The Bioscan 10(4): 2005-2010, 2015 (Supplement on Genetics and Plant Breeding) www.thebioscan.in
AN INTERNATIONAL QUARTERLY JOURNAL OF LIFE SCIENCES

ESTIMATION OF GENE EFFECTS BASED ON JOINT SCALING TEST AND MODEL FIT SCHEME FOR QUANTITATIVE TRAITS IN MELON

BIKRAMJIT SINGH, VINOD KUMAR VASHISHT AND SAYEED ABDULHAMID PATEL*
Department of Vegetable Science, Punjab Agricultural University, Ludhiana, Punjab - 141 004, INDIA
e-mail: sayeed-coavc@pau.edu

KEYWORDS
Muskmelon
Epistasis
Gene action
Heritability
Variance

Received on :
11.02.2015

Accepted on :
07.10.2015

***Corresponding author**

ABSTRACT
The study comprised of six basic generations *viz*., P_1, P_2, F_1, F_2, B_1 and B_2 of cross Punjab Sunehri × KP_4HM-15 (cross-I) and Punjab Sunehri × IC-267379 (cross-II). Scaling tests indicated epistasis for most of the traits. The results inferred additive gene effect (D) was lower than dominance gene effect (H) for most of the traits except days to first fruit ripening (DFF) (D= 1.46±0.31**; H= -2.69±0.79**) while rind thickness (RT) was non-significant in cross-I and DFF, fruit weight, flesh thickness (FT), RT and fruit cavity in cross-II. Duplicate epistasis was recorded for most of the traits. Variance analysis showed that additive genetic variance ($ó^2$D) was predominant for all traits in both crosses. Degree of dominance was >1 for DFF (1.12), fruit weight (1.45), fruit yield/vine (1.42) and polar (3.32) and equatorial diameter (7.48) in cross-I; for equatorial diameter (1.34) and FT (1.06) in cross-II. Moderate heritability was recorded for all traits except days to open first pistillate flower (84.30%), DFF (87.16%) and polar diameter (92.01%) in cross-I and equatorial diameter (89.07%) and FT (89.96%) in cross-II while genetic gain was found to be more for fruit number/vine (9.51%), RT (9.09%) and TSS (7.90%) in cross-I and FT (59.09%), RT (23.07%) and fruit number/vine (9.20%) in cross-II.

INTRODUCTION

Muskmelon (*Cucumis melo* L.) is an economically important, cross-pollinated and highly prized vegetable in advanced countries. It is a tropical old world species and availability of wild cross compatible races provides opportunities to enhance the quantity and quality. Moreover, most of this yield improvement can be credited to improved cultural practices, breeding for relatively simple traits such as resistance to diseases and pests and use of hybrids created from sparingly few elite lines (McCreight *et al.,* 1993; Robinson and Decker-Walters, 1997). Continuous increase in yield of melon will likely depend on the preservation, availability and use of genetic variability and breeding for yield or other important economic traits.

Both traits are quantitative and complex in nature. It means their expression is caused, not only by genetic factors, but also by environmental effects and genotype × environment interaction effects. The choice of selection and breeding procedures for genetic improvement of melon or any other crop depends largely on the knowledge of type of gene action for different characters in the plant materials under investigation.

Generation mean analysis, a biometrical method developed by Mather and Jinks (1971) method, is a useful technique for determining gene effects for polygenic traits. An understanding of the mode of inheritance of complex quantitative traits for an effective breeding program is essential for the improvement of a particular trait. Epistasis is a universal phenomenon for inheritance of quality and quantity in crop plants. Detection of epistasis become essential not only for obtaining unbiased estimates of additive and non-additive gene effects but also facilitates the breeders to decide about the breeders to the specific breeding methods to bring about improvement in melon.

Therefore, the present investigation was aimed to determine gene effects of different characters and to estimate the components of genetic parameters of different traits

MATERIALS AND METHODS

The experimental material consists of two crosses; Punjab Sunehri × KP_4HM-15 and Punjab Sunehri × IC-267379 and its progenies. Six generations *viz*., P_1, P_2, F_1, F_2, B_1 and B_2 were produced and raised in randomized complete block design (RCBD) with three replications during spring-summer season. F_1 (P_1 x P_2) was given by the Department of Vegetable Science, Punjab Agricultural University, Ludhiana, Punjab, India. P_1, P_2 and F_1 were sown and crosses were attempted by hand emasculation and pollination technique to produce F_2, B_1 (F_1 × P_1) and B_2 (F_1 × P_2). All yield and yield related traits were recorded at regular basis.

The means of different generation were analyzed by a joint scaling test using the weighted least squares method (Mather and Jinks, 1971; Kearsey and Pooni, 1996). The observed generation means were used to estimate the parameters of a model consisting only of mean (m), additive and dominance genetic effects. The estimated parameters were used in turn to calculate the expected generation means. The goodness-of-fit between observed and expected was tested; a significant chi square value indicate a significant difference between the observed and expected generation means, which implied that a simple additive model did not explain the data. When the

additive-dominance model was found to be insufficient, then additive × additive, additive × dominance and dominance × dominance di-genic epistatis parameters were added. If a di-genic epistatis parameter was not significant then it was omitted and the best fit model was applied. The weighted least-squares model that incorporates additive, dominance and digenic epistatic effects is formulated by (Hayman, 1958; Kearsey and Pooni, 1996):

In the complete six parameter model, χ^2 adequacy test was not possible, because the degrees of freedom were reduced to zero. In this situation, non-significant terms were eliminated from the full model to generate degrees of freedom for model adequacy χ^2 tests. Ideally, a satisfactory model would produce a non-significant χ^2 value whilst having each component significantly different from zero. The genetic parameters were estimated by applying joint scaling test and sequential model fitting after finding out best fit model.

The variances of the parameter estimates can be obtained from the diagonal elements of $(C'WC)^{-1}$. The expected means of the six generations were calculated using the parameter estimates, the goodness-of-fit of the observed generation means was tested with the chi-squared statistic. The significance of each parameter was determined by t-test.

Phenotypic, genotypic and environmental variances were estimated for each population using the model of Mather and Jinks (1971). Degree of dominance, narrow sense heritability and genetic gain was calculated by biometrical techniques (Chahal and Gosal, 2002; Sharma, 1998).

RESULTS AND DISCUSSION

Gene action

The data obtained for all characters were analyzed and found that the non-weighted scaling test approach identified significant additive (A), dominance (B) and non-allelic interaction (C) for all traits except B for days to open first pistillate flower, B and C for days to first fruit ripening, polar and equatorial diameter of fruit and rind thickness, A and C for TSS and all A, B and C for fruit cavity (table 1). These tests detected additive-dominance model and found to be operative in the inheritance of fruit cavity and TSS. Data for all traits did not adequately fit a simple additive-dominance model (three-parameter model) except TSS and fruit cavity. Sequential model fitting technique using a six-parameter model (*i.e.* additive, dominance and interactions) identified best-fit models with significant non-allelic interactions for most of traits. The estimates of parameters along with standard errors for studied traits are given in Table 1. The model having m, [*d*], [*h*], [*j*] and [*l*] components was found to be adequate for days to open first pistillate flower for both the crosses and days to first fruit ripening for cross-I was found to be best fit, but [*h*] component was non-significant in days taken to first fruit ripening.

In cross-I, all the scaling test are significant for number of fruits per vine, fruit weight, fruit yield per vine and flesh thickness which inferred the presence of all the non-allelic interaction while days to first fruit ripening, polar and equatorial diameter and rind thickness is significant at A scaling test *i.e.* only additive × additive [i] non-allelic interaction. This is in accordance with Eduardo *et al*. (2007). Fruit cavity is non-significant with all scaling test, this indicates absence of non-allelic interaction. In case of TSS, it is significant at B scaling test only which demonstrate non-allelic interaction additive × dominance [j] which is in contrast to the trait days to open first pistillate flower. These results are in consonance with Feyzian *et al*. (2009).

In cross-II, all the scaling test are significant for traits *viz*., days to open first pistillate flower, number of fruits per vine, fruit yield per vine and rind thickness while non-significant at fruit weight. Equatorial diameter, flesh thickness, fruit cavity and TSS. The trait like days to first fruit ripening shows negative significance at B scaling test and in polar diameter A scaling test is significant which denotes non-allelic additive × dominance [j] and non-allelic additive × additive [i] interaction respectively. This is in harmony with Lal *et al*. (2005). $\div^2$ value is highly significant for most of the traits except fruit cavity and TSS in cross-I while in cross-II, it is significant at days to open first pistillate flower, days to first fruit ripening, number of fruits per plant, fruit yield and rind thickness.

For cross-I, number of fruits per vine, fruit weight, fruit yield per vine, total yield per vine, polar diameter and rind thickness, best fit model identified was m, [*d*], [*h*] and [*l*]. Model having m, [*d*], [*h*] and [*i*] components was found to be adequate for equatorial diameter of fruit while m, [*d*], [*h*] and [*j*] for flesh thickness. The sum of additive effects ([*d*] + [*i*]), in terms of fixable component was higher than the sum of dominance effects ([*h*] + [*l*]) in terms of non-fixable component in all traits except for days to open first pistillate flower, days to first fruit ripening, fruit weight and fruit yield per vine. Duplicate type of epistasis was observed in most of traits except in equatorial diameter, flesh thickness, fruit cavity and TSS. While in cross-II, the best fit model for the trait number of fruits per vine and fruit yield per vine is m, [d], [h] and [l] while six parameter model for days to first fruit ripening. Five parameter model is best for days to open first pistillate flower and rind thickness. It is significant for all parameter except [d] and highly significant in all parameter respectively for this trait.

In this study, in addition to additive gene effects, [*h*] and [*l*] gene effects had high contributions in controlling the studied traits (Table 2). Gene interaction is considered to be complementary when the [*h*] and [*l*] estimates have the same signs and to be duplicating when the signs differ (Mather and Jinks, 1971). Gene interactions in this study were of duplicate type for all traits except equatorial diameter of fruit, flesh thickness, fruit cavity and TSS. Zalapa *et al*., (2006), reported that duplicate type of non-allelic interaction exists for fruit weight, total yield and days to open first pistillate flower. Negative sign of dominance [*h*] gene effect shows reductive alleles involving dominant phenotype otherwise increasing alleles include dominant phenotype. Also negative sign of dominance × dominance [*l*] interaction show ambi directional dominant. In the present study, for most traits, it was observed that direct dominance was unidirectional dominant and reductive alleles were involved in dominant phenotype. Similar case is reported by Khodambashi *et al*. (2012).

Variance components

Estimates of variance component (*i.e.* V_A, V_D, V_P and V_E) are presented in Table 3. Negative estimates were assumed to be zero (Robinson *et al*., 1955), but are reported herein as

Table 1: Scaling test and joint scaling test for the characters in two crosses

Cross-I

P	Days to open first pistillate flower	Days to first fruit ripening	Number of fruits per vine	Fruit weight	Fruit yield per vine	Polar diameter	Equatorial diameter	Flesh thickness	Rind thickness	Fruit cavity	TSS
Scaling test											
A	-7.81±3.26*	-4.97±1.56**	-1.25±0.54*	-189.00±47.75**	-808.60±261.89**	0.75±0.34*	0.49±0.25*	0.40±0.14**	-0.19±0.9*	0.40±0.47	-1.45±0.85
B	-2.04±1.62	-1.01±1.31	-1.30±0.42**	-256.00±67.39**	-1020.00±211.85**	0.58±0.56	0.11±0.54	-0.56±0.11**	0.03±0.02	0.05±0.07	-1.61±0.21**
C	-11.5±4.88*	2.27±6.27	-2.25±0.67**	-446.00±91.86**	-1652.00±364.74**	-0.41±0.73	-0.27±0.77	0.59±0.25*	-0.07±0.13	0.08±0.11	-1.31±0.75
Joint scaling test											
M	59.88±0.74**	100.74±0.32**	2.42±0.11**	341.56±16.36**	896.99±45.61**	7.81±0.15**	7.81±0.13**	1.39± 0.04**	0.32±0.01**	1.01±0.02**	10.01±0.36**
D	0.26±0.61	1.46±0.31**	0.12±0.12	-71.93±16.69**	-179.44±46.95**	0.12±0.13	0.11±0.09	-0.01±0.04	-0.01±0.01	-0.01±0.02	0.02±0.33
H	1.14±1.10	-2.69±0.79**	0.55±0.18**	175.97±25.34**	794.17±60.31**	1.56±0.28**	1.21±0.25**	0.14±0.05*	0.01±0.02	0.16±0.04**	1.66±0.82*
χ^2	7.72**	10.62**	12.54**	38.46**	46.88**	14.85**	5.86*	13.04**	5.84*	1.38	2.87

Cross-II

P	Days to open first pistillate flower	Days to first fruit ripening	Number of fruits per vine	Fruit weight	Fruit yield per vine	Polar diameter	Equatorial diameter	Flesh thickness	Rind thickness	Fruit cavity	TSS
Scaling test											
A	3.19±1.18**	0.84±2.62	-2.30±0.35**	-10.50±45.86	-724.25±123.82**	1.07±0.60*	-0.23±0.73	0.02±0.17	-0.13±0.05*	0.04±0.10	0.42±0.81
B	7.14±1.11**	-6.00±1.35**	-2.20±0.31**	-39.50±40.85	-726.67±123.76**	-0.10±0.83	0.14±0.69	-0.76±0.70	0.07±0.03*	-0.12±0.09	0.19±0.82
C	12.49±1.80**	1.19±2.65	-4.30±0.52**	50.50±64.58	-1216.25±202.39**	0.78±1.14	-0.30±1.01	-0.56±0.74	-0.24±0.05**	0.11±0.17	-0.16±1.31
Joint scaling test											
M	68.74±0.40**	102.70±0.57**	1.67±0.09**	336.06±9.79**	620.36±29.70**	7.46±0.22**	8.04±0.22**	1.24±0.07**	0.27±0.01**	0.98±0.02**	10.53±0.31**
D	-0.64±0.34	2.21±0.58**	-0.17±0.09	7.25±9.78	-32.65±29.38	0.07±0.20	-0.14±0.19	0.12±0.06*	0.02±0.01	0.08±0.02**	-0.44±0.30
H	12.49±0.77**	0.85±0.92	0.63±0.18**	3.90±19.71	151.89±59.89*	0.75±0.44	-0.09±0.43	0.12±0.14	-0.03±0.02	0.08±0.05	1.22±0.55*
χ^2	58.39**	23.62**	94.25**	2.42	66.12**	2.81	0.47	2.11.	39.11**	3.82	2.58

*, ** Significant at 5% and 1% level respectively, P- parameters

Table 2: Estimation of gene action parameter in best fit model for two crosses

Cross-I

P	Days to open first pistillate flower	Days to first fruit ripening	Number of fruits per vine	Fruit weight	Fruit yield per vine	Polar diameter	Equatorial diameter	Flesh thickness	Rind thickness	Fruit cavity	TSS
M	67.94±0.81**	99.59±0.65**	2.65±0.13**	399.82±18.91**	1026.26±49.40**	9.63±0.88**	8.26±0.62**	1.52±0.06**	0.44±0.06**	-	-
[d]	4.35±0.81**	2.29±0.65**	0.24±0.12	-94.30±17.08**	-210.07±47.18**	-0.36±0.14**	-0.31±0.15*	-0.11±0.07	0.17±0.01**	-	-
[h]	-24.50±2.74**	-4.52±2.45	-1.42±0.59*	-258.88±75.20**	-990.22±278.21**	-2.16±1.08*	0.60±1.03	0.13±0.11	-0.32±0.15*	-	-
[i]	-	-	-	-	-	-	0.13±0.06*	-	-	-	-
[j]	-12.47±1.98**	-6.17±2.07**	-	-	-	-	-	0.29±0.15*	-	-	-
[l]	18.65±2.72**	5.01±2.47*	1.96±0.56**	427.06±69.53**	1721.95±262.51**	2.87±1.47*	-	-	0.27±0.12*	-	-
$\div^2$	0.19	1.38	0.33	0.74	0.46	0.06	1.04	1.76	0.19	-	-
Epistasis	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	-	-	Duplicate	-	-

Cross-II

P	Days to open first pistillate flower	Days to first fruit ripening	Number of fruits per vine	Fruit weight	Fruit yield per vine	Polar diameter	Equatorial diameter	Flesh thickness	Rind thickness	Fruit cavity	TSS
M	66.74±0.50**	108.70±3.07**	2.18±0.11**	-	724.97±32.42**	-	-	-	0.20±0.02**	-	-
[d]	0.34±0.50	1.05±0.73	0.08±0.09	-	21.04±30.13	-	-	-	0.08±0.01**	-	-
[h]	13.14±1.75**	-15.70±8.33	-3.27±0.44**	-	-992.88±154.26**	-	-	-	0.06±0.03*	-	-
[i]	-	-6.35±2.98**	-	-	-	-	-	-	0.12±0.02**	-	-
[j]	-3.81±1.38**	6.85±2.80*	-	-	-	-	-	-	-0.23±0.04**	-	-
[l]	-11.49±1.69**	11.50±5.47*	4.38±0.45**	-	1343.91±166.89**	-	-	-	-	-	-
$\div^2$	2.72	-	0.21	-	1.26	-	-	-	1.11	-	-
Epistasis	Duplicate	Duplicate	Duplicate	-	Duplicate	-	-	-	Duplicate	-	-

*, ** Significant at 5% and 1% level respectively, P- parameters

Table 3: Estimates of variance components for studied characters in two crosses

Cross-I

Parameter	Days to open first pistillate flower	Days to first fruit ripening	Number of fruits per vine	Fruit weight	Fruit yield per vine	Polar diameter	Equatorial diameter	Flesh thickness	Rind thickness	Fruit cavity	TSS
$ó^2D$	0.6419	3.3970	0.0630	172.31	450.38	0.0371	0.0042	0.0026	0.0005	0.0007	0.2675
$ó^2H$	-0.1379	-1.9155	0.0115	183.04	457.98	-0.2048	-0.1177	0.0019	0.0001	0.0002	0.0099
$ó^2G$	0.5040	3.3976	0.0745	355.34	910.32	0.1607	0.1135	0.0045	0.0006	0.0009	0.2774
$ó^2E$	0.2574	0.5003	0.0155	168.67	44.490	0.0394	0.0121	0.0004	0.0003	0.0013	0.1070
$ó^2ph$	0.7614	3.8979	0.0900	524.01	954.81	0.2001	0.1256	0.0049	0.0009	0.0022	0.3844
$(H/D)^{1/2}$	0.65	1.12	0.60	1.45	1.42	3.32	7.48	0.33	0.40	0.76	0.27
Heritability $_{(n\ s)}$ (%)	84.30	87.16	70.00	31.52	47.16	92.01	34.71	53.07	55.00	31.81	69.58
Expected genetic gain (%)	2.15	3.51	9.51	3.96	3.15	4.58	0.98	5.19	9.09	2.56	7.90

Cross-II

Parameter	Days to open first pistillate flower	Days to first fruit ripening	Number of fruits per vine	Fruit weight	Fruit yield per vine	Polar diameter	Equatorial diameter	Flesh thickness	Rind thickness	Fruit cavity	TSS
$ó^2D$	0.0310	1.0600	0.0112	153.670	472.72	0.0244	0.0913	0.2390	0.0016	0.0016	0.0353
$ó^2H$	0.0060	-0.2960	0.0018	2.8600	39.86	0.0001	-0.0616	-0.1270	0.0002	-0.0001	0.0004
$ó^2G$	0.0371	1.0600	0.0130	156.53	512.58	0.0245	0.0301	0.1120	0.0018	0.0016	0.0357
$ó^2E$	0.0529	1.0825	0.0095	130.43	505.03	0.0239	0.0723	0.1796	0.0008	0.0009	0.1164
$ó^2ph$	0.0900	2.1425	0.0225	286.96	1017.61	0.0484	0.1024	0.2916	0.0026	0.0025	0.1521
$(H/D)^{1/2}$	0.622	0.558	0.567	0.193	0.411	0.001	1.342	1.063	0.250	0.003	0.022
Heritability $_{(n\ s)}$ (%)	34.44	49.47	49.77	53.55	46.45	50.41	89.07	89.96	61.53	64.00	23.21
Expected genetic gain (%)	0.30	1.45	9.20	5.60	2.99	2.78	6.91	59.09	23.07	4.35	1.58

$ó^2D$ = Additive variance, $ó^2H$ = Dominance variance, $ó^2g$ = Genotypic variance, $ó^2E$ = Environmental variance, $ó^2ph$ = Phenotypic variance, $(H/D)^{1/2}$ = Average degree of dominance

recommended by Dudley and Moll (1969) and Hallauer *et al*. (2010) for historical importance. The magnitude of the additive genetic variance estimated higher than the non-additive genetic variance for most of the traits except for fruit weight and fruit yield per vine in cross-I while it is higher for all traits in cross-II. The environmental variance was lower than genetic variance for all traits except for polar and equatorial diameter and fruit cavity in cross-I while it is higher for days to open first pistillate flower, days to first fruit ripening, fruit yield per vine and TSS in cross-II.

Genetic variance is a mean square of each locus effect and is not affected by gene dispersion and dominance direct. Thus, data of generation variances can be used to complete genetic information. Over dominance was observed for days to first fruit ripening, fruit weight, fruit yield per vine, polar and equatorial diameter in cross-I and for equatorial diameter and flesh thickness in cross-II. These characters can be improved by exploitation of non-additive genetic variance.

Heritability and expected genetic gain

As mentioned in Table 3, narrow sense heritability were relatively high for all traits and ranged from 92.01 to 31.52 per cent and 89.96 to 23.21 per cent and expected genetic gain ranged from 9.51 to 0.98 per cent and 59.09 to 0.30 per cent in cross I and cross II respectively. Polar diameter have observed highest heritability *i.e.* 92.01 per cent followed by days to first fruit ripening (87.16) and days to pen first pistillate flower (84.30) while the genetic gain is number of fruit thickness *i.e.* 9.51 followed by rind thickness (9.09) and TSS (7.90). Heritability in broad sense may play greater role about information of relative value of selection (Ramesh Kumar Jat *et al.*, 2014), but Johnson *et al*. (1955) had shown that heritability and genetic advance should be jointly considered for reliable conclusion. Heritability estimates along with genetic advance indicates more numbers of additive factors for which improvement is feasible through selection based on phenotypic observations (Barche *et al.*, 2014) than the heritability alone as observed in number of fruits per plant, TSS and rind thickness. Thus for these traits, there is maximum possibility of fruitful phenotypic selection. High heritability with moderate genetic gain attributed to additive gene effects (Panse, 1957) as observed in corss-I for traits like number of fruits per vine, rind thickness and TSS (Lal *et al.*, 2005) while in cross-II traits like number of fruit per vine, flesh thickness and rind thickness while Singh *et al.*, 1990 reported predominance of non-additive gene effects for these characters. On other hand high heritability with low genetic gain may attribute to non additive gene action. Those characters may be improved through hybridization while low heritability estimates suggest that selection for such traits under consideration will not be effective.

Overall studied characters, the phenotypic variance was greater than the genotypic variance in both the crosses. These results indicated that, the environment 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 sound breeding program (Magda *et al.*, 2013). The average degree of dominance $(H/D)^{1/2}$ (table 3) is more than unity for days to first fruit ripening (1.12), fruit weight (1.45), fruit yield per vine (1.42) and polar (3.32) and equatorial diameter (7.48) in cross-I; for equatorial diameter (1.34) and flesh thickness (1.06) for cross-II. These results back up indicate the presence of over dominance suggesting early selection might improve these traits. On the contrary, the same parameter is less than unity for days to open first pistillate flower (0.65), number of fruit per vine (0.60), flesh thickness (0.33), rind thickness (0.40), fruit cavity (0.76) and TSS (0.27) in cross-I and days to open first pistillate flower (0.622), days to first fruit ripening (0.558), number of fruit per vine (0.567), fruit weight (0.193), fruit yield per vine (0.411), polar diameter (0.001) and rind thickness (0.250) in cross-II. These results confirm the role of partial dominance gene effects in controlling these characters.

The difficulty exists in describing generation mean analysis when balance effects of all loci are segregating. It is found that, additive gene effect or interaction effect are subjected to the degree of increasing gene dispersion of traits between parents, while dominance gene effect is pure multiple of dominance directed in each locus. Therefore, additive gene effect may be little because of gene dispersion and also dominance gene effect can be little because of ambi directional dominant (ambi directional dominance occurs in a situation where multiple genes influence a phenotype and dominance is in different direction depending on the gene). High values of narrow-sense heritability and high expected genetic gain indicates that selection for these important economic traits is likely to be successful. Low narrow sense heritability and low expected genetic gain showed that selection of these traits will be difficult and high environmental inference will be a problem. To this end, study revealed that successful methods will be those that can map-up the gene to form superior gene combinations interacting in a favorable manner and at the same time maintain heterozygosity. This objective can be achieved by restricted recurrent selection (Joshi, 1979) methods.

Narrow-sense heritability is important to plant breeders, because effectiveness of selection depends on the additive portion of genetic variation in relation to total variance (Falconer, 1960). In our experiment, high values for narrow-sense heritability and moderate to high expected genetic gain suggested a considerable participation of genetics in the phenotypic expression of traits and that selection for all traits could be efficient and can be improved by accumulating genetic variance through inbreeding and selection. Based on these results, the cross-I could be selected for number of fruits per vine. Moreover, the cross-II is promising for selecting flesh thickness.

REFERENCES

Barche, S., Nair, R., Ramgiri, M. and Jain, P. K. 2014. Genetic variability in okra (*Abelmoschus esculentus* L. Moench). *The Ecoscan (Special issue)* **6:** 153-156.

Chahal, G. S. and Gosal, S. 2002. Principles and Procedures of Plant Breeding: *Biotechnological and Conventional Approaches. Narosa Publishing House*, New Delhi. pp. 311-33

Dudley, J. W. and Moll, R. H. 1969. Interpretation and use of heritability and genetic estimates in plant breeding.*Crop Sci.* **9:** 257-62.

Eduardo, I., Arús, P., Monforte, A. J., Obando, J., Fernández-Trujillo, J. P., Martínez, J. A., Alarcón, A. L., Álvarez, J. M. and Van der Knaap, E. 2007. Estimating the genetic architecture of fruit quality traits in melon using a genomic library of near isogenic lines. *J. Amer. Soc. Hort. Sci.* **132(1):** 80-89.

Falconer, D. C. 1960. Introduction to quantitative genetics. *Ronald Press*, New York. p. 365.

Feyzian, E., Dehghani, H. and Rezai A. M. and Jalali, J. M. 2009. Diallel cross analysis for maturity and yield related traits in melon (*Cucumis melo* L.). *Euphytica.* **168:** 215-223.

Hallauer, A. R., Carena M. J. and Miranda, J. B. 2010. Quantitative Genetics in Maize Breeding. *Iowa State University Press*, Ames. pp 169-221.

Hayman, B. I. 1958. The separation of epistatic from additive and dominance in generation means. *Heredity.* **12:** 371-390.

Johnson, H. W., Robinson, J. F. and Comstock, R. E. 1955. Estimation of genetic and environmental variability in soybean. *Agron. J.* **7:** 314-318.

Joshi, A. B. 1979. Breeding methodology for autogamous crops. *Indian J. Genet.* **39:** 567-578.

Kearsey, M. J. and Pooni, H. S. 1996. *The Genetical Analysis of Quantitative Traits*. 1st Edition, Chapman and Hall, London, p. 381.

Khodambashi, M., Bitaraf, N. and Hoshmand, S. 2012. Generation mean analysis for grain yield and its related traits in lentil. *J. Agr. Sci. Tech.* **14:** 609-616.

Lal, T., Kumar, R. and Vashisht, V. K. 2005. Genetics of some horticultural traits and resistance to downey mildew (*Pseudoperonospora cubensis* B&C) in muskmelon (*Cucumis melon* L.). *Crop Improv.* **32:** 209-213.

Magda, E., El-Naggar, A. A. M., Adam, A. I., El–Tony, F. E. Z. H., Moustafa, Y. A., El-Shehawi, A. M., Elhoffe, S. H., Hafez, E. S. E., Thanaa, H. A., El-Hussin, G. G. and Asmaa, A., 2013. Estimation of Some Genetic Parameters through Generation Mean Analysis in Three Bread Wheat Crosses. *Alex Journal of Agricultural Research*. **58(3):** 183-195.

Mather, K. and Jinks, J. L. 1971. *Biometrical Genetics*. Chapman and Hall, London. pp. 65-201.

McCreight, J. D., Nerson, H. and Grumet, R. 1993. Melon, *Cucumis melo* L. In: Kalloo G, Bergh BO (eds) Genetic improvement of vegetable crops. *Pergamon Press*, New York. pp. 267-294.

Panse, V. G. 1957. Genetics of quantitative characters in relation to Plant Breeding. *J. Genet. Plant Breed.* **17(2):** 318-328.

Ramesh Kumar Jat, Ameta, K. D. and Choudhary, R. C. 2014. Genetic variability, heritability and genetic advance for yield and yield attributing traits in valan kakri (*Cucumis sativus* var. *utilismus* L.). *The Ecoscan (Special issue)* **4:** 317-322.

Robinson, D. C., Comstock, R. E. and Harvey, P. H. 1955. Genetic variances in open- pollinated corn. *Genetics.* **40:** 45-60.

Robinson, R. W. and Decker-Walters, D. S. 1997. Cucurbits. *CAB Int.*, Wallingford, UK.

Sharma, J. R. 1998. Statistical and Biometrical Techniques in Plant Breeding. 1st Eds., New Age International, New Delhi, India, *ISBN*: 81-224-0888-5, pp. 17-24.

Singh, M. J., Lal, T. and Randhawa, K. S. 1990. Genetic analysis for fruit yield and quality traits in muskmelon. *J. Res. Punjab Agric. Univ.* **27:** 577-84.

Zalapa, J. E., Staub, J. E. and McCreight, J. D. 2006. Generation means analysis of plant architectural traits and fruit yield in melon. *Plant Breed.* **125:** 482-87.