GENETIC DIVERGENCE IN SOYBEAN (GLYCINE MAX (L.) MERR.)

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ABSTRACT

The genetic distance for 55 genotypes of soybean collected from different soybean growing states of India was estimated using D2 statistics. The results showed adequate diversity for all the traits among all possible 1485 pairs of genotypes with values ranging from 4.69 to 2324.12. The results revealed that 55 genotypes were grouped into eleven clusters I to XI with substantial genetic divergence between them. Cluster I was very large comprising 20 genotypes, while cluster X and XI were solitary clusters. The maximum inter cluster distance was obtained between cluster IX and XI (D = 43.58) followed by those between cluster II and XI (D = 40.11) which may serve as potential parents for hybridization programme. The genetic divergence had little to do with the geographic factor as noticed by the random distribution of genotypes into various clusters. Oil content, protein content and 100-seed weight were the major attributes governing the genetic divergence.

Knowledge on genetic distance is successfully utilized in soybean by several workers (Sharma et al. 1986; Tawar et al. 1987; Mehentre et al. 1994; Jangale et al. 1999 and Jain and Ramgiry, 2000) in the selection of parents to be used in hybridization programme for obtaining desirable segregants. Mahalanobis D2 technique is a unique tool for identifying degree of divergence in a biological population at genetic level. Therefore, an effort has been made to assess the genetic diversity using ten traits recorded in 55 genotypes of soybean.

The experimental material comprising of 55 diverse genotypes of soybean that were collected from different states viz., Madhya Pradesh, Uttar Pradesh, Maharashtra, Gujarat, Punjab, and New Delhi of India. The field experiment was laid out in randomized block design with three replications at Instructional Farm, College of Agriculture, Gujarat Agricultural University, Junagadh during Kharif 2001. Each entry was planted in a single row of 3 m length with inter and intra row spacing of 45 cm and 15 cm, respectively. The recommended agronomic practices and plant protection measures were followed for the successful raising of the crop. Five random plants were selected from each plot for recording the observations on seed yield/plant and its component traits viz., days to 50 % flowering, days to maturity, plant height, number of clusters/plant, number of pods/plant, 100-seeds weight, oil content, protein content. The data were subjected to the statistical analysis as suggested by Mahalanobis (1936). The criteria used by Torcher as described by Rao (1952) were followed for making group constellations.

The Mahalanobis D2 statistics showed adequate diversity between genotypes with values ranging from 4.69 to 2324.12. Based on D2 statistics, 55 genotypes were grouped into eleven clusters. The distribution of 55 genotypes in different clusters is given in Table 1. The D2 values have been used for grouping of genotypes in the clusters in such a way that the genotypes in the cluster had smaller D2 values than between clusters. Cluster I was very large and comprised of 20 genotypes, out of which 11 genotypes from Pantnagar, 4 from Jabalpur, 2 from New Delhi and one each from Pune, Parbhani and Vadodara. Cluster II included 8 genotypes from different parts of India, such as Pantnagar (3), Jabalpur (2), Punjab (2) and New Delhi (1). While cluster IV had 6 genotypes, cluster III and V had 5 genotypes each, cluster VI had 3 genotypes, cluster VII, VIII and IX had 2 genotypes each.
TABLE 1. Composition of clusters based on $D^2$ values in soybean

<table>
<thead>
<tr>
<th>Cluster No</th>
<th>No. of genotypes</th>
<th>Genotypes included in cluster</th>
<th>source</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>08</td>
<td>PK-719, PK-78, PK-942, JS-81-1625, JS(HS)-8612, Paredu-34, PB-1, DS-393A</td>
<td>Pantnagar, Jabalpur, Punjab, New Delhi</td>
</tr>
<tr>
<td>II</td>
<td>05</td>
<td>PK-960, PK-1031, JS-87-7, JS-87-28, J-482</td>
<td>Pantnagar, Jabalpur, Junagadh</td>
</tr>
<tr>
<td>IV</td>
<td>06</td>
<td>J-184, J-800, MACS-92, MACS-124, JS-79-411, KHSB-6</td>
<td>Junagadh, Pune, Jabalpur, Kanpur</td>
</tr>
<tr>
<td>V</td>
<td>05</td>
<td>MACS-57, MACS-66B, MACS-130, JS-81-716, KDS-5</td>
<td>Pune, Jabalpur, Kanpur</td>
</tr>
<tr>
<td>VI</td>
<td>03</td>
<td>BK-3, BK-10, B-16</td>
<td>Vadodara, Varanasi</td>
</tr>
<tr>
<td>VII</td>
<td>02</td>
<td>J-2750, FK-302, J-751, FK-824</td>
<td>Junagadh, Pantnagar, Junagadh, Pantnagar</td>
</tr>
<tr>
<td>VIII</td>
<td>02</td>
<td>MACS-267, PK-1046</td>
<td>Pune, Pantnagar</td>
</tr>
<tr>
<td>IX</td>
<td>01</td>
<td>JS-79-341</td>
<td>Jabalpur</td>
</tr>
<tr>
<td>X</td>
<td>01</td>
<td>MACS-308</td>
<td>Pune</td>
</tr>
</tbody>
</table>

and cluster X and XI comprised of single genotype only. The genotypes belonging to same state or origin were grouped into different clusters and the genotypes belonging to different origin were grouped into same cluster. So, the grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical distribution of the genotypes. Murty and Arunachalam (1966) stated that genetic drift and selection in different environments could cause greater genetic diversity than geographic distance. Further, the free exchange of seed materials among the different regions consequently causes character constellations because of human interference and material may lose its individuality. Kumar and Nadarajan (1994), Mehetre et al. (1994 and 1997), Dobhal (1995), Yadav (1999) and Das et al. (2000) also reported that genetic diversity was independent of geographic regions.

The average intra and inter cluster distance ($D$) between two populations varied from 0.00 to 16.58 and 12.94 to 43.58,
respectively. The maximum inter cluster distance appeared between clusters IX and XI (D = 43.58) followed by clusters II and XI (D = 40.11) and clusters VII and IX (D = 38.21). The last two clusters had only single genotype indicating solitary clusters so their intra cluster distances were zero. It has been well established that more genetically diverse parents used in hybridization programme, the greater will be the chance of obtaining high heterotic hybrids and broad spectrum of genetic variability (Arunachalam, 1981). Therefore, in the present study, based upon large cluster distances, it is advisable to attempt crossing of the genotypes from cluster IX and II with the genotypes of clusters XI which may lead to broad spectrum of favourable genetic variability for seed yield improvement in soybean.

The cluster means for ten characters are presented with their percent contribution towards the total genetic divergence. The results revealed that oil content contributed maximum (47.54) as a first ranker towards the total divergence with its average ranging from 14.57 % for cluster XI to 20.69 % for cluster II. The next major contribution came from protein content with 19.39 % and 100-seed weight with 16.90 % contribution towards divergence. The protein content ranged from 34.14 % (cluster III) to 44.82 % (cluster VII), while 100-seed weight ranged from 9.0 g (cluster X) to 14.43 g (cluster VII). On the other hand, rest of the traits had lower contribution (below 5 %) towards the total genetic divergence. A considerable diversity of 83.83 % was observed due to these three characters. Hence, selection for divergent parents based on these characters would be useful for heterosis breeding in soybean. Chikhale et al. (1992) and Kumar and Nadarajan (1994) also reported higher genetic diversity due to 100-seed weight.

The cluster X got desirable rating in respect of seed yield/plant, days to 50 % flowering, plant height, number of clusters/plant, while cluster XI had desirable rating for days to maturity and number of branches/plant. Cluster VI had also desirable value for days to maturity. Likewise, cluster VII had desirable rating for 100-seed weight and protein content, cluster II for oil content and cluster IV for number of pods/plant. The genotypes with high mean values of character in any cluster as well as high D² values between clusters can be used either for direct adoption or for hybridization programme in order to breed for better genotypes of soybean.

REFERENCES