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Genetics analysis and inheritance of different fruit characters in muskmelon (*Cucumis melo* L.) using different parental lines

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Abstract
When we starting breeding programme, there is need to know the inheritance of important characters. By study the genetics of economic traits and the accuracy of components of genetic variation, the convenient strategy can be formulated for their improvement. From the present investigation, it is inferred that two hybrids viz., MS-5 × MM-308 and MS-5 × MM-304 were found most promising. These two cross combinations were significantly better over Punjab Hybrid and Farmers' Glory for various traits. Dominance gene effects were observed for all the characters and days to first pistillate flower opening, days to fruit maturity and fruit cavity area and reaction to fusarium wilt disease were statistically significant. In the inheritance of the characters the predominance of dominance gene effects suggested that heterosis breeding may be advantageous to get quick gains in this crop.

Keywords: additive variance, dominanc variance, inheritance, gene effects, muskmelon

Introduction
Muskmelon (*Cucumis melo* L.) is an important cucurbitaceous crop relished as a dessert fruit for its sweet taste. It has gained commercial importance due to its short duration and high production potential. It is grown as spring-summer crop from mid February to end May in Punjab state._In Punjab, the area under this crop is 4.96 thousand ha and production 86.10 thousand tons with an average productivity of 17.37 tons ha^{-1}. In India, it is cultivated on an area of about 39.72 thousand ha with a production of 8.69 lac tons. In India, it is widely cultivated in hot and dry areas of Uttar Pradesh, Punjab, Rajasthan, Madhya Pradesh, Bihar and Karnataka. In 2016, the total production in the world was 29.5 million tons and area was 1.2 million ha with average yield of 24.9 tons ha^{-1}. The leading muskmelon producing countries of world are China, Iran, Turkey, Egypt, India, U.S.A and Spain.
Melon is a diploid species with 2n = 2x = 24 chromosomes. The species *Cucumis melo* L. is considered to be originated in Africa (Pitrat, 2008) [8]. Melon exhibits a wide range of morphological, physiological and biochemical diversity (Eduardo, 2007) [5]. Pitrat *et al.* (2008) [8] classified melon into 16 morphotypes based on fruit traits. It is also called sweet melon, muskmelon casaba and cantaloupe (Nayar and Singh, 1998) [7]. F_1 hybrids play an important role in increasing muskmelon production due to their early maturity,high yield potential, superior quality, disease and insect-pest resistance (Banga and Banga, 2000) [3]. Further, the development of F_1 hybrids is the quickest way of improving important economic traits and an easy way of introducing disease resistance governed by dominant genes.

Materials and Methods
The present investigation was carried out at Department of Vegetable Science, Punjab Agricultural University, Ludhiana (30 º 54' North, 75 º 48' East and 247 m above sea level) during the spring-summer season of year 2014 and 2015. The experimental materials comprised ten inbred lines and forty five F_1 hybrids and three standard checks. The crosses were attempted during spring-summer season of 2014. The hermaphrodite flowers were emasculated one day before opening of the flowers in the evening. Both the male and emasculated flowers were covered at bud stage with white parchment bags in the evening prior to anthesis. The emasculated flowers were used as female flowers during crossing. In the next morning, the bags from the freshly opened male flowers and emasculated flowers were

removed and emasculated flowers were pollinated with the pollens of the desired freshly opened male flowers. After pollination, each pollinated flower was tagged and again covered with parchment paper bag. Likewise, all the crosses were attempted and simultaneously each parent was selfed. Selfing was done by bagging the hermaphrodite flowers in the evening and these were pollinated by taking pollens from covered male flowers of the same plant. The F_1 seeds of different crosses and selfed seeds of parents were collected during June 2014.

The experiment was laid out in a Randomized Complete Block Design (RBD) with two replications. The package of practices recommended for the crop was followed to raise a healthy crop.

Following genetic parameters were estimated as suggested by Hayman (1954)

$D = V_{0L0}$-E

$H_1 = V_{0L0} - 4W_{0L01} - 4V_{1L1} - (3n-2)\ E/n$

$H_2 = 4V_{1L1} - 4V_{0L1} - 2E$

$F = 2V_{0L0} - 4W_{0L01} - 2(n-2)\ E/n$

$h^2 = 4(ML_1-ML_0)^2 - 4\ (n-1)\ E/n^2$

Where,

- D = components of variance due to additive effects of genes
- H_1 = components of variance due to dominance effects of genes
- H_2 = components of variance due to non-additive effects of genes correlated for gene distribution
- F = covariance of additive and non-additive gene effects in all the arrays
- E - environmental or non-heritable variation associated
- M'_e = with an individual mean and it's calculated by dividing the error mean squares of the design analysis by the number of replications
- h^2 = overall dominance effects of the heterosis loci accuracy of estimates of genetic parameters
- W_{0L01} covariance between the parents and the means of their offspring
- ML_1 = mean of all F_1's.
- ML_0 = mean of parents
- V_{1L1} = means of array variance
- V_{0L1} = variance of means of arrays
- V_{0L0} = variance of the parents

In order to estimate the S.E. of these components, the following equations were used

$$\text{Var D} = S^2 \frac{\left(n^5+n^4\right)}{n^5}$$

$$\text{Var F} = S^2 \frac{\left(4n^5+20n^4-16n^3+16n^2\right)}{n^5}$$

$$\text{Var H}_1 = S^2 \frac{\left(n^5+41n^4-12n^3+n^2\right)}{n^5}$$

$$\text{Var H}_2 = \frac{S^2}{n^5}\left(36n^4\right)$$

$$\text{Var E} = \frac{S^2\left(n^4\right)}{n^5}$$

$$\text{Var h}^2 = \frac{S^2}{n^5}\left(16n^4+16n^2-32n+16\right)$$

Where

S^2 = ½ Var (Wr-Vr)

n = number of parents involved in the diallel i.e. ten S.E.'s were calculated by taking the square root of these equations.

The following estimates and ratios were calculated by making use of significant genetic parameters

1. **$(H_1/D)^{1/2}$:** A weighted measure of dominance of each locus. It is equal to 1 in case of full dominance, more than 1 in case of over-dominance and less than 1 in case of partial- dominance.
2. **$H_2/4H_1$:** Provides an estimate of the value of **uv**, where u is the proportion of positive alleles and v is the proportion of the negative alleles and u + v = 1. The maximum value of $H_2/4H_1$ will be 1/4 or 0.25 when u = v = 1/2. If the value is close to 1/4, there is symmetry at the loci exhibiting dominance otherwise genes are considered to be asymmetrically distributed.
3. **$(4DH_1)^{1/2}$+F/ $(4DH_1)^{1/2}$-F:** This is the ratio of total number of dominant to recessive genes in all parents. If it is near unity, it implies equality between the number of dominant and recessive alleles in the parents. This is, of course, a necessary consequence of u = v = 1/2
4. **h^2/H_2:** Number of effective factor which control the character and exhibit dominance or number of gene blocks exhibiting dominance.

These proportions are evaluated and interpreted when the relevant components are significant.

Result and Discussion

This study showed that the values of dominance variance (H_1) were higher than the additive genetic variance for days to first female flower opening, days to first fruit maturity, fruit cavity area and reaction to fusarium wilt disease. This showed the presence of non-additive gene action (dominance) involved in the inheritance of these characters. The estimates of mean degree of dominance $(H_1/D)^{1/2}$ were much higher than unity for all the traits showing over-dominance. The positive values of F for days taken to 1st female flower opening, days to 1st fruit maturity, fruit weight, total fruit yield per plot, fruit shape index, rind thickness, flesh thickness, fruit cavity area, TSS content, β- carotene content, ascorbic acid content, acidity and reaction to fusarium wilt disease indicated more frequency of dominant alleles than recessive alleles in the parents. The proportion of genes with positive and negative effects ($H_2/4H_1$) in the parents was observed less than 0.25 for all the characters considering genes are to be asymmetrically distributed. The proportion of dominant and recessive genes $[(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F]$ in the parents were higher than unity in case of 1st female flower opening, days to 1st fruit maturity, total fruit yield per plot, rind thickness, flesh thickness, fruit cavity area, TSS content, β- carotene content, ascorbic acid content and acidity and values lower than unity in case of fruit weight and fruit shape index which indicated asymmetrical distribution of genes among the parents. Number of blocks of dominant genes (h^2/H_2) indicated that one group of genes showed dominance for all the traits under study. The results of analysis of components of variance are in conformity with findings of Zalapa *et al.* (2008) [13] and Pornsuriya and Pornsuriya (2009) [10]. Dominance variance was more prevalent than additive genetic variance along with over dominance for yield and earliness, while TSS content, number of fruits per plant and flesh thickness showed partial dominance concluding that the additive genetic variance was of sufficient magnitude needed for appreciable progress in the

improvement of these characters through selection among progenies Chadha *et al.* (1972) [4] and Singh *et al.* (1976) [11] reported the mode of inheritance of seven characters in a cross between Hara Madhu × Early Gold, where additive component of variance was high for days to appearance of first female flower, maturity, fruit number per vine and TSS content while dominance component was evident for fruit weight, flesh thickness and total fruit yield. The additive × additive gene effects were more important than additive × dominance or dominance × dominance effects for fruit maturity, number of fruits/vine and TSS content.

In the present study, the predominance of dominance gene effects in the inheritance of all the characters suggested that heterosis breeding may be advantageous to get higher gain in muskmelon.

Table 1: Inheritance of different characters of muskmelon

Characters	Additive (D)	Dominance (H_1)	Non-additive (H_2)	F	E	$(H_1/D)^{1/2}$	$H_2/4H_1$	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	h^2/H_2
Days to 1st female flower opening	2.28	6.45*	5.02*	1.63	0.151	2.822	0.195	1.057	0.039
Days to 1st fruit maturity	4.93	11.09**	7.94*	4.89*	0.166	2.247	0.179	1.046	0.377
Fruit weight (kg)	0.02	0.06	0.04	0.04	0.001	2.773	0.146	-1.316	0.201
TSS content (%)	1.42	7.00	5.72	0.87	0.134	4.943	0.204	1.045	0.365
Rind thickness (mm)	0.88	2.23	1.31	0.77	0.037	2.537	0.147	1.217	-0.008
Flesh thickness(cm)	0.21	0.51	0.38	0.24	0.008	2.369	0.184	3.484	0.412
Fruit cavity area(cm^2)	157.56**	394.35**	302.25**	180.92**	1.155	2.503	0.192	1.001	0.067
Fruit shape index	0.004	0.03	0.03	0.01	0.001	7.624	0.202	-1.216	0.022
β-carotene content(mg)	0.51	20.54	18.16	1.08	0.025	40.332	0.221	1.053	0.074
Ascorbic acid content(mg)	2.70	39.97	35.36	4.86	0.035	14.808	0.221	1.023	0.068
Acidity (mg)	0.001	0.002	0.00	0.00	0.000	1.513	0.166	-1.001	0.774
Total fruit yield per plot (kg)	24.74	61.00	37.71	32.41	1.84	2.465	0.155	1.011	-0.002
Reaction to fusarium wilt disease	26.14**	45.25**	37.98**	4.60	0.89	1.73	0.21	1.00	0.06
Reaction to viral disease	0.15	0.34	0.25	-0.05	0.02	2.31	0.19	0.62	0.36

*Significance at 5% level, ** Significance at 1% level

Conclusion

In the characters where dominance variance is more than an additive genetic variance and where a degree of dominance is more than one the heterosis breeding can be suitable option of breeding for genetic improvement of muskmelon in terms of both qualitative and quantitative characters. In the characters like days to first female flower opens days to fruit maturity and fruit cavity area and reaction to fusarium wilt disease.However, in other cases where an additive genetic variance is more than a dominance variance along with high heritability, it can be fixed in the inbred lines and inbred lines can be utilized for making new hybrids. The progenies should be evaluated at multi-locations to assess their performance properly by minimizing the genotypic-environment interaction. The population improvement programme should be carried out to improve the economically important quantitative characters in this crop. In population improvement, undesirable linkages are needed to be broken, releasing potential genetic variability and forming new recombinants, which can be used in breeding programme of muskmelon.

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