Genetic diversity studies for parental selection in bitter gourd (*Momordica charantia* L.)

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ABSTRACT

Nature and magnitude of genetic divergence assessed on twenty two bitter gourd genotypes assembled from different geographical locations showed the presence of wide genetic diversity. The genotypes were grouped into six clusters based on Mahalanobis D^2 statistics using Tocher's method. The clustering pattern of genotypes revealed that the genetic diversity was independent of the geographical diversity. Among the six clusters, maximum number of genotypes were found in cluster I and the clusters V and VI were found to be mono genotypic. Among the fourteen quantitative characters studied, individual fruit weight constituted a maximum of 26.83 per cent to the divergence, followed by yield of fruits per vine and length of fruit. Ranking of genotypes based on intra cluster mean performance for those characters which are major contributors of genetic diversity revealed its usefulness in selecting parents for heterosis breeding.

Bitter gourd (*Momordica charantia* L.) is one of the most nutritive and commercially important cucurbitaceous vegetables grown throughout the country for its tubercled, fleshy, unripe fruits. Bitter gourd, a crop with moderate degree of saline tolerance is also found to perform well in summer rice fallow and thus offers great scope for development of varieties/hybrids for such a situation. The knowledge on genetic diversity is an important factor for heritable improvement in any crop and the information pertaining to nature and degree of divergence would be of immense use in selecting desirable parents from available germplasm for a successful breeding programme. The nature and magnitude of genetic distance between the genotypes serve as an indication for hybridisation to exploit high degree of heterosis. Genetic diversity is important to applied plant breeding as it reduces vulnerability to pests, besides it helps in the choice of parental combinations of the greatest promise. Hence, the present study was aimed at ascertaining the nature and magnitude of genetic diversity present in a set of twenty two bitter gourd genotypes.

MATERIALS AND METHODS

The present study was carried out during *rabi* 2004 at Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal of Union Territory of Pondicherry, located along the East Coast at the tail end of the river Cauvery. The experimental material consisted of twenty two bitter gourd genotypes collected from different geographical locations of the country. They were evaluated in a Randomised Block Design with three replications. Observations were recorded on five randomly selected plants on fourteen important quantitative traits *viz.*, days to first male flower appearance, days to first female flower appearance, node of first male flower appearance, node of first female flower appearance, number of male flowers per vine, number of female flowers per vine, sex ratio (M/F), fruit length (cm), fruit girth (cm), individual fruit weight (g), vine length (m), number of primary branches per vine, number of fruits per vine and yield of fruits per vine (g). The D^2 analysis suggested by Mahalanobis (1936) was adopted to assess the genetic diversity among the twenty two genotypes and clustering of genotypes was performed using Tocher's method, as outlined by Rao (1952). The method suggested by Singh and Chaudhary (1977) was adopted for selection of genetically divergent parents from various clusters for use as parents to exploit high degree of heterosis.

RESULTS AND DISCUSSION
Clustering pattern of genotypes:

Mahalanobis's D^2 statistic, which measures the forces of differentiation at intra and inter cluster levels has been used as a powerful tool in quantifying the degree of divergence at genotypic level. The dispersion of these twenty two genotypes into six gene constellations indicated the presence of large amount of diversity in the population chosen for the study (Table 1). Two clusters *viz.*, cluster V and cluster VI were found to be mono genotypic, while the remaining clusters were found to constitute more than