# GENETIC ANALYSIS FOR SEED YIELD AND SOME RELATED CHARACTERS IN FOUR SOYBEAN CROSSES

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**ABSTRACT**

Six populations of four soybean crosses (L-86-K-96 × Ware), (Egyptian ×Ware), (H129 × Crawford) and (DR101× Giza 111) were conducted during three successive summer seasons 2019, 2020 and 2021 at the experimental farm of Sakha agricultural research station (SARS), Kafr El-Sheikh, Egypt for estimate the adequacy of genetic model and types of gene action for earliness, seed yield and its attributes. The scaling test provides evidence of non-allelic interaction in controlling all characters in all studies crosses. The additive, dominance and their digenic interaction types, additive x additive and dominance x dominance gene effects were significant and involved in the inheritance of days to 50% flowering in all crosses, days to 90% maturity and 100 seed weight in 1st cross, plant height in 3rd cross and number of pods/plant in 1st and 4th crosses. Duplicate type of epistasis was registered in 3rd cross for plant height; 4th cross for number of pods/plant; 1st and 2nd crosses for 100-seed weight and 1st cross for seed weight /plant. Heritability in narrow sense was high for plant height and seed weight /plant in 2nd cross and number of pods/plant in 3rd one. Positive and significant heterosis relative to mid and best parent were detected for number of pods/plant, number of seeds/plant and seed weight /plant in all crosses. Positive and significant correlation was detected between seed weight /plant and each of number of pods/ plant and number of seeds/plant. Number of seeds/plant, 100-seed weight and number of pods/plant had the highest direct effect on seed weight /plant.

## INTRODUCTION

Soybean (*Glycin max* L. Merril) is one of the important legume crops for oil and protein production. Soybean seeds have about 14 to 24% oil and about 45 to 48% protein (**Brim and Burton, 1979**). It is significantly used in Egypt for poultry and human consumption. The quantity of oil seeds produced in Egypt is away from the great request. Therefore, Egyptian plant breeders have glorified all efforts to improve soybean seed yield and to cover the rising demand for oil and protein consumption (**Talwar *et al.*, 1986**). Consequently, the plant breeder usually has

in mind an ideal plant that includes a maximum number of good characteristics. Improvement of seed yield and agronomic characters are the main objectives of soybean breeders. So, an understanding of the fundamental nature of the actions and interactions of genes involved in the inheritance of quantitative characters is very helpful to soybean breeders to choose the appropriate breeding procedure.

The generations mean analysis technique has been used to obtain considerable information on the types of gene action controlling earliness and seed yield as well as its attributes. Many quantitative characteristics in soybean may be governed

by additive and dominance gene actions, information on epistatic interactions would also be valuable to improve yield attributing traits in soybean (**Thakare *et al.*, 2017; Abou Sen, 2020**). Additive gene action was found predominant in the inheritance of yield and yield contributing characters *viz.*, number of primary branches /plant, number of clusters/plant, number of pods/cluster, 100 seed weight and yield/ plant. Both additive and non-additive gene effects were significantly involved in the expression of nine quantitative traits with duplicate epistasis (**Adsul *et al.*, 2016; Ramírez *et al.*, 2022**). Whereas **Nagarajan *et al.* (2022)** found that the adequacy of the additive dominance model was predominant to explain the inheritance of plant height in the crosses Co 3 × LP 5-1 and Co 3 × LP 13-1 and seed yield/plant in Co 3 × LP 5-2. The remaining crosses exhibited epistatic interactions with all other traits. **Krisnawati and Adie (2022)** revealed that heterosis according to mid-parent for $F_1$ crosses ranged from -61.20 to 27.57%, heterobeltiosis ranged from -71.17 to 9.84% and the degree of dominance ranged from 6.45 to 19.40. **Jain *et al.* (2018), Koraddi and Basavaraja (2019), Jandong *et al.* (2020) and Prathima *et al.* (2022)** observed high heritability coupled with high genetic advance for plant height and number of pods. The present investigation aimed to estimate the gene action, heritability, heterosis and predicated genetic gain for seed yield and some agronomic characters of four soybean crosses.

## MATERIALS AND METHODS

The present study was carried out at Sakha farm, Sakha Agricultural Research Station (SARS), Kafr El-sheikh, Egypt, during the three summer seasons of 2019, 2020 and 2021.

Seven soybean genotypes of wide divergent origin were used as parental material (L-86-K-96, Crawford, Giza 111, H129, Egyptian, Ware and D.R101) (Table 1).

In 2019 season, four crosses, I (L-86-K-96×Ware), II (Egyptian × Ware), III (H129 × Crawford) and IV (D.R101 × Giza 111), were made. In 2020 season, parents and $F_1$'s of each cross were planted and $F_1$ plants in each cross were self-pollinated and back-crossed to both parents to obtain the $F_2$'s and the back crosses seeds.. Crosses between the parental varieties were repeated to obtain additional hybrid seeds for further evaluation.

In 2021 season, the six populations (P1, P2, F1, BC1, BC2 and F2) of each cross were evaluated in randomized complete block design (RCBD) with three replications. Each replicate was consisted of two rows for P1, P2 and $F_1$ generations, four rows for back crosses and eight rows for $F_2$ generation. Each row was 4 m. long, and 60 cm width. Seeds were planted at 20 cm hill spacing on one side of the ridge with one seed per hill. Before flowering, 20, 40 and 80 plants were tagged for P1, P2 and $F_1$ generations, back-crosses and $F_2$ in each replicate, respectively. The total plants tagged for each cross was $P_1$, $P_2$, and $F_1$, 120 plants of $BC_1$ and $BC_2$, and 240 $F_2$ plants in the three replications to determine the studied characters *viz.*, number of days to 50% flowering, number of days to 90% maturity, plant height, number of branches / plant, number of pods/plant, number of seeds/plant, 100 seed weight and seed yield/plant.

### Statistical Analysis

Statistical analysis was used to calculate the means and variances for the six generations. Population means and variances were used to estimate the type of gene action for each character. A two-tail F-ratio was calculated to test the significance of the $F_2$ variance from environmental variance, as follows: F = $F_2$ variance/environmental variance, if the F-ratio was significant, Mather's procedure was used to calculate the components of genetic variance.

**Table 1. Pedigree, maturity group, origin, flower color and growth habit of the studied soybean genotypes**

| Cod. No. | Parent | Pedigree | Maturity group | Origen | Flower color | Growth habit |
|---|---|---|---|---|---|---|
| 1 | **L-86-K-96** | Williams 82 x L76.0279 | III | **USDA, ARS, Illinois | White | Indeterminate |
| 2 | **Crawford** | Williams x Columbus | IV | USA, Illinois | Purple | Indeterminate |
| 3 | **Giza 111** | Crawford X Celest | IV | *FCRI (Egypt) | Purple | Indeterminate |
| 4 | **H129** | D76-8070 X Giza 35 | IV | FCRI (Egypt) | white | Indeterminate |
| 5 | **Egyptian** | Franklin x J 74-5 | IV | Virginia, ***AES | White | Indeterminate |
| 6 | **Ware** | PI80-837xV63-76 (Hill x D53-354) | IV | Virginia, AES | Purple | determinate |
| 7 | **D.R 101** | Selected from Elgin | V | USDA, ARS, Illinois | Purple | determinate |

\*  FCRI = Field Crops Research Institute, Giza, Egypt.
\*\*USDA = U.S. Regional soybean laboratory at Urbana, Illinois, and Stoneville, Mississippi.
\*\*\* AES = Agricultural Experiment Station.

The following four tests for scale effects were estimated according to **Hayman and Mather (1955)** as follow:

$A = 2\,\overline{BC1} - \overline{P1} - \overline{F1}$     $V_A = 4V(BC1) + V(P1) + V(F1)$

$B = 2\,\overline{BC2} - \overline{P2} - \overline{F1}$     $V_B = 4V(BC2) + V(P2) + V(F1)$

$C = \overline{4F2} - 2\overline{F1} - \overline{P1} - \overline{P2}$    $V_C = 16V(F2) + 4V(F1) + V(P1) + V(P2)$

$D = 2\overline{F2} - \overline{BC1} - \overline{BC2}$     $V_D = 4V(F2) + V(BC1) + V(BC2)$

The adequacy genetic model estimated the various genetic component according to **Hayman (1958)** as follow:

m = Mean of F2

$d$ = Additive effect = $\overline{BC1} - \overline{BC2}$

$h$ = Dominance effect = $\overline{F1} - 4\,\overline{F2} - (1/2)\,\overline{P1}$ (1/2) P2 + 2BC1 + 2BC2.

$i$ = Additive x Additive type of gene interaction = 2 BC1 + 2BC2 – 4 F2

$j$ = Additive x Dominance type of gene interaction = BC1 - 1/2 P1 – BC2 + 1/2 P2.

I = Dominance x Dominance type of gene interaction

$= \overline{P1} + \overline{P2} + 2\overline{F1} + 4\overline{F2} - 4\overline{BC1} - 4\overline{BC2}$

Heterosis and inbreeding depression were determined according to **Mather and Jinks (1982)**. The two estimates of epistatic deviation ($E_1$) and ($E_2$) were calculated as the deviation of segregating populations *i.e.,* $F_2$, $BC_1$ and $BC_2$ from their nonsegregating populations ($F_1$ and parents). $E_1 = F_2 - \tfrac{1}{2} F_1 - \tfrac{1}{4} P_1 - \tfrac{1}{4} P_2$ ; $E_2 = BC_1 + BC_2 - F_1 - \tfrac{1}{2} P_1 - \tfrac{1}{2} P_2$

Where, $E_1$ is the epistatic deviation of $F_2$ and $E_2$ is the epistatic deviation of $BC_1 + BC_2$ (**Mather and Jinks, 1982**).

The relative of potence ratio (P) was used to determine the degree of dominance and its direction according to (**Mather and Jinks, 1982**) as follows: Potence ratio = ($F_1$ – M.P) / ½ ($P_2 - P_1$), where $P_1$ is the mean of the low parent and $P_2$ is the mean of the high parent.

The six population means in each cross were used to estimate the six parameters for gene effects using the relationships. Given by **Jinks and Jones (1958)**; namely, d, h, i,

j, and l. Where, d = additive effect, h = dominance effect, i = additive × additive type of epistasis, j = additive × dominance type of epistasis, and l= dominance × dominance type of epistasis. The estimates variances of additive (VD), dominance (VH), phenotypic (VP), environmental (VE), and genotypic (VG), from generations variances were calculated according to **Wright (1968)**.

**Mather (1949)** derived the expected genetic variance of $VBC_1$, $VBC_2$ and $VF_2$ interms of additive (1/2D) and dominance (1/4H) genetic variance as follows: ½ D = $2VF_2 − (VBC_1 + VBC_2)$ , while ¼ H = $VBC_1 + VBC_2 − VF_2 − VE$.

The variance of each of the genetic variance components was estimated as linear function of the variance of the mean squares. The variance of a mean square was calculated as given by **Anderson and Bancroft (1952)**. The standard error of the estimate is the square root of variance.

Heritability estimates were calculated in the $F_2$ generation as follows:

$$h^2 \text{ (broad sense)} = \frac{\frac{1}{2}D + \frac{1}{4}H}{\frac{1}{2}D + \frac{1}{4}H + E}$$

$$h^2 \text{ (narrow sense)} = \frac{\frac{1}{2}D}{\frac{1}{2}D + \frac{1}{4}H + E}$$

Where E = $VP_1 + VP_2 + VF_1$ / 3

Expected and predicated values of genetic advance (GS and GS %) were calculated according to **Johnson *et al*. (1955)** as GS = K × $h^2_{(ns)}$ × $\sigma$ ph where, K = selection differential (K = 2.06 when selection intensity 5%), and $\sigma$ Ph = phenotypic standard deviation of $F_2$. Genetic advance as a percent of the $F_2$ mean (GS %) was calculated as given by **Miller *et al*. (1958)** as GS% = (GS / $F_2$) × 100. Correlation coefficients calculated according to **Snedecor and Cochran (1981)**. Path coefficient analysis was computed according to **Dewey and Lu (1959)**.

## RESULTS AND DISCUSSION

### Mean Performance

Mean and standard error of the six populations ($P_1$, $F_1$, $F_2$, $Bc_1$, $Bc_2$ and $P_2$) of four soybean crosses for the studied characters are show in Table 2. The results revealed that, the $F_1$'s means were lower than the mean of parents for days to flowering and days to maturity in 2nd, 3rd and 4th crosses. These results provide evidence for the presence of heterotic effects and over-dominance gene effects and the decreasing alleles were more frequent than increasing ones in the genetic constitution of soybean genotypes. The 1st cross (L-86-K-96 × Ware) had $F_1$ mean higher than both parents for days to 90% maturity, suggesting the presence of over–dominance gene effects and the increasing alleles of this cases was predominant than decreasing ones.

The $F_2$ means were more than the $F_1$ values for days to flowering and days to maturity in all crosses, indicating the accumulation of increasing alleles for these characters.

The back cross population means are in the mid-way between the $F_1$ and the parental genotypes for days to flowering and maturity in 2nd and 4th crosses, suggesting absence of dominance and genes controlling these characters are independently segregated. But it deviated from the mid values of parents and their respective $F_1$ for the other cases. These results indicate that, polygenic and non-mendlian inheritance are more pronounced. Indicating that, these traits were quantitatively inherited. Similar results were recorded by **Adsul *et al*. (2016), Thakare *et al*. (2017), Abou Sen (2020) and Ramírez *et al*. (2022).**

Mean and standard error of the six population ($P_1$, $P_2$, $F_1$, $F_2$, $Bc_1$, and $Bc_2$) of four soybean crosses for yield and its

**Table 2. Means ± S.E. of the six populations for days to 50% flowering, days to 90% maturity, plant height, number of branches/plant and number of pods/plant of four soybean crosses during 2021 season**

| Crosses Populations | I (L-86-K-96 × Ware) | II (Egyptian × Ware) | III (H129 × Crawford) | IV (D.R101 × Giza 111) |
|---|---|---|---|---|
| **Days to 50% flowering** | | | | |
| $P_1$ | 40.58±0.156 | 50.25±0.174 | 41.25±0.358 | 52.64±0.247 |
| $P_2$ | 38.64±0.151 | 37.54±0.155 | 36.38±0.297 | 40.11±0.281 |
| $F_1$ | 40.84±0.138 | 42.35±0.188 | 37.54±0.416 | 42.34±0.390 |
| $F_2$ | 43.98±0.269 | 44.54±0.261 | 44.85±0.307 | 48.67±0.375 |
| $BC_1$ | 39.54±0.323 | 42.88±0.298 | 41.74±0.353 | 46.84±0.407 |
| $BC_2$ | 37.54±0.251 | 40.84±0.298 | 38.94±0.365 | 43.81±0.437 |
| LSD $_{0.05}$ | 2.3 | 2.15 | 1.46 | 2.55 |
| **Days to 90% maturity** | | | | |
| $P_1$ | 120.25±0.182 | 129.64±0.189 | 126.88±0.286 | 144.11±0.325 |
| $P_2$ | 124.84±0.196 | 125.84±0.218 | 122.97±0.253 | 128.69±0.352 |
| $F_1$ | 126.46±0.217 | 122.34±0.244 | 121.44±0.378 | 133.57±0.396 |
| $F_2$ | 133.85±0.279 | 127.95±0.255 | 135.98±0.358 | 138.69±0.368 |
| $BC_1$ | 122.81±0.323 | 125.64±0.308 | 130.11±0.387 | 140.67±0.406 |
| $BC_2$ | 126.06±0.281 | 123.67±0.308 | 128.61±0.409 | 135.67±0.444 |
| LSD. $_{0.05}$ | 3.15 | 2.95 | 2.37 | 3.48 |
| **Plant height (cm)** | | | | |
| $P_1$ | 70.85±0.189 | 104.45±0.237 | 122.01±0.388 | 79.67±0.325 |
| $P_2$ | 45.84±0.150 | 48.69±0.200 | 104.33±0.379 | 110.55±0.352 |
| $F_1$ | 88.11±0.207 | 100.84±0.287 | 116.64±0.427 | 115.38±0.396 |
| $F_2$ | 74.68±0.480 | 74.65±0.482 | 90.41±0.410 | 99.64±0.368 |
| $BC_1$ | 71.94±0.530 | 81.45±0.508 | 110.33±0.433 | 86.54±0.406 |
| $BC_2$ | 75.94±0.611 | 66.75±0.489 | 105.84±0.479 | 101.14±0.444 |
| LSD $_{0.05}$ | 8.10 | 7.5 | 6.34 | 8.53 |
| **Number of branches / plant** | | | | |
| $P_1$ | 4.64±0.101 | 5.07±0.119 | 4.49±0.102 | 5.02±0.117 |
| $P_2$ | 3.84±0.065 | 3.42±0.089 | 4.012±0.095 | 3.7±0.130 |
| $F_1$ | 6.5±0.117 | 6.012±0.133 | 4.76±0.179 | 4.22±0.178 |
| $F_2$ | 4.21±0.080 | 4.054±0.099 | 3.91±0.121 | 3.15±0.142 |
| $BC_1$ | 3.99±0.104 | 4.15±0.117 | 4.51±0.133 | 3.88±0.164 |
| $BC_2$ | 4.45±0.098 | 3.81±0.125 | 4.11±0.155 | 3.25±0.164 |
| LSD $_{0.05}$ | 1.5. | 1.62 | 1.1 | 1.2 |
| **Number of pods / plant** | | | | |
| $P_1$ | 119.67±0.691 | 111.35±0.751 | 133.25±0.752 | 99.74±0.961 |
| $P_2$ | 95.45±0.598 | 85.67±0.658 | 118.64±0.692 | 131.67±0.851 |
| $F_1$ | 194.84±0.96 | 189.81±1.13 | 166.99±0.865 | 215.88±1.01 |
| $F_2$ | 128.09±1.903 | 142.85±1.99 | 121.38±1.42 | 129.54±1.60 |
| $BC_1$ | 145.8±2..41 | 150.54±1.33 | 134.65±1.34 | 138.14±1.62 |
| $BC_2$ | 122.03±192 | 131.54±1.25 | 125.34±1.63 | 167.24±1.85 |
| LSD $_{0.05}$ | 15.3 | 14.78 | 15.4 | 16.2 |

**Table 3. Means ± S.E. of the six populations for number of seeds/plant, 100- seed weight and seed weight / plant of four soybean crosses during 2021 season**

| Populations \ Crosses | I (L-86-K-96 × Ware) | II (Egyptian × Ware) | III (H129 × Crawford) | IV (D.R101 × Giza 111) |
|---|---|---|---|---|
| **Number of seeds / plant** | | | | |
| $P_1$ | 270.98±2.17 | 332.54±1.77 | 255.37±1.77 | 187.41±1.90 |
| $P_2$ | 180.840±1.68 | 171.000±1.91 | 210.84±1.66 | 266.38±1.76 |
| $F_1$ | 408.640±2.28 | 433.650±2.50 | 374.35±1.88 | 318.46±2.01 |
| $F_2$ | 283.640±3.66 | 311.540±1.63 | 260.84±3.00 | 255.46±3.68 |
| $BC_1$ | 301.640±3.54 | 341.540±1.86 | 277.98±3.5 | 210.56±3.84 |
| $BC_2$ | 255.810±4.76 | 285.460±2.05 | 230.84±4.58 | 289.88±4.1 |
| $LSD_{0.05}$ | 22.4 | 23.78 | 21.47 | 25.14 |
| **100- seed weight (g)** | | | | |
| $P_1$ | 11.33±0.036 | 9.212±0.045 | 17.33±0.05 | 21.88±0.149 |
| $P_2$ | 18.540±0.064 | 18.650±0.063 | 15.38±0.086 | 17.24±0.170 |
| $F_1$ | 16.050±0.148 | 14.850±0.167 | 17.88±0.182 | 20.66±0.191 |
| $F_2$ | 14.550±0.116 | 14.250±0.135 | 16.89±0.135 | 17.14±0.163 |
| $BC_1$ | 15.021±0.133 | 11.330±0.158 | 17.06±0.158 | 19.64±0.169 |
| $BC_2$ | 16.650±0.120 | 15.850±0.143 | 16.11±0.152 | 17.85±0.201 |
| $LSD_{0.05}$ | 1.74 | 2.5 | 2.1 | 1.65 |
| **Seed weight / plant (g)** | | | | |
| $P_1$ | 28.97±0.266 | 28.345±0.307 | 45.92±0.368 | 39.45±0.506 |
| $P_2$ | 34.840±0.278 | 33.650±0.356 | 33.28±0.459 | 45.21±0.555 |
| $F_1$ | 68.940±0.868 | 65.840±0.806 | 58.46±1.01 | 60.38±0.790 |
| $F_2$ | 43.840±0.996 | 46.450±0.872 | 41.38±1.138 | 44.64±1.32 |
| $BC_1$ | 38.670±1.023 | 39.740±0.956 | 46.44±1.24 | 46.25±1.37 |
| $BC_2$ | 44.520±1.139 | 51.540±0.893 | 40.83±1.33 | 52.67±1.61 |
| $LSD_{0.05}$ | 6.4 | 3.98 | 2.47 | 5.46 |

attributes *i.e.* plant height, number of branches/ plant, number of pods/ plant, number of seeds/ plant, number of seeds/ plant, 100 seed weight and seed weight / plant are given in Tables (2 and 3). The four studied crosses varied greatly in the two parents involved in each cross and their populations of yield and its attributes. Such wide variation indicated the presence of the appreciable amount of genetic variability.

The results indicated that the $F_1$'s means were lower than $P_1$ and more than $P_2$ and mid-parents for plant height in the 2nd, and 3rd, crosses. These results provide evidence for the presence of heterotic effects and partial-dominance gene effects in the genetic constitution of soybean genotypes. Meanwhile, the $F_1$'s exceeding the high-performing parent for plant height in crosses 1st and 4th, all crosses for number of branches/ plant, number of pods/ plant, number of seeds/ plant and seed yield/ plant and in the 3rd cross for 100-seed weight. These results provide evidence for the presence of over-dominance gene effects and increasing alleles were more frequent than decreasing ones in the genetic makeup of soybean genotypes.

The $F_2$ means were lower than $F_1$ values for yield and its attributes in all crosses. These results suggest that decreasing alleles for these characters were more frequent than increasing ones, indicating the presence of inbreeding depression.

The backcross population means are in the mid-way between the $F_1$ and the parental genotypes for number of branches/ plant in the $3^{rd}$ cross, 100 seed weight and seed weight / plant in all crosses as well as plant height in the $1^{st}$ one. Also, the mid-way between the $F_1$ and the parental genotypes means were detected in $BC_1$ for number of pods/ plant in the $2^{nd}$ cross; $BC_2$ for plant height in the $1^{st}$ cross and number of seeds/plant in the $4^{th}$ one, suggesting the absence of dominance and genes controlling these characters are independently segregated. On the other hand, the backcross population means deviated from the mid values of parents and their respective $F_1$ for the other cases. These results are in harmony with those obtained by **Adsul** *et al.***, 2016; Thakare** *et al.***, 2017; Abou Sen, 2020 and Ramírez** *et al.***, 2022.**

## Scaling Test, Gene Effects and Heritability

### Flowering and to maturity dates

The scaling tests A, B, C and D were employed to test the presence of epistasis. The results given in Table 4 indicate significant non-allelic interactions for number of days to flowering and maturity in all crosses. These results indicated the presence of epistasis and the digenic model was adequate to explain the genetics of the aforementioned characters in the corresponding crosses. In this connection, the complex genetic model has controlled the inheritance of flowering and to maturity dates, **Adsul** *et al.* **(2016) and Ramírez** *et al.* **(2022)**.

The additive (d), dominance (h) and their digenic interaction types, additive x additive (i) and dominance x dominance (l) gene effects were significant in almost cases and involved in the inheritance of days to 50% flowering in all crosses and days to 90% maturity in $1^{st}$ cross. Hereby, recurrent selection system could be used for improving these characters in those crosses. In this respect, **Adsul** *et al.* **(2016) and Ramírez** *et al.* **(2022)** found that additive and dominance gene action were of primary importance in controlling flowering and to maturity dates characters.

The digenic interaction types additive × additive (i) and additive × dominance (j) in the $2^{nd}$ and $4^{th}$ crosses for days to 50% flowering and in the $1^{st}$ cross for days to 90% maturity were involved in the inheritance of theses traits. Additive × dominance (j) and dominance × dominance (l) were involved in the inheritance of days to 90% maturity only in the $4^{th}$ cross. These cross-combinations could be considered the most promising materials for recurrent selection programs for earliness. Similar results were recorded by **Thakare** *et al.* **(2017) and Abou Sen (2020).**

It is interesting to mention that, the additive (d) and dominance (h) gene actions were negative and significant for days to 90% maturity in the $1^{st}$ cross, indicating that decreasing alleles were more frequent than increasing ones in favor of decreasing days to 90% maturity.

It is noticeable that the dominance (h) and its digenic interaction type dominance × dominance (l) were significant and had different signs in all crosses for days to 50% flowering and in the $1^{st}$ and $2^{nd}$ crosses for days to 90% maturity, suggesting that interaction was predominantly of duplicate type.

**Table 4. Scaling tests and gene action for days to 50% flowering and days to 90% maturity using six populations of four soybean crosses during 2021 season**

| Crosses Estimates | I (L-86-K-96 × Ware) | II (Egyptian × Ware) | III (H129 × Crawford) | IV (D.R101 × Giza 111) |
|---|---|---|---|---|
| **Days to 50% flowering** | | | | |
| A | -2.34** | -6.84** | 4.69** | -1.3 |
| B | -4.4** | 1.79** | 3.96** | 5.17** |
| C | 15.02** | 5.67** | 26.69** | 17.25** |
| D | 10.88** | 5.36** | 9.02** | 6.69** |
| **Adequacy genetic model** | | | | |
| m | 43.98** | 44.54** | 44.85** | 48.67** |
| d | 2.00** | 2.04** | 2.8** | 3.03** |
| h | -20.53** | -12.27** | -19.32** | -17.42** |
| i | -21.76** | -10.72** | -18.04** | -13.38** |
| j | 1.03* | -4.315** | 0.365 | -3.235** |
| l | 28.5** | 15.77** | 9.39** | 9.51** |
| **Days to 90% maturity** | | | | |
| A | -1.09 | -0.7 | 11.9** | 3.66** |
| B | 0.82 | -0.84 | 12.81** | 9.08** |
| C | 37.39** | 11.64** | 51.19** | 14.82** |
| D | 18.83** | 6.59** | 13.24** | 1.04 |
| **Adequacy genetic model** | | | | |
| m | 133.85** | 127.95** | 135.98** | 138.69** |
| d | -3.25** | 1.97** | 1.5** | 5.0** |
| h | -33.75** | -18.58** | -29.96** | -4.91* |
| i | -37.66** | -13.18** | -26.48** | -2.08 |
| j | -0.955* | 0.07 | -0.455 | -2.71** |
| l | 37.93** | 14.72** | 1.77 | -10.66** |

*, ** significant at 0.05 and 0.01 probability levels, respectively.

### Seed yield and its attributes

The results in Tables 5 and 6 indicate significant non-allelic interactions for yield and its attributes in all crosses. These results indicated the presence of epistasis and the digenic model was adequate to explain the genetics of the aforementioned characters in the corresponding crosses. In this connection, the digenic model was found to be adequate to explain the genetics of plant height, number of branches/plant, number of pods/plant, number of seeds/ plant, 100 seed weight, and seed weight /

plant (**Adsul *et al.,* 2016; Ramírez *et al.,* 2022**).

The additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l) gene actions were significant for plant height in the 3rd cross, number of pods/plant in the 1st and 4th crosses and 100 seed weight in the 1st cross. Therefore, a recurrent selection procedures could be used for improving such characters.

It is interesting to mention that, the additive (d) and dominance (h) gene actions

**Table 5. Scaling tests and gene action for plant height, number of branches/plant and number of pods/plant using six populations of four soybean crosses during 2021 season**

| Crosses Estimates | I (L-86-K-96 × Ware) | II (Egyptian × Ware) | III (H129 × Crawford) | IV (D.R101 × Giza 111) |
|---|---|---|---|---|
| **Plant height (cm)** | | | | |
| **A** | -15.08** | -42.39** | -17.99** | -21.97** |
| **B** | 17.93** | -16.03** | -9.29** | -23.65** |
| **C** | 5.81** | -56.22** | -97.98** | -22.42** |
| **D** | 1.48 | 1.1 | -35.35** | 11.6** |
| **Adequacy genetic model** | | | | |
| **M** | 74.68** | 74.65** | 90.41** | 99.64** |
| **d** | -4.00** | 14.7** | 4.49** | -14.6** |
| **h** | 26.805** | 22.07** | 74.17** | -2.93 |
| **i** | -2.96 | -2.2 | 70.7** | -23.2** |
| **j** | -16.51** | -13.18** | -4.35** | 0.84 |
| **l** | 0.11 | 60.62** | -43.42** | 68.82** |
| **Number of branches / plant** | | | | |
| **A** | -3.16** | -2.782** | -0.23 | -1.48 |
| **B** | -1.44** | -1.812** | -0.552 | -1.42 |
| **C** | -4.64** | -4.298** | -2.382** | -4.56** |
| **D** | -0.02 | 0.148 | -0.8* | -0.83 |
| **Adequacy genetic model** | | | | |
| **M** | 4.21** | 4.054** | 3.91** | 3.15** |
| **d** | -0.46** | 0.34* | 0.4* | 0.63** |
| **h** | 2.3** | 1.471** | 2.11** | 1.52* |
| **i** | 0.04 | -0.296 | 1.6* | 1.66* |
| **j** | -0.86** | -0.485** | 0.161 | -0.03 |
| **l** | 4.56** | 4.89** | -0.818 | 1.24 |
| **Number of pods / plant** | | | | |
| **A** | 1.31 | 25.6** | -16.33** | -71.27** |
| **B** | -70.46** | -38.08** | -49.56** | 18.86** |
| **C** | -92.44** | -5.24 | -100.4** | -145** |
| **D** | -11.65* | 3.62 | -17.23** | -46.3* |
| **Adequacy genetic model** | | | | |
| **M** | 128.09** | 142.85** | 121.38** | 129.54** |
| **d** | 23.775** | 19.0** | 9.31** | -29.1** |
| **h** | 110.57** | 84.06** | 75.505** | 192.78** |
| **i** | 23.29* | -7.24 | 34.46** | 92.6** |
| **j** | 11.665** | 6.16** | 2.005 | -13.14** |
| **l** | 45.86** | 19.72* | 31.43** | -40.19** |

*, ** significant at 0.05 and 0.01 probability levels, respectively.

**Table 6. Scaling tests and gene action for number of seeds/plant, 100- seed weight and seed weight per plant using six populations of four soybean crosses during 2021 season**

| Crosses<br>Estimates | I (L-86-K-96 ×<br>Ware) | II (Egyptian ×<br>Ware) | III (H129 ×<br>Crawford) | IV (D.R101 ×<br>Giza 111) |
|---|---|---|---|---|
| **Number of seeds / plant** | | | | |
| A | 13.8 | 78.43** | -29.23** | -163.7** |
| B | -168** | -195.3** | -168** | 73.89** |
| C | -134.5** | -124.7** | -171.6** | -68.87** |
| D | 9.83 | -3.92 | 12.86 | 10.48 |
| **Adequacy genetic model** | | | | |
| M | 283.64** | 311.54** | 260.84** | 255.46** |
| d | 45.83** | 56.08** | 47.14** | -79.32** |
| h | 163.07** | 189.72** | 115.53** | 70.605** |
| i | -19.66 | 7.84 | -25.72 | -20.96 |
| j | 0.76 | -24.69** | 24.875** | -39.84** |
| l | 173.86** | 109** | 222.99** | 110.79** |
| **100- seed weight (g)** | | | | |
| A | -4.548** | -10.84** | 0.86* | 1.38** |
| B | 5.92** | 7.638** | **-2.99**\*\* | -6.84** |
| C | -3.77** | -0.562 | -0.91 | -11.88** |
| D | -2.571** | 1.32** | 0.61 | -3.21** |
| **Adequacy genetic model** | | | | |
| M | 14.55** | 14.25** | 16.89** | 17.14** |
| d | -1.629** | -4.52** | 0.95** | 1.79** |
| h | 6.257** | -1.721* | 0.305 | 7.52** |
| i | 5.142** | -2.64** | -1.22 | 6.42** |
| j | 1.976** | 0.199 | -0.025 | -0.53 |
| l | -6.514** | 5.842** | 3.35** | -0.96 |
| **Seed weight per plant (g)** | | | | |
| A | -26.44** | -20.01** | 1.14 | -13.09** |
| B | -8.87** | 8.895** | -22.72** | 5.51 |
| C | -26.33** | -7.875* | -30.6** | -26.86** |
| D | 4.49 | 1.62 | -4.51 | -9.64** |
| **Adequacy genetic model** | | | | |
| M | 43.84** | 46.45** | 41.38** | 44.64** |
| d | -5.85** | -11.8** | 5.61** | -6.42** |
| h | 28.055** | 31.603** | 27.88** | 37.33** |
| i | -8.98 | -3.24 | 9.02 | 19.28** |
| j | -2.915 | -9.148** | -0.71 | -3.54 |
| l | 44.29** | 14.355** | 12.56 | -11.7 |

*, ** significant at 0.05 and 0.01 probability levels, respectively.

were negative and significant for plant height in the $4^{th}$ cross, indicating that decreasing alleles were more frequent than increasing ones for plant height, on the other hand, it was positive and significant for a number of branches/ plant in the $2^{nd,}$ $3^{rd}$ and $4^{th}$ crosses, number of pods/ plant in the $1^{st}$, $2^{nd}$ and $3^{rd}$ crosses, number of seeds/ plant in all crosses, 100- seed weight in the $4^{th}$ cross and seed weight /plant in the $3^{rd}$ one, suggesting that increasing alleles were more frequent than decreasing ones for these traits.

It is noticeable that the dominance (h) and its digenic interaction dominance × dominance (l) were significant and have different signs in the $3^{rd}$ cross for plant height; the $4^{th}$ cross for number of pods plant; the $1^{st}$ and $2^{nd}$ crosses for 100-seed weight and the $1^{st}$ cross for seed weight /plant. These results indicate that interaction is predominantly of duplicate type. Whereas the sign of dominance (h) and dominance × dominance (l) was similar in the $2^{nd}$ cross for plant height, the $1^{st}$ and $2^{nd}$ crosses for number of branches/plant, the $1^{st}$, $2^{nd,}$ and $3^{rd}$ crosses for number of pods/ plant, all crosses for number of seeds/plant and the $1^{st}$ and $2^{nd}$ crosses for seed weight/plant, revealing that interaction is predominantly of complementary type.

### Heterosis, inbreeding depression, $F_2$ deviation and potence ratio

Results presented in Table 7 show that heterosis relative to mid and best parent for all traits were highly significant. Furthermore, useful heterosis relative to mid-parent was detected by the $2^{nd}$, $3^{rd,}$ and $4^{th}$ crosses for days to 50% flowering and days to 90% maturity as well as relative to best parent by the $2^{nd}$ and $3^{rd}$ crosses for days to 90% maturity and plant height, these results suggest that these crosses could be promising for earliness and plant height shortness through recurrent selection method.

Meanwhile, positive and significant heterosis relative to mid and best parent were detected for number of pods/ plant, number of seeds/ plant and seed weight / plant in all crosses and in the $1^{st}$, $2^{nd,}$ and $3^{rd}$ crosses for number of branches/plant. Moreover positive and significant heterosis relative to the mid parent was detected in all crosses and relative to the best parent in the $3^{rd}$ and $4^{th}$ crosses for 100- seed weight, these results suggest that, these crosses could be promising for seed yield and its components through selection in the advanced generation.

The inbreeding depression was negative and highly significant for days to 50% flowering in all crosses and for days to 90% maturity in the $1^{st}$ and $3^{rd}$ crosses. Meanwhile, positive highly significant inbreeding depression was detected in all crosses for all yields and its attributes. Significant effects for both heterosis and inbreeding depression seem logical since the expression of heterosis in $F_1$, s was followed by a considerable reduction in the $F_2$ performance. Also, a reduction in values of non-additive genetic components is expected caused through inbreeding depression. In addition, the conflicting estimates of heterosis and inbreeding depression were associated in most traits.

Potance ratio was less than unity but not equal to zero for days to 50% flowering in the $2^{nd}$, $3^{rd,}$ and $4^{th}$ cross; days to 90% maturity and number of branches/ plant in the $4^{th}$ cross; plant height in the $2^{nd}$ and $3^{rd}$ crosses and100 seed weight in $1^{st}$, $2^{nd,}$ and $4^{th}$ crosses, indicating partial dominance. Similar results were also reported by **Adsul *et al.* (2016)** as well as **Krisnawati and Adie (2022)**. Meanwhile, days to 50% flowering in the $1^{st}$ cross; days to 90% maturity and number of branches/ plant in the $1^{st}$, $2^{nd,}$ and $3^{rd}$ crosses; plant height in the $1^{st}$ and $4^{th}$ crosses; 100 seed weight in the $2^{nd}$ cross and number of pods/plant, number of seeds/plant and seed weight/plant

**Table 7. F$_2$ deviation (E1), back cross deviation (E2), heterosis, inbreeding depression percentage and potence ratio for the studied characters in four crosses of soybean**

| Character | Cross | (E1) | (E2) | Heterosis | | Inbreeding depression (%) | Potence ratio (P) |
|---|---|---|---|---|---|---|---|
| | | | | M.P. | B.P. | | |
| Days to 50% flowering | I | 3.76** | -3.37** | 3.11** | 5.69** | -7.67** | 1.27 |
| | II | 1.42** | -2.53** | -3.52** | 12.81** | -5.17** | -0.24 |
| | III | 6.67** | 4.33** | -3.28** | 3.19** | -19.47** | -0.52 |
| | IV | 4.31** | 1.94** | -8.70** | 5.56** | -14.95** | -0.64 |
| Days to 90% maturity | I | 9.35** | -0.13 | 3.19** | 1.30** | -5.84** | -1.71 |
| | II | 2.91** | -0.77 | -4.23** | -2.78** | -4.59 | -2.84 |
| | III | 12.80** | 12.36** | -2.79** | -1.24** | -11.97** | -1.78 |
| | IV | 3.71** | 6.37** | -2.07** | 3.79** | -3.83 | -0.37 |
| Plant height (cm) | I | 1.45* | 1.43 | 51.02** | 24.36** | 15.24** | 2.38 |
| | II | -14.01** | -29.21** | 31.70** | -3.46** | 25.97** | 0.87 |
| | III | -24.50** | -13.64** | 3.07 | -4.40** | 22.49** | 0.39 |
| | IV | -5.61** | -22.81** | 21.31** | 44.82** | 13.64** | -1.31 |
| Number of branches / plant | I | -1.16** | -2.30** | 53.30** | 40.09** | 35.23** | 5.65 |
| | II | -1.10** | -2.30** | 41.63** | 18.58** | 32.57** | 2.14 |
| | III | -0.60** | -0.39 | 11.97** | 6.01** | 17.86** | 2.13 |
| | IV | -1.14** | -1.45** | -3.21 | -15.94** | 25.36** | -0.21 |
| Number of pods / plant | I | -23.11** | -34.58** | 81.15** | 62.81** | 34.26** | -7.21 |
| | II | -1.31 | -6.24** | 92.68** | 70.46** | 24.74** | -7.11 |
| | III | -25.09** | -31.95** | 32.59** | 25.32** | 27.31** | -5.62 |
| | IV | -36.25** | -26.21** | 86.58** | 116.44** | 39.99** | 6.27 |
| Number of seeds / plant | I | -33.64** | -77.10** | 80.89** | 50.80** | 30.60** | -4.05 |
| | II | -31.17** | -58.42** | 72.24** | 30.41** | 28.16** | -2.25 |
| | III | -42.89** | -98.64** | 60.59** | 46.59** | 30.32** | -6.34 |
| | IV | -17.22** | -44.92** | 40.36** | 69.93** | 19.78** | 2.32 |
| 100- seed weight (g) | I | -0.94** | 0.69** | 7.47** | -13.43** | 9.35** | 0.31 |
| | II | -0.14 | -1.60** | 6.60** | -20.4** | 4.04** | 0.19 |
| | III | -0.23 | -1.07** | 9.32** | 16.25** | 5.54** | -1.56 |
| | IV | -2.97** | -2.73** | 5.62** | 19.84** | 17.04** | -0.47 |
| Seed weight /plant (g) | I | -6.58** | -17.66** | 116.08** | 97.88** | 36.41** | 12.62 |
| | II | -1.97* | -5.56** | 112.40** | 95.66** | 29.45** | 13.14 |
| | III | -7.65** | -10.79** | 47.63** | 75.66** | 29.22** | -2.98 |
| | IV | -6.72** | -3.79 | 42.64** | 33.55** | 26.07** | 6.27 |

I (L-86-K-96 × Ware), II (Egyptian × Ware), III (H129 × Crawford), and IV (D.R101 × Giza 111)

in all crosses were more than unity, showed over dominance. These results are in agreement with those reported by **Adsul *et al.* (2016)** as well as **Krisnawati and Adie (2022)**.

$F_2$ deviation (E1) and back cross deviation (E2) for all traits studied were either positive or negative significant or highly significant, however (E2) for days to 90% maturity in the 1st and 2nd crosses, plant height in the 1st cross, number of branches/ plant in the 3rd cross and seed weight / plant in the 4th cross as well as (E1) for number of pods/plant in the 2nd cross and 100 seed weight in the 2nd and 3rd crosses were non-significant.

### Heritability and genetic advance

Heritability values are important to the breeder since it quantifies the expected improvement upon selection to achieve genetic improvement through selection, heritability must be reasonably high. In the present investigation, the results in Table 8 show high values of heritability in broad sense.

The highest broad sense heritability values were recorded in the 1st cross for plant height (96.33%) and number of pods/ plant (95.96%), the 4th one for number of seeds/pod (93.41%), and seed weight / plant (94.28%). Furthermore, the highest narrow sense heritability values were observed for plant height (92.96%) in the 2nd cross, number of pods/ plant (89.88%) in the 3rd cross and seed weight / plant (87.59%) in the 2nd one. Meanwhile, the lowest broad sense heritability estimates were detected for number of seeds/ pod (59.09%) in the 2nd cross, number of branches/ plant in the 1st cross and days to 50% flowering (65.70%) in the 3rd cross. Moreover, the lowest narrow sense heritability estimates were recorded for number of seeds/pod (16.11%) in the 3rd cross, number of branches/plant in the 1st cross (39.75%) and the 2nd one (48.93%) and plant height (58.17%) in the 1st cross. The values of heritability in narrow sense which indicate

to the proportion of phenotypic variance that results from additive genetic variance, were high in magnitude but were lower than their corresponding broad sense values. Genetic advance estimates from selection 5% superior plants of the $F_2$ generation showed the highest values for number of seeds/ plant in the 1st cross (80.35) and in the 4th cross (98.31), number of pods/ plant in the 3rd cross (40.84) and the 4th one (41.79) and seed weight / plant in 3rd cross (26.47) and 4th one (30.05). While, low estimates were observed for number of branches/plant in all crosses (1.01, 1.54, 2.30 and 3.02, respectively) and 100 seed weight in all crosses (3.03, 3.24, 2.90 and 3.63, respectively). Genetic advance values as a percentage of $F_2$ mean (G.S/$F_2$%) were high for the number of branches/ plant in the 2nd cross (37.95), 3rd cross (58.80) and 4th one (96.01); number of pods/ plant in 1st cross (32.58), 3rd cross (33.64) and 4th one (32.26); number of seeds/ plant in the 4th cross (38.48) and seed weight / plant in all crosses.

The genetic advance under selection depends on the amount of genetic variability, the magnitude of the masking effect of the environment and the intensity of selection that is practiced. In terms of the progress expected, the confounding of non-additive with the additive genetic variance will have an effect in future generations, due to the non-additive variance included in the estimates. Therefore, the expected genetic advance for characters in this study was derived by using heritability in the narrow sense. These results are in harmony with the findings by, **Jain *et al.* (2018), Koraddi and Basavaraja (2019), and Prathima *et al.* (2022).**

### Correlation and path coefficient

Correlation results indicated that number of branches/plant, number of pods/ plant and number of seeds/ plant had significant positive correlation with seed weight / plant, whereas, days to 50% flowering had negative correlation with this parameter

**Table 8. Heritability in broad and narrow senses and genetic advance for studied characters in four crosses of soybean**

| Character | Cross | Heritability | | Genetic advance | |
|---|---|---|---|---|---|
| | | Broad sense | Narrow sense | Δ G | Δ G (%) |
| **Days to 50% flowering** | I | 92.39 | 84.06 | 7.21 | 16.40 |
| | II | 89.07 | 81.38 | 6.79 | 15.24 |
| | III | 65.70 | 63.60 | 6.24 | 13.91 |
| | IV | 69.84 | 67.37 | 5.13 | 10.54 |
| **Days to 90% maturity** | I | 87.31 | 82.11 | 7.31 | 5.46 |
| | II | 81.76 | 80.50 | 6.56 | 5.13 |
| | III | 81.28 | 76.88 | 8.80 | 6.47 |
| | IV | 82.66 | 73.19 | 8.75 | 6.31 |
| **Plant height (cm)** | I | 96.33 | 58.17 | 8.91 | 11.94 |
| | II | 93.57 | 92.96 | 14.29 | 19.14 |
| | III | 76.38 | 75.82 | 9.92 | 10.97 |
| | IV | 76.22 | 66.65 | 7.83 | 7.86 |
| **Number of branches / plant** | I | 63.06 | 39.75 | 1.01 | 23.97 |
| | II | 65.81 | 48.93 | 1.54 | 37.95 |
| | III | 71.00 | 59.32 | 2.30 | 58.80 |
| | IV | 74.59 | 66.74 | 3.02 | 96.01 |
| **Number of pods / plant** | I | 95.96 | 68.70 | 41.73 | 32.58 |
| | II | 86.79 | 83.99 | 32.14 | 22.50 |
| | III | 92.62 | 89.88 | 40.84 | 33.64 |
| | IV | 91.32 | 81.75 | 41.79 | 32.26 |
| **Number of seeds / plant** | I | 92.09 | 68.78 | 80.35 | 28.33 |
| | II | 59.09 | 55.90 | 29.09 | 9.34 |
| | III | 91.29 | 16.11 | 15.44 | 5.92 |
| | IV | 93.41 | 83.69 | 98.31 | 38.48 |
| **100- seed weight (g)** | I | 83.15 | 81.57 | 3.03 | 20.82 |
| | II | 84.34 | 75.40 | 3.24 | 22.73 |
| | III | 80.35 | 67.28 | 2.90 | 17.14 |
| | IV | 72.48 | 69.86 | 3.63 | 21.19 |
| **Seed weight/plant (g)** | I | 92.43 | 82.04 | 26.09 | 59.50 |
| | II | 90.48 | 87.59 | 24.39 | 52.50 |
| | III | 91.17 | 72.87 | 26.47 | 63.96 |
| | IV | 94.28 | 71.54 | 30.05 | 67.31 |

I (L-86-K-96 × Ware), II (Egyptian × Ware), III (H129 × Crawford), and IV (D.R101 × Giza 111)

(Table 9). Positive and significant correlation was recorded between days to50% flowering had negative correlation with this parameter (Table 9). Positive and significant correlation was recorded between days to 50% flowering with days to 90% maturity (0.771**); plant height with number of pods/plant (0.484*); days to 90% maturity with 100-seed weight (0.494*); number of branches/ plant with number of pods/ plant (0.401*), and number of seeds/ plant with number of branches/plant (0.628**) and number of pods/plant (0.783**). 100- seed weight exhibited negative and significant correlation with number of seeds/ plant (-0.424*). Number of branches (0.92) showed the uttermost correlation with seed yield (**Ghanbari *et al.* 2018**). **Santosh *et al.* (2020)** showed that number of branches/ plant and number of seeds/pod exhibited significantly positive correlation with seed weight/ plant. On the other side, **Kuswantoro *et al.* (2018)** reported that, the correlation of all seed yield components with yield was not significant, while plant height tended to have a higher number of branches.

Direct and indirect effects for some agronomic traits on seed yield/plant relative to correlation coefficients are showing in Table 10. The direct effect on seed weight /

plant for most studied traits was positive except days to 50% flowering (-0.300) and plant height (-0.072). The results displayed that number of seeds/ plant had the largest direct effect on seed weight / plant (0.906) followed by 100- seed weight (0.565), then days to 90% maturity (0.303), number of pods/plant (0.134), and number of branches /plant (0.040). Number of seeds/plant showed the highest positive indirect effects on seed weight /plant *via* number of pods/ plant (0.709), Number of branches/ plant (0.569), and Plant height (0.329). 100- seed weight had positive indirect effect on seed yield/ plant via and days to 90% maturity (0.279). On the other hand, days to 50% flowering, plant height and number of seeds/ plant showed negative indirect effect on seed weight / plant *via* 100- seed weight. Also, **Ferrari *et al.* (2018)** reported that, the number of branches and number of pods/plant had the greatest direct and indirect effects on seed yield.

Generally, the previous results revealed that number of seeds/plant, 100-seed weight, number of pods/ plant, number of branches/ plant, and days to 90% maturity were considered the major seed yield components and attributes that the soybean breeder should take into account for developing high yielding soybean genotypes.

**Table 9. Simple correlation coefficients for various metric traits in soybean genotypes**

| Trait | Days to 50% flowering | Days to 90% maturity | Plant height | Number of branches/ plant | Number of pods/ plant | Number of seeds/ plant | 100- seed weight | Seed weight / plant |
|---|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | 1 | | | | | | | |
| **Days to 90% maturity** | 0.771** | 1 | | | | | | |
| **Plant height** | 0.099$^{ns}$ | 0.136$^{ns}$ | 1 | | | | | |
| **Number of branches/ plant** | 0.069$^{ns}$ | -0.238$^{ns}$ | 0.185$^{ns}$ | 1 | | | | |
| **Number of pods/ plant** | -0.065$^{ns}$ | -0.083$^{ns}$ | 0.484* | 0.401* | 1 | | | |
| **Number of seeds/ plant** | 0.002$^{ns}$ | -0.341$^{ns}$ | 0.363$^{ns}$ | 0.628** | 0.783** | 1 | | |
| **100- seed weight** | 0.009$^{ns}$ | 0.494* | 0.052$^{ns}$ | -0.211$^{ns}$ | 0.054$^{ns}$ | -0.424$^{ns}$ | 1 | |
| **Seed weight / plant** | -0.072$^{ns}$ | 0.012$^{ns}$ | 0.37$^{ns}$ | 0.437* | 0.849** | 0.666** | 0.323$^{ns}$ | 1 |

ns, * and ** no significant, significant at 0.05 and significant at 0.01, probability levels respectively.

**Table 10. Direct (Diagonal) and indirect effect for studied traits on seed weight/plant**

| Trait | Days to 50% flowering | Days to 90% maturity | Plant height | Number of branches/ plant | Number of pods/ plant | Number of seeds/ plant | 100- seed weight |
|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | **-0.300** | 0.234 | -0.007 | 0.003 | -0.009 | 0.002 | 0.005 |
| **Days to 90% maturity** | -0.231 | **0.303** | -0.010 | -0.009 | -0.011 | -0.309 | 0.279 |
| **Plant height** | -0.030 | 0.041 | **-0.072** | 0.007 | 0.065 | 0.329 | 0.029 |
| **Number of branches/ plant** | -0.021 | -0.072 | -0.013 | **0.040** | 0.054 | 0.569 | -0.119 |
| **Number of pods/ plant** | 0.020 | -0.025 | -0.035 | 0.016 | **0.134** | 0.709 | 0.031 |
| **Number of seeds/ plant** | -0.001 | -0.103 | -0.026 | 0.025 | 0.105 | **0.906** | -0.240 |
| **100- seed weight** | -0.003 | 0.150 | -0.004 | -0.008 | 0.007 | -0.384 | **0.565** |

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# الملخص العربي

## التحليل الوراثى لمحصول البذور وبعض الصفات المرتبطه به لاربعة هجن من فول الصويا

إسماعيل أبوبكر الصديق اسماعيل محمد [1]، ثروت محب أبوسن[1]، محمد إبراهيم السيد عبد الحميد[2]

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أجريت هذه الدراسة خلال المواسم الزراعية الصيفية للأعوام 2019، 2020 و2021، تحت ظروف محطة البحوث الزراعية بسخا، كفر الشيخ، مصر. وذلك لتحديد الموديل الوراثي الملائم وطرز الفعل الجيني المتحكم في وراثة صفات التبكير وكذلك محصول البذور ومساهماته في العشائر الستة لأربعة هجن من فول الصويا هي,(Ware x96-K-86-L) I (Giza 111 x D.R101) IV (Crawford x H129) III ,(Ware x Egyptian) II وقد أظهرت نتائج اختبار المقياس (A, B, C and D) أن الموديل الوراثي المعقد هو الملائم لتفسير وراثة جميع الصفات في جميع الهجن تحت الدراسة. كان الفعل الجيني المضيف والسيادي والتفاعل (مضيف × مضيف)، (مضيف × سيادي) و(سيادي × سيادي) معنويا لصفات عدد الأيام حتى 50% تزهير في جميع الهجن، عدد الأيام حتى النضج ووزن 100 بذرة في الهجين الأول، ارتفاع النبات في الهجين الثالث، عدد القرون/النبات في الهجينين الأول والرابع. كان التفاعل غير الأليلى من النوع المتضاعف هو السائد في وراثة صفات ارتفاع النبات في الهجين الثالث، عدد القرون/النبات في الهجين الرابع، وزن 100 بذرة في الهجينين الأول والثاني. سجلت الصفات ارتفاع النبات ووزن البذور/النبات في الهجين الثاني وعدد القرون/النبات في الهجين الثالث أعلى القيم لكفاءة التوريث في المعنى الضيق. كانت قوة الهجين بالنسبة لمتوسط الآباء والأب الأفضل موجبة ومعنوية لصفات عدد القرون/النبات وعدد البذور/النبات ووزن البذور /النبات في جميع الهجن وعدد الأفرع /النبات في الهجن الأول والثاني والثالث. كان الارتباط موجب ومعنوى بين وزن البذور/النبات وبين كل من عدد القرون/النبات وعدد البذور/النبات. كان لعدد البذور/النبات، وزن 100بذرة وعدد القرون/النبات أعلى تأثير مباشر على كمية وزن البذور/النبات.

**الكلمات الاسترشادية:** فول الصويا، العشائر الستة، التبكير، محصول البذور.

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