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# Assessment of genetic diversity in soybean [*Glycine max* (L.) Merrill] germplasm under North-Western Himalayas

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**Abstract**
In order to assess the genetic diversity, an experiment was conducted with 31 soybean genotypes grown in randomized block design with three replications. The data were recorded on ten important quantitative traits. The genotypes could be grouped into 10 clusters which indicated the presence of sufficient diversity among the tested genotypes. The cluster II was the largest one with thirteen genotypes. Highest inter-cluster distance was observed between clusters III and IX followed by between clusters II and III and clusters V and IX. Cluster IV showed the highest number of pods per plant which suggested that the genotype falling in this cluster can be selected directly and used in hybridization programme. Days to 75 per cent maturity contributed maximum to the genetic divergence followed by days to 50 per cent flowering and 100-seed weight. The genotypes falling under clusters V and VII can be used as a source population for early flowering and better yield based upon cluster means.

**Keywords:** genetic diversity, $D^2$ statistic, inter-cluster distance, cluster means, soybean

## Introduction
Soybean [*Glycine max* (L.) Merrill], 2n= 40, is one of the versatile legume crop because of its extraordinary qualities and multiple uses. Soybean is a self-pollinated crop and belongs to the family *Fabaceae* under sub-family *Papilionaceae*. It has been originated in North Eastern China (Vavilov, 1951 and Leppik, 1971) [15, 8]. Soybean is an eminent source of nutritional vegetable oil and protein both which is used for human consumption, industrial purposes and for livestock feed. On an average, cultivated soybean contains about 40% high quality protein which supplies sufficient amount of various kinds of amino acids and 20% excellent oil comprising 85% poly unsaturated fatty acid with two essential fatty acids (linoleic and linolenic acid) which are not synthesized by the human body (Antalina, 2000; Balasubramaniyan and Palaniappan, 2003) [2, 3].
Therefore, soybean could be regarded as an ideal food crop for the people of poor and developing countries as it contains high quality protein and reasonable quantity of oil as a source of energy. In India, soybean has emerged as the major oilseed crop in a short span of time starting with a meager area of 0.03 million hectares in 1970. The crop has expanded with an unprecedented pace and touched the figure of 11.40 million hectares area with an estimated production of 11.40 million hectares with a productivity of 10.1 q/ha (Anonymous, 2017) [1].
The importance of genetic diversity in the improvement of both self and cross-pollinated crops is very well known (Murty and Anand, 1966; Gaur *et al*. 1978) [11, 5]. Estimates of genetic divergence provide the extent of diversity existed within the available germplasm and moreover, evaluation of genetic diversity is important to know the sources of genes for a particular trait. Selection of genetically diverse parents is a pre-requisite for any crop improvement programs as it improve the chances of selecting better segregants for various characters. Precise information on the nature and degree of genetic diversity helps the plant breeder to identify the diverse parents for future hybridization programme and to obtain desired recombinants with higher degree of heterosis. Keeping this in view, the present investigation was carried out to assess the nature and magnitude of genetic diversity in soybean germplasm which would help in selection of efficient genotypes with desirable traits for utilization in hybridization programme.

## Materials and Methods
The present investigation was carried out at the experimental farm area of Department of Crop Improvement, CSKHPKV, Palampur (H.P.) during *kharif* 2015. Out of 303 germplasm lines, 31 lines including four checks *viz*., Hara Soya, Him Soya, Palam Soya and Palam Early Soya-1 were evaluated in randomized block design with three replication.

Each genotype was raised in a plot consisting of 3 rows each of 1.5m length with spacings of 45cm between rows and 15cm between the plants. Five plants per genotype per replication were randomly selected for recording the observations at appropriate stages of crop growth on characters such as plant height, number of branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant. The observations on days to 50 per cent flowering and 75 per cent maturity were recorded on plot basis. The mean data over randomly selected plants from all the replications were subjected to the statistical analysis. Wilks criteria were used to test the significance of differences in mean values of correlated characters as per Rao, 1952. Genetic diversity was studied using $D^2$ statistic as per Mahalanobis, 1936. Intra- and inter-cluster distances and cluster means for different characters were also computed.

**Results and Discussion**

Genetic divergence analysis is used to assess the nature of genetic diversity which helps in identification of genetically diverse genotypes for hybridization programme and to obtain desired recombinants or transgressive segregants. $D^2$ statistic is a technique used in genetic divergence analysis which helps in categorizing genotypes into different groups based on the difference in the character expression. The more divergent the two genotypes are, more will be the probability of improving through selection and hybridization. A simultaneous test of significance based on Wilk's criterion and $D^2$ values obtained for each pair of populations were observed to be significant indicating the presence of sufficient genetic diversity among the genotypes studied. The $D^2$ statistic resulted in classifying the 31 soybean genotypes (including 4 checks) into ten clusters which indicated the presence of adequate genetic diversity among the tested genotypes. Cluster II formed the largest group with 13 genotypes followed by cluster I and cluster III with 4 genotypes each while clusters V and X had 3 and 2 genotypes each, respectively. Clusters IV, VI, VII, VIII and IX contained one genotype each (Fig1; Table 1).

In general, genetic diversity is associated with geographical diversity, but the former is not necessarily directly related to geographical distribution. In the present study, the genotypes within the same clusters were originated from different geographical regions of the country which indicated that the geographical distribution and genetic divergence did not follow the parallelism which might be due to the continuous exchange of soybean genetic material among different geographical regions. The results are in confirmatory with the earlier findings of Gohil *et al.* (2007) [6], Patil *et al.* (2011) [12], Shadakshari *et al.* (2011) [14] and Meena *et al.* (2017) [10] where the genetic divergence was independent of geographic regions.

The highest average intra-cluster distance $\sqrt{D^2}$ was observed in cluster III (2.43) followed by cluster X (2.35) and cluster II (2.33). Highest inter-cluster distance was observed between clusters III and IX (4.10) followed by between clusters II and III (4.02) and clusters V and IX (3.85). However, the distance between clusters IV and VI was minimum (2.12) indicating that the genotypes belonging to these clusters were comparatively less diverse (Table 2). Greater parental distance implies a large number of contrasting alleles at the desired loci to the extent that these loci recombine in the $F_2$ and $F_3$ generations following a cross of distantly related parents resulting in greater opportunities for the effective selection for yield factors. Thus, crosses involving genotypes of the clusters II, III, V and IX may produce higher amount of heterotic expression in the hybrids ($F_1$'s) and release wide range of variability in subsequent generations. Jency and Kalaimagal (2015) [7] observed highest intra-cluster distance (26.85) in cluster VI followed by cluster III (23.13), V (17.55) and IV (5.23) and highest inter-cluster distance was observed between clusters IV and V followed by cluster II and V suggesting more variability in genetic makeup of the genotypes included in these clusters. Patil *et al.* (2011) [12] reported maximum inter-cluster distance between clusters II and IV while Chavan *et al.* (2014) [4] reported maximum inter-cluster distance between the clusters VIII and X in soybean suggesting that the genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. The maximum contribution towards the genetic divergence was exhibited by days to 75 per cent maturity (36.99%) followed by days to 50 per cent flowering (29.03%) and 100-seed weight (13.33%) while the remaining characters contributes <10 per cent to the overall genetic divergence present in the soybean germplasm lines studied. Earlier, Jency and Kalaimagal (2015) [7] observed maximum contribution by number of seeds per pod followed by 100-seed weight and days to 50 per cent flowering towards genetic divergence in soybean.

The cluster means of soybean genotypes falling under different clusters are presented in Table 3. Among ten clusters, cluster IV showed the highest number of pods per plant and cluster V had the dwarf soybean genotypes which suggested that the genotypes falling in these clusters can be selected directly on the basis of these traits and used in hybridization programme. However, clusters VIII, IX and X showed the desirable cluster means for 100-seed weight and harvest index, less days to 75 per cent maturity and biological yield and number of branches per plant and number of seed per pod, respectively. Besides, these clusters also showed moderate mean values for other important characters.

Genotype falling in cluster V (Himso-14-126A, PS-1347 and Himso-14-145) and cluster VII (Himso-14-19) showed the desirable mean values for days to 50 per cent flowering (early) and seed yield per plant, respectively. The genotypes falling under these two clusters can be used as a source material for increasing yield coupled with early flowering.

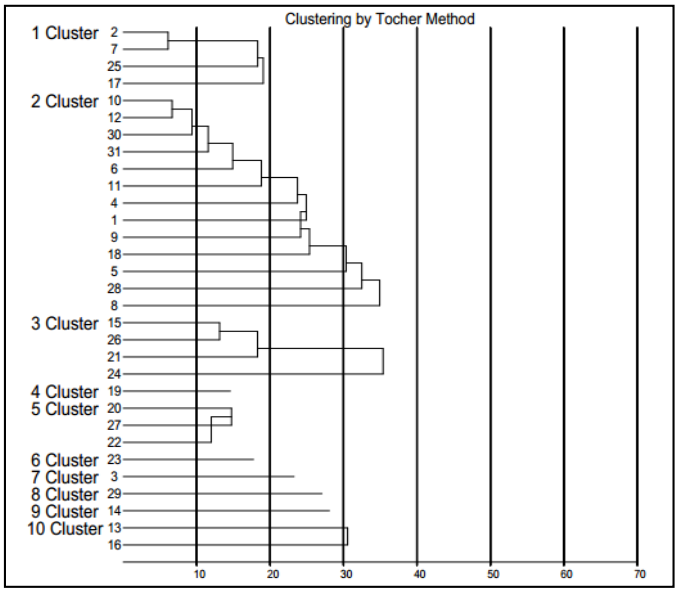


**Fig 1:** Phenogram showing diversity of soybean genotypes generated using Mahalanobis D²-cluster analysis

**Table 1:** Distribution of soybean genotypes among different clusters on the basis of Mahalanobis $D^2$ statistic

| Clusters | Number of genotypes | Genotypes |
|---|---|---|
| I | 4 | Himso-14-14A, Himso-14-39, Himso-14-158, Himso-14-115 |
| II | 13 | Himso-14-61A, Himso-14-86, Palam early soya 1, Him Soya, Himso-14-34, Himso-14-68, Himso-14-30, Himso-14-1, Himso-14-61, Himso-14-121, Himso-14-33, Hara Soya, Himso-14-52, Himso-14-52 |
| III | 4 | Himso-14-106, MAUS 162, Himso-14-142, Himso-14-157 |
| IV | 1 | Himso-14-132 |
| V | 3 | Himso-14-126A, PS-1347, Himso-14-145 |
| VI | 1 | Himso-14-146 |
| VII | 1 | Himso-14-19 |
| VIII | 1 | Palam soya |
| IX | 1 | Himso-14-100 |
| X | 2 | Himso-14-87, Himso-14-112 |

**Table 2:** Average intra- and inter-cluster values of $D^2$ and $\sqrt{d^2}$ among different clusters

| Cluster | I | II | III | IV | V | VI | VII | VII | IX | X |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 4.78 | 8.18 | 10.13 | 6.49 | 8.85 | 6.61 | 6.58 | 6.68 | 9.96 | 8.41 |
| | (2.19) | (2.86) | (3.18) | (2.55) | (2.97) | (2.57) | (2.58) | (3.16) | (2.90) | (2.19) |
| II | | 5.41 | 16.15 | 7.67 | 11.39 | 6.92 | 7.46 | 8.52 | 7.95 | 13.95 |
| | | (2.33) | (4.02) | (2.77) | (3.37) | (2.63) | (2.73) | (2.92) | (2.82) | (3.73) |
| III | | | 5.91 | 13.02 | 11.21 | 13.21 | 12.34 | 12.83 | 16.78 | 7.76 |
| | | | (2.43) | (3.61) | (3.35) | (3.63) | (3.51) | (3.58) | (4.10) | (2.79) |
| IV | | | | 0.00 | 7.81 | 4.50 | 6.37 | 9.69 | 11.33 | 12.06 |
| | | | | (0.00) | (2.79) | (2.12) | (2.52) | (3.11) | (3.37) | (3.47) |
| V | | | | | 4.11 | 7.74 | 8.76 | 12.52 | 14.80 | 13.25 |
| | | | | | (2.03) | (2.78) | (2.96) | (3.54) | (3.85) | (3.64) |
| VI | | | | | | 0.00 | 5.06 | 8.84 | 9.84 | 12.17 |
| | | | | | | (0.00) | (2.25) | (2.97) | (3.14) | (3.49) |
| VII | | | | | | | 0.00 | 7.31 | 9.70 | 11.80 |
| | | | | | | | (0.00) | (2.70) | (3.11) | (3.44) |
| VIII | | | | | | | | 0.00 | 7.64 | 10.37 |
| | | | | | | | | (0.00) | (2.76) | (3.22) |
| IX | | | | | | | | | 0.00 | 13.11 |
| | | | | | | | | | (0.00) | (3.62) |
| X | | | | | | | | | | 5.53 |
| | | | | | | | | | | (2.35) |

Values in bold figures are intra-cluster distances; Values in parentheses are $\sqrt{D^2}$ values

**Table 3:** Cluster means for different traits in soybean

| Clusters Traits | I | II | III | IV | V | VI | VII | VIII | IX | X | Mean | Maximum | Minimum |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | 56.92 | 51.13 | 63.25 | 50.00 | 50.00* | 51.00 | 53.00 | 57.00 | 54.33 | 65.33** | 55.196 | 65.33 | 50 |
| Days to 75% maturity | 116.00 | 111.49 | 125.92** | 117.33 | 125.78 | 116.67 | 118.33 | 110.33 | 108.33* | 117.67 | 116.785 | 125.92 | 108.33 |
| Plant height (cm) | 77.70 | 61.79 | 73.95 | 90.27** | 60.08* | 72.19 | 61.44 | 67.74 | 60.59 | 84.01 | 70.976 | 90.27 | 60.08 |
| No. of branches / plant | 5.29 | 4.41* | 6.45 | 6.12 | 5.29 | 6.06 | 5.16 | 4.71 | 5.93 | 6.64** | 5.606 | 6.64 | 4.41 |
| No. of pods / plant | 53.65 | 48.87 | 55.33 | 78.36** | 42.48* | 44.93 | 58.42 | 47.98 | 50.15 | 61.02 | 54.119 | 78.36 | 42.48 |
| No. of seeds / pod | 2.20 | 2.26 | 2.37 | 2.21 | 2.28 | 2.23 | 2.33 | 2.20* | 2.21 | 2.39** | 2.268 | 2.39 | 2.2 |
| 100 - seed weight (g) | 12.96 | 13.90 | 12.26 | 11.11 | 12.92 | 10.05* | 13.68 | 14.08** | 12.86 | 10.60 | 12.442 | 14.08 | 10.05 |
| Biological yield / plant(g) | 30.83 | 40.12 | 34.83 | 38.12 | 33.63 | 39.69 | 43.31 | 24.34* | 70.74** | 44.60 | 40.021 | 70.74 | 24.34 |
| Harvest Index (%) | 38.08 | 30.62 | 38.29 | 32.96 | 34.69 | 38.82 | 43.71 | 62.79** | 21.68* | 26.65 | 36.829 | 62.79 | 21.68 |
| Seed yield / plant((g)) | 11.63 | 12.09 | 12.97 | 12.44 | 11.51* | 15.33 | 18.65** | 15.07 | 15.26 | 11.65 | 13.66 | 18.65 | 11.51 |

## Conclusion

It can be concluded from present study that considerable genetic variability was found in the present material. All genotypes under study were grouped into 10 clusters which indicated the presence of sufficient diversity among the germplasm lines. The clustering revealed that there was no correlation between geographical diversity and genetic divergence. The genetic divergence had little to do with the geographic factor as noticed by the random distribution of genotypes into various clusters. The clusters II, III, V and IX exhibited large inter-cluster distances thus, indicating more chances of developing good segregants by crossing the genotypes of the these clusters. Himso-14-132 falling under Cluster IV showed the higher cluster means for plant height and number of pods per plant which suggested that it can be selected directly on the basis of these traits and used in hybridization programme. Three genotypes such as Himso-14-126A, PS-1347 and Himso-14-145 of cluster V and Himso-14-19 of cluster VII exhibited the genes for higher seed yield potential and early flowering. Therefore these genotypes can be used as source population for higher seed yield coupled with earliness.

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