

Studies on genetic divergence on cucumber (*Cucumis sativum* L.)

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Evaluation of 41 diverse genotypes of cucumber was carried out in a randomized block design. Among the 41 genotypes studied, Mahalanobis D² analysis confined the presence of wide genetic diversity through the formation of seven clusters. The clustering pattern showed the lack of parallelism between geographic and genetic diversities. Among the clusters, intercrossing the genotypes in the cluster I, II, IV and V had high mean values for many characters studied is likely to result in an enlargement of spectrum of variability facilitating the selection for higher yield. The ranking D² values revealed that tender fruit yield per vine, tender fruit girth, tender fruit weight and number of tender fruit per vine contributed high genetic divergence. Hence, these characters could respond favourably for phenotypic selection.

Key words : Cucumber, Genetic diversity, Intra and inter cluster

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INTRODUCTION

Cucumber (*Cucumis sativus* L.) is an important vegetable and one of the most popular members of the *Cucurbitaceae* family (Lower and Edwards, 1986; Thoa, 1998). It is one of the oldest vegetable cultivated by man with historical records dating back 5,000 years (Wehner and Guner, 2004). The crop is the fourth most important vegetable after tomato, cabbage and onion in Asia (Tatlioglu, 1997), the second most important vegetable crop after tomato in Western Europe (Phu, 1997). Growers, buyers and processors all demand uniformity in plant type, fruit type, and maturity, so it is necessary that cultivars developed for sale to meet commercial standards. The scope of selection in the improvement of cucumber depends upon the genetic diversity available in the germplasm. Since, a considerable amount of variability exists in this crop, a germplasm collection is essential for any rational plant breeding programme. To formulate a sound and successful breeding programme, the importance of the study of genetic variability in the population and the pattern of correlation existing among the traits needs emphasis.

RESEARCH METHODOLOGY

The present experiment was conducted at the

Department of Horticulture, Agriculture College and Research Institute, Madurai, Tamil Nadu. A total of 41 cucumber genotypes were collected from different district of Tamil Nadu. The experiment was laid out in a Randomized Block Design with two replications. Fourteen biometric observations were recorded on five randomly selected plants in each genotype per replication for all the characters (vine length, number of primary branches per vine, days to first male flowering, days to first female flowering, node number of first male flower production, node number of first female flower production, number of male flowers per vine, number of female flowers per vine, sex ratio, number of tender fruits per vine, tender fruit length, tender fruit girth, tender fruit weight and tender fruit yield per vine.

The genetic diversity existing between different populations with respect to a set of correlated variables were measured using Mahalanobis's statistics. The data were computerized and the D² values were obtained. For determining the clusters, the criterion suggested by Tocher as quoted by Rao (1952) was followed. The average intra and inter-cluster distances were computed according to the method described by Singh and Chaudhary (1979). The relative contribution of each character to genetic divergence was determined according to the method described by Singh and Chaudhary (1979).