

A DIALLEL ANALYSIS OF TOTAL SOLUBLE SOLIDS IN MUSKMELON (*CUCUMIS MELO* L.)

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The genetic system governing the inheritance of total soluble solids (TSS) was investigated in a 10 parent diallel cross of muskmelon (*Cucumis melo* L.) by applying the graphical and variance component methods. Overdominance was observed for TSS. Both additive and dominance genetic components were found to be important, the latter being predominant. There was some asymmetry of distribution of genes with positive and negative effects. The proportion of dominant and recessive genes was almost equal in the parents. More than seven groups of genes were found for TSS. A selection scheme which involves a certain degree of intercrossing and hybridization followed by selection has been indicated to bring about an acceptable level of improvement in TSS.

The diallel analysis has been used to study the quantitatively inherited characteristics of crop plants. Frequent use has been made of the Hayman (1954 a, b) and Jinks (1954) approach, which provides a rapid evaluation of the genetic relationships among several parental lines. The determination of the genetic variation and the partition of variance provide information on the type of gene action associated with a particular trait (Nga, 1975). Muskmelon (*Cucumis melo* L.) is an important desert crop of India and hence must meet certain minimum standards in terms of quality. The total soluble solids concentration (TSS) is a major concern in muskmelon eating quality (Davis, Baker and Kasmire, 1964). The studies on the inheritance of

quality characters in this crop are not many. The present investigation was taken up with the objective of studying the genetic system governing TSS using the diallel technique involving ten parental lines.

MATERIALS AND METHODS

Ten diverse parental lines of muskmelon viz., Mainstream (1), Muskotaly (2), Gulfstream (3), Hara Madhu (4), Arka Rajhans (5), Arka Jeet (6), UFG 515 (7), PI 126114 [8], Punjab Sunheri [9], and Durgapura Madhu [10] were selected and they were selfed for two generations before being used in this study. They were crossed in all possible combinations excluding reciprocals. The 45 F₁ crosses along with 10 parents were grown in a randomized

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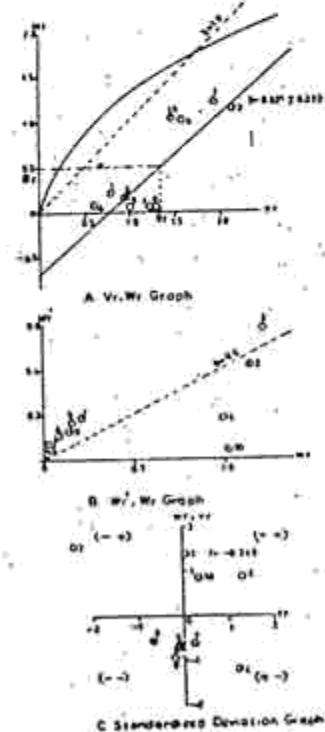
block design with three replications. Each treatment was sown in single row plots of 3.5m length. A spacing of 2.5m was kept between rows. In each row hills were prepared at a distance of 75 cm. In each hill 5 seeds were sown and only 2 seedlings were retained, 25 days after sowing. Usual cultural practices were followed. Fruits were harvested at full slip stage from 5 randomly selected plants in each plot. Total soluble solids [TSS] in percentage was determined with the help of a hand refractometer. The diallel analysis was done as per the methods of Jinks [1954] and Hayman [1954a, b] after testing the validity of assumptions by 't'² test. The variance [v_r] of each array, covariance [w_r] between the parents and their progenies in each array and covariance (W 's) between the parents and the array mean were calculated. Variance-covariance [V_r, W_r] and covariance-covariance (W_r, W_r) graphs were drawn according to Hayman (1954a) and Allard (1956). In the absence of non-allelic gene interaction and with independent distribution of genes among the parents, W_r is related to V_r by a straight regression line of unit slope in V_r, W_r graph. The distance between the origin and the point where the regression line cuts the W_r axis provides measure of mean degree of dominance. The order of the array points along the regression line provides information on the distribution of dominant and recessive genes among the parents. The array points in W_r, W_r

graph when compared with those in V_r, W_r graph give an indication about the type of epistasis.

The relationship of the order of dominance ($W_r + V_r$) among the parents was determined by the standardised deviation graph of parental measurement (Y_r) and ($W_r + V_r$) values of the parents (Johnson and Aksel, 1959). The narrow-sense heritability was estimated using appropriate formula [Singh and Chaudhary, 1979].

RESULTS AND DISCUSSION

Analysis of variance for the experimental design revealed highly significant differences among parents and progenies with respect to TSS. Non-significant t^2 value and non-significant regression coefficient from unity, indicated the validity of assumption thereby providing adequate



justification for the extension of diallel analysis to the material in question.

Graphical analysis [Vr,Wr graph] indicated the absence of epistatic interaction, as the regression coefficient [$b=0.931 \mp 0.222$] was not significantly different from unity. Over-dominance was observed for this trait as the regression line intercepted the Wr axis below the point of origin [Fig. 1A]. Parent Hara Madhu had the maximum number of dominant genes, being nearest to the origin. On the other hand, Muskotaly possessed more recessive genes, being farthest to the origin. The array points of various parents were scattered along the regression line, suggesting wide genetic diversity between parents under study. The parabola curve intercepted the regression line away from the last array point showing prominent role of environmental factors in the expression of TSS. This holds good for a complex character like TSS which includes glucose, fructose and sucrose.

Judging from the distribution of array points in Vr,Wr graph [Fig.1A] and Wr,W'r grap (Fig.1B), genic interactions appear to be made up mostly of the complementary type, as most of the array points which were lying below the unit slope in Vr,Wr graph were found distributed above the one half unit slope in Wr,W'r graph.

The standardised deviation graph of parental order of dominance ($Wr+Vr$) and parental measurements (Yr) showed that the parents, Gulfstream, Durgapura Madhu and Arka Jeet had recessive genes and parents UFG 515 and Hara Madhu had dominant genes for increased TSS. For decreased TSS, parents Punjab Sunheri, Mainstream, Arka Rajhans and PI 126114 had dominant genes and parent Muskotaly had recessive genes (Fig. 1C), when the parental means for TSS were correlated with ($Wr+Vr$) values, the correlation coefficient (r) was negative and non-significant (-0.349). This indicated that there is no correlation between the percentage TSS of a parent and the number of dominant genes that it possesses. This could be interpreted as meaning that there are dominant genes for high TSS and dominant genes for low TSS present.

The variation developed in the diallel cross population was split into different genetic components, viz., D , H , H_2 , h^2 , F and E , which were further utilized to estimate different ratios (Table 1). Both additive (D) and dominance (H_1 and H_2) components were significant. But H_1 and H_2 components were higher, indicating predominant role of dominance effects in the inheritance of TSS. The ratio $(H_1/D)^{1/2}$, which measures the mean degree of dominance, falls in the range of over dominance, confirming the higher magnitude of dominance component. However this

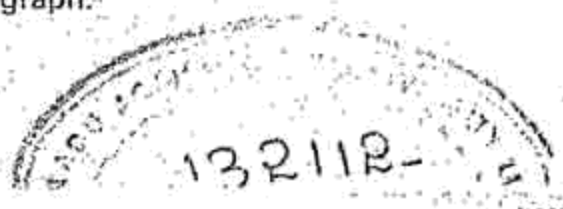


Table 1. Estimates of genetic components of variation and related ratios for total soluble solids in muskmelon.

Genetic Parameters	Estimate	SE
D	0.74*	0.23
H ₁	2.19**	0.48
H ₂	2.36**	0.41
F	-0.11	0.53
E	1.02**	0.07
h ²	17.90**	0.30
$(H_1/D)^{\frac{1}{2}}$	1.72	
$(H_2/4H_1)$	0.24	
(KD/KR)	0.92	
(h^2/H_2)	7.59	
h ₂ (ns)	0.17	
$\overline{F_1-P}$	0.73	

*P=0.05; ** P=0.01.

Where,

D=additive component.

H₁=dominance component.
 $H_2 = H_1 [1 - (u-v)^2]$, where u=proportion of positive genes in the parent
and v=proportion of negative genes in the parent.

F=mean of Fr over all arrays.

 $E_{\overline{2}}$ =expected environmental component.h²=dominance effect. $(H_1/D)^{\frac{1}{2}}$ =mean degree of dominance. $H_2/4H_1$ =proportion of genes with positive and negative effects in the parents. $KD/KR = \frac{(4DH_1)^{\frac{1}{2}}}{(4DH_1)^{\frac{1}{2}} + F}$ =proportion of dominant and recessive alleles in the parents. $\frac{(4DH_1)^{\frac{1}{2}}}{(4DH_1)^{\frac{1}{2}} + F}$ h²/H₂=gene group of number of effective factors.h²(ns)=narrow-sense heritability. $\overline{F_1 - P}$ =overall F₁ mean-overall parental mean.

figure is somewhat inflated if there is non-allelic interaction or epistasis. Subtracting the overall parental mean from the overall F_1 mean provides an indication of the mean degree of dominance. A value of 0.73 was obtained for $\overline{F_1} - \overline{P}$, which is an indication for dominance of high TSS. Kalloo and Dixit (1983) have also reported similar results for TSS in muskmelon. The symmetry of genes with positive and negative effects in parents, measured by $H_2 / 4H_1$, which should theoretically be equivalent to 0.25, was 0.24. This indicated that there was some asymmetrical distribution of positive and negative genes in the parents. The value of KD/KR (0.92) showed that parents had almost equal proportion of dominant and recessive genes. The ratio h^2 / H_2 , which provides an estimate of number of effective factors exhibiting dominance indicated that more than 7 groups of genes control TSS. Arasimovitch (1936) also reported polygenic control of TSS in muskmelon. The heritability (narrow-sense), as expected, was low mainly because of the high magnitude of dominance component. A highly significant role of environment in modifying the phenotype was observed as the estimate for 'E' was significant.

The results indicated the presence of both additive and non-additive genetic components with the preponderance of the latter. Therefore, it would be worth making selection for high yield and high TSS in fur-

ther generations for the simultaneous exploitation of fixable and non-fixable components.

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