plant	N	0.79	26.57	-2.26	0.88	0.18	7.90
	R	0.39	19.68	0.76	0.93	0.07	2.38
Plant height (cm)	N	1.34	964.48	-96.02	0.99	0.25	6.99
	R	1.13	1251.45	-146.01	0.99	0.30	9.98
No. of pods/plant	N	3.15	4105.01	-462.15	0.99	0.29	16.90
	R	6.05	4327.28	-520.69	0.99	0.31	18.84
Main root length (cm)	N	1.93	51.55	-3.64	0.85	0.14	5.98
	R	0.26	113.92	-12.90	0.99	0.29	12.59
100- seed weight (g)	N	0.31	11.33	-0.84	0.89	0.15	3.32
	R	0.03	5.24	-0.24	0.98	0.10	1.39
Seed yield /plant (g)	N	1.69	762.24	-76.26	0.98	0.25	17.03
	R	0.67	807.56	-95.65	0.99	0.31	21.85

N= Normal irrigation   R= Reduced irrigation.

The additive gene action (d) was significant for all traits under normal and reduced irrigations except for main root length in normal

irrigation and 100-seed weight in reduced irrigation followed by the epistasis gene action from the type additive x additive (i) where it gave significant values for maturity date and main root length in both irrigation treatments, number of pods/plant and seed yield/plant in normal irrigation and plant height under reduced irrigation. According to the significant additive (d) and additive x additive (i) gene action, the pedigree method of selection will be excellent for selecting the superior genotypes for these traits in this cross. These findings are in agreement with Sayad *et al* (2005). While, the dominance x dominance gene action (l) was significant for plant height in normal irrigation, 100-seed weight in reduced irrigation, number of pods/plant in reduced irrigation and main root length in normal irrigation. Finally, the significance of dominance gene (h) was absent in all traits under both irrigation treatments. The epitasis type was duplicate for maturity date and 100-seed weight in normal irrigation and number of empty pods/plant and main root length in both irrigation treatments. This type was undesirable in breeding programs but the significant additive x additive non-allelic interaction with duplicate epistasis may consider an evidence for the possibilities of obtaining transgressive segregates in later generations (Ghassemi and Yazdi-Samadi, 1987). While the desirable type of epitasis (complementary) was presented in all other traits. These findings may be clear evidence about the great role of selection for improvement of these traits (Sayad *et al* 2005 and Datt *et al* 2011). From the previous results it could be clear that pedigree selection in the early segregating generations was an excellent breeding program for this cross, where it help the breeder in selecting excellent lines with high genetic stability for most should traits, especially seed yield.

Cross DR101-937 x Line 164
1. Scaling test II:
Most studied traits in this cross showed significant values for both C and D scales or one of them in both treatments, indicating non-allelic interacting mode of inheritance for these traits. These findings consider a great indicator at the presented non-allelic interacting mode of inheritance of these traits. Similar results were obtained by Maloo and Nair (2005).
2. Genetic parameters:
Scaling test II for cross DR101-937 x Line 164 is presented in Table 3. Results indicated that the C measure was significant for number of empty

pods/plant, plant height, number of pods/plant, main root length and seed yield/plant under normal and reduced irrigation. These findings refer to the importance of epistasis gene action (dominance x dominance) in the inheritance of these traits. On the other side, the scale measure D was significant for number of pods/plant and seed yield/plant in both irrigation treatments and main root length in normal irrigation; this may refer to the importance of the gene action additive x additive in the inheritance of these two traits. The F_2 mean values (m) of the cross DR101-937 x Line 164 were highly significant for all studied traits under normal and reduced irrigations (Table 3). The additive gene action (d) was highly significant for all traits under normal and reduced irrigations, except for main root length in normal irrigation followed by the epistasis gene action from the type additive x additive (i) where it gave significant values for maturity date and 100-seed weight in both irrigation treatments and main root length under reduced irrigation and these values were exceeded the same additive values (d). Raut *et al* (2002) and Sayad *et al* (2005) indicated that additive effects could facilitate fixation of the combination of genes and therefore, selection for traits with the highly significant additive gene would give better response. While, the dominance gene action (h) was significant and exceeded all other gene actions for No. of empty pods/plant and plant height in both irrigation treatments. These refer to non-fixable components of genetic variation, reciprocal recurrent selection or bi-parental mating was suggested for improving these traits (Sayad *et al* 2005 and Shinde 2010). Finally, the significance of (dominance x dominance) gene (h) was absent in most traits under both irrigation treatments. The epistasis types were duplicate for number of empty pods/plant in both irrigation treatments, number of pods/plant and main root length in normal irrigation and 100-seed weight under reduced irrigation. This shape was undesirable in breeding programs. While the desirable type of epistasis (complementary) was presented in all other traits. From the previous results, it could be clear that pedigree selection in the early segregation generations was an excellent method in breeding program of this cross where it help the breeder to select excellent lines with highly genetic stability for most traits especially seed yield. These results suggest the potential for obtaining further improvements for these characters by using pedigree selection program. Similar results were obtained by Abd-Allah *et al* (2008) and Abdel-Nour and Hassan (2009).

1538

Components of variation (D, H and E) were computed on the basis of additive-dominance model are presented in Table (4). Based on the calculation of components of variation, environmental variation (E) was found out as the mean of P_1. P_2 and F_1 variances and the values for D (additive variation) and H (dominance variation) were estimated from the variances of F_2 and F_3 generations. Having only three parameters (D, H and E), a perfect fit of solution was possible and thus neither the standard deviation of the estimates or test of the goodness of fit could be done.

The presented data in Table 4 indicated that the dominance variances (H) were higher than the additive variances (D) in all traits under normal and reduced irrigations for both crosses. The variances of D and H were positive for all traits in both crosses under normal and reduced irrigations, except for dominance variance (H) of main root length in Giza 21 x Line 164 under normal irrigation.

Heritability in both broad and narrow senses are presented in Table 4. The higher heritability values in broad sense for cross Giza 21 x Line 164 were detected for all studied characters under both normal and reduced irrigations which ranged from 98% to 66%, except for main root length and seed yield/plant under normal irrigation and 100-seed weight under reduced irrigation, where the broad sense heritability in these three traits ranged from 46% to 57%. The higher broad sense heritability may be useful for the breeder in these characters. This could be identify and illustrate the importance of straight forward phenotypic selection for the improvement of these traits. With regard to broad sense heritability for the cross DR101-937 x Line 164, it is clear that the high broad sense heritability were presented in all studied traits under both normal which reduced irrigations and it ranged from 99% to 85%. The increase of broad sense heritability in these traits considers a clear evidence about the ability of the breeder to use the phenotypic selection to select the superior genotypes (Table 4).

With respect to narrow-sense heritability for Giza 21 x Line 164 (Table 4), the results indicated that the narrow sense heritability were very low in most should traits which ranged from 8% for maturity date to 36% for main root length under normal irrigation, while it ranged from 10% for 100-seed weight to 31% for plant height under reduced irrigation. In the same line, the narrow sense heritability for the cross DR101-937 x Line 164

were also, very low in all studied traits, which ranged from 14% for main root length to 29 % for number of pods/plant under normal irrigation, while it ranged from 7% for number of empty pods to 31% for number of pods/plant and seed yield/plant under reduced irrigation. The highly significant differences in magnitude of both broad and narrow sense in all studied characters may consider an evidence for the presence of both additive and non-additive gene effects in the inheritance of these characters. Also, this difference considers an evidence on a large part of genetic variation due to dominance variance. These results are in harmony with those obtained by Reddy *et al* (2001) and Pandini *et al* (2002).

Genetic advance % (ΔG %) of all studied traits in both crosses under normal and reduced irrigations is presented in Table 4. The genetic advance % of Giza 21 x Line 164 ranged from 1.66% in plant height to 12.99% in main root length under normal irrigation, while genetic advance % in the same cross ranged from 1.42% in 100-seed weight to 12.71% in seed yield/plant under reduced irrigation. The cross DR101-937 x Line 164 exceeded the cross Giza 21 x Line 164 in genetic advance% in most studied traits where, ΔG % of DR101-937 x Line 164 ranged from 3.32% for 100-seed weight to 17.03% for seed yield/plant under normal irrigation and ranged from 1.39% in 100-seed weight to 21.85% in seed yield/plant under reduced irrigation. The percentage of genetic advance was associated with narrow sense heritability in all studied traits. Similar results were obtained by Reddy *et al* (2001) and Pandini *et al* (2002).

REFERENCES

Abd-Allah, Soheir M.H and S.A Abdel- Dayem (2008). Determination of gene   effects and variance in three bread wheat crosses. Ann. Agri. Sci. Moshtohor 46(1): 23-31.

Abdel-Nour, Nadya A.R. and Manal A. Hassan (2009). Determination of gene effects and variance in three bread wheat crosses for low water (Drought). Egypt J. Plant Breed.13:235-249.

Bhor, T.J., V. P. Chimote and M. P. Deshmukh (2014). Genetic analysis of yield and yield components in soybean [*glycine max (l.) Merrill*]. Indian J. Agric. Res. 48 (6) 446-452.

Burris, R.H. and G.P. Roberts (1993). Biological nitrogen fixation. Annul. Rev. Nutr. 13:317-335.

Cavalli, L.L. (1952). An analysis of linkage in quantitative inheritance. Ed. E.C.R. Review and H. Waddington. HMSO London.135-144.

Datt, S., S. K. Noren, V.P. Bhadana and P.R. Sharma (2011). Gene action for yield and its components in soybean (*Glycine max* (L.) Merrill). VEGETOS 24 (1): 89-92.

Dogan, E., H.Kirnak and O. Copur (2007). Deficit irrigations during soybean reproductive stages and CROPGRO-soybean simulations under semi-arid climatic conditions. Field Crops Res. 103:154-159.

FAOSTAT (2017). Soybean cultivated area and total production. Food and Agriculture Organization of the United Nation, November,

Ghassemi, F. and B. Yazdi-Samadi (1987). Genetic estimation of eight quantitative characters in soybean [(*G. max* (L.) Merrill)]. Iran J Agri. Sci. 17(3-4): 31-43.

Hayman, B. I. (1958). The separation of epistasis from additive and dominance variation in generation means. Heredity 12: 371- 390.

Hayman, B.I. and K. Mather (1955). The description of gene interaction in continuous variation. Biometrics 11:69-82.

Heatherly, L.G. and R.W. Elmore (2004). Managing inputs for peak Production. In: Specht JE, Boerma HR, editors. Soybeans: Improvement, Production, and Uses. Agronomy Monographs, 3rd ed. No. 16. Madison, WI: ASA-CSSA-SSSA; 2004. p. 451-536.

Johanson, H. W.; H. F. Robinson and R. E. Comstock (1955). Estimates of genetic and environmental variability in soybean. Argon. J. 47: 314.

Livestock's Long Shadow (2016). Environmental issues and options. www.fao.org. Retrieved 2016-01-15.

Malik, M. F. A; A. S. Qureshi; M. Ashraf and A. Ghafoor (2006). Genetic variability of the main yield related characters in soybean. International J. of Agri. & Biology 6: 815–819.

Maloo, S. R. and Nair Sandeep (2005). Generation mean analysis for seed yield and its components in soybean. Indian J. Genet. 65(2): 139-140.

Mather, K. (1949). Biometrical Genetics. Methuen Co. Ltd., London.

Miller. P. A., T. C. Williams; H. F. Robinson, and R. E. Comstock (1958). Estimates of genotypes and environmental variances in upland cotton and their implications in selection Agro. J. 50: 126 – 131.

Nguyen, H.T., R.C. Babu and A. Blum (1997). Breeding for drought resistance in rice: physiology and molecular genetics considerations. Crop Sci. 37:1426-1434.

Pandini, F., N. Antonio and A. Almeida lopes (2002). Heterosis in soybean for seed yield components and associated traits. Braz .Arch .Biol. Technol. 45(4).

Panthee, D. R., V. R. Pantalone, D. R. West, A. M. Saxton and C. E. Sams (2005). Quantitative trait loci for seed protein and oil concentration, and seed size in soybean Crops. 45 (5): 2015-2022.

Pathan, M.S., J.D. Lee, J.G. Shannon and H.T. Nguyen (2007). Recent advances in breeding for drought and salt stress tolerance in soybean. In : Jenks M.A., Hasegawa P.M. and Jain. S.M. editors. Advances in Molecular Breeding Toward Drought and Salt tolerant Crops. New York: Springer p 339-773.

Pimentel, D. and T. Patzek (2008). Ethanol Production Using Corn, Switch grass And Wood; Biodiesel Production Using Soybean. In: Pimentel D, editor. Biofuels, Solar and Wind as Renewable Energy Systems. New York: Springer, p. 373-394.

Raut, V. M., and S.P. Taware, and G. B. Halvankar (2002). Gene effects for quantitative characters in soybean crosses. Indian J. of Agric. Sci. 70(5): 334-335.

1541

Reddy, P., M. Sekar, A. Raganatha and A. Dhanraj (2001). Genetic variability and heritability for seed yield and its components in sesame *(Sesam indicum L.)*.Journal of Oil Seeds Research 18(2): 173-175.

Sayad, Z.S., M.M.Soliman, S.A. Mokhtar, H.M.G. Shaboury and G.A.A. Hafez (2005). Heterosis, combining ability and gene action in F_1 and F_2 diallel crosses among six soybean genotypes. Annals Agri. Sci. Moshtohor 43 (2) : 545-559.

Sharma, K.K. and M. Lavanya (2002).Recent developments in trans-genic for abiotic stress in legumes of the semi-arid tropics.; JIRCAS Working Report p. 61-73.

Shinde, S.R. (2010). Inheritance of resistance to leaf rust caused by *Phakopsora Pachyrhizi Syd.* and quantitative characters in soybean [(*Glycine max* (L.)]. Ph. D. thesis submitted to Mahatma Phule Krishi Vidyapeeth, Rahuri 90-104.

Soy Facts (2017). Soya tech. Archived from the original on January 12, 2017. Retrieved January 24, 2017.

Specht, J.E.; D.J. Hume and S.V. Kumudini (1999). Soybean yield potential-a genetic and physiological perspective. Crop Sci. 39:1560-1570.

Zhu, J. C. (1992). Study on the heritability, genetic advance and correlation of primary agronomic traits of spring soybean varieties sown in spring and autumn. Soybean Sci. 11: 322–328.

الفعل الجينى للمحصول و مكوناته في هجينين من فول الصويا تحت ظروف الري المعتاد و الري الناقص

فايز السيد والى, طارق صابر محمد السيد و أبو زيد عبد المحسن أبو زيد

قسم بحوث المحاصيل البقولية ، معهد بحوث المحاصيل الحقلية ، مركز البحوث الزراعية.

أجريت هذه الدراسة في المزرعة البحثية لمحطة البحوث الزراعية إيتاي البارود ، مركز البحوث الزراعية خلال موسمي ٢٠١٧ و ٢٠١٨ لتحديد الفعل الجينى ، درجتى كفاءة التوريث بالمعنى الواسع والضيق والنسبة المئوية للتحسين الوراثى للعشائرالخمسة (P1) و P2 و F1 و F2 و F3 لهجينين وهما (جيزة ٢١ × سلالة ١٦٤) و (937-DR101 × سلالة ١٦٤) تحت ظروف الرى الكامل و الناقص. تم زراعة العشائر الخمسة في تجربتين للري العادي (العدد الكامل للريات) والرى المرشد (نصف عدد الريات) صممت كل تجربة في نظام القطاعات الكاملة العشوائية من ثلاث مكررات. أظهرت النتائج أن تباين الأجيال الإنعزالية F2 و F3 كان أعلى من تباين الاجيال غير الإنعزالية P1 و P2 و F1 تحت الري الكامل و الناقص لكلا الهجينين. كان للري الناقص تأثيرات سلبية على محصول البذور ومكوناته في العشائر الخمس للهجين (جيزة ٢١ × سلالة ١٦٤)، مما أدى إلى زيادة عدد القرون الفارغة/النبات ، وانخفاض عدد القرون/النبات أيضاً و كذلك محصول البذور فى P1 ، P2 ، F1 , F2 و F3 حيث انخفضت قيم تلك الصفات بشكل حاد تحت الرى الناقص. بينما لم يتأثر المحصول و

مكوناته فى جميع عشائر الهجين (٢١ Giza x 937 -DR101) بنقص مياه الرى باستثناء عدد القرون وإنتاجية البذور لل P2 حيث انخفضت هذه الصفات انخفاضًا حادًا تحت الري الناقص. لوحظ وجود معنوية لواحد او اكثر من C او D او كليهما معا لجميع الصفات في الهجينين (جيزة ٢١ × سلالة ١٦٤) و (جيزة ٢١ DR101-937 x) في الري العادي والإجهاد مما يشير إلى وجود تفاعل غير أليلي فى كلا الهجينين ، كان فعل الجين المضيف (d) و التفوق من النوع مضيف x مضيف (i) ذا أهمية بالنسبة لمعظم صفات المحصول تحت ظروف الري العادي و الاجهاد. أخيرًا ، كان الفعل الجينى السيادى غير معنوى لمعظم الصفات تحت معاملتى الرى. كان طراز التفوق المرغوب حاضرا في معظم الصفات في كلا الهجينين. كان من الواضح أن النسبة المئوية للتحسين الوراثي فى الهجين (Giza 21 x Line 164) تراوحت بين ١,٦٦٪ في ارتفاع النبات إلى ١٢,٩٩٪ في طول الجذر الرئيسي في ظل ظروف الرى الطبيعى وتراوحت بين ١,٤٢٪ في وزن ١٠٠ بذرة و ١٢,٧١٪ في محصول البذرة/نبات تحت حالة الاجهاد. فى حين تجاوز التحسين الوراثى للهجين (-DR101 937 x Line 164)(الهجين جيزة ٢١ × سلالة ١٦٤) في معظم الصفات حيث تراوحت نسبة التحسين الوراثى المتوقع (∆G) ٪ فى (DR101-937 x Line 164) من ٣,٣٢٪ لوزن ١٠٠ بذرة إلى ١٧,٠٣٪ في محصول البذور/النبات تحت الري العادى وتراوحت بين ١,٣٩٪ في وزن ١٠٠ بذرة إلى ٢١,٨٥٪ في محصول البذور/النبات تحت ظروف الإجهاد. من النتائج السابقة ، يتضح أن طريقة اختبار النسب في الاجيال الانعزالية المبكرة تعتبر طريقة ممتازة لانتخاب سلالات مميزة مما يساعد مربى في اختيار سلالات ممتازة ذات ثبات وراثي عالي لمعظم الصفات وخاصة محصول البذور.