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Gene action of nutritional and quality traits in muskmelon (*Cucumis melo* L.)

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Abstract

A study of twenty one F_1 hybrids of Muskmelon (*Cucumis melo* L.) in a half-diallel set involving seven parents showed over-dominance and low narrow-sense heritability for acidity, vitamin c, TSS, sodium, potassium, zinc, manganese, copper, iron, magnesium, calcium, respiration rate and ethylene emission rate. In all these characters, the dominance component of genetic variance (H_1) was higher than the additive component of genetic variance (D) indicating predominance of dominant gene action over additive gene action and commercial exploitation of heterosis for improvement of these traits.

Keywords: Gene action, nutritional, quality traits, muskmelon

Introduction

Muskmelon (*Cucumis melo* L., 2n=2x=24) is one of the most nutritive and commercially important cucurbit extensively cultivated in hot and arid areas of Uttar Pradesh, Punjab, Rajasthan, Madhya Pradesh, Bihar and Karnataka and being grown in cultivable land as well as in marginal land of riverbed areas. The centre of origin of muskmelon was earlier considered as African continent but recent studies showed that cucumber and muskmelon both are of Asian origin and wide diversity of wild species of *Cucumis melo* L. exists in India and China (Sebastian *et al.* 2010) [7]. *Cucumis melo* L. is considered as one of the most diverse and highly polymorphic species in Cucurbitaceae family (Danin-Poleg, *et al.* 2001, Decker-Walters, *et al*. 2002) [3, 1] and it comprises of a large number of botanical varieties or horticultural groupings which may be consequence of higher genetic diversity in this species (Mliki *et al.* 2001) [5]. The improvement programme of Muskmelon is based mainly on exploiting natural sources of germplasm by means of selection and hybridization followed by selection.

For development of promising high yielding varieties, the identification of genetically superior plants is an important pre-requisite.

The knowledge of gene effects for different traits is of prime importance before starting a breeding programme. Determination of the most suitable breeding method and selection strategy for improvement of a trait would depend on the knowledge of gene actions operating in breeding population. In plant breeding, gene action is usually measured in terms of components of genetic variances or combining ability variances and effects. In heterosis breeding, a knowledge of combining ability, gene action and relative amount of additive and non-additive components of genetic variance present in cross combination helps to determine the feasibility of its utilization and identification of best combiners. Selection and hybridization are two basic methods for crop improvement. The success of selection mainly depends upon the extent of genetic variability present it. Therefore, a higher genetic base should be utilized for faster and higher magnitude of success. Utilization of divergent germplasm in hybridization creates such broad genetic base (Singh, 1998) [8].

A detailed knowledge about the magnitude and nature of genetic variation in a specific population is of prime importance for the effective prediction of the most effective breeding programme. The numerical analysis of diallel provides detailed account of additive and dominance components and the allied statistics. The genetics largely depends upon the relative magnitude of these two components. The genetic model on which the analysis of diallel tables is based involve certain assumptions *viz.* (i) segregation is diploid; (ii) there are only environmental differences between reciprocal crosses; (iii) absence of epistasis; (iv) the parents are homozygous; (v) there are no multiple alleles (vi) that the genes are independently distributed and that there is no genotype interaction with locations and years (Walton, 1968).

In spite of exhibiting considerable amount of genetic diversity with respect to different characters little attention has been given for improvement of this crop. Hence, an attempt was made to investigate the gene action (inheritance pattern) of yield and yield attributing traits.

Materials and Methods

The present investigation was carried out during spring summer and *kharif* season of 2015 at research farm of Division of Vegetable Science of Indian Agricultural Research Institute, New Delhi. Seven genetically diverse inbreds of Muskmelon *viz,* DHM-163 (P_1), DHM-162 (P_2), DMM-159 (P_3), DCM-31 (P_4), Pusa Madhuras (P_5), Kashi Madhu (P_6) and Hara Madhu (P_7) were crossed in 7 x 7 half-diallel (excluding reciprocals) mating scheme (Hayman, 1954). The resulting 21 F1 hybrids along with 7 parental lines were evaluated in a randomized block design with three replications. The seeds were sown in rows of 2.5m with 0.75 m spacing between the plants. All the recommended package of practices was followed to grow a successful crop. Out of 12 plants, 10 were marked for taking observations. Observations on individual fruit basis were recorded on thirteen nutritional and quality characters *viz.* acidity, vitamin c, TSS, sodium, potassium, zinc, manganese, copper, iron, magnesium, calcium, respiration rate and ethylene emission rate. Gene action was studied by the diallel method of numerical approach given by Hayman (1954). If the estimates of average degree of dominance [(H1/D)½] is '0' denote no dominance, 0 to 1, partial dominance; 1, complete dominance and > 1, over dominance. The maximum values of H2/4H1 shall be 0.25 when u = v = 0.05. If the relative frequency of dominant and recessive genes [(4DH1)½ + F/ (4DH1)½ - F] in parents =1, means nearly equal proportion i.e. symmetrical distribution; u = v = 0.5. Any deviation from 1 shows asymmetry of distribution (u > v) as > 1 refers to excess of dominant genes and minority of recessive genes (u > v) and <1 means minority of dominant genes and excess of recessive (u < v).

Results

The estimates of genetic components of variation and various statistical parameters for different characters were represented in Table 1. The genetic components of variation for sodium (Na) revealed that estimate of D, H_1 and H_2 were highly significant. The value of H_1 was higher than D indicating the presence of more dominant genes. The value of $(H_1/D)^{½}$ was higher (1.93) indicating over-dominance. The proportion of genes with positive and negative effects ($H_2/4H_1$) in parents was found to be 0.20 (less than 0.25), which denoted asymmetry at loci showing dominance. The narrow sense heritability (28.22%) indicated that non-additive type of gene action played an important role in the inheritance of this trait.

Results pertaining to components of genetic variation for potassium (K) revealed that estimate of H_1 and H_2 were highly significant. The value of H_1 was higher than D indicating the presence of more dominant genes. The value of $(H_1/D)^{½}$ was higher (2.96) indicating over-dominance. The proportion of genes with positive and negative effects ($H_2/4H_1$) in parents was found to be 0.19 (less than 0.25), which denoted asymmetry at loci showing dominance. The narrow sense heritability (24.27%) indicated that non-additive type of gene action played an important role in the inheritance of this trait.

Results pertaining to components of genetic variation for zinc (Zn) revealed that estimate of H_1 and H_2 were highly significant. The value of H_1 was higher than D indicating the presence of more dominant genes. The value of $(H_1/D)^{½}$ was higher (2.48) indicating over-dominance. The proportion of genes with positive and negative effects ($H_2/4H_1$) in parents was found to be 0.23 (less than 0.25), which denoted asymmetry at loci showing dominance. The narrow sense heritability (13.43%) indicated that non-additive type of gene action played an important role in the inheritance of this trait.

Results pertaining to components of genetic variation for Manganese (Mn) revealed that estimate of H_1 and H_2 were highly significant. The value of H_1 was higher than D indicating the presence of more dominant genes. The value of $(H_1/D)^{½}$ was higher (1.75) indicating over-dominance. The proportion of genes with positive and negative effects ($H_2/4H_1$) in parents was found to be 0.20 (less than 0.25), which denoted asymmetry at loci showing dominance. The narrow sense heritability (30.92%) indicated that non-additive type of gene action played an important role in the inheritance of this trait.

Results pertaining to components of genetic variation for iron (Fe) revealed that estimate of H_1 and H_2 were highly significant. The value of H_1 was higher than D indicating the presence of more dominant genes. The value of (H_1/D)½ was higher (2.08) indicating over-dominance. The proportion of genes with positive and negative effects ($H_2/4H_1$) in parents was found to be 0.22 (less than 0.25), which denoted asymmetry at loci showing dominance. The narrow sense heritability (23.20%) indicated that non-additive type of gene action played an important role in the inheritance of this trait.

The value of $(H_1/D)^{½}$ was higher in case of cupper, magnesium (Mg), calcium (Ca), acidity and TSS (3.21, 3.57, 2.49, 1.61 and 3.79 respectively) indicating over-dominance. The proportion of genes with positive and negative effects (H2/4H1) in parents was found to be less than 0.25, which denoted asymmetry at loci showing dominance. The narrow sense heritability (10.62%, 7.76%, 15.61%, 37.75% and 6.94%) indicated that non-additive type of gene action played an important role in the inheritance of these traits.

Results pertaining to components of genetic variation for vitamin C revealed that estimate of H_1 and H_2 were highly significant. The value of H_1 was higher than D indicating the presence of more dominant genes. The value of (H_1/D)½ was higher (2.74) indicating over-dominance. The proportion of genes with positive and negative effects ($H_2/4H_1$) in parents was found to be 0.20 (less than 0.25), which denoted asymmetry at loci showing dominance. The narrow sense heritability (8.44%) indicated that non-additive type of gene action played an important role in the inheritance of this trait.

For respiration rate, the estimated value of D, H_1, H_2 and F were highly significant. The estimated value of H_1 was greater than D which revealed that non-additive genes were more than additive genes. Positive value of F indicated predominance of dominant alleles. The mean degree of dominance $(H_1/D)^{½}$ being 1.13 showed over dominance. The proportion of genes with positive and negative effects ($H_2/4H_1$) was 0.20, which denotes asymmetry at loci. The proportion of dominance and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 2.47 whereas number of group of genes exhibiting dominance and controlling character was 0.32. The narrow sense heritability (75.18%) indicated the partial dominant type of gene action for expression of this character

For ethylene emission rate, the estimated value of D, H^2 H_1, H_2 and F were highly significant. The estimated value of H_1 was greater than D which revealed that non-additive genes were more than additive genes. Positive value of F indicated predominance of dominant alleles. The mean degree of dominance $(H_1/D)^{½}$ being 0.78 showed partial dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was 0.18, which denotes asymmetry at loci. The proportion of dominance and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 3.17 whereas number of group of genes exhibiting dominance and controlling character was 1.47. The narrow sense heritability (84.22%) indicated the partial dominant type of gene action for expression of this character.

Table 1: Estimates of genetic components of variation and various statistical parameters for nutritional and quality traits.

Genetic parameter	Acidity(%)	Vitamin C (mg/100g)	Na (mg/g)	K (mg/g)	Zn (µg/g)	Mn (µg/g)
D(Additive effect)	0.00	3.13	0.82*	84.33	0.45	0.08
SE±	0.00	3.60	0.35	68.65	0.46	0.05
F(Gene distribution)	0.00	-8.14	1.21	223.00	-0.02	0.08
SE±	0.00	8.63	0.85	164.70	1.11	0.12
H_1	0.00	23.49**	3.05*	739.03**	2.76*	0.24*
SE±	0.00	8.66	0.85	165.28	1.11	0.12
H_2	0.00	18.62**	2.45*	560.95**	2.56**	0.20*
SE±	0.00	7.63	0.75	145.64	0.98	0.10
h^2	0.00	7.99	-0.03	257.99**	0.54	0.00
SE±	0.00	5.13	0.50	97.82	0.66	0.07
E(Environmental effect)	0.00	0.54	0.06	1.92	0.03	0.00
SE±	0.00	1.27	0.12	24.27	0.16	0.02
$(H_1/D)^{1/2}$	1.61	2.74	1.93	2.96	2.48	1.75
$H_2/4H_1$	0.19	0.20	0.20	0.19	0.23	0.20
((4DH1)^.5+F)/((4DH1)^.5-F)	0.00	0.36	2.24	2.61	0.98	1.81
h^2/H_2	0.00	0.43	-0.01	0.46	0.21	0.00
r	0.65	0.88	-0.23	-0.18	0.58	0.25
Heritability (narrow sense)	37.75	8.44	28.22	24.27	13.43	30.92

*Significant at P=0.05

**Significant at P=0.01

Table 1: Estimates of genetic components of variation and various statistical parameters for nutritional and quality traits.

Genetic parameter	TSS (°Brix)	Cu (µg/g)	Fe (µg/g)	Mg (mg/g)	Ca (mg/g)	Respiration rate (ml.CO_2/kg/hr)	Ethylene emission rate((µl/kg/hr)
D(Additive effect)	0.06	0.00	19.15	0.00	0.00	15.85**	6825.70**
SE±	0.29	0.00	10.72	0.00	0.00	2.60	284.52
F(Gene distribution)	0.49	0.00	19.93	0.00	0.00	15.11**	5556.48**
SE±	0.83	0.00	25.71	0.00	0.00	6.23	682.55
H_1	0.73	0.02	82.74**	0.00	0.00	20.11**	4184.36**
SE±	2.00	0.00	25.80	0.00	0.00	6.25	684.96
H_2	7.04**	0.01	71.74**	0.00	0.00	16.13**	2946.91**
SE±	2.00	0.00	22.73	0.00	0.00	5.51	603.55
h^2	5.77**	0.01	41.48**	0.00	0.00	5.20	4330.17**
SE±	1.76	0.00	15.73	0.00	0.00	3.70	405.37
E(Environmental effect)	0.20	0.00	0.14	0.00	0.00	0.06	0.27
SE±	1.18	0.00	3.79	0.00	0.00	0.92	100.59
$(H_1/D)^{1/2}$	3.79	3.21	2.08	3.57	2.49	1.13	0.78
$H_2/4H_1$	0.20	0.16	0.22	0.20	0.21	0.20	0.18
((4DH1)^.5+F)/((4DH1)^.5-F)	1.49	0.00	1.67	0.00	0.00	2.47	3.17
h^2/H_2	0.03	1.00	0.58	0.00	0.00	0.32	1.47
r	-0.10	-0.85	-0.05	-0.51	-0.23	0.74	0.74
Heritability (narrow sense)	6.94	10.62	23.20	7.76	15.61	75.18	84.22

*Significant at P=0.05

**Significant at P=0.01

Discussion

A detailed knowledge about the magnitude and nature of genetic variation in a specific population is of prime importance for the effective prediction of the most effective breeding programme (Debnath, 1988) [2]. Diallel analysis is most balanced and systemic experimental design to examine continuous variation. The genetic information related to parental population becomes available quite in early generation i.e. in F_1 and it is thus useful to define breeding strategy without losing much time. In diallel cross system, there is no need for parents to be strictly inbred or to have uniformity. The knowledge of gene effects for different traits is of prime importance before starting a breeding programme. Determination of the most suitable breeding method and selection strategy for improvement of a trait would depend on the knowledge of gene actions operating in breeding population. In plant breeding, gene action is usually measured in terms of components of genetic variances or combining ability variances and effects. Since most of the characters, which showed heterosis, are governed by polygenes, the study of gene action (inheritance pattern) of these characters is of valuable importance in ascertaining the genetic basis of heterosis.

The results of diallel analysis of present study revealed over-dominance for all the characters studied. In all these characters, the dominance component of genetic variance (H_1) was higher than the additive component of genetic variance (D) indicating predominance of dominant gene action over additive gene action. This was also confirmed by the values of narrow sense heritability which were found to be less than 50% for all the characters (except respiration rate and ethylene emission rate). The positive sign of ‘F’ value in most of the characters showed an excess of dominant genes in the parents. The negative ‘F’ value for Zn content and vitamin C indicated predominance of recessive genes for these characters. The proportion of genes with positive and negative effects in parents was found to be less than 0.25 for all these characters denoting asymmetry at loci showing dominance. The mean degree of dominance $(H_1/D)^{½}$ which was also found to be more than 1 for all the characters (except ethylene emission rate) confirmed the presence of over-dominance. Sirohi and Yayasani (2006) [9] reported predominance of non-additive genetic variance (over-dominance) and low narrow sense heritability for nutritional and quality characters. These results were also on conformity with the findings consonance of Pandey *et al.* (2010) [6] and Sit and Sirohi (2001) [10] in pumpkin. The results of the present investigation showed over-dominance for majority of the traits. The predominance of non-additive gene action and low to moderate narrow sense heritability for majority of the characters studied suggested that heterosis breeding might be advantageous to get higher gain in muskmelon.

Conclusion

The results of present investigation revealed over-dominance for all the characters studied. In all these characters, the dominance component of genetic variance (H_1) was higher than the additive component of genetic variance (D) indicating predominance of dominant gene action over additive gene action. Thus, in the present investigation, the predominance of non-additive gene action and low narrow sense heritability was observed for most of the important yield contributing characters which suggested the importance of heterosis breeding to get higher gain in muskmelon.

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