Exploiting Genotypic Variability in Relation to Genetic Divergence Among Advanced Lines of Soybean [*Glycine max* (L) Merrill]

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Sixty eight advanced soybean lines derived from 19 crosses, involving diverse parents, along with two varieties, were evaluated for seed yield and its components to assess genotypic variability in relation to genetic divergence. Analysis of variance revealed significant differences among the lines for all the traits studied. On the basis of D^2 analysis, the lines were grouped into 14 clusters. The patterns of distribution of genotypes in different clusters indicated that genetic divergence was not related to parentage. Maximum intercluster distance was obtained between clusters II and VIII followed by clusters VIII and IX. These clusters included the genotypes Himso 1610, Himso 1629, Himso 1630, Himso 1631, Himso 1606, Himso 1655, Himso 1636, Himso 1650, Himso 1609 and Himso 1669, derived from the crosses Himso 330 x Punjab-1, Himso 1520 x Himso 330, Punjab -1 x DS 74-22, P7-1-1 x Punjab-1, PK 1053 x Punjab-1 and Himso 330 x Hardee . These genotypes may be utilised in the future breeding programme.

Key words: Genetic divergence, Soybean, Advanced breeding lines

The success in genetic improvement of a crop depends on extent of genetic variability. It is evident that genetically diverse parents are likely to produce high heterotic effects and yield desirable segregates. Soybean is the world's most important oilseed crop in terms of total production and trade. A considerable amount of the existing genetic variability in this crop has been exhausted in developing improved varieties in the country. Since the development of a variety is based on the extent of variability for desired characters, the locked genetic variability in respect of linked genes can be released by hybridization and thus breaking gene linkages by crossing over (Fahr, 1978). Earlier studies have revealed the genetic diversity in soybean only of germplasm lines of different geographic origin. Whereas, information on genetic diversity among soybean lines generated though hybridization is meager, therefore, the present investigation was undertaken to unzip the genetic divergence among the advanced lines of soybean following Mahalanobis D^2 statistics which is a powerful tool to quantify the variability at genotypic level.

Materials and Methods

Sixty eight advanced lines of soybean derived through hybridisation from 19 different crosses, along with two commercial varieties, were grown in a randomized block design with two replications during *kharif,* 2004 at the experimental farm of the Department of Plant Breeding & Genetics, Chaudhary Sarwan Kumar (CSK) Himachal Pradesh Krishi Vishvavidyalaya, Palampur. Selection in the segregating generations was practiced on the basis of yield contributing traits and as a result more than one breeding line having different combination of traits from the same cross were isolated. Each line was sown in a single row plot of 2m length with row- to- row spacing of 30 cm and plant- to- plant spacing of 5 cm. Recommended package of practices were followed for raising the crop. Observations on different traits were recorded on five random competitive plants from each genotype in each replication. To assess the genetic divergence among the lines, Mahalanobis D^2 statistics (Singh and Chaudhary, 1977) was used and grouping of lines was done following Tocher's method (Rao, 1952).

Results and Discussion

Analysis of variance indicated significant variability between the lines for all the traits under study, thereby revealing that sufficient genetic variability has been generated through hybridisation in the present material. Based on the magnitude of D^2 values, sixty eight lines were grouped into 14 clusters, the lines present in the same cluster have smaller D^2 values among themselves than those belonging to different clusters. The parentage of different advance lines have been given in Table 1. As many as 26 lines were grouped in cluster I; 12 in cluster III; 6 each in cluster II and IV; 4 in cluster V, 3 each in cluster VI and X, 2 each in cluster VII, VIII and IX and one each in cluster XI, XII, XIII and XIV (Table 2). The pattern of distribution of genotypes in different clusters indicated that genetic divergence was not related to parentage. Many advanced

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Table 1. Parentage of different soybean lines

Parentage	Number of lines	Code of lines
DS83-20 x Punjab-I	2	Himso 1607, Himso 1608
Himso 330 x Hardee	2	Himso 1609, Himso 1668
Himso 330 x Punjab-I	1	Himso 1610
Himso 333 x NRC2	17	Himso 1611, Himso 1612, Himso 1613, Himso 1614, Himso 1615, Himso 1616, Himso 1617, Himso 1618, Himso 1619, Himso 1620, Himso 1621, Himso 1622, Himso 1623, Himso 1624, Himso 1625, Himso 1626, Himso 1627
Himso 558-A x Bragg	1	Himso 1628
Himso 1520 x Himso 330	4	Himso 1629, Himso 1630, Himso 1631 Himso 1606
Himso 1520 x Punjab-1	3	Himso 1632, Himso 1633, Himso 1634
NRC2 x Hardee	1	Himso 1635
P7-1-1 x Punjab-1	5	Himso 1636, Himso 1637, Himso 1638, Himso 1639 Himso 1640
PK 1053 x Himso 107	7	Himso 1641, Himso 1642, Himso 1643 Himso 1644, Himso 1645, Himso 1646 Himso 1647
PK 1053 x Punjab-1	4	Himso 1648, Himso 1649, Himso 1650 Himso 1651
Punjab-1 x VLS2	3	Himso 1652, Himso 1653, Himso 1654
Punjab-1 x DS 74-22	1	Himso 1655
VLS 2x Lee	2	Himso 1656 Himso 1657
SL 284 x Bragg	6	Himso 1658, Himso 1659, Himso 1660, Himso 1661, Himso 1662 Himso 1663
SL 284 x Punjab-1	3	Himso 1664, Himso 1665 Himso 1666
Palam Soya x PK 416	1	Himso 1667
Hardee x JS 78-53	2	Himso 1669 Himso 1670
Hardee x Punjab-1	3	Himso 1671, Himso 1672 Himso 1673
Palam Soya, Bragg (Commercial varieties)	2	69, 70

Table2. Clustering of 68 soybean lines based on D^2 statistics

Cluster	Number of lines	Code of lines
I	26	Himso 1611, Himso 1616, Himso 1618 Himso 1624, Himso 1626, Himso 1627 Himso 1635 Himso 1637 Himso 1639 Himso 1641 Himso 1642 Himso 1643 Himso 1644 Himso 1645 Himso 1646 Himso 1647 Himso 1649 Himso 1651 Himso 1652 Himso 1653 Himso 1654 Himso 1658 Himso 1659 Himso 1666 Himso 1670 Himso 1672
II	6	Himso 1610, Himso 1629, Himso 1630, Himso 1631, Himso 1606, Himso 1655
III	12	Himso 1612, Himso 1619, Himso 1620, Himso 1621, Himso 1622 Himso 1628 Himso 1638 Himso 1660Himso 1661 Himso 1662Himso 1664 Himso 1669
IV	6	Himso 1607, Himso 1608, Himso 1663, Himso 1668, Palam Soya, Bragg
V	4	Himso1613,Himso 1617, Himso 1640, Himso 1665
VI	3	Himso 1632, Himso 1634, Himso 1671
VII	2	Himso 1623, Himso 1625
VIII	2	Himso 1636, Himso 1650
IX	2	Himso 1609, Himso 1669
X	3	Himso 1614, Himso 1615, Himso 1657
XI	1	Himso 1633
XII	1	Himso 1648
XIII	1	Himso 1656
XIV	1	Himso 1673

lines derived from the same cross were grouped into different clusters and *vice-versa*. Such type of clustering may have been resulted from recombination coupled with selection for different combinations of desirable traits in segregating generations.

Intra-cluster distances ranged from zero (in monogenotypic clusters) to 37.21 (cluster among genotypes of cluster X), indicating that the lines present in this cluster have maximum genetic dissimilarity among themselves. The intra-cluster distances of clusters III, IV and V (28.68, 29.58 and 29.19, respectively) indicated close relationship and almost parallel genetic diversity among the genotypes included in the respective clusters. Similarly, intra-cluster distances of clusters I and II (31.56 and 32.95), clusters VIII and IX (26.20 and 27.58), clusters VI and X (36.90 and 37.21) exhibited narrow genetic diversity among the genotypes in the respective clusters.

Maximum inter-cluster distance (Table 3) was observed between clusters II and VIII (656.61), followed by clusters VIII and IX (587.99), indicating thereby that the progenies derived from crossing the lines of these clusters, will be expected to throw out a broad

Table3. Intra-cluster (diagonal and bold) and inter-cluster distances among fourteen clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	**31.6**													
II	253.7	**32.9**												
III	55.5	298.0	**28.7**											
IV	80.2	128.8	74.1	**29.6**										
V	78.8	394.8	129.7	205.5	**29.2**									
VI	140.7	249.7	244.6	228.4	95.9	**36.9**								
VII	66.9	437.5	61.6	141.9	117.4	294.4	**12.8**							
VIII	209.0	656.6	319.8	445.5	71.9	151.8	261.5	**26.2**						
IX	352.0	121.5	499.7	297.2	422.8	212.7	575.9	587.9	**27.6**					
X	58.9	393.8	69.2	161.3	56.0	161.2	92.6	159.1	526.9	**37.2**				
XI	80.7	103.7	110.6	68.5	131.4	84.3	206.2	305.1	208.6	123.8	**0.0**			
XII	97.4	358.4	58.1	132.5	136.2	226.0	127.8	307.1	567.9	53.1	104.0	**0.0**		
XIII	158.1	427.5	221.6	302.2	69.6	84.6	276.2	89.2	469.4	108.1	148.6	193.7	**0.0**	
XIV	94.5	315.4	207.5	216.1	50.6	50.5	187.6	94.2	245.3	129.7	125.8	228.7	117.9	**0.0**

spectrum of genetic variability and thus providing greater chances for isolating high- yielding segregates in the succeeding generations. New and hitherto unknown gene combinations could be produced by crossing genotypes from highly diverse groups. Hybridization between genetically diverse groups to generate promising breeding material has been suggested frequently (Raut *et al.*, 1984). The minimum inter- cluster distance was observed between clusters XIV and VI (50.48), followed by clusters XIV and V (50.62), indicating the minimum diversity between the genotypes included in these clusters. Such results suggest to avoid selection of parents from these clusters (genetically closer) which may narrow down the genetic base and result in inbreeding depression.

Cluster means showed that maximum and minimum values for different characters were; 72.50 days (cluster XIII) and 60.50 days (cluster VII) for days to flowering; 128 days (cluster IX) and 119.17 days (cluster X) for days to maturity; 18.15g (cluster II) and 8.88 g (cluster VIII) for 100-seed weight, 45.50 (cluster XII) and 23.83 (cluster II) for pods per plants, 235g (cluster IX) and 155 g (cluster VIII) for seed yield (Table 4). As such, it was observed that the 100-seed weight was maximum in cluster II but the number of pods per plant the minimum in cluster II, indicating thereby inverse relationship between these traits. So, lower the pod number, bolder the seed. Cluster VIII had the minimum 100-seed weight (8.88g) and simultaneously the lowest yield (155g)

Table 4. Cluster mean values for different traits among the lines

Cluster/Trait	Plant height	Days to flowering	Days to maturity	Pods per plant	100 seed weight	Seed yield
I	65.8	64.0	121.0	29.5	12.0	225.5
II	73.0	64.0	122.0	23.8	18.2	226.7
III	64.7	62.0	118.0	30.5	12.1	221.3
IV	66.0	61.0	120.0	27.4	14.5	233.3
V	70.4	68.0	122.0	32.1	10.8	208.8
VI	67.8	70.0	124.0	31.5	13.8	181.7
VII	66.3	61.0	120.0	29.8	9.6	165.0
VIII	63.3	71.0	124.0	31.0	8.9	155.0
IX	81.3	66.0	128.0	25.0	17.6	235.0
X	88.3	66.0	119.0	35.8	11.2	221.7
XI	75.0	67.0	121.0	33.0	15.2	190.0
XII	65.0	65.0	118.0	45.5	12.8	190.0
XIII	64.0	73.0	120.0	24.5	10.9	150.0
XIV	73.5	68.0	126.0	34.0	11.9	240.0

among all clusters which indicated direct relationship between 100-seed weight and seed yield. Genetic divergence studies in soybean has been carried out by earlier workers only on germplasm lines of soybean of different geographic origin (Raut *et al.*, 1984; Ghatge and Kadu, 1993; Kumar and Nagarajan, 1994; Mehetre *et al.*, 1994), suggesting that majority of economically important characters including seed yield and its components are amenable for genetic improvisation through intense breeding, among genetically diverse parents.

In the present study, maximum intercluster distance was observed between clusters II and VIII followed by clusters VIII and IX. These cluster involved the genotypes Himso 1610, Himso 1629, Himso 1630, Himso 1631, Himso 1606, Himso 1655, Himso 1636, Himso 1650, Himso 1609 and Himso 1669, derived from the crosses Himso 330 x Punjab-1, Himso 1520 x Himso 330, Punjab -1 x DS 74-22, P7-1-1 x Punjab-1, PK 1053 x Punjab-1 and Himso 330 x Hardee. These genotypes may be utilised in the future breeding programme as hybridisation between divergent genotypes is likely to produce wide variability and transgressive segregants.

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