

and maximum in EC-389813-F (23.5) whereas frame size ranged between 36.2 cm (EC-490190) to 66.5 cm (EC-490167). Minimum and maximum stalk length was recorded in EC-490196 (0.55 cm) and 490194 (2.10 cm), respectively. Maximum head size index of 306.45 cm² was recorded in EC-490186 and minimum of 78.30 cm² in EC-490157. Gross weight per plant ranged between 0.45 kg (EC-490157) to 2.77 kg (EC-490189). Maximum net head weight was recorded in EC-490201 (1.25 kg/head) and minimum in EC-490157 (0.30 kg/head). It is, therefore, evident that considerable amount of variability was available for all the traits under study.

Based on the overall performance with respect to head shape (round), compactness of head, early heading, smaller frame size (<50 cm) and average net head weight

(>0.75 kg/head), 7 lines viz., EC-490162, 490165, 490174, 490176, 490185, 490191 and 490200 were selected. Although EC-490201, 490204, 490180, 490167, 490186, 490179, 490183 and 490193 also had better net head weight but they had either oval head shape or resembled with savoy type of cabbage or both and therefore, not selected. Similarly EC-490189 and EC-389805 were also rejected due to their bigger frame size and flat head shape, respectively. The selected collections will be exploited in the on-going breeding programme on cabbage.

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Genetic Variability and Association Analysis in Exotic Cherry Tomato

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Key Words: Cherry Tomato, Genetic Divergence, Intertrait Correlation

Tomato is one of the most widely grown and commercially important vegetable crops. The numerous varieties differ greatly in plant form and fruit type, the latter ranging from a small currant size through cherry, plum, and pear forms to the large, nearly round fruits. Tomatoes are a valuable source of minerals and vitamins, particularly vitamins A and C. The cherry tomatoes are widely used in salads, with dip as an appetizer or as garnishing. In order to incorporate desirable characters to maximize marketable yield, the information on the nature and extent of genetic variability in a population of cherry tomato for desirable characters and inter trait relationship are the basic requirement. The material of the present study consisted of thirty two exotic genotypes of cherry tomato and evaluated in randomized complete block design at research farm of IIVR Varanasi during 2004.

The observations on nine morphological traits were analysed statistically. The variance analysis showed that the genotypes differed significantly among themselves for all the characters under study. The phenotypic coefficients of variation (PCV) were

slightly higher than their corresponding genotypic coefficient of variation (GCV) due to environmental influence. The higher estimates of heritability coupled with the higher genetic advance for number of fruits per plant (98.9, 79.6) and plant height (98.8, 69.8) indicated that preponderance of additive effects and the direct selection would be rewarding for such traits. High heritability accompanied with low genetic advance for flesh thickness (99.2, 0.13) and number of locules (97.3, 1.2) is indicative of non-additive gene action.

Correlation studies showed that for most of the character pairs, genotypic and phenotypic associations were in the same direction and genotypic correlations estimates were higher than the phenotypic ones, indicating an inherited association between the characters. Yield per plant the most important economic trait, exhibited positive association with average fruit weight (0.53) and number of fruits per plant (0.38). The negative correlation was observed for number of fruits per plant with average fruit weight (-0.54), number of locules (-0.45) and flesh thickness (-0.34). Therefore simultaneous

improvement for all the traits associated with yield would be difficult in the population.

Multivariate hierarchical analysis revealed total of six clusters. It was concluded that 32 genotypes were mainly divided at first node into two clusters with 24 and 8 genotypes. Cluster with 24 genotypes was further divided into 3 groups with 9, 7 and 8 genotypes respectively.

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Studies on Genetic and Biochemical Parameters of Introduced and Indigenous Germplasm in Snap Melon (*Cucumis melo* L var. *momordica* Duth. and full.)

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Key Words: GCV, Genetic Advance, Heritability, PCV, Variability

Snap melon (*Cucumis melo* L. var. *momordica*) belongs to family cucurbitaceae and is grown in many parts of India. The tender fruits are used as a vegetable and ripe fruits are used as dessert. The fruits are rich in vitamins and minerals. Besides it has got enormous medicinal value. India, being a secondary centre of origin of snap melon, has accumulated a wide range of variability with respect to different quantitative and qualitative characters. The critical assessment of nature and magnitude of variability is a prerequisite for any efficient breeding programme and provides an opportunity to identify superior lines with desirable yield and quality characters. Heritability along with genetic advance will be helpful in assessing the reliability of a character for selection. Hence, the present investigation was undertaken to study variability, heritability and genetic advance for 19 important quantitative and biochemical characters in 30 genotypes of Snap melon.

The present investigation was carried out at the research farm of The Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi, during the spring-summer season of 2003. The experimental

materials consisted of 30 indigenous and exotic genotypes of snap melon collected from different sources. The experiment was laid out in a randomized block design with three replications. Each treatment comprised ten hills and two plants were allowed to grow per hill. The observations were recorded on five randomly selected plants per replication for each entry on nineteen quantitative and biochemical characters. The analysis of variance were carried out as suggested by Panse and Sukhatme (1967) and were used for calculating other genetic parameters. Genotypic and phenotypic coefficient of variation was calculated as per the formula suggested by Burton (1952). Heritability in broad sense and expected genetic advance were calculated as per the formula given by Allard (1960) and Johnson *et al.* (1955), respectively.

The extent of variability present in thirty genotypes of snap melon was measured in terms of phenotypic variance (V_p), phenotypic coefficient of variation (PCV), genotypic variance (V_g), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance (GA). A perusal of data in Table 1 revealed that maximum