Genetic components for yield and its contributing traits in muskmelon (*Cucumis melo* L.)

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ABSTRACT

The estimates of D which measures the variance due to additive genetic effects was significant for number of node on which first female flower appears in E_2 and on pooled basis, days to first female flower open in E_1, number of primary branches per plant on pooled basis and days to first harvesting in both the environments and on pooled basis. While, H_1, which measures the variance due to non-additive effects was significant for all the characters in both the environments and on pooled basis except for number of node on which first female flower appears in E_1. The above findings indicate that both additive and dominance components were important in the inheritance of these traits. However, additive component was lower in magnitude than dominance component for most of the traits in both environments, suggesting the preponderance of non-additive gene action. The narrow sense heritability estimated for all the non-significant characters was either medium or low suggesting that non-additive genetic variance was largely predominating.

Key words : Gene action, Narrow sense heritability, Muskmelon.

Muskmelon (*Cucumis melo* L.) is an important vegetable crop of family cucurbitaceae. Being a dessert fruit, it is not only the yield, but quality characters of hybrid over improved population should be a major objective in heterosis breeding programme. In spite of wide genetic variability available in this crop especially for fruit characters, meagre emphasis has been given to the improvement of quality characters and also on the genetics (gene action) of quality traits of this vegetable. Hence, an attempt was made to investigate the gene action of some important quality characters.

MATERIALS AND METHODS

Ten varieties of muskmelon, *viz.* Punjab Sunehri, Pusa Madhuras, AMM- 00-25, AMM- 00-11, AMM- 01-18, DM-1, AMM- 02-26, PMM- 96-20, Hara Madhu and RM-50 were crossed in all possible combinations excluding reciprocals. The resulting 45 F_1 hybrids alongwith their parents were sown in randomized block design with three replications at spacing of 150 cm and 90 cm in two environments created by sowing dates (E_1=15th October, 2003 and E_2=15th February, 2004). All the recommended cultural practices were followed during experimentation. Observations were recorded on number of node on which first female flower appeared, days to first female flower opened, number of primary branches per plant, days to first harvesting, fruit length (cm), fruit girth (cm), fruits per plant, fruit weight (g), fruit yield per plant (kg), flesh thickness (cm), moisture content (Per cent), total soluble solids (TSS in per cent), acidity (Per cent) and total soluble sugars (mg g^{-1}). These genetic

components of variation were calculated from the diallel table following the methods outlined by Hayman (1954, 1954 a, b; 1957, 1958 and 1960) and Jinks (1954 and 1956) as described in detail by Mather and Jinks (1982) and Singh and Chaudhary (1985). To test failure of either of the assumption of diallel analysis, 't²' was applied as suggested by Hayman (1954 a).

RESULTS AND DISCUSSION

The validity of hypothetical assumptions underling diallel analysis as postulated by Hyman (1954 a) was tested by t² test. The non-significant value of t² estimated probably suggested fulfillment of the assumptions and confirm the validity of the hypothesis. The estimated 't²' value for different characters indicated non-significance for most of the characters except fruit length, fruit weight, fruit yield per plant, moisture content, acidity and total soluble sugars. However, for characters total soluble solids 't²' value was non significant in E_1, while E_2 and on pooled basis this trait was significant. For these characters, one or few assumptions of diallel analysis could not be fulfilled.

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