Genetic diversity studies in okra [*Abelmoschus esculentus* (L.) Moench]

K. PRAKASH*, M. PITCHAIMUTHU[1], R. VENUGOPALAN[1], SHIVANAND HONGAL[1] AND K. JAINAG

University of Horticultural Sciences, PG and Zonal Horticultural Research Station, G.K.V.K. Campus, BENGALURU (KARNATAKA) INDIA (Email : prakash837@gmail.com)

ABSTRACT

Fourty four okra genotypes were assessed for genetic divergence using Mahanalobis D^2 statistics. The population was grouped in to twelve clusters. The cluster III was the largest with eight genotypes followed by cluster I and VIII with seven, cluster II with five, cluster XII with three while, clusters IV, V, VI, IX, X and XI included only two genotype in each. The clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. The intra-cluster distance was maximum in cluster XII (28.14), while inter-cluster distance was maximum between cluster VI and VIII (35.57) followed by I and IX (35.31), thus being a good source for attempting hybridization. The characters namely days to 50% flowering (35.62%), 100 seed weight (28.44%), number of seeds per fruit (17.23%) and average fruit weight (8.14%) were directly contributed towards maximum divergence and, therefore, selection of divergent parents based on these characters is recommended for getting good hybrids or segregants in okra.

Key words : Okra, Genetic divergence, D^2 statistics

INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench] is an economically important vegetable of tropical and sub-tropical part of India. It is mainly grown for its tender fruits, which are cooked and consumed as vegetable. For any crop improvement program it is essential that sufficient variability or diversity exist for economically important traits in the germplasm. The importance of genetic diversity in selecting the parents for recombination breeding in crops has been repeatedly emphasized by many workers (Murthy and Anand, 1996; Pillai, 2002). Hence, estimation of genetic divergence of economically important characters based on sound statistical procedures like Mahanalobis D^2 statistics is required to identify diverse genotypes for crossing. Therefore, the present study was carried out to examine the nature and magnitude of genetic divergence in 44 genotypes of okra collected from different geographical areas.

MATERIALS AND METHODS

The experimental material consisted of 44 diverse genotypes of okra. The experiment was laid out in Randomized Block Design with three replications during *Kharif* season 2009 at Vegetable Breeding Block, Indian Institute of Horticultural Research (IIHR), Bangalore, Karnataka. Each entry was sown at 30 x 15 cm spacing, accommodating 30 plants in each row per replication. All the recommended package of practices was followed for raising a healthy crop. The observations were recorded from five competitive plants from each replication on twelve parameters *viz.*, plant height (cm), inter-nodal length (cm), days to 50 % flowering, days to 80 % maturity, stem girth (mm), fruit length (cm), fruit width (mm), number of fruits per plant, average fruit weight (g), number of seeds per fruit, hundred seed weight (g) and total fruit yield per plant (g). Genetic diversity between groups was estimated by using D^2 statistics given by Mahalanobis (1936) following the procedure given by Rao (1952). The mean values were computed to calculate D^2 values between all possible pairs of genotypes. The grouping of genotypes was done using Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed that the genotypes varied significantly for all the characters under study. After compiling D^2 values for all the possible pairs, the 44 genotypes were grouped in to twelve clusters (Table 1). Number of genotypes per cluster ranged from two to eight. The cluster III was the largest with eight genotypes

* **Author for correspondence.**
[1]Indian Institute of Horticulture Research, Hessaraghatta, BENGALURU (KARNATAKA) INDIA