Araştırma Makalesi/*Research Article (Original Paper)*

# Genetic Analysis of Yield Components, Early Maturity and Total Soluble Solids in Cantaloupe (*Cucumis Melo* L. subsp. *melo* var *cantalupensis* Naudin)

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**Abstract**: Analysis of genetic main effects and genotype×environment interaction effects for quantitative traits of cantaloupe were conducted based on a genetic model containing additive-dominance and their interactions with environments. A set of 21 diallel $F_1$ hybrids and their parents were evaluated during two the springs of 2011 and 2012. The average weights per fruit, (WT), maturity (DM), flesh thickness (F), total soluble solids content (TSS) and total fruit yield (TY) were measured. The additive genetic variance component was significant for WT, F, DM and TSS, the dominance genetic variance for WT, TY, DM and TSS. However, dominance×year interaction was significant for all traits under investigation except for TSS. Additive gene effects were most important with respect to WT, F, DM and TSS, while genetic dominance effects mainly controlled TY. The parent, Dastjerdi had the highest additive effect for WT and DM, while the parents, Tiltorogh and Savei had the highest additive effects for F and TSS, respectively. Tiltorogh×Savei and Rishbaba×Tiltorogh was the best specific combiner for the traits, WT, F and TY. Favorable heterosis over the better parent heterobeltiosis was found for TY. Thus, there is the potential to generate superior cultivars in segregate generation and hybrid production.

**Key words**: Cantaloupe, Diallel, Genetic effects, Selection, Heterosis

## Kantalop Kavunlarda (*Cucumis Melo* L. subsp. *melo*. var *cantalupensis* Naudin) Verim Bileşenleri, Erken Olgunluk ve Toplam Suda Çözünür Kuru Maddenin Genetik Analizi

**Özet:** Kantalop kavunlarda kantitatif özellikler için genetik ana bileşenler ve genotip-çevre etkileşimi etkilerinin analizi eklemeli-dominans genetik modelleme ve bunların çevre ile etkileşimlerini içeren bir genetik modele dayalı olarak gerçekleştirilmiştir. Yirmibir (21) adet diallel $F_1$ melez ve ebeveynlerini içeren bir set 2011 ve 2012 yıllarında iki yıl incelenmiştir. Ortalama meyve ağırlığı (OMA), olgunluk (O), meyve eti kalınlığı (MEK), toplam suda çözünür kuru madde (SÇKM) ve toplam meyve verimi (TMV) ölçüm ve gözlemleri yapılmıştır. Eklemeli genetik varyans bileşeni, OMA, MEK, O ve SÇKM bakımından istastistiki olarak önemli bulunurken, dominans gentik varyans bileşeni, OMA, TMV, O ve SÇKM ibakımından istastistiki olarak önemli bulunmuştur. Bununla birlikte, dominans-yıl etkileşimi SÇKM hariç bütün incelenen özellikler bakımından istastistiki olarak önemli çıkmıştır. Eklemeli gen etkisi özellikle OMA, MEK, O ve SÇKM bakımından en önemli olarak bulunurken, dominans gen etkisi başlıca TMV'yi kontrol etmiştir. Ebeveynlerden Dastjerdi OMA ve O bakımından en yüksek eklemeli gen etkisine sahip olurken, ebeveynlerden Tiltorogh ve Savei, MEK ve SÇKM bakımından en yüksek eklemeli gen etkisine sahip olmuşlardır. OMA, MEK ve TMV bakımından en iyi özel kombinasyonlara Tiltorogh×Savei ve Rishbaba×Tiltorogh sahip olmuştur. TMV bakımından en iyi ebeveyni geçen olumlu heterobeltiosis gözlenmiştir. Bu yüzden, açılım gösteren jenerasyonlarda ve hibrit üretiminde üstün özelliklere sahip çeşitlerin geliştirilmesi potansiyeli bulunmaktadır.

**Anahtar kelimeler:** Kantalop, Diallel, Genetik etkiler, Seleksiyon, Heterosis

## Introduction

Cantaloupe (*Cucumis melo* L. var *cantalupensis* Naudin) is a commercially important crop in Iran. Cantaloupe is a species of melon that has been developed into many cultivated varieties. Although it

thought to have originated in Africa, new data suggest that melon may probably be of Asian origin (Sebastian et al. 2010). Iran is a secondary diversity centre for melon (Kerje and Grum 2000). Iranian germplasm has a large genetic variability, because of the environmental conditions of cultivation. The major producers are China, Turkey, Iran, The United States and Spain.

High yield, early maturity and uniform fruit shape and size, as well as excellent quality, are important objective of melon breeding programs (Zalapa et al. 2006). In melon, yield is associated with several traits including primary branch number, days to anthesis, fruit number and average weight per fruit. Although presently planted cultivars are capable of high yield, early maturity and good quality, interest still exists in pursuing further improvement of melon through breeding activities, because genetic gains can be performed without a concomitant increase in crop management costs. Economic traits including fruit weight, fruit yield, early maturity, flesh thickness and total soluble solids content are quantitative traits affected by the genotype, environment and genotype×environment interaction. The complexity of these traits is a result of different processes that happen during plant development. Exploitation of genetic variability is critical for making further genetic improvement of economically important traits. Knowledge of type and amount of genetic effects will improve an efficient use genetic variability.

There are many genetic models which have been developed based on the analysis of variance procedure. Some of these models such as North Carolina designs (Hallauer and Miranda 1988) and Hayman, Griffing's methods of diallel analysis (Hayman 1954; Griffing 1956; Gardner and Eberhart 1966), have been widely used by plant breeders to provide reliable information for genetic improving of different crops (Lippert and Legg 1972; Feyzian et al. 2009). Although using the ANOVA approaches results in good success in breeding progress of many crops, these procedures have some deficiencies in handling unbalanced data, or non-integer values of coefficients, or correlated random factors (Radhakrishna 1971; Zhu and Weir 1994a, b, 1998). Therefore, the further development of quantitative genetics has been restrained in some ways by its prevailing dependency on ANOVA-based procedures. Mixed linear models developed by statisticians (Hartley and Rao 1967; Rao 1970; Miller 1974) can be applied in quantitative genetics for estimating genetic parameters in plant breeding. These methods can overcome the shortcomings of ANOVA approaches for analyzing genetic models with unbalanced data or complicated models. Zhu and Weir (1994b) suggested a genetic model of diallel crosses based on the mixed linear models for estimating additive, dominance variance components, as well as their interactions with environments. They used a minimum norm quadratic unbiased estimation (MINQUE) approach to estimate the variance components for a single trait and covariance components for multiple traits of random factors (Zhu and Weir 1994b). The linear unbiased prediction (LUP) method was also applied to predict the random effects including additive, dominance and environment effects, etc. Abderrahmane and Zhu (2001) considered particularly on the effect of the environment and on the interaction between genetic and environment effects. They stated that an understanding of the inheritance of these effects is of basic significance in the study of evolution and in the application of genetics to plant breeding.

The main objective of the present study was genetic analysis of the economic traits in cantaloupe using a diallel mating design thorough additive-dominance genetic method of mixed model developed by Zhu and Weir (1996).

## Material and Methods

### Plant materials

Seven Iranian endemic populations of cantaloupe were crossed in 7×7 diallel crosses to produce the 21 $F_1$ hybrids without reciprocals in 2010. The genotypes including Rishbaba, Shahabadi, Samsori, Dastjerdi, Magasi, Tiltorogh and Savei were used as parents. These genotypes were selected based on their considerable variability in early maturity, sweetness, yield and yield related traits.

### Experiment

Twenty eight entries including seven parents and their 21 $F_1$ hybrids were evaluated at Tarbiat Modares University agricultural research filed, Tehran, Iran during two the springs of 2011 and 2012. The site is at 35º, 44' N latitude; 51º, 9' E longitude; and 1,280 m elevation. The experiment was carried out in layout

of the lattice design with three replications. Sowings in the first year were performed on April 9th, 2011 and on the second year on April 22nd, 2012 with 2 m spacing between rows and 0.5 m spacing between plants, respectively. Fertilizer treatments were accomplished uniformly on the all furrows (150 kg ha^{-1} NPK (2:2:1) and 10 tons ha^{-1} cow manure prior to plowing, with an additional 100 kg ha^{-1} of N top-dressed 45 days after sowing). Plants were thinned 3 weeks after sowing. The agronomic traits were measured on five plants per genotype and means of each trait was used in statistical analysis. Weeds were controlled by hand as needed. Mature fruits were harvested every day during the growing season.

*Data collection*

The average weight (kg) (WT) per fruit was measured for each plant by dividing the total number of fruit per plant by the total weight per plant. The average day to maturity of fruits (DM) was assessed for each plant by dividing the total number of fruits per plant by the total days to maturity of fruits per plant. Total yield (TY) was estimated by the total production of each plant. The average flesh thickness (F; cm) was calculated on the radial cross section by dividing the total number of fruit per plant by the total flesh thickness per plant. Total soluble solids content (TSS) was measured using Atago hand refractometer. Five freshly cut fruits were used for each genotype. The data for all traits were collected in both years.

*Statistical analysis*

A genetic model based on the mixed linear models (Zhu and Weir 1996) was applied to study the genetic analysis of measured traits as follows:
$$Y_{ijkl}=\mu+Y_i+A_j+A_k+D_{jk}+AY_{ij}+AY_{il}+DY_{ijk}+B_{l(i)}+e_{ijkl}$$
where $y_{ijkl}$ is the yield of hybrid jk for replicate l and year i; $\mu$ is the grand mean; $Y_i$ is the ith year effect; $A_j$ is the additive effect of parent j; $A_k$ is the additive effect of parent k; $D_{jk}$ is the dominance effect of parent j in combination with parent k; $AY_{ij}$ and $AY_{il}$ are the additive×year interaction effects of parents j and k; $DY_{ijK}$ is the dominance×year interaction effects of parent j in combination with parent k; $B_{l(i)}$ is the block effect and $e_{ijkl}$ is the residual effect. All of the genetic effects in the model were considered as random effects. A minimum norm quadratic unbiased estimation (MINQUE) method (Zhu 1992; Zhu and Weir 1994b) was applied to estimate the variance components of traits. The jackknife resampling method (Miller 1974; Zhu and Weir 1996) was employed to derive the standard errors of estimated components of variances or predictors. Furthermore, method for predicting random effects including additive, dominance and environment effects was Adjusted Unbiased Prediction (AUP) (Zhu 1992). Heterosis (MP: mid-parent) and heterobeltiosis (BP: better parent) values were, respectively predicted by using an approach proposed by Zhu (1993). All of the statistical analyses were carried out using QGAStation software developed by Chen and Zhu (2003).

**Results and Discussion**

The analysis of variance indicated highly significant differences among genotypes for all the traits (data were not shown). The genotype×year interaction effect was also significant for all the studied traits except for TSS, suggesting that the genotypes were influenced by the year and there could be a certain degree of heterosis in the $F_1$ genotypes.

The predicted phenotypic variance and genetic variance components were summarized in Table 1. The additive genetic variance components ($V_A$) were significant for the traits, WT, F, DM and TSS and the dominance variances ($V_D$) were also significant for the characters, WT, TY, DM and TSS. The significant narrow sense heritability was also obtained for WT, F, DM and TSS. It was indicated, by significant narrow sense heritability for all the traits excluding TY, that the selection could obtain apparent genetic gain for these traits. Dominance×year interaction ($V_{D×Y}$) variance was significant for the traits, WT, F, TY and DM. It was suggested that the utilization of heterosis could be applied to obtain genetic gain for these traits in special environment. It was founded that the four agronomic traits (WT, F, TY and DM) were controlled by genotype×year interaction effect. Thus, the results of this study indicated this fact that the genotype×year interactions are not avoidable in agriculture investigation (Allard and Bradshaw 1964; Yan and Kang 2002). Some researchers have also suggested that environmental conditions and genotype×environment interaction can modify melon fruit development (Bhella 1985; Kultur et al. 2001; Zalapa et al. 2006). The variation in the performance of the genotypes across environments can be

ascribed to significant changes in the General combining ability (GCA) of parents and Spesific combining ability (SCA) of crosses across the environments.

Table 1. Analysis of additive, dominance, their interaction genetic effects with environment and heritability estimates for measured characters in cantaloupe

| Sources | WT | F | TY | DM | TSS |
|---|---|---|---|---|---|
| $V_A$ | $0.024^{**}$ | $0.035^{**}$ | $0.000^{ns}$ | $8.756^{**}$ | $0.605^*$ |
| $V_D$ | $0.017^{**}$ | $0.001^{ns}$ | $0.050^*$ | $1.973^{**}$ | $0.253^*$ |
| $V_{A \times Y}$ | $0.000^{ns}$ | $0.000^{ns}$ | $0.042^*$ | $0.000^{ns}$ | $0.000^{ns}$ |
| $V_{D \times Y}$ | $0.002^*$ | $0.011^*$ | $0.007^{**}$ | $1.552^{**}$ | $0.000^{ns}$ |
| Error | 0.105 | 0.147 | 0.268 | 7.249 | 1.199 |
| $V_A/V_D$ | 1.41 | 35 | 0.0 | 4.44 | 2.39 |
| $V_{ph}$ | $0.148^{**}$ | $0.194^{**}$ | $0.367^{**}$ | $19.530^{**}$ | $2.057^{**}$ |
| $h_N^2$ | $0.160^{**}$ | $0.182^{**}$ | $0.000^{ns}$ | $0.448^{**}$ | $0.294^{**}$ |
| $h_B^2$ | $0.274^{**}$ | $0.185^{**}$ | $0.137^{**}$ | $0.549^{**}$ | $0.417^{**}$ |
| $h_{NY}^2$ | $0.000^{ns}$ | $0.000^{ns}$ | $0.114^{**}$ | $0.000^{ns}$ | $0.000^{ns}$ |
| $h_{BY}^2$ | $0.015^{ns}$ | $0.058^{ns}$ | $0.134^*$ | $0.079^*$ | $0.000^{ns}$ |

$V_A$: Additive variance, $V_D$: Dominance variance, $V_{A \times Y}$: Additive×Year interaction variance, $V_{D \times Y}$: Dominance×Year interaction variance, $V_{ph}$: Phenotypic variance $h_N^2$: Narrow sense heritability, $h_B^2$: Broad sense heritability, $h_{NY}^2$: Narrow sense heritability×year interaction, $h_{BY}^2$: Broad sense heritability×year interaction. *WT:* fruit weight, *F:* flesh thickness, *TY:* Total yield, *DM:* days to maturity of fruits, *TSS:* total soluble solids. *, ** significant at 5% and 1% probability levels, respectively.

Estimated additive effects of genetic components were presented in Table 2. The parent, Dastjerdi had the highest positive additive effect for WT and significantly higher than that measured for all of the other parents. Furthermore, the highest negative additive effect was estimated for Dastjerdi, while Magasi had the highest additive positive effect for late maturity. Having large additive effect of WT and DM, Dastjerdi could serve as a good parent in selection for favorable traits with high WT and DM. Two parents, Tiltorogh and Rishbaba had positive significant additive effect for F. It was implied that these parents could be used as candidate parents to increase flesh thickness of offspring. Because the additive×year interaction ($V_{A \times Y}$) variance was significant for TY, we examine the additive effect for each year separately. For this trait, the highest additive effect was recorded for Rishbaba in the first year, while Samsori had the highest additive effect in second year. There was significantly additive effect of TSS for Savei, then the having of large additive effect of TSS for the Savei might be a promising cross with high TSS.

Table 2. Estimation of additive effects in the parents for measured traits for cantaloupe

| Parent | WT (kg) | F (cm) | TY (kg) Year 1 | TY (kg) Year 2 | DM | TSS |
|---|---|---|---|---|---|---|
| Rishbaba (1) | $0.049^{ns}$ | $0.146^*$ | $0.262^{**}$ | $-0.203^*$ | $0.199^{ns}$ | $0.127^{ns}$ |
| Shahabadi (2) | $-0.165^{**}$ | $-0.189^{**}$ | $-0.198^{ns}$ | $0.056^{ns}$ | $-0.571^*$ | $0.212^{ns}$ |
| Samsori (3) | $-0.020^{ns}$ | $-0.074^{ns}$ | $-0.113^{ns}$ | $0.256^*$ | $-0.105^{ns}$ | $0.190^{ns}$ |
| Dastjerdi (4) | $0.159^*$ | $0.049^{ns}$ | $0.107^{ns}$ | $-0.010^{ns}$ | $-4.014^{**}$ | $-1.184^{**}$ |
| Magasi (5) | $-0.016^{ns}$ | $0.022^{ns}$ | $0.012^{ns}$ | $-0.069^{ns}$ | $2.826^{**}$ | $0.084^{ns}$ |
| Tiltorogh (6) | $0.085^*$ | $0.163^{**}$ | $0.033^{ns}$ | $-0.095^*$ | $1.287^{**}$ | $0.014^{ns}$ |
| Savei (7) | $-0.091^*$ | $-0.118^*$ | $-0.102^{ns}$ | $0.067^{ns}$ | $0.375^{ns}$ | $0.557^*$ |

*WT:* fruit weight, *F:* flesh thickness, *TY:* Total yield, *DM:* days to maturity of fruits, *TSS:* total soluble solids. *, ** significant at 5% and 1% probability levels, respectively.

Predicted dominance effects of genetic components were given in Table 3. Because the traits, WT, F, TY and DM had the significant dominance×year interaction ($V_{D×Y}$) variances, the dominance effects for these traits were examined by each year separately. For WT, there were positive dominance effects for the three crosses, 1×6, 5×7 and 6×7 in both years. Having large dominance effect of WT, these crosses might be a promising cross with high WT. The genotypes 1×2 and 6×7 had the positive significant effect for F in both years. So, these crosses could be useful for breeding higher flesh thickness genotypes. For TY, the crosses 1×6, 5×7 and 6×7 had the positive significant dominance effect in both years and might be the promising crosses with high yield. The crosses 3×4 and 4×6 had the high negative dominance effects for early maturity in both years, while for TSS, there were the significant dominance effects for the genotypes, 1×2 and 5×7.

Table 3. Estimation of dominance effects in the $F_1$ generation for measured traits for cantaloupe

| Cross | WT (kg) | | F (cm) | | TY (kg) | | DM | | TSS |
|---|---|---|---|---|---|---|---|---|---|
| | Year 1 | Year 2 | Year 1 | Year 2 | Year 1 | Year 2 | Year 1 | Year 2 | |
| 1×2 | 0.038** | -0.041** | 0.065* | 0.096* | 0.145** | -0.046** | -0.019ns | -0.939* | 0.369** |
| 1×3 | 0.030** | -0.006* | 0.191* | -0.200* | 0.210** | -0.119** | -0.437* | 1.986** | 0.092ns |
| 1×4 | -0.001ns | 0.030* | 0.003ns | 0.085ns | -0.025** | 0.069** | 0.909* | -0.500* | -0.269** |
| 1×5 | -0.010ns | 0.037* | -0.002ns | 0.079ns | -0.005ns | 0.097** | -1.527** | 1.401** | 0.417ns |
| 1×6 | 0.041* | 0.036* | -0.100ns | 0.078ns | 0.050** | 0.037** | -1.232** | -0.047ns | -0.423* |
| 1×7 | 0.023** | -0.017* | 0.108* | -0.110ns | 0.053* | -0.007ns | 0.399ns | -1.498** | 0.108ns |
| 2×3 | 0.000ns | 0.018** | -0.072** | 0.157** | -0.072** | 0.108** | -0.795* | 0.327ns | -0.727ns |
| 2×4 | 0.047** | -0.011* | 0.052ns | 0.010ns | 0.178** | -0.068** | 0.512ns | -0.536ns | 0.317ns |
| 2×5 | 0.033* | -0.027* | 0.035ns | -0.012ns | 0.036* | -0.047** | -0.472ns | -1.467* | -0.254ns |
| 2×6 | -0.002ns | -0.040** | 0.020ns | -0.136* | 0.026ns | -0.063* | -0.227ns | -1.043* | 0.362ns |
| 2×7 | -0.016** | -0.002ns | 0.016ns | -0.025ns | -0.062** | -0.061** | -1.847* | 1.737* | 0.159ns |
| 3×4 | -0.040* | 0.135* | -0.194ns | 0.282ns | -0.083** | 0.083** | -1.022* | -2.794** | -1.068* |
| 3×5 | 0.050* | -0.031* | 0.126ns | -0.044ns | 0.067** | -0.018** | -0.628ns | -0.130ns | -0.576ns |
| 3×6 | 0.048* | -0.017ns | 0.045ns | -0.063ns | 0.002ns | -0.049** | 1.036** | -0.024ns | 0.242ns |
| 3×7 | -0.083* | 0.036* | -0.184* | 0.094* | -0.156* | 0.115* | -2.161** | 1.715* | -0.258ns |
| 4×5 | 0.132* | -0.096* | 0.171ns | -0.096ns | 0.163** | -0.136** | -0.852ns | 1.631* | 0.370ns |
| 4×6 | -0.013* | -0.014ns | -0.081ns | 0.051ns | -0.046** | 0.022** | -1.782** | -3.605** | -0.100ns |
| 4×7 | -0.053* | 0.003ns | -0.081* | 0.067ns | -0.019** | -0.028** | 1.426* | -0.634ns | 0.014ns |
| 5×6 | -0.077* | 0.008ns | -0.134ns | -0.018ns | -0.062* | -0.027** | 0.054ns | 0.097ns | -1.075ns |
| 5×7 | 0.009** | 0.019* | 0.069ns | -0.078ns | 0.029** | 0.064* | 0.978** | 1.363* | 0.699** |
| 6×7 | 0.094* | 0.022* | 0.022* | 0.042* | 0.153** | 0.078* | -0.009ns | 0.408ns | 0.381ns |

1: Rishbaba, 2: Shahabadi, 3: Samsori, 4: Dastjerdi, 5: Magasi, 6: Tiltorogh, 7: Savei. *WT:* fruit weight, *F:* flesh thickness, *TY:* Total yield, *DM:* days to maturity of fruits, *TSS:* total soluble solids. *, ** significant at 5% and 1% probability levels, respectively.

Predicted heterosis for measured traits was given in Table 4. Beneficial heterosis was found only over the mid- parent for fruit weight. Six $F_1$ hybrids expressed heterosis over the better parent. Feyzian et al. (2009) reported favorable heterosis for fruit weight over the mid- and better parent (17.52 and 1.56%, respectively). Kalb and Davis (1984) also found the beneficial heterosis for fruit weight. Favorable heterosis over the mid- and better parent was not observed for F. Only one hybrid showed heterosis over the better parent for this trait. For TY, there was the beneficial heterosis over the mid- and better parent (0.139 and 0.094 respectively). Feyzian et al. (Feyzian et al. 2009) also reported favorable heterosis for yield over the mid- and better parent (24.67 and 12.90% respectively). Furthermore, favorable heterosis was not obtained over the mid- and better parent for the traits, DM and TSS.

Knowledge of the mechanisms that control the main economic traits of a species is fundamental to genetic improvement and can be obtained through diallel cross methodologies. Although some interpretations of the diallel mating design may be prone to error, this method has applied useful in providing basic information about the genetic mechanism that control the traits measured for this study. This information could be effectively used in selecting special crosses for more comprehensive testing of genetic mechanisms controlling the traits studied. For estimating additive, dominance and their interactions with environment effects, Zhu and Weir (1994b) developed an additive-dominance genetic method of mixed model. The application of such models may help improve the melon breeder's understanding of the underlying gene action, and provide a better predict of the heritability of a given

trait. In the present study, additive genetic effects played a major role in the inheritance of the all traits, except for TY, but did not interact with years. The dominance effects, on the contrary, affected some traits especially TY, but were of little importance due to its smaller main effects. The major role of additive effects in controlling most of the measured traits, suggests that selection in early segregating generations should be effective in bringing desirable changes in these traits. There was the large dominance effect for the trait, TY. It was suggested that the utilization of heterosis could obtain apparent genetic gain for this trait. The dominance×year interaction effects were also significant for all of the traits except for TSS. The dominance×year interaction provides a degree of the stability of the effects of dominance interaction over years (Allard 1956). Its variance ratio in the present study suggested moderate instability for the traits, WT and F and relatively high instability for TY and DM. Thus, dominance associations in the genetic control of these traits appeared to modify with environmental changes. Furthermore, high values of $V_{D \times Y}$ for TY and DM indicated that utilization of heterosis could be feasible when selection is based on the evaluation of genotypes in number of environments. The involvement of non-additive genetic effects in the inheritance of yield in melon has been previously reported (Zalapa et al. 2008; Feyzian et al. 2009). There were the significant narrow sense heritability for the traits, WT, F, DM and TSS.

Table 4. Predicted heterosis values over the mid-parent (MP) and better parent (BP) for measured characters, in cantaloupe

| Cross | WT (kg) | | F (cm) | | TY (kg) | | DM | | TSS | |
|---|---|---|---|---|---|---|---|---|---|---|
| | MP | BP | MP | BP | MP | BP | MP | BP | MP | BP |
| 1×2 | 0.084[ns] | -0.019[ns] | 0.001[ns] | -0.107[**] | 0.300[*] | 0.207[ns] | -0.034[**] | -0.034[**] | 0.050[*] | 0.035[*] |
| 1×3 | 0.175[**] | 0.128[ns] | 0.004[ns] | -0.069[**] | 0.256[*] | 0.129[ns] | 0.009[ns] | 0.006[ns] | -0.061[**] | -0.150[**] |
| 1×4 | 0.148[**] | 0.038[ns] | 0.017[ns] | -0.020[*] | 0.211[*] | 0.098[ns] | 0.014[**] | -0.058[**] | -0.011[ns] | -0.185[**] |
| 1×5 | 0.139[**] | 0.137[*] | 0.011[ns] | -0.029[**] | 0.307[*] | 0.230[ns] | -0.013[*] | -0.045[**] | 0.040[*] | 0.025[ns] |
| 1×6 | 0.231[**] | 0.167[**] | -0.012[*] | -0.028[**] | 0.289[*] | 0.199[*] | -0.024[**] | -0.032[**] | -0.067[**] | -0.077[**] |
| 1×7 | 0.104[ns] | 0.046[ns] | 0.001[ns] | -0.082[**] | 0.245[*] | 0.165[*] | -0.015[**] | -0.024[**] | 0.033[*] | -0.009[ns] |
| 2×3 | 0.124[**] | 0.068[**] | 0.018[*] | -0.017[ns] | 0.094[**] | 0.060[*] | -0.027[**] | -0.030[**] | -0.166[**] | -0.241[**] |
| 2×4 | 0.119[**] | -0.093[**] | 0.017[**] | -0.055[*] | 0.200[*] | 0.180[*] | -0.001[ns] | -0.072[**] | 0.056[**] | -0.133[**] |
| 2×5 | 0.060[**] | -0.041[*] | 0.008[ns] | -0.059[ns] | 0.087[*] | 0.071[*] | -0.047[**] | -0.080[**] | -0.047[ns] | -0.047[*] |
| 2×6 | -0.026[ns] | -0.193[**] | -0.019[*] | -0.142[**] | 0.041[**] | 0.037[ns] | -0.033[**] | -0.041[**] | 0.025[ns] | 0.020[ns] |
| 2×7 | 0.020[ns] | -0.025[ns] | 0.003[ns] | -0.022[**] | -0.056[**] | -0.069[**] | -0.011[**] | -0.020[*] | 0.035[**] | 0.008[ns] |
| 3×4 | 0.267[**] | 0.111[*] | 0.021[*] | -0.016[**] | 0.029[**] | 0.015[ns] | -0.030[**] | -0.098[**] | -0.192[**] | -0.454[**] |
| 3×5 | 0.123[**] | 0.077[**] | 0.016[*] | -0.017[ns] | 0.127[*] | 0.077[ns] | -0.022[**] | -0.058[**] | -0.164[**] | -0.238[**] |
| 3×6 | 0.148[**] | 0.037[*] | -0.007[ns] | -0.096[**] | -0.006[ns] | -0.044[**] | 0.007[ns] | -0.004[ns] | -0.067[**] | -0.146[**] |
| 3×7 | 0.011[ns] | 0.000[ns] | -0.005[ns] | -0.014[ns] | 0.010[ns] | -0.036[**] | -0.007[ns] | -0.013[ns] | -0.093[*] | -0.141[*] |
| 4×5 | 0.117[**] | 0.005[ns] | 0.017[**] | 0.013[*] | 0.114[*] | 0.077[*] | 0.019[**] | -0.085[**] | 0.047[**] | -0.142[**] |
| 4×6 | 0.006[**] | -0.039[**] | -0.007[ns] | -0.059[**] | 0.038[*] | 0.014[ns] | 0.038[**] | -0.041[**] | -0.015[**] | -0.198[**] |
| 4×7 | -0.032[ns] | -0.199[**] | 0.005[*] | -0.041[*] | 0.018[ns] | -0.015[ns] | 0.030[**] | -0.032[**] | 0.034[**] | -0.182[**] |
| 5×6 | -0.077[**] | -0.143[**] | -0.024[*] | -0.081[**] | -0.007[*] | -0.020[*] | -0.004[ns] | -0.028[**] | -0.167[**] | -0.172[**] |
| 5×7 | 0.103[**] | 0.047[**] | 0.002[*] | -0.040[*] | 0.228[*] | 0.224[*] | 0.032[**] | -0.010[**] | 0.086[**] | 0.059[**] |
| 6×7 | 0.264[**] | 0.142[**] | -0.003[ns] | -0.101[*] | 0.387[*] | 0.378[*] | 0.010[**] | -0.007[ns] | 0.043[**] | 0.011[*] |
| Mean | 0.100[**] | 0.012[ns] | 0.003[ns] | -0.051[**] | 0.139[**] | 0.094[**] | -0.005[ns] | -0.038[**] | -0.029[**] | -0.112[**] |

1: Rishbaba, 2: Shahabadi, 3: Samsori, 4: Dastjerdi, 5: Magasi, 6: Tiltorogh, 7: Savei.
*WT:* fruit weight, *F:* flesh thickness, *TY:* Total yield, *DM:* days to maturity of fruits, *TSS:* total soluble solids.
*, ** significant at 5% and 1% probability levels, respectively.

The significance of $V_A$ and $V_D$ for the traits, WT, F, DM and TSS indicated that both additive and non-additive gene action were important in controlling these traits, but the $V_A/V_D$ ratio confirmed the importance of additive gene action (Table 1). The superiority of additive genetic variation suggested that the parent could be selected based on $V_A$ values for these traits. The advantage of additive genetic variances for these traits also mean that, aside from hybrid and synthetic breeding, the opportunity exists for genetic improvement by collecting favorable alleles through selection. These findings are in contrast with those of Zalapa et al. (Zalapa et al. 2006, 2008) who reported that the dominance and epistatic genetic effects mainly control average weight per fruit, but consistent with Feyzian et al. (Feyzian et al. 2009) who expressed the importance of additive gene action for this trait. For DM, similar results have been reported by Kalb and Davis (Kalb and Davis 1984) who emphasized the importance of additive gene action in determining days to fruit maturity. The additive effect was significant for F. It's confirmed the

importance of additive gene action; hence selection will bring genetic improvement for this trait. The magnitude of additive genetic effect in the inheritance of flesh thickness in melon was previously reported by Lippert and Hall (1982). The dominance genetic effect and dominance×year interaction effect had the major role in controlling TY. It suggests that selection will bring no or slow desirable changes, while production of hybrid and synthetic breeding could be effective in bringing genetic improvement for this trait.

This study demonstrated that the development of cultivars with high yield, early maturity fruits and excellent quality is possible. In the present study, genetic analysis of economic traits in cantaloupe was investigated using a diallel mating design thorough additive-dominance genetic method of mixed model. The significant narrow sense heritability indicated that additive gene effects were more important in explaining variation in WT, F DM and TSS while non-additive gene effect was more important in explaining variation in TY. The parent, Dastjerdi had the highest additive effect for WT and DM, while the parents, Tiltorogh and Savei had the highest additive effects for F and TSS, respectively. Tiltorogh×Savei for the, WT, F and TY traits, Rishbaba×Tiltorogh for the WT and TY traits and Magasi×Savei for the WT, TY and TSS traits were the best specific combiner and indicated the most hetosis except for the F trait in Tiltorogh×Savei. Thus, they could be a good indicator to identify the most promising genotypes to be used either as $F_1$ hybrids or as a resource population for further selection in cantaloupe breeding. Favorable heterosis over the better parent was found for TY over the all crosses. Thus, there is the potential to generate superior cultivars in segregate generation and hybrid production. The significant genotypes×environment (G×E) interaction obtained for WT, F, TY and DM was an indication of the lack of stability across environments, and suggested that the hybrids must be evaluated in more than one environment.

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