Inheritance of some Important Characters in Summer Squash (*Cucurbita pepo* L.)

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ABSTRACT

The present investigation was carried out during the period from 2013 to 2015 at the Agricultural Experiment Station of the Faculty of Agriculture, University of Cairo, Giza, Egypt to determine the genetic basis of the inheritance of some vegetative growth, flowering and fruit characters of summer squash. The crosses were between parents having high and low values for each studied character. The first cross was accession PEP 1672 (cv. Early Sugar) × accession PEP 1692(cv. White Bush Scallop) for studying plant length, number of branches/plant, internode length, number of nodes to the first female flower, date of the first female flower anthesis, stem thickness, tendril appearance and fruit peduncle. The second cross was PEP 11 (cv. Early Summer Crockneck) × PEP 1763(cv. Royal Acorn Large) for studying plant length, internode length, tendril appearance and mature fruit color. Genetic populations of the two crosses, viz*.,* P_1, P_2, F_1, F_2, BCP_1 and BCP_2 were evaluated during the 2015 winter season, under greenhouse conditions. Results indicated that partial dominance controlled the inheritance of low levels of plant length, internode length, number of branches/plant, stem thickness and fruit peduncle and also controlled high levels of number of nodes to the first female flower and date of the first female flower anthesis .Complete dominance controlled the inheritance of short internode length in the second cross. The minimum number of genes controlling various characters was 2-6 for plant length, 5 for number of branches/plant, 1-3 for internode length, 5 for number of nodes to the first female flower, 2 for date of the first female flower anthesis, 2 for stem thickness, 1 for tendril appearance and 3 for fruit peduncle. Broad sense heritability estimates were from 80.47 % to 90.36 % for plant length, 66.84 % for number of branches/plant,84.11 % to 89.18for internode length, 71.68 % for number of nodes to the first female flower,85.57 %for date of the first female flower anthesis,69.77 % for stem thickness and61.76 % for fruit peduncle. Narrow sense heritability estimates were from39.77 % to77.39 % for plant length,80.34 %for internode length,48.16 % for stem thickness and22.29 % for date of the first female flower anthesis.

Introduction

Summer squash is the edible immature fruits of *Cucurbita pepo* L., which belongs to the economically important family Cucurbitaceae. It is a short-season crop adapted to tropical and subtropical regions. Some *C. moschata* Duchesne varieties are grown for their edible immature fruits. Some *C. maxima* Duchesne varieties are grown for this purpose in South America (Whitaker and Robinson, 1986; Paris, 1996 and 2008).

Fruit shape can vary from round to disc shaped to very long. The fruits can be smooth or warted, with or without longitudinal ribs, longitudinal grooves, furrows, or wavy lobes. Exterior color can be green, orange, or yellow, but range in shading and intensity from almost black to almost white and can appear in patterns of longitudinal striping, which can be broad and contiguous, narrow and noncontiguous, irregular, and/or in latitudinal bicolour patterns, all superimposed on barely discernable to obvious light-colored speckling. The color of the mature fruit flesh is most often light yellow-orange, but can range from greenish white to intense orange; it can be relatively thick or thin, and coarsely fibrous and tough to finely fibrous and tender (Paris, 2008).

Whitwood (1975) studied the inheritance of tendril development and mature fruit color in *Cucurbita pepo*. Tendril development was inherited as a single gene in some crosses, while in others, two genes controlled tendril expression. The inheritance of mature fruit color in most crosses was simply inherited with cream dominant to white, white dominant to yellow and yellow dominant to green. In crosses among yellow and green fruit skin lines, yellow segregated 3 to 1 in all cases except those involving precocious yellow which had a 15 to 1 ratio indicating duplicate dominant epistasis.

Edelstein *et al*. (1989) evaluated vegetative and reproductive characteristics using bush and vine habit squash accessions and their reciprocal F_1s to study dominance degree for these characters. A single complete dominant gene for bush habit and the symbol 'Bu' has been assigned to this gene.

Abd El-Hadi *et al.* (2005) studied the genetic behavior of plant length of squash. The broad sense heritability (BSH) was 83.18 % and narrow sense heritability (NSH) was 81.17 %.

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El-Sherbeny *et al.* (2005) studied nature of gene action for some economic traits of summer squash. The values of NSH for vegetative and earliness traits were 11.56% and 38.51% for days to first male flower and leaf area, respectively.

Al-Zabaee (2006) evaluated gene action for some vegetative (plant length), fruit quality (average fruit weight, fruit length and fruit diameter) and yield characters. Dominance degree was more than unity for all studied traits, indicating the presence of over-dominance except fruit diameter which hadpartial dominance. BSH was high for all studied traits, while NSH was moderate for all studied traits except yield /plant and plant length which were low.

Obiadalla-Ali (2006) estimated BSH and NSH for some vegetative, flowering and yield characters in summer squash. BSH was high for all studied traits. BSH was 85.39 % for date to 1st female flower anthesis; 99.02 % for plant length and 98.85 % for number of branches. NSH was 27.25 % for date to 1st female flower anthesis; 12.32 % for plant length and 13.46 % for number of branches.

Al-Kummer *et al.* (2009) estimated BSH for some vegetative (plant length and number of leaves) and flowering (sex ratio, date to 1st female flower anthesis and date to 1st male flower anthesis) characters. High BSH estimates were found for all studied characters.

Mohamed (2009) studied BSH and NSH for some vegetative, flowering, yield and seed characters. BSH and NSH estimates for plant length and first female flower appearance were 97.90 and 69.21% and 91.41and 60.79%, respectively.

Al-Araby (2010) studied heritability and degree of dominance for stem length, days to 1st female flower anthesis, date of first male flower anthesis and nodes to 1st female flower. High BSH estimates were detected for all studied traits. NSH estimates were moderate for stem length, number of days to first female flower opening and number of nodes to first female flower. Over dominance controlled the inheritance of stem length, date to first female flower anthesis and number of nodes to first female flower.

Al-Hamadany and Al-Lelah (2010) studied BSH, NSH and dominance degree for some vegetative (plant length and number of leaves), flowering (sex ratio, fruit set ratio, date to 1st female flower anthesis and date to 1st male flower anthesis),fruit characters (fruit length, fruit diameter and average fruit weight) and yield (early and total) in summer squash. Broad sense heritability estimates were moderate to high for all studied traits, except for sex ratio, average fruit weight and early yield that were low. Narrow sense heritability was low for all studied characters. Over dominance controlled the inheritance of all studied traits, except plant length which showed partial dominance.

Hussien (2015) studied nature of gene action for some vegetative (plant height), flowering (date to first female flower anthesis and number of fruits/plant), fruit quality (average fruit weight, fruit length and fruit diameter) and yield characters (early yield/plant and total yield/plant) in summer squash. Dominance degree was more than unity for all studied traits, indicating the presence of over-dominance. BSH was high for all studied traits. NSH was 68% for plant height and ranged from 30 % to 43% for number of fruits/plant, total yield/plant, early yield/plant and flowering date. Narrow sense heritability was low and valued 13% (fruit length), 21% (fruit diameter) and 27% (average fruit weight).

This study aimed at determining the genetic basis of the inheritance of some vegetative growth, flowering and fruit quality characters of summer squash.

Materials and Methods

These studies were carried out during the period from 2013 to 2015 at the Agricultural Experiment Station (AES) of the Faculty of Agriculture, University of Cairo, Giza, Egypt.

Two crosses were chosen for the genetic studies of some vegetative growth, flowering and fruit characters. The crosses were between parents having high and low values for each studied character. The first cross was accession PEP 1672 (cv. Early Sugar)×accession PEP 1692(cv. White Bush Scallop)for studying plant length, number of branches/plant, internode length, number of nodes to the first female flower, date of the first female flower anthesis, stem thickness, tendril appearance and fruit peduncle. The second cross was PEP 11(cv. Early Summer Crockneck) × PEP 1763(cv. Royal Acorn Large) for studying plant length, internode length, tendril appearance and mature fruit color. Vegetative characters were measured at the end of plant life and fruit peduncle was measured 3 days after anthesis. Mature fruit color was measured more than 30 days after anthesis. Internode length and stem thickness were measured in the middle of the main stem.

Seeds of these genotypes were kindly provided by IPK-Gatersleben Gene Bank, Germany. Seeds ofF_1s were produced during 2013 winter season under greenhouse conditions.F_1 plants of the two crosses were planted during 2014 winter season under greenhouse conditions and were selfed to obtain F_2 seeds, and were crossed with their parents to obtain the backcross seeds. Seeds of genetic populations of each cross, viz., P_1, P_2, F_1, F_2, BCP_1 and BCP_2 were sown on October 15, 2015 and seedlings were field-transplanted into the greenhouse after two weeks in a randomized complete block design with three replicates. Each plot consisted of 1 bed 1.2 m-

wide and 5 m-long. Plants were set 50 cm apart in the bed and were subjected to the common agricultural practices.

Data recorded for the studied characters were taken on individual plant basis. Data obtained were used in calculating the following genetic parameters:

a. Potence ratio:

Potence ratio (P) was used to determine the direction of dominance and was calculated according to Smith (1952) as follows:

$$P = (\overline{F}_1 - MP)/[1/2(\overline{P}_2 - \overline{P}_1)]$$

Where: $\overline{F}_1$ = First generation mean; $\overline{P}_1$ = Mean of the smaller parent; $\overline{P}_2$ =Mean of the larger parent; and

MP= Mid parent value $= 1/2(\overline{P}_1 + \overline{P}_2)$.

The absence of dominance was assumed when the difference between the parents was significant and

$\overline{F}_1 - MP$ was not significant. Complete dominance was assumed when potence ratio equaled to or did not differ from ± 1.0. Meanwhile, partial dominance was considered when potence ratio was between +1.0 and -1.0, but was not equal to zero. Over dominance (heterosis) was assumed when potence ratio exceeded ± 1.0.

b. The minimum number of genes controlling the character:

The minimum number of genes was calculated using Castle-Wright equation (Castle and Wright, 1921) as follows:
N = $D^2 / 8(VF_2 - VF_1)$
Where: N = Number of genes controlling the character; D = Difference between parental means; and VF_1 and VF_2 = Variances of the F_1 and F_2 populations, respectively.
Chi-square test was used to estimate number of genes controlling the qualitative characters.

c. Broad sense heritability:

Broad sense heritability (BSH) was calculated using the equation:
BSH = $(V_G / V_P) 100$ (Allard, 1960)
Where: V_G = Genetic variance which was calculated by subtracting the environmental variance (V_E) from phenotypic variance (V_P); V_P = VF_2; and V_E = Environmental variance which was calculated as the arithmetic mean of thenon-segregating populations, i.e., parents and F_1.

d. Narrow sense heritability:

Narrow sense heritability (NSH) was calculated using the equation:
NSH = $(V_A / V_P) 100$ (Warner, 1952)
Where: $V_A = 2V_{F2} - (V_{B1} + V_{B2})$; and V_P = VF_2.

Results and Discussion

Vegetative characters:

Plant length:

Data obtained on plant length of parental, F_1, F_2, and backcross populations of the crosses PEP 1672 (Early Sugar) × PEP 1692(White Bush Scallop) and PEP 11 (Early Summer Crockneck) × PEP 1763 (Royal Acorn Large) are presented in Tables 1 and 2, respectively. In both crosses, parents were significantly different in plant length. F_1 mean of the first cross was close to that of the mid-parent, Meanwhile, F_1 mean of the second cross was very close to that of the lower parent.

In both crosses, F_2 mean was very close to that of the lower parent. F_2 plants were distributed between their two respective parents with a high tendency towards the lower one. Plants of the backcrosses to the tall parents, *i.e.*, PEP 1672 or PEP 1763 were distributed with a tendency towards them, while plants of the backcrosses to short parents, *i.e.*, PEP 1692 or PEP 11were very close to them.

Genetic parameters obtained for plant length in the crosses PEP 1672 × PEP 1692 and PEP 11 × PEP 1763 are presented in Tables 3. In the two crosses, bush plant type was partially dominant. These results agree with those of Aldiab (1994) and Aldiab and Kasrawi (1996) who reported that bush habit was incompletely dominant over viny habitat at late growth stages. Also, Edelstein *et al*. (1989) reported that bush habit was completely dominant over viny habitat.

Table 1: Distribution, mean, and variance of plant length of parental, F_1, F_2 and backcross populations of the cross PEP1672× PEP1692.

Population	Frequency of plant length (cm) in class^z															Total no. of plants	Mean $\overline{x} \pm S_{\overline{x}}$	Variance (σ^2)
	59.5	99.5	139.5	179.5	219.5	259.5	299.5	339.5	379.5	419.5	459.5	499.5	539.5	579.5	619.5			
PEP 1672(P_1)												2	9	8	1	20	555.5 ±6.74	909.47
PEP 1692(P_2)	17	3														20	65.5 ± 3.27	214.73
F_1				9	10	1										20	243.5 ±5.35	572.63
F_2	10	17	7	19	11	8	3	1		1						77	166.5 ± 8.73	5871.22
BCP_1							1		1	3	1	2	6	12	5	31	538.20 ± 14.18	6238.28
BCP_2		3	7	10	4	5	2									31	188.5 ±10.11	3169.03

^{z}*Each class represents a range of 40 cm and class values represent class centers:*

Table 2: Distribution, mean, and variance of plant length of parental, F_1, F_2 and backcross populations of the cross PEP11× PEP1763.

Population	Frequency of plant length(cm) in class^z												Total no. of plants	Mean $\overline{x} \pm S_{\overline{x}}$	Variance (σ^2)
	25.5	45.5	65.5	85.5	105.5	125.5	145.5	165.5	185.5	205.5	225.5	245.5			
PEP 11(P_1)	17	3											20	28.5 ±1.63	53.68
PEP 1763(P_2)				1	1	3	5	6	2	1		1	20	174.5 ± 7.32	1072.63
F_1			6	12	2								20	61.5 ± 2.75	151.57
F_2	22	24	11	4	2	5	3	1		2	1		75	63.9 ± 5.39	2181.18
BCP_1	20	7	2	4									33	39.43 ± 3.63	437.12
BCP_2		2	7	8	3		2	2	1	2			27	102.53 ± 9.10	2237.03

^{z}*Each class represents a range of 20 cm and class values indicated represent class centers*

The minimum number of genes controlling plant length was 6 and 2 pairs in the first and second crosses, respectively. These results disagree with those of Aldiab (1994) and Aldiab and Kasrawi (1996) who reported that a single gene controlled bush habit over viny habitat and these results also disagree with those of Edelstein *et al*. (1989) who reported a single complete dominant gene for bush habit.

In both crosses, estimates of BSH were high, being 90.36 % and 80.47 % in the first and second crosses, respectively. These results are in agreement with those obtained by Al-Araby (2010) and Hussien (2015) who, respectively, estimated BSH for this trait as 91.6 % and 99.3 %. On the contrary, Al-Hamadany and Al-Lelah (2010) reported medium BSH (53.17 %). In the present study, estimates of NSH were low (39.77 %) and moderate (77.39 %) in the first and second crosses, respectively. These results are in harmony with those of Al-Araby (2010), Al-Hamadany and Al-Lelah, (2010) and Hussien (2015) who estimated NSH ranging from 47.55 % to 68.39 %.

Tendril appearance:

This trait was studied in the crosses PEP 1672 × PEP 1692 and PEP 11× PEP 1763. Plants of the parents PEP 1672 and PEP 1763 had tendrils, while plants of both PEP 1692 and PEP 11 had no tendrils. All F_1 plants of the first cross had tendrils indicating dominance of this trait. On the contrary, all F_1 plants of the second cross had no tendrils indicating recessiveness of this trait. In the first cross, 58 of 79 F_2 plants had tendrils, while 21 plants had no tendrils. The number of plants that having tendrils to those without tendrils in the F_2 did not deviate significantly from the ratio 3:1. These results proved that tendril development is controlled by a single dominant gene. In the second cross, 39 of 75 F_2 plants had tendrils, while 36 plants had no tendrils. The number of plants having tendrils to those without tendrils in the F_2 did not deviate significantly from the ratio 9:7. These results indicated that this trait was controlled by two recessive duplicate epistatic genes. These results agree with those obtained by Whitwood (1975) who reported that tendril development was inherited as a single gene in some crosses, while in others, two genes controlled tendril expression.

Table 3: Quantitative genetic parameters obtained for the characters studied in the crosses PEP 1672 × PEP 1692 and PEP 11× PEP 1763.

Character	Potence ratio	No. of genes	BSH %	NSH %
PEP 1672 × PEP 1692				
Plant length	-0.27	5.66	90.36	39.77
Internode length	-0.3	2.69	84.111	80.34
Number of branches	-0.85	4.8	66.84	—
Stem thickness	-0.48	1.37	69.77	48.16
No. nodes to 1st Female flower	0.21	4.34	71.68	—
Date of 1st female flower anthesis	0.14	1.33	85.57	22.29
Fruit peduncle length	-0.4	2.12	61.76	—
PEP 11× PEP 1763				
Plant length	-0.54	1.31	80.47	77.39
Internode length	-0.95	0.91	89.18	—

Table 4: Segregation for tendril trait of parental, F_1 and F_2 populations of the crosses PEP 1672 × PEP 1692 and PEP 11× PEP 1763.

Population	Number of plants		Total No. of plants	Expected ratio	Chi-square	*P*
	Tendril	No tendril				
PEP 1672 × PEP 1692						
PEP 1672(P_1)	20		20			
PEP 1692(P_2)		20	20			
F_1	20		20			
F_2	58	21	79	3:1 9:7 15:1 13:3	0.105 9.46 55.73 3.18	0.50 - 0.95 < 0.05 < 0.05 0.05-0.10
PEP 11× PEP 1763						
PEP 11(P_1)		20	20			
PEP 1763(P_2)	20		20			
F_1		20	20			
F_2	39	36	75	3:1 9:7 15:1 13:3	29.16 2.07 267.9 54.42	< 0.05 0.10 - 0.20 < 0.05 < 0.05

Internode length:

Data obtained on internode length of parental, F_1, F_2, and backcross populations of the crosses PEP 1672 (Early Sugar) × PEP 1692 (White Bush Scallop) and PEP 11 × PEP 1763 are presented in Tables 5 and 6,

respectively. In the two crosses, parents were highly significantly different in internode length. F_1 and F_2 meanswere lower than thatof the mid- parent. F_2 plants were distributed between the two parents with a high tendency towards the lower values. Distribution of plants of the backcrosses to the high parents, *i.e.*, PEP 1672 and PEP 1763 was close to that of these parents, while plants of the backcrosses to the parents having short internodes, *i.e.*, PEP 1692 and PEP 11 were distributed with a tendency towards these parents.

Genetic parameters obtained for internode length in the crosses PEP 1672 × PEP 1692 and PEP 11 × PEP 1763 are presented in Table 3. Short internode length was partially dominant in the first cross and completely dominant in the second one.

Minimum number of genes controlling internode length was 3 pairs and one pair in the first and second crosses, respectively. These results disagree with those of Paris *et al.* (1984) who reported that a single recessive gene and one or more modifier genes, as well as environmental factors are involved in determining short internode length.

In both crosses, estimates of BSH were high, while NSH were high in the first cross.

Table 5: Distribution, mean, and variance of internode length of parental, F_1, F_2 and backcross populations of the cross PEP 1672× PEP 1692.

Population	Frequency of internode length (cm) in class[z]															Total no. of plants	Mean $\bar{x} \pm S_{\bar{x}}$	Variance (σ^2)
	2.00	3.33	4.67	6.00	7.33	8.67	10.00	11.33	12.67	14.00	15.33	16.67	18.00	19.33	20.67			
PEP 1672(P_1)										1	2	5	5	2	5	20	18 ±0.45	4.11
PEP 1692(P_2)	17	3														20	2.2 ± 0.10	0.23
F_1				5	9	3	2	1								20	7.66 ±0.33	2.22
F_2	9	13	16	8	9	5	3	8	5	1	1		1			79	6.64 ± 0.41	13.80
BCP$_1$					1		3	2	1	4	6	5	4	5		31	15.24 ± 0.57	10.42
BCP$_2$	13	5	4	4	1	1	2									30	4.04 ±0.45	6.09

[z]*Each class represents a range of 1.33 cm and class values represent class centers*

Table 6: Distribution, mean, and variance of internode length of parental, F_1, F_2 and backcross populations of the cross PEP 11× PEP 1763.

Population	Frequency of internode length (cm) in class[z]											Total no. of plants	Mean $\bar{x} \pm S_{\bar{x}}$	Variance (σ^2)
	1.33	2.33	3.33	4.33	5.33	6.33	7.33	8.33	9.33	10.33	11.33			
PEP 11(P_1)	20											20	1.33 ±0.00	0
PEP 1763(P_2)						3	1	6	2	5	1	18	8.77 ± 0.36	2.37
F_1	17	3										20	1.48 ± 0.08	0.13
F_2	14	21	12	10	4	1	2	3	1	3	3	74	3.95 ± 0.32	7.74
BCP$_1$	15	6	5	3	1	2		1				33	2.72 ± 0.31	3.24
BCP$_2$			1	11	2	3	3	2	2	3		27	6.25 ± 0.43	5.07

[z]*Each class represents a range of 1 cm and class values represent class centers:*

Number of branches:

Data obtained on number of branches of parental, F_1, F_2, and backcross populations of the cross between summer squash accession PEP 1672, as a female parent, and accession PEP 1692, as a male parent, are presented in Table 7.

Parents were highly significantly different from each other in the number of branches. F_1 and F_2 means were very close to that of the parent having lower number of branches. F_2 plants were distributed between the two parents with a high tendency towards the lower one. Distribution of plants of the backcross to accession PEP 1672 was close to that of the mid- parent, while plants of the backcross to the accession PEP 1692 were distributed with a high tendency towards the lower parent.

Genetic parameters obtained for number of branches in the cross PEP 1672× PEP 1692 are presented in Table 3. The low number of branches was partially dominant over the high one.

The number of branches was found to be controlled by 5 pairs of genes.

Estimate of BSH was 66.84%. NSH was considered zero due to its negative value. These results partially agree with those of Obiadalla-Ali (2006) who reported that BSH for this trait was 98.85%, while NSH was 13.46%. It also agree with those of Al-Jebory (2006) who reported that BSH was 83%, while NSH was neglected due to its negative value.

Table 7: Distribution, mean, and variance of number of branchesof parental, F₁, F₂ and backcross populations of the cross PEP1672× PEP1692.

Population	Frequency of number of branches in class^z									Total no. of plants	Mean $\overline{x} \pm S_{\overline{X}}$	Variance (σ^2)
	1.2	3.5	5.8	8.1	10.4	12.7	15.0	17.3	19.6			
PEP 1672(P₁)						3	8	7	2	20	15.92 ±0.45	4.12
PEP 1692(P₂)	15	5								20	1.77 ± 0.22	1.04
F₁	7	12	1							20	2.81 ± 0.29	1.72
F₂	31	20	19	4	2	1				77	3.67 ± 0.29	6.92
BCP₁	1	2	7	4	3	7	2	2	3	31	10.47 ± 0.91	25.91
BCP₂	10	12	7	1		1				31	3.72 ± 0.45	6.47

^{z}*Each class represents a range of 2.3 branch and class values represent class centers.*

Stem thickness:

Data obtained on stem thickness of parental, F₁, F₂, and backcross populations of the cross between summer squash accession PEP 1672, as a female parent, and accession PEP 1692, as a male parent, are presented in Table 8.

Parents were highly significantly different in their stem thickness.F₁ and F₂ means were intermediate between their respective parents with a low tendency towards the high parent. Plants of the backcross to the accession PEP 1672were distributed between the two parents with a tendency towards the thinnest stem parent, whereas plants of the backcross to PEP 1692 were widely distributed with a tendency towards the high parent.

Genetic parameters obtained for stem thickness are presented in Table 3. Thinner stem was partially dominant over thick stem.

Stem thickness was found to be controlled by 2 pairs of genes.

The estimate of BSH was 69.77% and NSH was 48.16%. These results are the first record on the inheritance of stem thickness.

Table 8: Distribution, mean, and variance of stem thickness of parental, F₁, F₂ and backcross populations of the cross PEP1672× PEP1692.

Population	Frequency of stem thickness (mm) in class^z											Total no. of plants	Mean $\overline{x} \pm S_{\overline{X}}$	Variance (σ^2)
	6.75	8.25	9.75	11.25	12.75	14.25	15.75	17.25	18.75	20.25	21.75			
PEP 1672(P₁)		10	8	2								20	9.15 ±0.22	1.04
PEP 1692(P₂)						3	4	10		2	1	20	17.02 ± 0.43	3.85
F₁		1	5	10	2	2						20	11.17 ± 0.33	2.24
F₂	6	16	7	16	11	17	2	3				78	11.36 ± 0.31	7.87
BCP₁	3	10	3	5	3	1	1					26	9.86 ± 0.47	5.74
BCP₂		1		6	4	12	2	2	1	1		29	13.88 ± 0.46	6.21

^{z}*Each class represents a range of 1.5 mm and class values represent class centers.*

Flowering characters:

Number of nodes to the first female flower:

Data obtained on number of nodes to the first female flower of parental, F_1, F_2, and backcross populations of the cross between summer squash accession PEP 1672, as a female parent, and accession PEP 1692, as a male parent, are presented in Table 9.

Parents were highly significantly different in the number of nodes to the first female flower. F_1 mean was close to that of the mid-parent. F_2 plants were distributed between the two parents with a tendency towards the low parent. Plants of the backcross to accession PEP 1692 were distributed with a tendency towards the smaller parent, while plants of the backcross to PEP 1672 were very close to it.

Genetic parameters obtained for number of nodes to the first female flower in the cross PEP 1672 × PEP 1692 are presented in Table 3. High number of nodes to the first female flower was partially dominant. These results disagree with those of Al-Jebory (2006) and Al-Araby (2010), who reported that large number of nodes to the first female flower showed over dominance.

The minimum number of genes controlling number of nodes to the first female flower was 5 pairs.

The estimate of BSH was moderately high, being 71.68 % and NSH was neglected because it was estimated as a negative value. These results partially agree with those of Metwally (1985) who reported high BSH and low NSH for this trait. Meanwhile, results disagree with those of Al-Jebory (2006), who reported that estimates of BSH and NSH were low and also with Al-Araby (2010),who reported that BSHand NSH were 94.76 % and 47.11%, respectively.

Table 9: Distribution, mean, and variance of number of nodes to the first female flower of parental, F_1, F_2 and backcross populations of the cross PEP1672× PEP1692.

Population	Frequency of number of nodes to the first female flower in class[z]											Total No. of plants	Mean $\bar{x} \pm S_{\bar{x}}$	Variance (σ^2)
	7	9	11	13	15	17	19	21	23	25	27			
PEP 1672(P$_1$)								5	7	3	5	20	23.8 ±0.51	5.22
PEP 1692(P$_2$)	15	5										20	7.5 ± 0.19	0.78
F$_1$					4	10	4	2				20	17.40 ± 0.40	3.2
F$_2$	8	8	16	20	14	9	3	1				79	12.72 ± 0.37	10.84
BCP$_1$				1	5	5	7	7	5	1		31	21.12 ± 0.54	9.31
BCP$_2$	3	2	5	8	1	5	4					28	13.35 ± 0.71	14.23

[z]*Each class represents a range of 2 nodes and class values represent class centers.*

Date of first female flower anthesis:

Data obtained on date of first female flower anthesis of parental, F_1, F_2, and backcross populations of the cross between summer squash accession PEP 1672, as a female parent, and accession PEP 1692, as a male parent, are presented in Table 10.

Parents were highly significantly different in their date of first female floweranthesis. F_1 mean was intermediate between the two parents with a low tendency towards the high parent. F_2 meanwas also intermediate between the two parents but with a low tendency towards the low parent. F_2 plants were widely distributed between the two parents with a low tendency towards the lower parent. Plants of the backcross to accession PEP 1672 were distributed with a tendency towards its values, while plants of the backcross to PEP 1692 were close to it.

Genetic parameters obtained for date of first female flower anthesis in the cross PEP 1672 × PEP 1692 are presented in Table 3. Late date of first female flower anthesis was partially dominant over the early date. These results partially agree with those of Al-Jebory (2006) and Al-Araby (2010), who reported that late date of first female flower anthesis was over dominant over the early one.

Date of first female flower anthesis was found to be controlled by 2 pairs of genes. Broad sense heritability for date of first female flower anthesis was high being 85.57 %, while NSH was 22.29%. These results are in agreement with those of Obiadalla-Ali (2006), who estimated BSH for this character as 85.39 % and NSH as 27.25 %, but partially agree with those of Al-Jebory (2006), who estimated BSH and NSH for this character as 67 % and 4 %, respectively.

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Fruit peduncle length:

Data obtained on fruit peduncle length of parental, F_1, F_2, and backcross populations of the cross between summer squash accession PEP 1672, as a female parent, and accession PEP 1692, as a male parent, are presented in Table 11.

Parents were highly significantly different in fruit peduncle length. F_1 mean was intermediate between the two parents but it tended more towards parent with low values, Meanwhile, F_2 mean was very close to the mid-parent. F_2 plants were distributed between the two parents. Plants of the backcross to accession PEP 1672 were distributed with a tendency towards the low parent, while plants of the backcross to accession PEP 1692 were distributed between the two parents with a tendency towards to its values.

Genetic parameters obtained for fruit peduncle length in the cross PEP 1672 × PEP 1692 are presented in Table 3. Short fruit peduncle was partially dominant. These results disagree with those of Merie *et al.* (2012), who reported that long fruit peduncle was partially dominant. .

The minimum number of genes controlling fruit peduncle length was 3 pairs.

The estimate of BSH was 61.76%, while NSH was considered zero due to its negative value. On the contrary, Marie *et al.* (2012) reported high BSH and moderate NSH for this trait.

Table 10: Distribution, mean, and variance of date of 1st female flower anthesis of parental, F_1, F_2 and backcross populations of the cross PEP1672× PEP1692.

Population	Frequency of date of 1st female floweranthesis in class[z]									Total No. of plants	Mean $\overline{x} \pm S_{\overline{x}}$	Variance (σ^2)
	41.3	46.0	50.7	55.4	60.1	64.8	69.5	74.2	78.9			
PEP 1672(P_1)							2	8	10	20	75.86 ±0.71	10.08
PEP 1692(P_2)		9	11							20	48.56 ± 0.53	5.67
F_1			1	1	1	12	2	1		18	64.14 ± 1.18	25.33
F_2	2	8	6	12	10	21	5	9	5	78	61.31 ± 1.10	94.97
BCP$_1$	1			1	4	5	13	1	5	30	67.62 ± 1.44	62.30
BCP$_2$	1	9	3	6	2	4		1	2	28	55.33 ± 1.94	106.46

[z]Each class represents a range of 4.7 day and class values represent class centers.

Table 11: Distribution, mean, and variance of fruit peduncle length of parental, F_1, F_2 and backcross populations of the cross PEP1672× PEP1692.

Population	Frequency of fruit peduncle length (cm) in class[z]											Total No. of plants	Mean $\overline{x} \pm S_{\overline{x}}$	Variance (σ^2)
	3	5	7	9	11	13	15	17	19	21	23			
PEP 1672(P_1)	18	2										20	3.25 ±0.17	0.59
PEP 1692(P_2)				1	3	3	8	3	1		1	20	15.2 ± 0.70	9.8
F_1	3	5	8	3	1							20	6.82 ± 0.51	5.24
F_2	2	20	15	18	14	3	4	1	1		1	79	9.15 ± 0.41	13.63
BCP$_1$	5	15	7	2	1			1				31	6.38 ± 0.51	8.22
BCP$_2$	1	4	4	5	7	1	3	1	2	1		29	11.06 ± 0.86	21.81

[z]Each class represents a range of 2 cm and class values represent class centers.

Mature fruit color:

Data obtained on mature fruit color of the cross PEP 11× PEP 1763 are presented in Table 12. Plants of PEP 11 (n=20) had yellow fruit color, while plants of PEP 1763 (n=20) had green fruit color. All F_1 plants (n=20) had yellow fruit color indicating the dominance of yellow fruit color. In the F_2, 69 of the 77 plants had yellow fruit color, while 8 plants had green fruit color. The number of plants that had yellow fruit color in the F_2 did not deviate significantly from the ratio 15:1. These results showed that yellow fruit color was controlled by two dominant duplicate epistatic genes. These results agree with those obtained by Whitwood (1975) who reported that in crosses among yellow and green fruit skin lines, yellow segregated 3 to 1 in all cases except those involving precocious yellow which had a 15 to 1 ratio indicating duplicate dominant epistasis.

Table 12: Segregation for mature fruit color trait of parental, F_1, F_2 and backcross populations of the cross PEP 11× PEP 1763.

Population	Number of plants		Total No. of plants	Expected ratio	Chi-square	p
	Yellow	Green				
PEP 11 (P$_1$)	20		20			
PEP 1763 (P$_2$)		20	20			
F$_1$	20		20			
F$_2$	69	8	77	3:1	8.76	< 0.05
				9:7	34.82	< 0.05
				15:1	2.25	0.10 - 0.20
				13:3	3.53	0.05- 0.10

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