

Genetic divergence in soybean [*Glycine max* (L.) Merrill]

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Accepted : December, 2008

SUMMARY

Fifty genotypes of soybean collected from different geographic sources were analyzed by using Mahalanobis's D^2 statistics for eight characters. These genotypes were grouped into ten clusters. Canonical analysis indicated genetic divergence for number of pods/plant, days to 50% flowering, plant height and seed yield/plant. The clustering pattern revealed that genetic diversity was not necessarily associated with geographical diversity in this crop.

Key words : Genetic divergence, D^2 , Canonical analysis, Soybean.

The importance of genetic diversity in selecting genetically diverse parents either to exploit heterosis or to get desirable recombinants has been recognized by plant breeders. The genetic diversity, which is the basis of plant breeding, is produced due to inherent genetic differences in plant species and is of major interest to plant breeder. Soybean is a self-pollinated crop, the selection of parents for hybridization influences the success of breeding programme. The genetically diverse parents are likely to produce high heterotic effects and yield desirable segregants. The Mahalanobis's D^2 technique is found to be a powerful tool to measure genetic divergence among a set of genotypes. The present study gives genetic diversity in 50 soybean genotypes.

MATERIALS AND METHODS

Fifty genotypes of soybean having different geographical origins were obtained from NBPGR center of Akola. Out of 50, 41 genotypes were exotic and remaining 9 were Indian. The material was grown on the farm of Regional Research Center Amravati during *khari*-2005 in a randomized block design with two replications. The genotypes were sown with spacing 45 cm x 10 cm with single row plot. Data were recorded on five competitive plants of each genotype for days to 50 per cent flowering, plant height, number of pods/plant, number of primary branches, 100 seed weight, yield/plant, yield/plot and oil content.

The analysis of variance for the individual characters was carried out. Genetic divergence was estimated by using Mahalanobis's D^2 statistics as described by Rao (1952). On the basis of D^2 values obtained, the genotypes

were ground into different clusters by using Tocher's method described by Rao (1952).

RESULTS AND DISCUSSION

Result of D^2 analysis revealed the presence of wider genetic diversity for all the characters under study. Fifty genotypes were grouped into ten clusters. Cluster I comprised of highest number of genotype (21). The smallest clusters are IV, VI, VIII, IX and X with single genotype. Distribution of 50 genotypes in different clusters and their geographic origin are presented in Table 1. It is apparent that genotypes coming from different eco-geographic area were grouped into same clusters (I, II, III, V and VII) and genotypes belonging to same geographic origin were included in different clusters (II, III, VI), similar results were reported by Agrawal *et al.* (2001) and Murty and Arunchalam (1996).

Average intra and inter-cluster distance between the ten clusters are given in Table 2. The highest inter-cluster distance was recorded between cluster II and V (49.60) where as, the minimum average inter-cluster distance was recorded between clusters V and VI (16.24). Thus, hybrids between genotypes belonging to II and V clusters may result in higher heterotic effects and desirable segregants. Thus, as suggested by Bhatt (1970), the mean statistical distance (27.11) in the present study may be considered as guideline and crosses between parents belonging to clusters showing an inter-cluster distance of 27.11 or more may be attempted.

The cluster means (Table 3) for different characters showed that the genotype included in cluster V were early flowering (34.30 days). The maximum mean value for plant height was observed in cluster IX (89.35cm.). Cluster VII showed the highest mean for number of pods/plant (94.30). The varieties included in cluster VII were characterized by highest seed yield/plant (11.99gm.). Genotype EC-232051 (Cluster VII) exhibited high value

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