IV - EXPERIMENTAL RESULTS

Nature of gene action, degree of dominance, heterosis, inbreeding depression, minimum number of operating genes, and heritability were estimated for the economic characters studied in the interspecific hybrid.

The following is the results obtaind in this study.

1- Inheritance of days to flowering : (Number of days from planting to anthesis of the first male and female flowers)

a) Male flower. The mean day to flowering variance, standard error, C.V % and the arithmetic mean for days to flowering are given in Table (3) for the parents : Cucurbita pepo and Cucurbita moschata), F_1, F_2 , BC_1 and BC_2 populations. Significant difference was found among the two species, therefore, genetic difference among the two species was probable. C.pepo (p_1) was earlier in flowering (mean 35.00 $\pm$ 0.14) days than C.moschata (p_2) with a mean of (41.27 $\pm$ 0.14) days. Greater variability was encountered in F_2 , BC_1, and BC_2 than in F_1 and both parents.

The difference between the observed and arithmetic mean (mid-parent) of F_1 population was highly significant. Moreover, the scaling tests (A and B) were highly significant compared zero. Therefore, the additive-dominant

model is not adequate. The estimates of the different kinds of the gene effects were shown in table (5) along with their standard errors. Each value of different types of gene effects was higher than its standard error. However, all values negative sign except of the dominance x dominance gene interaction (l) which was positive (48.59 ± 12.18).

The difference between F_1 and P_2 (the late flowering sp. C. moschata) was significant indicating over-dominance for late flowering. This evidence for over-dominance in this cross was substantiated by both potence ratio ($3:48^{**}$) and $\sqrt{H/D}$ (-1.44) value.

The variances of backcrossing of the F_1 to C. pepo and C. moschata were 8.38 and 6.74, respectively. Thus, the late parent C. moschata must had a preponderance of dominant genes.

The value of $\sqrt{HD}$ (-24.03) is not equal to the value of dh (1.65) indicating that all the h alleles are not with the same sign, Table (4). The parent C. moschata must has a preponderance of dominance genes and some of them must be recessive to their allels from C. peop.

Partitioning phenotypic variance into its components showed that the additive (½ D), the domenance (¼ H)and environmental (E) variances were (-4.18) , (8.64) and (1.02) , respectively, table (4).

The estimations of heterosis over the mid-parents and the better parent were (28.59%) and (40.10%) , respectively, table (5).

The inbreeding depression was (19.67%) and (-2.30%) as compared to the mean of F_1 and the mid-parents, respectively, Table (5).

Heritability values in broad sense were (81.41%), 81.48% and 81.53% as obtained by using the variance of the F_1as environmental variance, square root of the two parental variances and cube root of P_1 , P_2 and F_1 variances, and F_1 variances, respectively. Heritability in narrow sense could not be estimated due to negative value of additive gentic variance (D) , Table (6).

The Castle-Wright and Wright's formula gave (1.10) and (2.24) pair of genes respectively.

b) Female Flower : The data on the mean number of days to opening of the first female flower for C. pepo and C. moschata are given in table (3).

Significant difference was found between the means of the two species as regard to mumber of days-to-flowering, therefor, genetic differences among the two species were expected The species C. pepo is earlier in flowering than C. moschata, the means of days-to-flowering were 38.86 ± 0.16 and 51.57 ± 0.12 days , respectively.

Data on the means of F_1 and the segregating populations, e.g., F_2 , BC_1 , and BC_2 together with their variances, S.E., and C.V% are given in, Table (3).

Greater variabilities were found in the segregating populations than that in the F_1 generation and the two parents.

The difference between the observed F_1 mean and the arithmetic one was highly significant (t = 77.86), Table(3). Moreover, the scaling tests (A and B) were highly significant different from zero, (-29.23 ± 6.05 and 31.51 ± 6.48, respectively). Accordingly, the additive - dominant model is not adequate to interpret gene effects.

The estimates of the different kinds of gene effects (six parameter model) are shown in Table (5). Each value of the additive (d), dominant (h), additive x additive (i) , and dominant x dominant (l) gene effects was higher

than its standard error.

Besides, all values had negative signs except that for dom. x dom. gene effects which had a positive value of 103.94 ± 14.40. The value for add. x dom. gene effects was equal to its standard error.

The difference between the mean of the F_1 (59.27 ± 0.15 days) and that of the late flowering species, i.e., C. moschata (51.57 ± 0.12 days) was significant. This might be an indication of overdominance for late flowering character. The presence of overdominance is substantiated by a significant value (2.21^{**}) of potence ratio and a negative value (-0.60) of $\sqrt{H/D}$, Table (2).

Accordingly, preponderance of dominant genes are presented in the late flowering parent , i.e., C. moschata. Moreover, the value of $\sqrt{HD}$ was (-24.03) , and it was not equal to the dh value (1.65) which indicated that all of h alleles are not with the same sign, Table (2), nd the parent C. moschata must have a preponderance of dominant genes, however, some of them may be recessive to their alleles from C. pepo parent .

The mean days-to-flowering of the F_2 generation is

47.86 with variance of 5.12 , Table (1). Partitioning of the phenotypic variance into its components using the two backcrosses and F_2 variances gave value of (-8.25) for the additive ($\frac{1}{2}D$) , 3.05 for dominance ($\frac{1}{4}H$), and 1.18 for the environmental variance (E), Table (2).

Heterosis over mid-parents was 31.08% and was 52.53% as estimated from the better parent, Table (3). Besides, the inbreeding depression values were (19.24%) and (-5.85%) as compared with the mean of the F_1 and the mid-parent, respectively, Table (3).

Heritability in broad sense was quite high (78.64%) when the variance of the F_1 was used as an environmental variance. When variances of the two parents were used, heritability was 76.67% . And when variances of P_1 , P_2, and F_1 were used, heritability was 75.76 % , However, heritability in narrow sense could not be estimated by using Warner's (1952) formula.

The minimum number of genes were 5.02 and 17.27 pairs as it was estimated using Castle-Wright and Wright formula, respectively.

2- Inheritance of number of flowers per plant :

The two species C. pepo and C. moschata are monoecious

plants and both male and female flowers are important for sitting fruits. However, female flowers are related more to fruit yield.

a) Number of male flowers per plant:

The species C.pepo produced more male flowers (20.00 ± 0.56) per plant than C. moschata (15.0 ± 0.10). The plants of the F_1 generation carried intermediate number of flowers per plant (17.77) , Table (1), and the mean number of male flowers per plant were (15.88 ± 0.30), (14.87 ± 0.29), and (18.42 ± 0.15) for the BC_1 , BC_2, and F_2 generations, respectively. More variabilities were found in the segregating generation than for the parents and F_1 generations, Table (1).

The difference between the observed and the arithmetic means of the F_1 population was insignificant. Moreover, the scaling tests (A, B, and C) were insignificantly different from zero, Table (1). Therefore , the additive dominant model is adequate to interpret gene effects for that trait . However, the six parameter model was also used to detect other types of gene effects. Data in Table (3) showed the five types of gene effects along with their standard errors. All kinds of gene effects had negative values except that of the additive gene

effects (d) which had positive and significant value (2.50 ± 0.46) and dom x dom (l) which gave value of (21.24 ± 8.39).

The mean of the F_1 generation was 17.77 and lays between both parents . And it was significantly different from that of both parent means. Moreover, the mean of the F_1 is slightly higher than the mid-parent value, Table (3) , Therefore, dominance was partial for more-numbered male flowers. Potence ratio was 0.11 which indicated partial dominance, Table (5). However, the $\sqrt{H/D}$ degree of dominance gave a high value (3.27), Table, (5).

The variance of BC_1 (F_1 x C. pepo) was (5.13) which was higher than the variance of BC_2 (4.47), (F_1 x C. moschata). Both parents possessed dominant alleles, however C. pepo must has some recessive alleles. The value of $\sqrt{H.D}$ was (1.18) and it was greater than the value of dh (0.23), therefore, the h alleles are not with the same sign, Table (4).

Partitioning of the phenotypic variance showed that the additive variance ($\frac{1}{2}D$) , dominance variance ($\frac{1}{4}H$), and environmental variance (E) were (0.18) , (0.97), and (0.87), respectively, Table (4).

Heterosis values of 1.54 and 18.47 as a percent deviated from mid-parent and C.moschata parent, respectively.

The inbreeding depression was (0.65%) and (0.95%) , as a deviation from F_1 and mid-parent respectively.

Heritability estimats were 85.03% , 83.11% , and 93.25% , when calculating environmental variances from F_1, the two parents, and the cubic root of $P_1 + P_2 + F_1$ variances, respectively. However, heritability in narrow sense was 3.63% , Table (5).

The minimum number of genes were estimated by Castle-Wright and Wrigh's formulae and the number reached to be 0.75 and 0.76 pair, respectively.

b) Number of female flowers per plant :

Data on the mean number of female flowers per plant, standard error, variance and C.V% are given in Table (3). Significant differences had existed between C. pepo (8.52 ± 0.15) and C.moschata (4.95 ± 0.13). Therefore, genetic differences are probable between the two species. The mean of the F_1 generation was 10.68 ± 0.12 which significantly exceeded the better parent (C. pepo) . Besides, the mean of the BC_1 (backcross to C. pepo) was higher than the

mean of the BC_2 (backcross to C. moschata), Table (3). Meanwhile the mean of the F_2 generation (6.6 ± .16) intermediated the two parental means.

The expected F_1 mean was significantly lower (6.73) than the observed one (10.68 ± 0.12). Accordingly, the additive - dominant model is not adequate. However scaling tests (A,B and C) were lower than their standard errors.

Estimation of different kindSof gene effects gave positive and significant values for the additive effects (d) and dominant effects (h) . And all types of gene interactions values had insignificantly differed from zero, Table (5).

Hybrid vigour is expected since the mean of the F_1 generation was significantly higher than the mean of the highest parent C. pepo , and potence ratio was also significant (2.21^{**}) . This proved to be an evidence for over-dominance. Dominant genes seemed to be alike with the same sign since the values of $\sqrt{H.D}$ and dh are almost equal.

Estimation of heterosis was 58.61% and 25.37% over the mid-parent and better parent, respectively.

Values of inbreeding depression were (-38.20%) and (-1.98%) calculated from the F_1 and mid-parent, respectively.

Heritability values in the broad sense were 84.86%, and 95.52% as the environmental variance was used respectively from F_1 variance, the variance of the two parents, and the cubic root of $p_1 + p_2 + F_1$. Narrow sense heritability was also high (81.36%), Table (5).

The minimum number of genes was (0.37) and (1.25) as it was estimated by Castle-Wright and Wright formulae, respectively, Table (5).

3- Inheritance of six ratio : The ratio between number of male flowers to female flowers are obtained for each plant in each population. Sex ratio means, variance, standard errors, coefficient of variation, and arithmetic F_1 means are given in Table (3) for the parents F_1, F_2 and the two backcrosses.

Significant difference was found between the mean of the C. pepo (2.41 $\pm$ 0.08) and C. moschata (3.14 $\pm$ 0.12). Thus genetic difference among the two species was probable. Slight difference was found between the observed and airthmetic mean of the F_1 generation. Moreover, scaling tests

A, B and C had insignificantly differed from zero.

The estimated parameters of gene effects using the population means, were given in table (4). All values had negative sign except the additive gene effect d and dominance x dominance gene interaction l which were positive. And all values did not differ from zero.

The difference between F_1 and P_2 was significant. However, the F_1 mean was likely to be intermediate between the parental means. This result explained the presence of dominance, potence ratio had value of (-3.0), and degree of dominance was (3.26).

The variances of backcrosses of the F_1 to C. pepo and C. moschata were (3.50) and (3.81), respectively, therefore the genes from C. pepo may show the dominance effects.

The difference between the $\sqrt{H.D}$ (4.33) and dh(0.31) was significant indicating that the (h) alleles did not have the same sign, Table ( ).

Mather (1949) method was used for partitioning phenotypic variance in the F_2 into its components . This showed

that the additive variance ($\frac{1}{2}$ D), dominance ($\frac{1}{4}$ H) and environmental (E) were (0.66) , (3.71) and (0.98) respectively , Table (4).

Means percentage of heterosis over the mid-parents and the better parent were (-39.80%)and (14.97%) respectively, Table (5).

The estimation of inbreeding depression were (-3.96%) and (-25,54%) compared to the means of F_1 and the mid-parents, respectively, table (5).

The values of broad sense heritability were (91.81%), (92.55%) and (92.75%) respectively. However, heritability in narrow sense was 88.82, Table (5).

Results indicated that there was one pair of genes controlling the difference between the two parents, table (5).

4- Inheritance of number of mature fruits / plant :

Completely mature fruits per plant were counted. Mean variances, standard errors, and coefficients of variation for the number of mature fruits per plant are given in table (3) for the parents, F_1 , F_2 , BC_1 and BC_2 generations.

C. moschata produced mature fruits per plant with a mean of (3.00 ± 0.12) which is more than C. pepo (1.60 ± 0.11). Therefore, genetic difference is probable between the two species.

The variances of the parents and the F_1 generations were lower than that of the segregating generations, while the mean of the F_1 was lower than the mean of the better parent, C. moschata, Table (3).

The difference between the observed and arithmetic means of the F_1 population was insignificant. Moreover, the scaling tests (A, B and C) did not differ from zero. Hence the additive - dominant model is adequate. The estimates of the different kinds of gene effects are shown in table (5), along with the standard errores. All values had positive sign except the additive x dominance type of epistasis j and dominance x dominance type of epistasis (l) which had negative values : (-2.01 ± 1.12) and (-6.56 ± 5.41) , respectively, Table (5). Types of gene interaction (i) , (j) , and (l) did not differ from zero, Table (5).

Dominance was partial, since the mean of the F_1 was

lower than the better parent and this was substantiated by both potency ratio (0.49) and $\sqrt{H/D}$ value (-0.99).

The variances of backcrosses of the F_1 to C. pepo and C. moschata were (1.82) and (1.53) , Therefore the genes from C. moschata showed to be dominant.

The estimation of $\sqrt{H.D}$ was (-1.42) which is non equal to dh (0.29) , Therefore, all h alleles were not with the same sign, Table (6). The parent C. moschata must have a preponderance of dominance genes and some of them must be recessive to their alleles from C. pepo.

The results of partitioning phenotypic variance into its components, showed that the additive variance ($\frac{1}{2}D$), dominant effect ($\frac{1}{4}H$) and environmental action (E) were (o.75) , (0.35) and (0.64), respectively, Table (4).

The expression of heterosis in the F_1 over the mid-parents and the better parent were (14.78 %) and (-12%), respectively, Table (5).

The inbreeding depression were (0.38%) and (-14.35%) when determined by using the means of F_1 and midparents.

Broad-sense heritability value was 57.77 % when F_1 variance was used as environmental variance, while narrow-sense heritability could not be estimated.

The estimated number of genes determined by using Castile - Wright and Wright's formulae gave (0.43) and (0.46) pair of genes, respectively.

5- Inheritance of fruit weight: The fully matured fruits of each single plant in the parental species, F_1 , F_2 , BC_1 and BC_2 were weighted and the mean of fruit weight in kelograms are given in Table (3).

Plants of C. pepo bear small fruits (1.08 $\pm$ 0.02Kg), where plants of C. moschata beared heavier fruits with a mean weight of (5.35 $\pm$ 0.08) . Mean of fruit weight in the F_1 was (1.09 $\pm$ 0.09 Kg).

The average fruit weight in the F_2 generation was (2.35 $\pm$ 0.17 Kg) . Variances of the F_2 gnd backcrosses was greater than those of the F_1 and the parents. Table (3).

Significant difference was found between the mean of the F_1 and the arithmetic (mid - parent) mean (3.21 Kg).

Also, there were insignificant values of scaling tests A , B , and C which . indicates the adequcy of the additive dominant model.

The six parameter model is shown in table ( ). Significant value was found for the parameter (d), the additive gene effects had gave value of (2.13 $\pm$ 0.28).

Insignificant values for the other parameters were obtained and had negative signs except that of the mean and the dominant x dominant gene interaction (l) which had positive signs.

Insignificant difference was found between the mean of the F_1 and the light fruited parent C.pepo. (Mean of 1.09 $\pm$ 0.09 and 1.08 $\pm$ 0.02 , respectively) This could indicate presence of complete dominance of the light fruit. And potency ratio was (1.96^{**}) and the degree of dominance was (0.83) which suggested presence of complete dominance.

The variances of BC_1 and BC_2 (crosses of the F_1 plants to P_1 and P_2 , respectively) were (1.50) and(1.85), respectively. And the value of $\sqrt{H.D}$ was (2.33) and that was not equal to the difference of the variance of the two backcrosses (dh = -0.35) , Table (6).

Partitoning of phenotypic variance for the F_2 into its components showed that the additive variance ($\frac{1}{2}D$), dominance variance ($\frac{1}{4}H$), and environmental variance (E) were 1.41, 0.48 and 0.49 , respectively, Table (6).

Broad sense heritability values were 54.22% , 97.22%, and 83.99% when variance of the F_1 , the two parents variance, and the variances of the three were used as an

environmental variance respectively. Heritability in narrow sense was 59.24% , Table (5).

The minimum numbersof effective factorsas estimated by Castle Wright and Wright formulae were 1.55 to 1.86 pairs of genes, respectively.

6- Inheritance of fruit length: The mean for fruit length in P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 were (24.52 ± 0.12), (52.64 ± 0.19), (36.52 ± 0.13) , (22.06 ± 0.37), (39,66 ± 0.31). and (56.78 ± 0.13) and the coefficient of variation were 3.99%, 2.67%, 2.66%, 12.65%,5.85%and 28.83%respectively. Besides, the expected means were 38.73 and 37.63 for F_1 and F_2 respectively, Table (3).

Significant difference was found between (P_1) C. pepo and (P_2) C. moschata, therefore genetic difference among the two species was apparent. The species C. moschata (P_2) was greater in fruit length (mean 52.64 ± 0.19 cm). Than C. pepo (P_1) with a mean (24.82 ± 0.12 cm) and greater variability were found between F_2 , BC_1 and BC_2 than in F_1 and both parents.

The difference between the observed and arithmetic means of F_1 population was highly significant, moreover,

the scaling test (A and C) had highly significantly differed from zero , therefore, the additive - dominant model is not adequat.

Estimating of the different kinds of the gene effects were shown in table (4) , along with their standard errors.

All values were significant and had negative signs e except the additive (d) and dominance x dominance gene interactions (l) which had positive signs (13.91 $\pm$ 2.65) and (130.77 $\pm$ 29.20), respectively, Table (4).

The difference between F_1 and (P_1) the short fruited parent. Sp (C. pepo) was significant and showing partial dominance for short fruits. The potency ratio was (-0.56) and degree of dominance was (2.23).

The variances of backcrosses (BC_1 and BC_2) were (7.79) and (5.37), respectively. And the value of $\sqrt{H.D}$ was nearly equal to the value of (dh).

Partitioning phenotypic variance in F_2 into its components showed that the additive variance ($\frac{1}{2}D$), dominant effect ($\frac{1}{4}H$) and environmental (E) where (2.49), (0.25) and (1.31), respectively , Table (6).

Heterosis over the mid-parents and the better parent

were (-5.71%) and (30.62%) respectively, Table (5).

The inbreeding depression were (+5.86 %) and (0.94%) as compared with the mean of F_1 and mid-parents, respectively, Table (5).

The broad sense heritability values of fruit length were (87,92%) by using the F_1 variance, (82.14%) by using the squar root of variance of the two parents, and (84.6&%) by using the three variances of the parents and F_1, and narrow sense heritability by using Warner method was (31.93%), table (5).

The estimated minimum number of effective factors using Castle-Wright and Wright formulaegave (14.06) and (14.23) pair of genes, respectively.

7- Inheritance of fruit width : The mean of fruit width, variance, standard error, C.V % and the mid parent value of fruit width are given in Table (3), for the parnets C. pepo (P_1) , C. moschata (P_1) , F_1 , F_2 , BC_1 and BC_2

Significant difference was found among the two species was probable. C. Moschata (P_2) was greater in fruit width (mean 26.13 ± 0.19 cm) than C.pepo (P_1) with a mean

(10.36 $\pm$ 0.17 cm), Greater variability was encountered in F_2, BC_1 and BC_2 than F_1 and both parents.

The difference between the observed mean of the F_1 and the mid-parent was insignificant, and the scaling tests A, B, and C did not differ from zero.

The estimates of the different kinds of gene effects are shown in table (4). Values of the additive (d), dominance (h), and additive x dominance (j) values had significantly differed from zero. And all parameters had negative signsexcept the additive (d) and dominance x dominance gene interaction (l) were positive, table (4).

The difference between F_1 and P_2 parent Sp C. moschata was significant indicating partial dominance of the wide fruit, this evidence for partial dominance in this cross was substantiated by degree of dominance value of (0.98), table (6).

The average variances of backcrosses of the F_1 to C. pepo (P_1) and C. moschata (P_2) are (4.06) and (5.31), respectively. And the value of $\sqrt{H.D}$ (6.39) is not equal to the value of dh (-1.25), table (6).

Partitioning phenotypic variance in F_2 into its components showed that the additive variance ($\frac{1}{2}D$), dominance

variance ($\frac{1}{4}$H) and environmental (E) were (3.28), (1.56) and (1.57), respectively , Table (6).

The estimations of heterosis over the mid-parents and the better parent were (-1.81 %) and (45.66%) respectively , table (5). The inbreeding depression were (-16.69%) and (-14.58%) as compared with the mean of F_1 and mid-parents. The number of gene difference between two the parents were seven pairs of Genes.

8- Inheritance of fruit shape index : The data of this character are given in Table (3). The observed means and standard erros for P_1 , P_2 F_1 BC_1 , BC_2 and E_2 were (2.48 $\pm$ 0.09) , (1.74 $\pm$ 0.05) , (2.13 $\pm$ 0.05), (2.02 $\pm$ 0.13), (2.70 $\pm$ 0.13) and (2.59 $\pm$ 0.07) , respectively.

The coefficients of variability for these populations were 25.31% 19.31% 15.92% 47.85% , 35.04% and 38.89% respectively.

A great difference was found between the mean of the two species (C. pepo) and C. maschata , Table (3).

The great variation was found in F_2 , BC_1 and BC_2 than F_1 and parents.

The comparisons between the actual mean of F_1

generation and its mid-parent mean was insignificant. There were insignificant values for the three scaling tests, i.e, A, B and C which indicated the adequancy of the additive dominant model.

The determination of the different kinds of the gene effects are shown in table (4) , along with their standard error. All values had negative sign except the additive gene effect (d) and dominance x dominance gene interaction (l) were positive (0.37 $\pm$ 0.50) and (3.07 $\pm$ 8.86) respectively. All values had insignificantly differed from zero except that for dominant gene effects (h) which had value of (-15.94 $\pm$ 5.92), Table (4).

The different between the means of F_1 and (P_2) sp (C.pepo) was significant . Moreover the mean of F_1 was greater than the mid- parent which indicated the presenee of partial dominance for clynder fruit shape . However, potency ratio was (-2.5) and degree of dominance (2.23), table (6) , which revealed an over dominance.

The variations of backcrosses of the F_1 to (C. pepo) P_1 and (C. moschata) P_2 were (0.94) and (0.90), respectively.

The $\sqrt{H.\ D}$ value (1.04) was not equal to the (dh) value (1.83), Table (6).

Partitioning of phenotypic variance of F_2 generation into its componant D, H and E are given in Table (6).

The data showed that the additive variance ($\frac{1}{2}D$), dominance variance ($\frac{1}{4}H$) and environmental (E) were (0.23), (0.58) and (0.21), respectively.

Positive values of heterosis as estimated over the mid-parents was (1.09%). However, heterosis over the better parent was negative (-22.42%).

The values of inbreeding depression were (-21.69%) and (-22.90%) as compared with the mean of F_1 and the mid-parents, respectively, table (5).

Estimates of heritability in broad sense reached (88.8%), (79.59%) and (80.57%) by using the F_1 using the F_1 variance beside using the F_1 variance beside using square root of the two parental variances and cube root of P_1, P_2 and F_1 variances, respectively. Besides heritability estimate in narrow sense was (22.58%).

Number of genes involved as calculated by Castle-Wright and Wrights formulae were (0.08) and (0.14) pairs

of genes respectively, Table (5).

9- Inheritance of weight of 100 seeds : Data on this character are given in Table (3), which included means, standard errors, and the coefficients of variability of the six populations.

The difference between the means of the two species C. pepo and C. moschata was significant and the parent C. moschata (P_2) had heavier seed (means 8.78 ± 0.07 gram) than C. pepo (mean 7.87 ± 0.06 gram).

Coefficient of variation in segregating generations, i.e F_2, BC_1 and BC_2 was greater than that of F_1 and both parents.

The comparison between the actual and arithmetic means of F_1 generation was highly significant. Moreover, the mean of the F_1 was greater than that of the better parent C. moschata. The scaling test (A) had negative value and it was highly significant than zero. However, scaling tests (B and C) had insignificantly differed from zero, Table (3).

The estimates of the different kinds of the gene effects were shown in table (4), along with the standard erros. All values had negative sign except the

additive gene effect (d) had a positive value (0.68 ± 0.27). And it had significantly differed from zero.

The difference between F_1 and P_2 the better for the weight of 100 seeds, sp C.moschata, was significant indicating presence of over-dominance for heavy weight seeds, and potency ratio was (-0.04), while the degree of dominance was (0.94), Table (6).

Variances of the backcrosses of the F_1 to C. pepo and C. moschata are (2.11) and (3.74), respectively, Table (5). And the value of $\sqrt{H.D}$ (4.26) was not equal to the value of dh (-1.01), Table (6). Therefore, the parent (C. moschata) must had a preponderance of dominance genes and some of them must be recessive to their allels from C. pepo.

Partitioning phenotype variance in F_2 into its components showed that the additive variance ($\frac{1}{2}D$), dominant variance ($\frac{1}{4}H$) and environmental (E) variance were (2.27), (1.01) and (0.48), respectively, Table (6).

Heterosis percentages were (11.98%) and (18.45%), over the mid-parents and the better parent, respectively, Table (5).

Inbreeding depression were 17.71% and 7.86% as compared with the mean of F_1 and the mid-parents, respectively, Table (5).

The estimated values of heritability in broad sense were (74.69%) , (93.61%) and (98.92%) as obtained by using the variance of F_1 as environmental variance, squar of the two parental variances, and cube-root of P_1 , P_2 and F_1 variances, respectively. Besides, heritability in narrow sense was (60.39%) , Table (5).

The minimum number of effective factors was one pair of genes as it was obtained by Castle-Wright and Wright's formulae Table (5).

10- Inheritance of plant hight : The mean of stem length variance , standard error, C.V % and the arithmetic F_1 mean of the six families for stem length are given in Table (3).

Highly significant difference was found among the two species. Therefore, genetic difference among the two species was probable . C. moschata was longer in stem length (mean 519.64 ± 0.74 cm) than C. pepo (mean 49.39 ± 0.19 cm). Greater variability was encountered in F_2 , BC_1

and BC_2 , than in F_1 and both parents.

The difference between the observed and arithmetic means of F_1 population was highly significant. Moreover, the scaling tests (A, B and C) were highly significant than zero . Therefore, the additive -dominant model is not adquate. The estimates of the different kinds of the gene effects are shown in Table (5). All values had negative sign except the additive gene effect (d) and dominance gene effect (h) were possitive. And all parameters were highly significant, Table (5).

The difference between F_1 and (P_1) C. pepo, which had short stem length was highly significant,and it was shorter than the arithmetic mean (mid-parent). This could indicated partial dominance for short stem. This evidence of partial dominance was substantiated by both potency ratio (0.06) and degree of dominance (-0.74). Table(6).

The variances of backcrosses of the F_1 to C. pepo and C. moschata were (55.82) and (73.67), respectively. Thus the genes from C.pepo showed the preponderante of dominant allels.

The value of $\sqrt{H.D}$ (-336.42) is not equal to the

value of dh (-17.85) indicating that all the h allels are not with the same sign, Table (6). The parent C.pepo must has a preponderance of dominance genes and some of them must be recessive to their allels from C. moschata.

Partitioning phenotypic variance in F_2 into its components showed that the additive variance ($\frac{1}{2}D$), dominance variance ($\frac{1}{4}H$) and environmental variance (E) were (229.78), (-62.30) and (12.16), respectively, Table (5).

The estimations of heterosis over the mid-parents and the better parent were (-46.28%) and (-70.59%) respectively, Table (5').

The inbreeding depressions were (-120.75%) and (18.59%) as compared with the mean of F_1 and the mid-parents, respectively, Table (5).

Heritability values in broad sense were (97.49%), (96.38%) and (95.80%) as obtained by using the variance of the F_1 as environmental variance, square root of the two parental variance, and cube root of p_1, p_2 and F_1 variances, respectively, Table (5). Heritability in narrow sense could not be calculated, Table (5).

The Castle-Wright and Wright's formulae gave (1.58) and (1.84) pair of genes respectively.

11- Cytological studies : The species studied with their chromosome number are shown in Table (1) including classification of pair of chromosomes, localities and habitats of collection , Table (2) , shows approximate measurements of somatic chromosomes. Observations on the genomes of the two species can be summarized as follows:

I. C. moschata (Fig. 1) The 24 chromosomes were classified into three types as follows :

(1) Metacentri chromosomes : This catogary included :

Sex pair of chromosomes

(2) Nearly telocentric chromosomes. This group included two pair of chromosomes.

(3) Telocentric chromosomes.

This category involved four pair of chromosomes.

II. C. pepo . (Fig 22) : The 20 chromosomes were classified into the following three types:

i Four pairs with median centromeres (metacentric)

ii Two pairs with subtelocentric as rod shap.

iii Four pairs with telocentric.

Table (3) : Mean , S.E expected mean, C.V % and "t" test for some quantitative characters in the cross : C. pepo x C. moschata

Genotypes	N	Male flowers earliness					Female flowers earliness				
		X ± S.E	σ^2	arth mean	C.V %	+	X ± S.D	σ^2	exp mean	C.V %	+
P_1	56	35.00 ± 0.14	1.02		2.88		38.86 ± 0.16	1.48		3.13	
P_2	56	41.27 ± 0.14	1.01		2.43		51.57 ± 0.12	0.96		1.87	
F_1	56	49.04 ± 0.13	1.02	38.14	2.65	77.86	59.27 ± 0.15	1.10	45.22	3.31	93.67
BC_1	56	31.70 ± 0.39	8.38		9.12		34.45 ± 0.39	8.52		8.47	
BC_2	56	39.14 ± 0.35	6.74		6.63		39.67 ± 0.42	9.97		7.96	
F_2	212	39.39 ± 0.16	5.47	43.59	5.94	-26.25	47.86 ± 0.16	5.12	52.24	4.73	27.38

Scaling

A	- 20.65 ± 5.96	- 29.23 ± 6.05
B	- 12.02 ± 5.38	31.51 ± 6.48
C	- 16. ± 9.67	-17.53 ± 9.42

Table (3) : Continue.

Genotypes	Number of male flowers					Number of female flowers				
	X ± S.E	σ^2	arth mean	C.V %	t	X ± S.E	σ^2	exb mean	C.V%	t
P_1	20.00 ± 0.56	1.36		5.64		8.52 ± 0.15	1.26		13.14	
P_2	15.00 ± 0.10	0.50		4.71		4.95 ± 0.13	0.90		19.12	
F_1	17.77 ± 0.12	0.73	17.50	4.82	0.0	10.68 ± 0.12	0.12	6.73	8.28	32.92
BC_1	15.88 ± 0.30	5.13		14.29		7.50 ± 0.25	3.60		19.70	
BC_2	14.87 ± 0.29	4.47		14.22		7.41 ± 0.26	3.81		26.33	
F_2	18.42 ± 0.15	4.90	17.63	12.00	5.27	6.60 ± 0.16	5.17	8.71	34.44	-13.19
	- 6.020 ± 4.76					- 0.20 ± 4.06				
	- 3.03 ± 4.37					- 0.81 ± 4.11				
	3.14 ± 9.12					- 8.42 ± 9.38				

Table (3) : Contenue

Genotypes	N	sex ratio					Number of fruits / plant				
		X ± S.E	σ^2	arith means	C.V%	+	X ± S.E	σ^2	exp mean	C.V%	+
P_1	56	2.41 ± 0.08	1.25		24.13		1.60 ± 0.11	0.62		49.31	
P_2	56	3.14 ± 0.12	0.90		28.48		3.00 ± 0.12	0.73		28.52	
F_1	56	2.67 ± 0.05	0.78	2.78	22.40		2.64 ± 0.12	0.55	2.30	11.51	2.83
BC_1	56	1.92 ± 0.14	3.50		55.75		2.64 ± 0.18	1.82		21.00	
BC_2	56	2.64 ± 0.17	3.81		48.03		2.95 ± 0.17	1.53		41.98	
F_2	212	3.49 ± 0.09	5.17	2.22	37.52	14.11	2.63 ± 0.08	1.30	1.81	43.35	0.25

Scaling

A = - 0.24 ± 4.01 1.04 ± 2.91

B = 0.47 ± 4.11 0.25 ± 2.72

C = 5.05 ± 9.38 0.64 ± 4.94

P_1 = C. pepo

P_2 = C. moschata

Table (3) . Continue

Genotypes	N	Mean of fruit weight					Length of fruit				
		X ± S.E	σ^2	arth mean	C.V%	t	X ± S.E	σ^2	exp mean	C.V %	t
P_1	56	1.08 ± 0.02	0.01		9.72%		24.82 ± 0.12	0.99		3.99	
P_2	56	5.35 ± 0.08	0.31		11.68%		52.64 ± 0.19	1.99		1.67	
F_1	56	1.09 ± 0.09	1.07	3.21	21.79%	-9.65	36.52 ± 0.13	0.95	38.75	2.66	- 17
BC_1	56	1.29 ± 0.18	1.50		58.82%		22.06 ± 0.37	7.79		12.65	
BC_2	56	1.31 ± 0.14	1.85		31.65%		39.66 ± 0.31	5.37		5.85	
F_2	212	2.35 ± 0.17	2.38	2.152	52.97%	4.97	56.78 ± 0.13	7.83	37.63	28.83	147.31

Scaling

A = 0.41 / 0.400 / -1.82 ± 2.66 — - 17 ± 5.75

B = -3.82 / -3.21 ± 2.26 — -9.84 ± 4.94

C = 0.78 ± 6.54 — 76.62 ± 11.49

Table (3) : Continue

Genotypes	Mean of fruit width						Fruit Shape Index					
	X ± S.E	σ^2	arth mean	C.V %	t		X ± S.E	σ^2	exp mean	C.V %	t	
P_1	10.36 ± 0.17	1.65		12.41			2.48 ± 0.09	0.39		25.31		
P_2	26.13 ± 0.19	1.95		5.34			1.74 ± 0.05	0.11		19.31		
F_1	17.91 ± 0.19	1.93	18.24	7.76	-1.74		2.13 ± 0.05	0.12	2.11	15.92	0.4	
BC_1	14.16 ± 0.27	4.06		14.24			2.02 ± 0.13	0.94		47.85		
BC_2	23.26 ± 0.31	5.31		9.91			2.70 ± 0.13	0.90		35.04		
F_2	20.(o ± 0.18	6.40	18.08	12.09	15.67		2.59 ± 0.07	1.07	2.12	38.89	6.72	

0.06 ± 4.46

2.49 ± 5.01

11.30 ± 12.16

- 0.56 ± 2.06

1.53 ± 1.95

1.77 ± 4.18

Table (3) : Continue

Genotypes	Weight of 100 seeds					Stem length.				
	X ± S.E	σ^2	arth mean	C.V %	t	X ± S.E	σ^2	exp mean	C.V%	t
P_1	.87 ± 0.06	0.20		5.73		49.39 ± 0.19	1.90		2.79	
P_2	8.78 ± 0.07	0.28		6.04		519.64 ± 0.74	30.06		1.06	
F_1	9.22 ± 0.13	0.95	8.33	10.44	6.85	152.86 ± 0.29	4.52	284.52	1.39	-454
BC_1	5.29 ± 0.20	2.11		27.47		264.91 ± 1.00	55.82		2.82	
BC_2	6.68 ± 0.24	3.12		26.44		406.43 ± 1.15	73.67		2.11	
F_2	7.67 ± 0.13	3.74	8.81	25.23	-8.77	337.43 ± 0.92	179.64	218.69	3.97	129.07
	- 6.62 ± 3.10					327.57 ± 15.15				
	- 4.75 ± 3.70					140.36 ± 18.15				
	- 4.61 ± 8.01					474.77 ± 54.08				

Table (4) Mean estimatates of six parameter modele of gene effects for cross: C.pepo x C. moschata.

No	Characters studies	Gene effects					
		m ± S.E	d ± S.E	h ± S.E	i ± S.E	j ± S.E	l ± S.E
1	Male flowers earli ess	54.02 ± 8.55	-3.14 ± 0.05	-53.53 ± 13.74	-15.89 ± 5.20	- 8.63 ± 2.56	48.59 ± 12.18
2	Female flowers earliness	88.42 ± 2.93	-6.36 ± 0.36	-133.10± 18.19	-43,20 ± 2.82	2.25 ± 2.51	103.94 ± 14.40
3	Number of male flowers	29.69 ± 6.36	2.50 ± 0.46	-33.16 ± 5.21	-12.19 ± 6.33	- 2.99 ± 1.34	21.24 ± 8.39
4	Number of female flowers	-0.69 ± 7.32	1.79 ± 0.30	17.79 ± 8.35	- 8.39 ± 7.29	0.61 ± 1.10	- 6.42 ± 5.53
5	Sex ratio	7.59 ± 7.35	0.36 ± 0.30	-10.51 ± 8.56	- 4.82 ± 7.31	- 2.16 ± 1.26	4.59 ± 5.85
6	Number of fruits / plant	1.64 ± 2.78	0.70 ± 0.17	2.96 ± 1.79	0.66 ± 2.72	- 2.01 ± 1.12	- 6.56 ± 5.41
7	Mean of fruit weight	7.41 ± 6.25	2.13 ± 0.14	2.00 ± 7.29	- 4.20 ± 6.24	2.23 ± 2.03	7.62 ± 4.42
8	Length of fruit	142.42 ± 48.62	13.91 ± 2.65	-236.67± 83.14	-103.69±48.54	- 63.04 ±17.32	130.77 ± 29.20
9	Mean of fruit width.	26.99 ± 4.98	7.89 ± 0.27	-15.30 ± 5.78	- 8.76 ± 4.97	- 33.97 ± 1.30	6.22 ± 3.30
10	Fruit shap index	10.58 ± 9.84	0.37 ± 0.50	-15.94 ± 5.92	- 8.47 ± 8.52	- 2.09 ± 2.95	3.07 ± 8.86
11	Weight of 100 seeds	2.59 ± 8.11	0.68 ± 0.27	- 0.90 ± 9.07	- 0.92 ± 8.06	- 1.05 ± 2.30	- 0.05 ± 6.02
12	Plant height	291.54 ± 3.15	235.13 ± 0.27	322.23 ± 1.87	- 7.02 ± 3.12	-753.29 ± 0.35	-460.91± 3.37

able (5) : Heterosis by M.P and B.P , Inbreeding depression, Heritability in Narrow and Broad sence and number of genes in the interspecific cross : C. pepo & C. moschata.

Characters studies	Heterosis %		Inbreeding depression.		Heritability H^2 %				Number of genes	
					Broad sense			Narrow sense		
	$\overline{M.P}$ %	$\overline{B.P}$ %	by $\overline{F_1}$	by $\overline{M.P}$	1	2	3		$\overline{1}$	2
Male flowers earlines	28.59	4..10	19.67	- 3.30	81.41	81.48	81.53	-76.42	1.10	2.24
Female flowers earlines	31.08	52.53	19.24	- 5.85	78.64	76.67	75.76	-	5.02	17.27
Number of male flowers	1.54	18.77	-3.66	- 5.26	85.03	83.11	93.25	3.68	0.75	0.76
Number of female flowers	58.61	25.37	-38.20	- 1.98	84.86	79.86	95.52	81.36	0.37	1.25
Sex ratio.	-39.80	14.97	- 3.96	-25.54	91.80	92.55	92.79	88.82	0.02	0.24
Number of fruits/plant.	14.78	-12.00	0.38	-14.35	57.77	-	-	-57.39	0.43	0.46
Mean fruit weight.	66.07	-79.62	-115.14	26.99	54.22	97.22	83.99	59.31	1.55	1.86
Fruit length	-5.71	30.62	-5.86	0.94	87.92	82.14	84.67	31.93	14.06	14.23
Fruit width.	-1.81	45.66	-16.69	-14.58	69.77	71.91	96.60	51.17	6.98	6.98
Fruit shap index.	1.09	-22.42	-21.69	-22.90	88.86	79.56	80.57	22.57	0.08	0.14
Weight of 100 seeds.	11.98	18.45	17.71	7.86	74.69	93.61	98.92	60.39	0.04	0.40
Plant height.	-46.28	-70.59	-120.75	18.59	97.49	96.38	95.80	-	1.58	1.84

1 : by using VF_2
2 : by using $V p_1 - Vp_2$
3 : by using $V F_1 . Vp_1 . Vp_2$

1 : Castle - Wright formula.
2 : Wright's formula.

Table (6) : Estimation of ½D, ¼H, E H/D, H.D , dh and potance ratio in sone quantitative characters in the interspecfic cross : C. pepo x C. moschata

N	Characters studied	½ D	¼ H	E	Degree of dominance y			
					Potance ratio	$\sqrt{H.D}$	$\sqrt{H.D}$	dh
1	Male flowers earlines	- 4.18	8.64	1.02	3.48 **	-1.44	-24.03	1.65
2	Female flowers earlines	- 8.25	3.05	1.18	2.21 **	-0.61	-20.05	-1.46
3	Number of male flowers	0.18	0.97	0.87	0.11	3.27	1.27	0.23
4	Number of female flowers	4.21	0.0.	0.98	2.21 **	-0.04	-0.04	-0.21
5	Sex ratio	0.66	3.71	0.98	-3 *	3.26	4.33	-0.31
6	Number of fruit / plant	0.75	0.35	0.64	0.49	-0.99	-1.42	0.29
7	Mean of fruit weight	1.41	0.48	0.49	1.96**	0.83	2.33	-0.35
8	Fruit length	2.49	0.25	1.31	-0.56	2.23	2.24	2.41
9	fruit width	3.28	1.56	1.57	-0.10	0.98	6.39	-1.25
10	Fruit shap index	0.23	0.58	0.21	-2.05	2.23	1.04	1.83
11	Weight of 100 seeds	2.27	1.01	0.48	-0.04	0.49	4.26	-1.01
12	Plant heigh	229.78	-62.30	12.16	0.06	-0.74	-336.42	-17.85

y Degree of dominance.

* signifficant

** hightly signifficant.