

## **GENETIC BEHAVIOR OF YIELD AND QUALITY TRAITS IN SWEET MELON ESMALAWI VARIETY (CUCUMIS MELON – VAR AGYPTIACUS)**

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### **ABSTRACT**

The highly polymorphic in sweet melon for many commercial traits providing seemingly endless possibilities for genetic improvement. The main objective of current study was to estimate of genetic behavior and obtain the genetic parameters of sweet melon advanced lines (*Cucumis melo* L. var. *aegyptiacus*). Eight inbred lines were developed from previous study using a pedigree selection method. The selected inbred lines were crossed according to factorial mating design generated 16 crosses. The additive genetic variance played an important role in the inheritance of yield and most yield component traits. Female variance ( $\sigma^2_i$ ) appeared to be larger than male variance ( $\sigma^2_m$ ) for the most quality traits except for taste. The magnitudes of additive genetic variance ( $\sigma^2_A$ ) were lower than their non-additive including dominance ( $\sigma^2_D$ ) for all studied yield traits, except for number of male flowers per plant and fruit length. The MAGD105, MAGD106 and MAGD107 are promising lines that could be used in farther improvement programs.

**Keywords:** *Cucumis melo* var. *aegyptiacus*, heterosis, genetic variance, fruit quality.

### **INTRODUCTION**

Sweet melon (*Cucumis melo* L. var. *aegyptiacus*) belongs to the family *Cucurbitaceae* is an important horticultural crop worldwide, where the introgression of unadapted germplasm continues to be critical to plant breeding efforts. Wild forms (e.g., ssp. *agrestis*) and landraces of *C. melo* can be found in the Middle East and Asian (Staub *et al.* 1987) that are cross-compatible, but genetically, distant from commercial melon (Mliki *et al.* 2001, Staub *et al.* 2004). However, such genotypes have been historically important in plant breeding. Although, it can not compare with watermelon or cantaloupe as a desirable vegetable fruit. Some farmers grow sweet melon for the local consumption using uncertified seeds from unknown origins. Sweet melon show a great variability determines horticultural market class designations that include differences in mature fruit vary in shape, sweetness, color, exocarp characteristics, diameter, and weight (Silberstein *et al.* 2003, Monforte *et al.* 2005). The highly polymorphic for fruit traits, providing seemingly endless possibilities for genetic improvement through introgression and recombination (Burger *et al.* 2006).

Despite of the large diversity that has been observed among melon germplasm, the efforts for characterization and utilization these germplasm still limited in genetic improvement programs (Neitzke *et al.* 2009). The recent findings by Pereira *et al.* (2011) found that the potential of melon to grow under partial restriction of light that fact could be exploited to improve the ability to produce melon in the regions that have a limited period of light. EI-

Adl *et al.* (1996), revealed that additive and non-additive genetic variances were important in the inheritance of most studied yield traits in *Cucumis melo* var chate. Moreover, additive genetic variances composed the largest portion of genetic variability for yield per plant, shape index, taste and flesh thickness. Similarly, Kim-Moon Soo *et al.* (1996) studied combining ability for yield (fruit weight) and other agronomic traits in muskmelon (*Cucumis melo*). They mentioned that the line “west” was the best general combiner when used as female and male parent. Moreover, Queiroz *et al* (2001) reported that the lines involved in hybrid combinations should be used in the next cycle of selection, synthesizing as many hybrid combinations as possible in order to select the best pair of lines to produce the desirable hybrids.

This study was conducted to evaluate new lines of sweet melon through its offspring with great emphasis on fruit quality; estimation of the genetic parameters in order to define the appropriate strategy for improving Ismailawy sweet melon. Finally, investigation the efficiency of factorial desing in the determination of the relative importance of additive genetic and non-additive genetic effects.

## **MATERIALS AND METHODS**

### **Genetic materials**

Eight lines of sweet melon i.e., Magd<sub>101</sub>, Magd<sub>102</sub>, Magd<sub>103</sub>, Magd<sub>104</sub>, Magd<sub>105</sub>, Magd<sub>106</sub>, Magd<sub>107</sub> and Magd<sub>108</sub> were selected from a previous study using a pedigree selection method. The selected inbred lines were crossed according to factorial mating design (4x4) resultred in 16 crosses. The inbred lines Magd<sub>101</sub>, Magd<sub>102</sub>, Magd<sub>103</sub>, and Magd<sub>104</sub> were used as testers while the remainder were used as lines. In the growing season of 2009, the parents and their offspring were evaluated for yield and fruit quality traits through field experiment in randomized complete blocks design with three replications. The experiment was conducted at Elbaramoon Horticulture Research Station, Horticulture Research Institute. Mansoura Governorate, the yield and its components were evaluated as the number of male flowers/plant (NMF/P) and the number of female flowers/plant (NFF/P), number of fruits/plant (NF/P), average fruit weight (AFW) in Kg, yield/plant (Y/P) in Kg, fruit length (FL) in cm, fruit diameter (FD) in cm and shape index (SI). In addition traits to yield components traits, were estimated

flesh thickness (FT) in cm and total soluble solids (TSS) %.

### **Statistical analysis**

Factorial mating design (4x4) was applied to obtain 16 F<sub>1</sub> crosses to estimate the additive and non-additive genetic variances. The procedures of this analysis were described by Comstock & Robinson design II (1952). The genetic variances components could be estimated as follow:

$$\sigma^2_m = \sigma^2_f = \text{Cov.hs} = \frac{1}{2} \sigma^2_A$$

$$\sigma^2_{mf} = \text{Cov.fs} - \text{Cov.hs(m)} - \text{Cov.hs.(f)} = \sigma^2_D$$

$\sigma^2_D = \sigma^2_{mf}$  :  $\sigma^2_D$  is non-additive genetic variances including dominance.

$\sigma^2_G = \sigma^2_A + \sigma^2_D$  and  $\sigma^2_{ph} = \sigma^2_A + \sigma^2_D + \sigma^2_{e/k}$ , Estimates of heritability values in broad and narrow senses were obtained as follow:

$$h^2_{b.s} = \frac{\sigma^2 A + \sigma^2 D}{\sigma^2 A + \sigma^2 D + \sigma^2 e} / K$$

$$h^2_{n.s} = \frac{\sigma^2 A}{\sigma^2 A + \sigma^2 D + \sigma^2 e} / K$$

## RESULTS AND DISCUSSION

Eight inbred lines of sweet melon were developed from the Balady variety (Esmalawi) through a pedigree selection program. An extensive study of the genetic capacity of these inbred lines resulted in identification as Magd<sub>101</sub>, Magd<sub>102</sub>, Magd<sub>103</sub>, Magd<sub>104</sub>, Magd<sub>105</sub>, Magd<sub>106</sub>, Magd<sub>107</sub>, and Magd<sub>108</sub>. The F<sub>1</sub> hybrids among these inbred lines would yield an important information concerning the inheritance and the nature of gene action in sweet melon. In addition, the amounts and the manifestation of heterosis, heritabilities would be also investigated.

The results indicated that the differences between the means of the crosses were highly significant for most studied traits. The results cleared that the cross 2 x 7 was the best (215.0) for NMF/P trait while the mean values of the other yield studied traits ranged from (9.3 to 33.3), (1.59 to 4.01), (1.51 to 3.06), (3.98 to 11.28), (16.5 to 35.2), (12.5 to 20.4) and (1.21 to 1.72) for the number of female flowers/plant (NFF/P), number of male flowers/plant (NF/P), average fruit weight (AFW), yield/plant (Y/P), fruit length (FL), fruit diameter (FD) and shape index (Sh.I), respectively. The mean values of fruit quality traits taste, flesh thickness FT and total soluble solids TSS% over the crosses ranged from (2.50, 2.97 and 2.84) to (4.64, 4.50 and 7.13) respectively (Table 1). Similar results were demonstrated by Paiva *et al.* (2000), they showed that the average inbred lines soluble solid content was similar compared to that observed in the commercial varieties in the same study. In general, late inbred lines produced fruits with higher soluble solids content. The mean squares of the genotypes showed highly significant for all studied traits except for shape index (Sh.I), which was significant at 5%. The magnitudes of variation illustrated the existence of genetic variation for yield traits (Table 2). The mean squares of males, females and males x females interaction showed highly significant for most yield traits except fruit diameter of males which was significant at 5% of probability. The results showed that the large magnitude of the mean squares of females and (males x females) components from the factorial mating design indicated the importance and the sizable presence of non-additive genetic variances including dominance in current material (Ferreira *et al.* 2002)

**Table 1. Mean performances of 16 crosses of sweet melon for yield traits during the growin season of 2009.**

Crosses	Yield traits							Quality traits			
	NMF/P	NFF/P	NF/P	AFW (Kg)	Y/P (Kg)	FL (cm)	FD (cm)	Sh.I	Taste	FT (mm)	TSS (%)
1 x 5	126	9.7	3.70	3.06	11.28*	19.9	14.8	1.34	3.04	3.37	5.07
1 x 6	97	33.3*	3.36	2.69	9.05	28.7	20.0	1.43	4.21	4.23	7.01
1 x 7	146	32.0	1.90	2.43	6.62	17.4	13.8	1.25	4.10	4.13	2.96
1 x 8	172	32.7	3.16	1.67	5.27	18.9	13.3	1.42	3.17	2.97	3.19
2 x 5	193	13.3	4.01*	2.69	10.75	19.8	15.0	1.32	2.50	3.13	4.40
2 x 6	94	28.7	3.55	2.46	8.73	23.8	19.2	1.26	3.97	3.57	6.92
2 x 7	215*	24.0	1.76	2.34	4.12	17.8	12.5	1.42	4.22	3.67	3.20
2 x 8	200	21.7	3.49	1.51	5.29	19.0	13.0	1.46	3.31	3.03	3.05
3 x 5	184	9.3	3.75	2.59	9.71	19.5	14.6	1.32	3.40	3.37	5.58
3 x 6	99	22.0	2.99	2.41	7.20	35.2*	20.4*	1.72*	4.64*	4.03	7.13*
3 x 7	200	24.7	1.59	2.49	3.98	16.5	13.7	1.21	4.59	4.50*	3.26
3 x 8	207	28.7	3.30	2.75	6.10	17.6	12.6	1.39	3.48	3.13	2.96
4 x 5	103	12.7	3.59	2.66	9.65	20.0	14.6	1.40	3.26	3.47	5.63
4 x 6	88	30.0	2.96	2.69	7.96	23.0	17.7	1.30	4.59	4.10	7.00
4 x 7	167	26.0	1.96	2.37	4.64	16.7	13.1	1.29	4.56	3.80	2.84
4 x 8	192	25.0	3.29	1.97	6.42	18.5	14.0	1.31	3.40	3.10	3.21
LSD	0.50	1.39	0.03	0.29	1.12	1.22	1.12	0.87	0.34	0.12	2.98
0.05	0.66	1.85	0.17	0.39	0.50	1.63	1.49	1.16	0.46	0.16	3.98
0.01											

<sup>†</sup>NMF/P: number of male flowers/plant; NFF/P: number female flowers/plant; NF/P: number of fruits/plant; AFW: average fruit weight; Y/P: yield/plant; FL: fruit length; FD: fruit diameter; SI: shape index; FT: flesh thickness; TSS: total soluble solids.\*Significant at 0.05% level; + Best cross; - Lowest cross.

**Table 2. The analysis of variances and the mean squares for studied yield traits according to factorial mating design.**

Sources	Df	M.S. for yield traits†							Quality traits			
		NMF/P	NFF/P	NF/P	AFW (Kg)	Y/P (Kg)	FL (cm)	FD (cm)	Sh.I	Taste	FT (mm)	TSS (%)
Reps	2	92.271	1.896	0.001	0.004	0.120	0.113	0.297	0.005	0.002	0.015	0.015
Geno	15	6544.7**	195.3**	1.814**	0.540**	18.30**	73.42**	21.43	0.043*	1.002**	0.704**	8.835**
Male	3	5673.8**	78.18**	0.203**	0.117**	1.320**	16.92**	1.215	0.015*	0.398**	0.371**	0.269**
Female	3	23318.**	789.0**	8.594**	2.379**	84.86**	270.2**	98.74	0.041*	4.355**	2.786**	43.00**
M x F	9	1243.7**	36.52**	0.091**	0.068**	1.337**	26.64**	1.813	0.053*	0.085**	0.121**	0.301**
Error	30	31.093	2.89	0.004	0.004	0.101	0.373	0.325	0.004	0.003	0.004	0.006

<sup>†</sup>NMF/P: number of male flowers/plant; NFF/P: number female flowers/plant; NF/P: number of fruits/plant; AFW: average fruit weight; Y/P: yield/plant; FL: fruit length; FD: fruit diameter; SI: shape index; FT: flesh thickness; TSS: total soluble solids.\*Significant at 0.05% level.; \*\* Significant at 0.01% level.

The results cleared also that the variance of female ( $\sigma^2_f$ ) appeared to be larger than those the variance of males ( $\sigma^2_m$ ) and the variance of males by females ( $\sigma^2_m \times \sigma^2_f$ ) for all studied yield traits, although both of them considered as indicator to additive gene effect (Table 3). The results showed that  $\sigma^2_m$  was negative in yield/plant (Y/P), fruit diameter (FD) and shape index (Sh.I), while  $\sigma^2_f$  was positive in all studied yield traits. The results also indicated that the magnitudes of  $\sigma^2_{mf}$  were larger than those  $\sigma^2_m$  for all studied yield traits, except for fruit length (FL). These results indicated that additive genetic variances played an important role in the inheritance of yield

and yield component traits although non-additive genetic variances not be neglected. These results were in accordance with Kosba & El-Diasty (1991) and El-Adl *et al.* (1996). As regards to fruit quality traits, the results revealed that the  $\sigma^2_f$  which contained additive and maternal effect appeared to be larger than those  $\sigma^2_m$  for the majority studied quality traits, except for taste band, although both of them considered as an indicator to additive variances. The results also showed that  $\sigma^2_m$  was negative in total soluble solids (TSS %) while  $\sigma^2_f$  was positive for all studied quality traits (Table 3). Kosba and El-Adl *et al.*(1996) reported similar findings.

**Table 3. The genetic parameters and their standard error for studied yield and quality traits.**

Sources	Yield traits								Quality traits		
	NMF/P	NFF/P	NF/P	AFW (Kg)	Y/P (Kg)	FL (cm)	FD (cm)	Sh.I	Taste	FT (mm)	TSS (%)
$\sigma^2_f$ ± SF	1839.6* ± 1230.0	62.7* ± 41.6	0.71 ± 1.43	0.19 ± 0.40	6.96 ± 14.16	20.30 ± 45.16	8.08 ± 16.47	0.001 ± 0.003	0.030 ± 0.73	0.22 ± 0.47	3.55 ± 7.17
$\sigma^2_m$ ± SF	369.2* ± 302.3	3.5 ± 4.3	0.009 ± 0.010	0.004 ± 0.006	-0.001 ± 0.07	0.81 ± 1.11	-0.06 ± 0.08	-0.003 ± 0.004	0.052** ± 0.02	0.021 ± 0.022	-0.003 ± 0.015
$\sigma^2_{mf}$ ± SF	404.2** ± 65.6	11.2** ± 5.2	0.03** ± 0.003	0.02* ± 0.01	0.41** ± 0.008	0.11 ± 14.33	0.50** ± 0.06	0.016 ± 0.024	0.024** ± 0.01	0.039 ± 0.17	0.98** ± 0.04

<sup>†</sup>NMF/P: number of male flowers/plant; NFF/P: number female flowers/plant; NF/P: number of fruits/plant; AFW: average fruit weight; Y/P:yield/plant; FL:fruit length; FD: fruit diameter; SI: shape index; FT: flesh thickness; TSS: total soluble solids.\*Significant at 0.05% level.; \*\* Significant at 0.01% level. \* Significant at 0.05% level.; \*\* Significant at 0.01% level.

The magnitudes of additive genetic variance ( $\sigma^2_A$ ) were lower than their corresponding non-additive genetic variances including dominance ( $\sigma^2_D$ ) for all studied yield traits, except for number of male flowers per plant and fruit length. The results also revealed that the highest values of additive variance ( $\sigma^2_A$ ) were (738.4) for number of male flowers per plant while the lowest value was (-0.12) for fruit diameter. On the other hand, the highest value of dominance genetic variance ( $\sigma^2_D$ ) was (404.2) for number of male flowers per plant while the lowest value was (0.016) for shape index, respectively.Thus these results also account for the relatively quite amounts of heterosis obtained for yield traits (Table 4).

**Table 4. The relative magnitudes of the genetic parameters for yield and quality traits for crosses according to the factorial mating design.**

Sources	Yield traits								Quality traits		
	NMF/P	NFF/P	NF/P	AFW (Kg)	Y/P (Kg)	FL (cm)	FD (cm)	Sh.I	Taste	FT (mm)	TSS (%)
$\sigma^2_A$	738.4	7.0	0.018	0.008	-0.002	1.62	-0.12	-0.006	0.104	0.042	-0.006
$\sigma^2_D$	404.2	11.2	0.03	0.02	0.41	0.11	0.50	0.016	0.024	0.039	0.980

<sup>†</sup>NMF/P: number of male flowers/plant; NFF/P: number female flowers/plant; NF/P: number of fruits/plant; AFW: average fruit weight; Y/P:yield/plant; FL:fruit length; FD: fruit diameter; SI: shape index; FT: flesh thickness; TSS: total soluble solids.\*Significant at 0.05% level.

Similarly, El-Adl *et al.* (1996) obtained results in the same trend. The results indicated that the highest value of additive genetic variance ( $\sigma^2_A$ ) was (0.104) for taste while the lowest value was (-0.006) for TSS%. On the other hand, the highest value of dominance genetic variance ( $\sigma^2_D$ ) was (0.98) for total soluble TSS%, while the lowest value was (0.024) for taste, respectively (Table 4). Similar findings were obtained by Kosba & El-Diasty (1991) and El-Adl *et al.* (1996).

The estimated values of heritability in broad sense were (97.35%, 86.27%, 93.31%, 92.31%, 80.16%, 82.26%, 53.90% and 71.43%) for number of male flowers/plant, number female flowers/plant, number of fruits/plant, average fruit weight, yied/plant, fruit length, fruit diameter and shape index, respectively (Table 5). These results indicated the importance of both additive ( $\sigma^2_A$ ) and non-additive genetic variance including dominance ( $\sigma^2_D$ ) in the inheritance of many yield and its component traits. There is general agreement that GCA and associated heterotic effects are important determinates of parental choice during hybrid melon development (Ferreira *et al.* 2002; Souza *et al.* 2002). Moreover, heterosis, as a function of performance, is often related to degree of genetic relatedness and is ramatically influenced by growing environment. The estimated values of heterosis in broad sense ( $h^2_b\%$ ) were (97.14%, 95.24% and 94.0%) for taste band, flesh thickness and TSS%, respectively. In the same time, the highest values of heterosis in narrow sense ( $h^2_n\%$ ) was 68.57% for taste (Table 5). In a similar study on watermelon, Souza *et al.* (2005) found that the most hybrids showed positive heterosis for most studied quality traits in relation to the parent mean and the standard cultivar. Generally, similar results concluded that selection could be effective to improve most economical traits of *Cucumis melo*, Eladl *et al.*1996, Queiroz *et al.* 2001).

**Table 5. The heritability values in broad and narrow senses for yield and quality traits for the F<sub>1</sub> hybrids.**

Source s	Yield traits							Quality traits			
	NMF/P	NFF/P	NF/P	AFW (Kg)	Y/P (Kg)	FL (cm)	FD (cm)	Sh.I	Taste	FT (mm)	TSS (%)
$h^2_b\%$	97.35	86.27	92.31	87.50	80.16	82.26	53.90	71.43	97.14	95.24	94.00
$h^2_n\%$	62.91	33.18	34.62	25.00	00.00	77.03	00.00	00.00	68.57	47.62	0.00

<sup>†</sup>NMF/P: number of male flowers/plant; NFF/P: number female flowers/plant; NF/P: number of fruits/plant; AFW: average fruit weight; Y/P: yield/plant; FL: fruit length; FD: fruit diameter; SI: shape index; FT: flesh thickness; TSS: total soluble solids.\*Significant at 0.05% level.

Through the estimation of heterosis values from the mid-parents and the better parent for yield and its traits, it was observed that the average means of the F<sub>1</sub> hybrids significantly exceeded the mid-parents (MP) for most studied yield traits (Table 6). The amounts of heterosis estimated from the F<sub>1</sub> hybrids against the mid-parents (MP) ranged from (-7.69 to 70.93%) for number of female flowers/plant and yield/plant, respectively. Paiva *et al.* (2000), estimated the yield of melon lines that ranged from 16.2 t/ha up to 65.1 t/ha, whereas in commercial varieties produced 28.0 t/ha. The negative values of heterosis, which estimated for number of male flowers/plant and

number of female flowers/plant were expected and desirable where these traits considered as a measure of earliness. The estimated values of heterosis from the average of the F<sub>1</sub> hybrids significantly exceeded the better parent (BP) for all studied traits. The results indicated that the highest values of heterosis from the better parent were 41.05% for number of male flowers/plant. On the other hand, the lowest heterosis values of F<sub>1</sub> versus the better parent were 19.68% for number of fruits/plant. Similar results were obtained by Kosba & El-Diasty (1991), Awny *et al* (1992) and Kosba *et al.* (1993). It was also noticed that the highest values of heterosis versus the mid-parent were 65.14% for TSS and the lowest values of heterosis of the F<sub>1</sub> hybrids from the mid-parent were -2.43% for flesh thickness. The means of the F<sub>1</sub> hybrids significantly exceeded the better parent for flesh thickness and TSS%. The results also showed that the highest amounts of heterosis values estimated from the better parent (BP) was 12.13 for taste trait. Whereas, the lowest heterosis values for flesh thickness in the F<sub>1</sub> hybrids from the better parent were 4.90. These results were in agreement with the results obtained by Kosba *et al.* (1993).

**Table 6. The estimates of mid parents (M.P.), better parent (B.P.), the means of F<sub>1</sub> hybrids and heterosis values versus the (M.P.) and (B.P.) for quality traits.**

Parameter	Quality traits		
	Taste	FT	T.S.S. %
M.P.	3.13	3.29	4.59
B.P.	4.37	4.03	7.01
F <sub>1</sub>	3.84	3.21	7.58
H (M.P.)	22.68**	-2.43	65.14**
H (B.P.)	12.13	-5.17**	8.13**
LSD	0.05	0.12	2.98
	0.01	0.16	3.98

\*Significant at 0.05% level; \*\* Significant at 0.01% level.

In the current study factorial design applied to estimate the additive genetic variances including dominance which could be obtained from the (males x females) component, and additive genetic variances which could be obtained from  $\sigma^2_m$  and/or  $\sigma^2_f$ . Since, the factorial mating design is commonly used in plant breeding studies. Mating design was generally developed to partition genetic variances into its components. In factorial mating design, the total genetic variance is divided into males, females and males by females components. The first two portions of variance, i.e., male and/or female are an estimation of additive genetic variance, while the latter portion males by females component is an estimation of non-additive genetic variance including dominance. The magnitudes of additive genetic variance relatively to non-additive genetic variance have an important implication to determine the breeding program, which could be followed. As for heterosis in sweet melon, little investigations were reported. Since little information were obtained with respect to the amounts of heterosis in sweet melon. The large magnitudes of the mean squares of both yield and quality traits obtained from

the factorial mating design indicated the importance of the additive and non-additive (including dominance) genetic variances, although the mean squares of the female were high for most studied traits. It could be concluded that it is possible to improve sweet melon traits through the selection for new inbred lines. The hybridization among these inbred lines could produce superior F<sub>1</sub> hybrids.

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### السلوك الوراثي لصفات المحصول والجوده في الشمام الاسميلاوى

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يمثل التباين غير المحدود في الشمام الاسميلاوى وتنوع اشكاله لعديد من الصفات الهامه اقتصادياً عامل هام في برامج التحسين الوراثي لهذا المحصول. كان الهدف الرئيسي من الدراسة الحاليه هو تقييم السلوك الوراثي لصفات المحصول والجوده للثمار والحصول على بعض المعايير الوراثية لبعض سلالات الشمام الاسميلاوى (*Cucumis melo* L. var. *aegyptiacus*). تم في هذه الدراسة استخدام ثمانى سلالات متقدمه من الشمام الاسميلاوى ناتجه عن طريق انتخاب النسل. تم تهجين هذه السلالات بنظام التزاوج العاملى منتج ١٦ هجين. تم تقدير مكونات التباين الوراثي لكل من الاباء والهجن. التباين الاضافي كان له الدور الاساسي في وراثه معظم صفات المحصول ومكوناته. بينما كان التباين في الامهات اكبر مقارنة بنظيره في خطوط التربية الاباء في معظم صفات الجوده للمحصول فيما عدا صفه التذوق. التي زاد فيها التباين في الاباء عن نظيره في الامهات اهميه كل من التباين الاضافي وغير الاضافي بوجه عام تباين في كل من صفات المحصول والجوده للثمار. اظهرت كل من السلالات MAGD105, MAGD106 و MAGD107 احتوائها على اعلى نسبة من تكرارات الاليلات المفيده و التي يمكن استغلالها في برامج انتاج الهجن للشمام الاسميلاوى.

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