

## Estimation of some genetic parameters through generation mean analysis in melon

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### ABSTRACT

This study was done to determine the types and magnitude of gene effects and heritability of some yield and physiological traits in melon (*Cucumis melo* L.). After generating of F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations from the meeting of the two parents, Tashkandi (P<sub>1</sub>) and Alien (P<sub>2</sub>), the six generations were used in the generation mean and variance analysis. The experiment was carried out in a randomized complete block design with three replications. The results indicated that, additive gene effect was significant for fruit length, seed length and TSS. The significant additive and dominance effects was observed in fruit diameter, fruit length/diameter ratio, flesh thickness and skin thickness. Significant additive×additive effects was detected for all traits except TSS. Additive×dominance gene effects was significant for fruit length, fruit diameter, fruit length/diameter ratio and seed length. Dominance×dominance significant effects were detected for flesh thickness, skin thickness and TSS. The additive genetic variance estimates for fruit length, fruit length/diameter ratio, flesh thickness, skin thickness and seed length were positive and the dominance variance estimates for these traits were negative or small. In contrast, in fruit diameter and TSS dominance variances were high. So, narrow sense heritability was high for all traits except fruit diameter and TSS. These results indicate that selection may be more effective for improving traits of genotypes in early generations

**Key words:** Additive, *Cucumis melo*, Dominance effects, Generation mean analysis.

### INTRODUCTION

Melon (*Cucumis melo* L.) is a cross-pollinated plant and an economically important crop species of Cucurbitaceae family. Some researchers in botany consider Iran as the most important center of secondary diversity and localization of this plant (Mallic and Masui, 1986).

During melon domestication levels many traits related to yield and fruit qualities are determined. The genetic control of fruit shape, sex expression, gelatinous sheath around the seeds, sutures, number of placentas and white flesh color are determined as a recessive genetic control (Pitrat, 2013). About fruit traits, several reports (Eduardo *et al.*, 2007; Pitrat, 2013; Pornsuriya and Pornsuriya, 2009) suggested that the genetic control of fruit traits at unripe and ripe stage are mono and oligogenic characters. Several authors detected additive and non-additive effects in the genetic control of the fruit weight in melon (Lippert and Legg, 1972; Kalb and Davis, 1984; Singh and Randhawa, 1990; Monforte *et al.*, 2004). Feysian *et al.*, (2009) observed a predominance of additive effects of average fruit weight in a diallel of local populations from Iran. Lippert and Legg (1972) evaluated the gene action of yield traits in melon, and determined that additive and non-additive variance

components were important in the genetic control of yield-associated traits. High yield with uniform fruit shape, size and excellent quality are prerequisites for the release of superior melon varieties. In this crop, yield is associated with several traits, including primary branch number, days to anthesis, fruit number, weight per plant and average weight per fruit (Lippert and Hall, 1982; Kultur *et al.*, 2001; Abdalla and Aboul\_Nasr, 2002; Taha *et al.*, 2003). However, few studies have examined the inheritance of traits affecting yield in this vegetable crop species (Lippert and Legg, 1972; Lippert and Hall, 1982; Shahikumar *et al.*, 2016). This study was designed to determine: (i) gene action, (ii) components of variance and (iii) broad and narrow-sense heritability.

### MATERIALS AND METHODS

This experiment was conducted at Agricultural Research Station, University of Tehran, Alborz, Iran. Two advanced and morphologically distinct melon, Tashkandi (P<sub>1</sub>) and Alien (P<sub>2</sub>) as parents with F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> were used in the generation mean and variance analysis. The experiment was arranged in a randomized complete block design. Field plot consisted of 2 m long rows with 10 plants. Each plot was arranged in three randomized blocks with unequal number of plots for each generation. The P<sub>1</sub>, P<sub>2</sub> and F<sub>1</sub>

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generation planted in two plots per block, F<sub>2</sub> generation planted in eight plots per block and BC<sub>1</sub> and BC<sub>2</sub> generations planted in four plots per block. The final number of plants varied in all the generations. The spacing was 2.0 m between rows and 60 cm between plants. In each block, 10 plants for parent and F<sub>1</sub> hybrid, 25 plants for backcrosses and 30 plants for F<sub>2</sub> generations were taken for study. The normal recommended cultural practices were adopted during experimentation. The fruits were evaluated for the traits: fruit weight (g), fruit length (cm), fruit diameter (cm), fruit length/diameter ratio, flesh thickness (cm), skin thickness (cm), internal cavity size (cm), seed length (cm) and total soluble solid (TSS: Brix percent). Total soluble solid (°Brix) of melons were measured by a handheld refractometer (Atago Co., PR-1 Brix-Meter, Tokyo, Japan).

Analysis of weighted variance and mean comparison were performed using SAS software. For the generation mean analysis, at first, additive-dominance model was conducted using weighted least squares. The joint scaling test was carried out to verify the goodness of fit of the model (Kearsey and Pooni, 2004). Generation mean analysis was done using the Mather and Jinks model (1982). Additive, dominance, environmental variance and additive-dominance covariance components were estimated using the weighted least square test with the observed variance of the six basic generations been used as the initial weights ( $df/(2 \times S^2)^2$ ) until the chi-squared test value reached a minimum (Lynch and Walsh, 1998).

## RESULTS AND DISCUSSION

Analysis of weighted variances and means comparisons for studied traits in different generations is shown in Table 1. Analysis of variance showed significant differences among generations (except for internal cavity size). Therefore, the significant difference between generations makes possible generation mean and variance analysis and surveys of gene action and their inheritance (Due to the low differences observed in parents for the fruit weight and internal cavity size, genetic analysis of these traits was not performed).

The results of A, B, C and D scaling test for traits (Table-2) revealed that significance of any of these tests indicates the presence of non-allelic gene interactions or epistasis on the scale of measurement used. Although scaling test does not fail to detect non-allelic interaction for all of the traits, the inadequacy of the additive-dominance model suggests the presence of non-allelic interactions too. Results of scaling test, showed that additive-dominance model is inadequate for explaining the inheritance of all studied characters, indicating the presence of non-allelic gene interaction.

The results of generation mean analysis provide estimates of the main and first order interaction gene effects (Table 3). Significant chi square value expressed the presence of non-allelic interaction in studied traits. The significant mean parameters [m] for all studied traits indicate that the contribution due to the overall mean plus the locus effects

**Table 1:** Analysis of variance and mean comparison for various characters investigated.

	Fruit Weight	Fruit Length	Fruit Diameter	Fruit Length/Diameter Ratio	Flesh Thickness	Skin Thickness	Seed length	Internal Cavity Size	TSS
Replication	0.126	0.005	0.0503	0.0257	0.0344	0.024	0.147	0.24	0.055
Generations	1.92**	6.39**	2.232**	20.102**	0.602**	1.76**	4.095**	0.37	8.855**
Error	0.255	0.152	0.224	0.1366	0.076	0.158	0.206	0.26	0.17
CV%	0.32	2.26	3.93	28.62	9.52	39.25	33.18	4.95	3.039
P1	0.828b	21.46a	10.85b	2.054a	2.69c	0.4488cd	1.1177a	5.41ab	10.756b
P2	1.001b	12.35c	12.045ab	1.024d	2.94ab	0.5409bc	0.854c	5.01b	14.904a
F1	1.516a	17.99b	12.71a	1.423b	3.057ab	0.4782bc	1.0519ab	5.64ab	14.7a
F2	1.773a	18.65b	13.26a	1.392bc	2.84bc	0.7452a	1.092ab	6.05a	15.166a
BC1	1.57a	18.27b	12.216a	1.488b	3.095a	0.3452d	1.08ab	5.31ab	15.658a
BC2	1.501a	16.91b	13.29a	1.299c	3.13a	0.5783b	1.009b	5.97a	14.569a

\*,\*\*,:Significant at 5% and 1% levels of probability, respectively, TSS: Total soluble solid.

**Table 2:** Estimates of scaling test for investigated traits.

Traits	A	B	C	D
Fruit Length	6.405**±0.84	-5051**±0.8	6.047**±2.14	2.57±9.3
Fruit Diameter	-0.248±0.504	3.239**±0.482	5.03**±0.904	1.02±4.24
Fruit Length/Diameter Ratio	0.557**±0.034	-0.881**±0.054	-0.166±0.14	0.0783±0.581
Flesh Thickness	0.1316±0.152	0.45**±0.158	-0.307±0.32	-0.44±1.47
Skin Thickness	-0.3008±0.048	0.209**±0.057	1.008**±0.108	0.55±0.474
Seed Length	0.24**±0.029	-0.172**±0.03	0.279**±0.071	0.106±0.309
TSS	1.74**±0.18	3.34**±0.604	5.618**±0.86	0.268±4.21

\*,\*\*,:Significant at 5% and 1% levels of probability, respectively, TSS: Total soluble solid

and interaction of the fixed loci was significant. Additive gene effect [d] was significant for fruit length, seed length and TSS, indicating potentiality of improving the performance of these characters using the pedigree selection program may be more effective. The significant [d] and [h] in the inheritance of rest traits (fruit diameter, fruit length/diameter ratio, flesh thickness and skin thickness) revealed that both types of additive and dominance effects are involved in the genetics of these traits. The negative value of [h] observed in some cases indicated that the alleles responsible for less value of the traits were dominant over the alleles controlling high value.

According to Ajay *et al.*, (2012), inter-allelic interactions play a key role in the expression of a character and additive-dominance alone is not sufficient. Significant epistatic additive×additive [i] gene effects was detected for all traits except TSS. Additive×dominance [j] epistatic type of gene effects were found to be significant for fruit length, fruit diameter, fruit length/diameter ratio and seed length. The negative sign of additive×dominance [j] interaction in fruit diameter also suggested dispersion of genes in the parents. Concerning the third type of epistatic effect i.e. dominance×dominance [l], highly significant effects were detected for flesh thickness, skin thickness and TSS. Paris *et al.*, (2008) reported the presence of additive and non-additive effects for the longitudinal diameter trait, diverging from this study. Concerning flesh thickness, Kalb and Davis (1984), Singh and Randhawa (1990) and Kitroongruang *et al.*, (1992) observed significant effects for GCA and SCA and the presence of additive and non-additive effects of

internal cavity size. Paris *et al.*, (2008) mentioned the same fact for flesh thickness.

The signs of [h] and [l] were opposite in flesh thickness, skin thickness and TSS suggests duplicate types of non-allelic interaction (15:1) in these traits. Hence, it is appropriate to follow recurrent selection. The existence of such epistasis and higher magnitudes of [h] and [l] in the population generally reduces efficiency of selection. Usually selection would be effective after several generations once a high level of gene fixation is attained for the traits showing significant gene interactions. The results obtained here revealed the importance of epistatic types of gene effects in the inheritance of all traits studied, and cannot be ignored when establish a new breeding program to improve melon populations. The inheritance of all studied traits was controlled by additive and non-additive genetic effects, with greater values of additive gene effect than the dominance one in most cases that will also be seen in the variance analysis of generations. When additive effects are larger than the no additive, it is suggested that selection in early segregating generations would be effective, while, if the non-additive portion are larger than additive, the improvement of the characters needs intensive selection through later generation. On the other hand, this should also be taken into account that such gene effects cancelled due to the simultaneous presence of positive and negative components. Most of the traits indicated negative alleles dispersed in the parents of the cross for the inheritance of these traits. Therefore, selection for such traits should be done in later generation that the desired recombinants become available in the population (Shashikumar *et al.*, 2016).

**Table 3:** Estimation of gene effects for investigated traits.

	[m]±S <sub>d</sub>	[d]± S <sub>d</sub>	[h]± S <sub>d</sub>	[i]± S <sub>d</sub>	[j]± S <sub>d</sub>	[l]± S <sub>d</sub>	X <sup>2</sup>
Fruit Length	19.119**±0.787	-4.66**±0.3	-1.175±0.92	-2.134*±0.89	12.11**±1.1	—	2.256
Fruit Diameter	14.01±0.37	0.688**±0.154	-1.364**±0.42	-2.62**±0.41	-3.508**±0.678	—	0.39
Fruit Length/ Diameter Ratio	1.302**±0.04	-0.49**±0.022	0.11**±0.052	0.214**±0.056	1.408**±0.059	—	8.9
Flesh Thickness	1.93**±0.356	0.112*±0.043	2.61**±0.83	0.911**±0.35	—	-1.484**±0.49	2.27
Skin Thickness	1.667**±0.114	-0.06**±0.017	-2.49**±0.269	-1.12**±0.113	—	1.304**±0.159	49.29**
Seed Length	1.109**±0.028	-0.14**±0.101	-0.06±0.033	-0.12**±0.031	0.412**±0.039	—	2.15
TSS	13.91**±1	1.85**±0.13	4.27±2.45	-1.014±0.99	—	-3.49*±1.504	4.97

\*,\*\*.:Significant at 5% and 1% levels of probability, respectively, TSS: Total soluble solid.

**Table 4:** The estimates of variance components and heritability for different traits.

	V <sub>E</sub>	V <sub>A</sub>	V <sub>D</sub>	V <sub>AD</sub>	V <sub>G</sub>	V <sub>P</sub>	H <sup>2</sup> <sub>n</sub>	H <sup>2</sup> <sub>b</sub>
Fruit Length	5.54	23.76	-10.92	-2.23	23.76	29.3	0.81	0.81
Fruit Diameter	1.4848	0.681	0.9472	-0.19	1.628	3.1128	0.22	0.523
Fruit Length/ Diameter Ratio	0.0116	0.136	-0.0687	-0.001	0.136	0.1476	0.92	0.92
Flesh Thickness	0.163	0.281	-0.034	-0.019	0.281	0.444	0.63	0.63
Skin Thickness	0.0236	0.0328	-0.0134	0.0018	0.0328	0.0564	0.581	0.581
Seed Length	0.0089	0.021	-0.01	-0.002	0.021	0.0299	0.7	0.7
TSS	1.62	-0.959	2.1377	1.91	2.1377	3.7577	0	0.57

V<sub>A</sub> : Additive variances, V<sub>D</sub> : Dominance variances, V<sub>AD</sub> : Additive-dominance variances, V<sub>E</sub> : Environmental variances, V<sub>G</sub> : Genotypic variance, V<sub>P</sub> : Phenotypic variance, H<sup>2</sup><sub>n</sub> : Narrow-sense heritability, H<sup>2</sup><sub>b</sub> : Broad sense heritability, TSS: Total soluble solid.

Variance components, broad sense and narrow sense heritability are presented in Tables 4. The additive genetic variance estimates for fruit length, fruit length/diameter ratio, flesh thickness, skin thickness and seed length were positive and the dominance variance estimates for these traits were negative or small in magnitude when compared to their additive variance estimates. In contrast, the magnitude of additive genetic variance for fruit diameter and TSS was small when compared to their associated dominance variances. Mohammadi *et al.*, (2014) recorded that analysis of variance indicated highly significant differences among genotypes for TSS in Cantaloupe (*Cucumis melo* L. Subsp. *melo* var. *cantalupensis* Naudin). El-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. The obtained results indicated that  $V_A$  played the greatest role for inheritance of these traits.  $V_{AD}$  is an indicator of association between  $V_A$  and  $V_D$  over all loci. If  $V_{AD}$  is zero, it means that dominant genes are in the parent with high performance, while negative  $V_{AD}$  denotes that dominant genes are in the low performance parent. Negative estimates of variance components were assumed zero (Robinson *et al.*, 1955). Some researchers reported these negative signs in their studies for special purposes (Dudley and Moll, 1969; Hallauer and Miranda, 1988). It seems that, shortage of data in some generations leads to negative variances. Kearsey and Pooni (2004) stated that due to the small effects of dominance effects in some traits, usually the contribution of these effects has been estimated low and small. In all traits, the genotypic variance was greater than environmental variance. These results indicated that, genetic had an important role in the expression of these characters. There is enough scope for selection based on these characters and the diverse genotypes can provide materials for a breeding program.

Heritability indicates the effectiveness with which selection of genotypes can be done on the basis of its phenotypic variation in the experimental population (Samlined Sujin *et al.*, 2017). Narrow sense heritability was high for all traits except fruit diameter and TSS. These results indicate that selection may be more effective for improving traits of genotypes in early generations. On the contrary, low narrow sense heritability was estimated for fruit diameter and TSS indicate that environmental effects have a larger contribution than genetic effects for these traits and selection for end-generations or hybrid selection can be effective.

Iban *et al.*, (2007) on melon found that heritability estimates for fruit weight, TSS, diameter, length and shape index were 19%, 35%, 31%, 29% and 62% respectively. Pornsuriya (2009) on oriental pickling melon showed that the estimates of broad sense heritability for fruit: length,

width and shape index were 65%, 55% and 88% respectively. Abou Kamer *et al.*, (2015) showed that high broad sense heritability for the fruit flesh thickness and TSS. On the other hand, the fruit flesh thickness showed high narrow sense heritability. Ibrahim (2012) on sweet melon showed that broad sense heritability estimates among all the traits were very high (>90%), and the high heritability estimates indicate the presence of a large number of fixable additive factors and hence these traits may be improved by selection. He found that high heritability associated with high genetic advance was found in the characters like fruit weight and this indicated this character was mostly controlled by additive gene action. He also showed a high heritability accompanied by low genetic advance for gene action predominance that could be exploited through heterosis breeding.

For TSS the additive genetic variance ( $V_A$ ) was zero, but the dominance variance ( $V_D$ ) was also significant. The broad sense heritability was moderate for TSS. These results do not agree with those of Abadia *et al.*, (1985), Kitroongruang *et al.*, (1992), Zhihua (1995), Monforte *et al.*, (2005), Bayoumy *et al.*, (2014) and Shashikumar and Pitchaimuthi (2016). They recorded that additive gene effects in melon control TSS. Moreover, Kalb and Davis (1984), Singh, Randhawa (1990), Barros *et al.*, (2011), and Mohammadi *et al.* (2014) on melon reported additive and non-additive gene actions controlling TSS trait. On the contrary, Monforte *et al.*, (2004) found that non-additive gene effects control TSS. El-Adl *et al.*, (1996) obtained the lowest additive and a highest dominance value of genetic variance for TSS, respectively (Table 4). Kosba and El-Diasty (1991) obtained similar findings.

In general, when quantitative characters are governed by additive or dominance gene actions, hybrid breeding methods may be easily improved. However, when interaction effects influence these characters, it becomes very difficult to improve characters by simple selection programs (Sunil Kumar, 2005). Jhanavi *et al.*, (2018) stated that the characteristics that have a heritability of over 60% and controlled by additive effects, can play an important role in plant breeding programs. Selection of suitable breeding methods for better exploitation of the potential of various agronomic traits in a plant depends on the type of gene action and heritability. Moreover, knowing the type of gene action involved in the expression of a trait in breeding methods of plant communities has special importance.

## CONCLUSION

Results of the present study exhibited that genetic variability were an important factor for all traits like fruit length, fruit diameter, fruit length/diameter ratio, flesh thickness, seed length and TSS. Therefore, generations mean analysis through scaling tests was functional for estimation of gene action for these traits. Scaling tests (A, B, C and D) were found to be important for these attributes. Therefore,

epistasis played a role in inheritance of these traits. Both additive and non-additive gene actions play a key role in the expression of the quantitative traits. Additive-dominance model did not explain the observed variation for all of the studied traits, thus the evidence for presence of digenic or higher order epistatic interactions. In general, genetic effects were not of single type, but were a combination of different interaction effects for all the traits. Finally, the high heritability in fruit length, seed length and fruit length/diameter ratio represented that these traits were less affected by environment indicating either this simply inherited and

were controlled by a few main genes or additive gene effects. Therefore, selection of these traits would be more effective. On the other hand, the lower heritability showed low penetration of the additive genetic variance and a large penetration of the environmental effect, which it proposes selection based on early selective generation, would not be effective for them. This study corroborated that it is feasible to produce new melon hybrids under the Iranian environments which can he compete with the import hybrids, meet the needs of agronomist and diminish a lot of fees annually spend to buy the foreign hybrid seeds.

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