# Assessment of Genetic Variability Based on Morphometric Characteristics in Soybean (*Glycine max* L. Merrill) Germplasm

KAVERI CHAWAN, P. RAVISHANKAR, S. RAMESH AND T. ONKARAPPA

Department of Genetics and Plant Breeding, College of Agriculture, UAS, GKVK, Bengaluru - 560 065
e-Mail : kaverichawan1@gmail.com

### AUTHORS CONTRIBUTION

KAVERI CHAWAN :
Conceptualization,
investigation and original
draft preparation;
P. RAVISHANKAR :
Conceptualization and draft
correction;
S. RAMESH :
Conceptualization, original
draft preparation and
analysis;
T. ONKARAPPA :
Supervision and editing

***Corresponding Author :***
KAVERI CHAWAN
Department of Genetics and
Plant Breeding,
College of Agriculturre,
UAS, GKVK, Bengaluru

### ABSTRACT

The present study is aimed at assessing the extent and pattern of genetic variability present among soybean germplasm accessions (2000) obtained from IISR (Indian Institute of Soybean Research), Indore, Madhya Pradesh. It was studied at University of Agricultural Sciences (UAS), Bangalore for 7 quantitative traits and 13 qualitative traits. The germplasm accessions along with three check entries were sown in augmented design in 21 compact blocks during 2021 summer season at the experimental plots of Zonal Agricultural Research Station (ZARS), UAS, GKVK, Bengaluru. Substantial variability among the accessions for quantitative traits and polymorphism for qualitative traits were documented. The germplasm accessions could be grouped into 10 clusters following K-means clustering approach. The variability parameters like mean, range of variation, GCV, PCV, heritability and genetic advance were estimated for all traits. The differences between GCV and PCV estimates were narrow for all traits indicating less contribution of environmental factors in traits expression. High estimates of heritability coupled with high genetic advance were observed in all traits. The traits with higher heritability and GA value may indicate their variability and high selective value. Some of the germplasm accessions were superior to the check KBS 23, JS 335 and DSB 21. The accessions contrasting for individual and multiple traits were identified. These results are discussed in relation to suitable strategies to be adopted for breeding soybean for improved productivity.

SOYBEAN (*Glycine max* L. Merril) is an annual self-pollinated diploid legume (subfamily Fabaceae), which is an important source of high quality protein and oil in the world. It contains about 42 per cent protein, 20 per cent oil and 33 per cent carbohydrate (Zhang *et al.,* 2001). Cultivated soybean has a genome size of 1.1 to 1.15 GB with chromosome pair of twenty (2n=40). Owing to its amino acids composition, the protein of soybean is called a complete protein. Among the various soybean growing countries in the world, USA stands first in both production and productivity with 96.62 m.t. and 3157 kg/ha respectively from 306.03 lakh ha of area. Whereas, India in the fifth position

produces 9.00 m.t. with productivity of 800 kg/ha from 112.5 lakh ha of area (USDA Foreign agricultural service, 2020). India's contribution to the world soybean area is 10 per cent, but the contribution to total world soybean grain is only 4 per cent indicating the poor level of productivity of the crop in India as compared to other courtiers (world average 2.2 t/ha). Hence it necessitates broadening the genetic base through enhanced use of diverse germplasm accessions.

Precise information on genetic variability and diverse sources of germpalsm for traits of economic importance is a prerequisite for enhanced use of

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germplasm for continued genetic improvement and to cater to the needs of changing consumer preferences. The remarkable progress made in plant genetic resource management in recent days has resulted in the collection of a huge set of plant germplasm that hinders the very purpose for which they exist (Odong *et al.,* 2013). Frankel and Brown (1984) proposed the concept of core collection that could be established from an existing collection for better management and utilization of plant genetic resources. Characterization of a core set is an efficient approach for exploring and capturing the genetic diversity of large populations, as it represents the maximum genetic diversity of the whole collection and become a powerful tool for evaluation and identification of trait-specific accessions in germplasm (Gireesh *et al.,* 2015).

Therefore, an investigation was carried out to assess the variability for morpho-metric traits among germplasm accessions at the University of Agricultural Sciences (UAS), Bangalore which in turn helps in understanding the limitations of the domesticated germplasm and potential use of its wild relatives in crop improvement.

## MATERIAL AND METHODS

The material for the study comprised of 2000 germplasm accessions obtained from IISR (Indian Institute of Soybean Research), Indore, Madhya Pradesh and three check entries (KBS 23, JS 335 and DSB 21). The 2000 germplasm accessions and three check entries were sown in an augmented design (Federer 1956) in 21 compact blocks during 2021 summer season in the experimental plots of Zonal Agricultural Research Station (ZARS), UAS, GKVK, Bengaluru (930 m above mean sea level; 12°C 58' north latitude and 77°C 35' east longitude). Each block consisted of 100 germplasm accessions and three checks (replicated twice). The seeds of each entry were dibbled in a single row of 1.5-meter length, using a row spacing of 45 X 10 cm. At the time of sowing, a basal dose of 25:50:25 Kg NPK ha$^{-1}$ was applied to the experimental plot. Recommended agronomic and plant protection practices were followed to raise a healthy crop.

Using five randomly tagged plants, data were recorded on 13 qualitative traits (hilum color, seed coat color, early plant vigour, hypocotyl color, flower color, leaf shape, leaflet color, plant pubescence, plant pubescence color, plant pubescence density, plant pubescence type, stem determination, pod color) visually. Data were also recorded on 7 quantitative traits *viz.* days to 50 per cent flowering, plant height (cm), number of secondary branches$^{-1}$, number of pods$^{-1}$, days to 80 per cent maturity, 100 seed weight (g), seed yield$^{-1}$ (g) based on counting/measurement using appropriate scale depending on the trait following the descriptors developed by IISR. Quantitative trait means of each of the 2003 accessions were adjusted for block effect. Block effect was estimated as difference between trait mean of check entries included in the i$^{th}$ block and trait mean of check entries of all the blocks (Federer, 1956). The number and per cent accessions belonging to each class were counted and computed.

## Statistical Analysis

Adjusted mean values of quantitative traits data recorded on five random plants were subjected to statistical analysis. Descriptive statistics such as range and variance and their standardized values standardized range (maximum-minimum/mean), coefficient of variation (standard deviation/mean) x 100 were estimated (Snedecor and Cochran, 1994) to quantify variability and compare across traits. The 2003 soybean accessions were grouped into 10 clusters following model-based 'K means' clustering (Mac Queen, 1967) approach. The significance of difference among the clusters for means and variances of 7 quantitative traits was examined using 't' and Levene's (Levene, 1960) tests, respectively.

## RESULTS AND DISCUSSION

An attempt was made to study the variability in the soybean germplasm accessions by using 20 morph metric characteristics and substantial variability was documented for both qualitative and quantitative traits.

TABLE 1
Variability for qualitative characteristics and their frequency in soybean germplasm

| Traits | Score | Class | Frequency | Percentage |
|---|---|---|---|---|
| Hypocotyl color | 1 | Green | 498 | 24.86 |
| | 2 | Purple | 1505 | 75.14 |
| Early plant vigour | 1 | Poor | 89 | 4.44 |
| | 2 | Good | 1608 | 80.28 |
| | 3 | Very good | 306 | 15.28 |
| Leaf shape | 1 | Broad | 500 | 24.96 |
| | 2 | Indeterminate | 1015 | 50.67 |
| | 3 | Narrow | 488 | 24.36 |
| Leaf color | 1 | White | 561 | 28.01 |
| | 2 | Light green | 959 | 47.88 |
| | 3 | Green | 254 | 12.68 |
| | 4 | Dark green | 229 | 11.43 |
| Plant pubescence | 0 | Absent | 51 | 2.55 |
| | 1 | Present | 1952 | 97.45 |
| Plant pubescence color | 0 | Absent | 51 | 2.55 |
| | 1 | Grey | 146 | 7.29 |
| | 2 | Light tawny | 502 | 25.06 |
| | 3 | Tawny | 1304 | 65.1 |
| Plant pubescence density | 0 | Absent | 51 | 2.55 |
| | 1 | Glaborus | 100 | 4.99 |
| | 3 | Sparse | 535 | 26.71 |
| | 5 | Semi-sparse | 380 | 18.97 |
| | 7 | Normal | 922 | 46.03 |
| | 9 | Dense | 15 | 0.75 |
| Plant pubescence  type | 0 | Absent | 51 | 2.55 |
| | 1 | Errect | 1109 | 55.37 |
| | 3 | Semi-appressed | 436 | 21.77 |
| | 5 | Appressed | 277 | 13.83 |
| | 7 | Curly | 113 | 5.64 |
| | 9 | Retrose tip | 17 | 0.85 |
| Stem determination | 1 | Determinate | 1205 | 60.16 |
| | 2 | Semi-determinate | 369 | 18.42 |
| | 3 | Indeterminate | 429 | 21.42 |
| Flower color | 1 | White | 393 | 19.62 |
| | 2 | Light purple | 233 | 11.63 |
| | 3 | Purple | 1067 | 53.27 |
| | 4 | Dark purple | 310 | 15.48 |

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| Traits | Score | Class | Frequency | Percentage |
|---|---|---|---|---|
| Pod color | 1 | Light brown | 625 | 31.2 |
|  | 2 | Brown | 600 | 29.96 |
|  | 3 | Dark brown | 778 | 38.84 |
|  | 4 | Black | 0 | 0 |
| Hilum color | 1 | Yellow | 34 | 1.7 |
|  | 2 | Buff | 66 | 3.3 |
|  | 3 | Brown | 626 | 31.25 |
|  | 4 | Green | 2 | 0.1 |
|  | 5 | Grey | 187 | 9.34 |
|  | 6 | Imperfect black | 153 | 7.64 |
|  | 7 | Black | 935 | 46.68 |
| Seed coat color | 1 | Yellowish white | 266 | 13.28 |
|  | 2 | Yellow | 1246 | 62.21 |
|  | 3 | Green | 126 | 6.29 |
|  | 4 | Buff | 3 | 0.15 |
|  | 5 | Reddish brown | 81 | 4.04 |
|  | 6 | Grey | 0 | 0 |
|  | 7 | Imperfect black | 69 | 3.44 |
|  | 8 | Black | 212 | 10.58 |

## Qualitative traits

Determinate type of accessions dominated the collection (60.16%) followed by indeterminate (21.42%) and semi-determinate (18.42%) types (Table 1). Although an indeterminate growth habit is attractive to develop high-yield soybean varieties with higher number of pods, lodging in indeterminate varieties remains a problem in India. As the determinate and semi-determinate varieties have shorter main stem length than the indeterminate varieties, this trait can be useful to improve varieties with high yield and low lodging risk hence determinate growth habit always had an advantage. Predominance of determinate types of accessions and lower frequency of semi determinate or indeterminate accessions in the USDA Soybean Germplasm Collection database at National Plant Germplasm System (NPGS) of 89 soybean germplasm accessions have been documented (Zhixi *et al.,* 2010).

Soybean is now being cultivated extensively for commercial purpose, determinate type cultivars are gaining popularity among the farmers. Determinate type cultivars have more compact growth habit, reduced branching, shorter internodes, reduced above ground biomass and accelerated and synchronized flowering and reduced period of pod production leading to more uniform pod maturity and stable harvest index. Further, determinate types do not require support system (in contrast to indeterminate types which require staking) enabling high density planting to harness complete productivity potential of cultivars. Hence, breeding for determinacy is one of the major objectives of soybean breeding to optimize allocation between vegetative and reproductive phases. Shannon *et al.,* (1971) and Weaver *et al.,* (1991) have reported a higher yield of determinate type soybean lines.

Purple flowers (53.27%) dominated the collection followed by white (19.62%), dark purple (15.48%) and light purple (11.63%) flowers (Table 1). Genotypes with purple hypocotyl (75.14%) were highest compared to green hypocotyl (24.86%).

Indeterminate leaf shape (50.67%) with light green (47.88%) leaves type of accessions dominated the collection followed by broad leaves (24.96%) and narrow leaves (24.36%) with white (28.01%), green (12.68%) and dark green (11.43%) leaves. Good plant vigour type of accessions dominated the collection (80.28%) followed by very good plant vigour (15.28%) and poor plant vigour (4.44%) types. High seedling vigour is considered a decisive factor for the success of most field crops, as these parameters contribute to uniform plant growth maturity, better competition with weeds and high productivity (Bewley *et al.,* 2013 and Schuch *et al.,* 2009).

Accessions bearing pubescent (97.45%) pods which of tawny (65.1%) and light tawny (25.06%) colored pubescence were higher compared to non-pubescent pods (2.5%) and grey colored pubescence (7.29%). Dark brown pod color type of accessions dominated the collection (38.84%) followed by light brown (31.2%) and brown (29.96%) types. Genotypes with yellow (62.21%), yellowish white (13.28%) colored seed coat were found to be prominent over black (10.58%), green (6.29%), reddish brown (4.04%), imperfect black (3.44%) and buff (0.15%) colored seed coat accessions. Further, seeds with black colored hilum (46.68%) were higher followed by brown (31.25%), imperfect black (7.64%), grey (9.34%), buff (3.3%) and yellow (1.7%) hilum colored genotypes. The dominance of yellow seeded genotypes in the collection may be due to higher directional selection for yellow seeded ones owing to their high yield potential and consumer preference (Akito Kaga *et al.,* 2012).

**Quantitative Traits**

Analysis of variance represents the variability among the germplasm accessions and it exhibited a highly significant mean sum of square values for all quantitative traits (Table 2). Mean squares due to check varieties were significant for all traits except for number of pods plant⁻¹, while those due to 'accessions vs. check varieties' were significant for all traits except for days to 80 per cent maturity. These results suggested significant differences among the accessions and they differ from the checks.

TABLE 2

Analysis of variance of Soybean germplasm accessions for quantitative traits

| Sources of variation | df | Mean sum of squares (MSS) | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | Days to 50% flowering | Plant height (cm) | Number of secondary branches plant⁻¹ | Number of pods plant⁻¹ | Days to 80% maturity | 100 seed weight (g) | Seed yield plant⁻¹ (g) |
| Blocks | 19 | 895.89 ** | 988.00 ** | 1.48 ** | 749.22 ** | 1277.91 ** | 49.00 ** | 14876.25 ** |
| (Accessions + Checks) | 2002 | 69.21 ** | 90.65 ** | 0.43 ** | 155.06 ** | 87.53 ** | 7.56 ** | 2397.24 ** |
| Accessions | 1999 | 76.97 ** | 93.33 ** | 0.43 ** | 160.04 ** | 98.11 ** | 7.87 ** | 2531.20 ** |
| Checks | 2 | 112.90 ** | 5707.96 ** | 7.45 ** | 17.05 | 939.15 ** | 142.19 ** | 5985.45 ** |
| Accessions *vs* Checks | 1 | 1280.87 ** | 1934.45 ** | 7.27 ** | 4437.68 ** | 157.12 | 41.14 ** | 9159.47 ** |
| Error | 38 | 12.44 | 10.2 | 0.13 | 7.95 | 46.65 | 0.41 | 38.38 |

*Significant at P= 0.05 level, **Significant at P= 0.01 level

**Descriptive Statistics of Quantitative Characters**

It indicated the components of genetic variability, heritability and genetic advance and it was computed using first and second-degree statistics. Presence of genetic variability *per se* is of less significance in crop breeding programmes. Knowledge on relative contribution of genetic and non-genetic sources on the quantitative trait variability is useful in formulating appropriate selection strategies to breed improved soybean cultivars. The estimates of standardized range provide clues about the occurrence of accessions with extreme expression which varied with the trait. However, standardized range *per se* does not reflect variability in the expression of all the accessions. The estimates of GCV and PCV which reflect average inter-accession differences are more useful statistics to understand variability among the germplasm accessions.

The accessions were highly variable for plant height (cm), number of pods plant⁻¹, 100 seed weight (g), seed yield plant⁻¹(g), hilum color, seed coat color, early plant vigour, hypocotyl color, flower color, leaf shape, leaf color, plant pubescence, plant pubescence color, plant pubescence density, plant pubescence type, stem determination, pod color traits as indicated by the estimates of PCV (>20%) (Table 3), the accessions were moderately variable (10.1% < PCV < 19.9%) for days to 50 per cent flowering and number of secondary branches plant⁻¹ traits. The accessions were least variable for days to 80 per cebt maturity (PCV=8.29%). Relatively narrow difference between PCV and GCV estimates for these traits has amply reflected in higher broad-sense heritability estimates. The differences between GCV and PCV estimates were narrow for all the traits indicating less contribution of environmental factors in character expression (Karnwal and Singh, 2009 and Aditya *et al.,* 2011). Thus selection based on the phenotypic performance of these characters would be an effective way to bring about considerable improvement of these characters (Akram *et al.,* 2016).

TABLE 3

Descriptive statistics for quantitative traits in Soybean germplasm

| Traits | Mean ± Std. Error | Range | | Standar-dized Range | Coefficient of variablility | | Broad-sense h² (%) | Expected genetic advance as % mean |
|---|---|---|---|---|---|---|---|---|
| | | Min | Max | | GCV% | PCV% | | |
| Days to 50% flowering | 58.37 ± 0.2 | 43.73 | 77.39 | 33.67 | 13.62 | 14.9 | 83.56 | 21.92 |
| Plant height (cm) | 46.81 ± 0.22 | 31.65 | 83.31 | 51.67 | 19.29 | 20.46 | 88.86 | 31.97 |
| Number of secondary branches plant⁻¹ | 4.94 ± 0.01 | 3.4 | 7 | 3.6 | 10.98 | 13.26 | 68.37 | 16.08 |
| Number of pods plant⁻¹ | 41.92 ± 0.28 | 22.38 | 93.44 | 71.07 | 29.13 | 29.9 | 94.94 | 49.94 |
| Days to 80% maturity | 118.81 ± 0.22 | 94.91 | 138.58 | 43.67 | 5.98 | 8.29 | 51.95 | 7.58 |
| 100 seed weight (g) | 13.28 ± 0.06 | 6.01 | 23.29 | 17.29 | 20.36 | 20.93 | 94.6 | 34.85 |
| Seed yield plant⁻¹ (g) | 110.02 ± 1.12 | 36.5 | 294.77 | 258.27 | 44.92 | 45.27 | 98.45 | 78.45 |

*Significant at P= 0.05 level, **Significant at P= 0.01 level

Broad-sense heritability was higher (> 60%) for all the traits, except for days to 80 per cent maturity (51.95%), hypocotyl color (38.24%), leaf shape (39.8%) and plant pubescence (39.94%). Plant pubescence density (99.93%) followed by seed yield plant[-1] (98.45%) and hilum color (98.16%) were more heritable than the other traits. Soybean is predominantly a self-pollinated crop. Hence the accessions used in the study are a mixture of pure lines whose expression predominantly determined by additive genetic effects and additive x additive type of epistasis. Consequently, broad-sense heritability is a reflection of narrow-sense herit ability Thus selection of desired accessions for any of the traits considered in the present investigation would be effective as all the traits were highly heritable.

In the present study, the estimates of expected GAM were higher for seed yield plant[-1] and plant pubescence density (78.45 and 72.22%, respectively), hilum color (63.21%), seed coat color (59.99%), plant pubescence type (59.71%), stem determination (54.37%), number of pods plant[-1] (49.94%), while they were lower for number of secondary branches plant[-1] (16.08%) and days to 80 per cent maturity (7.58%). Thus higher estimates of expected genetic advance which takes into account of variability and heritability are conformity evidence for scope and effectiveness of a selection of genotypes (Patil *et al.,* 2011). One of the major applications of estimating heritability and the genetic parameters that compose the heritability estimate is to compare the expected genetic gains from selection based on alternative selection strategies and different experimental designs (Falconer and Mackay, 1996). The information elicited from such comparisons could be used to design optimal breeding strategies (Milligan *et al*., 1990).

**Organization of Variability**

The efficiency and pace of soybean improvement programmes hinges on the precise information on magnitude of fixable (additive and additive based epitasis) component of genetic variability, g×e (both spatial and temporal) interaction and DNA marker-assisted chromosomal localization and mode of action of genes controlling traits of economic importance. The identification of accessions contrasting for traits of economic importance is a prerequisite for eliciting such information. Cluster analysis helps in grouping of accessions sharing similar characters in different clusters and to identify genetically diverse and desirable genotypes.

The quantitative traits mean differences between clusters were significant for all the traits (Table 4). The trait variances among six clusters were significant for all traits (Table 5). These results suggested K-means clustering approach was efficient to minimize with-in cluster variance and maximize between-cluster variance as a result of inclusion of diverse accessions into different clusters. The estimates of the means of the quantitative traits such as Days to 50 per cent flowering, plant height, secondary branches plant[-1], number of pods plant[-1], days to 80 per cent maturity, 100 seed weight, seed yield plant[-1] (g) were highest among the accessions included in cluster X and Cluster VI and were least among the accessions included in cluster VIII.  It is desirable to choose germplasm accessions from among those included in Cluster X and Cluster VI for various applications in soybean breeding research such as those already indicated.

Significant variability among the accessions for quantitative traits was expected as they are landraces which have evolved over millennia through a combination of natural and human selection on the variation originated by mutations and distributed by recombination (Allard, 1999). These landraces poses different combination of traits and hence have better adaptability to different production environment and / or a combination of production environments. Through increased use of landraces, efficiency of breeding soybean cultivars that are suitable for diverse production constraints especially that of terminal drought, a most frequently occurring abiotic stress in regions where soybean is extensively grown could be maximized.

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TABLE 4

Estimates of quantitative traits means of the soybean accessions belonging to different clusters

| Size of the cluster | $C_1$ | $C_2$ | $C_3$ | $C_4$ | $C_5$ | $C_6$ | $C_7$ | $C_8$ | $C_9$ | $C_{10}$ | Mean of clusters | | F Statistic | Probability |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | 221 | 284 | 170 | 340 | 141 | 182 | 231 | 209 | 154 | 71 | | | | |
| Days to 50% flowering | 61.26 | 54.15 | 69.97 | 54.51 | 70.28 | 60.5 | 53.54 | 53.05 | 58.16 | 59.47 | | | 29.65 | 0.00 |
| Plant height (cm) | 49.54 | 42.12 | 56.14 | 42.74 | 53.72 | 49.11 | 41.81 | 41.19 | 52.05 | 55.98 | | | 25.39 | 0.00 |
| Number of secondary branches plant$^{-1}$ | 4.99 | 4.83 | 5.03 | 4.9 | 5.12 | 4.91 | 4.92 | 4.89 | 5 | 5.05 | | | 177.44 | 0.00 |
| Number of pods plant$^{-1}$ | 48.48 | 43.24 | 39.66 | 37.18 | 28.5 | 54.23 | 31.1 | 25.82 | 63.11 | 76.08 | | | 8.82 | 0.00 |
| Days to 80% maturity | 121.48 | 115.24 | 127.78 | 115.93 | 129.1 | 119.86 | 115.04 | 112.56 | 119.97 | 122.16 | | | 69.32 | 0.00 |
| 100 seed weight (g) | 13.09 | 13.89 | 11.94 | 13.58 | 11.89 | 13.57 | 14.11 | 13.59 | 12.78 | 12.61 | | | 53.07 | 0.00 |
| Seed yield plant$^{-1}$ (g) | 135.52 | 105.52 | 93.31 | 86.73 | 61.36 | 167.55 | 70.75 | 53.44 | 203.04 | 242.05 | | | 6.05 | 0.00 |

TABLE 5

Estimates of quantitative traits variances among the soybean accessions belonging to different clusters

| Size of the cluster | $C_1$ | $C_2$ | $C_3$ | $C_4$ | $C_5$ | $C_6$ | $C_7$ | $C_8$ | $C_9$ | $C_{10}$ | Variance of clusters | | F Statistic | Probability |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | 221 | 284 | 170 | 340 | 141 | 182 | 231 | 209 | 154 | 71 | | | | |
| Days to 50% flowering | 77.27 | 28.59 | 42.61 | 29.54 | 43 | 67.91 | 28.28 | 34.56 | 62.09 | 46.65 | | | 8.32 | 0.00 |
| Plant height (cm) | 108.3 | 33.57 | 103.63 | 35.73 | 79.39 | 109.78 | 25.53 | 18.85 | 114.88 | 104.84 | | | 5.79 | 0.00 |
| Number of secondary branches plant$^{-1}$ | 0.47 | 0.33 | 0.47 | 0.43 | 0.39 | 0.56 | 0.42 | 0.41 | 0.47 | 0.44 | | | 22.89 | 0.00 |
| Number of pods plant$^{-1}$ | 2.86 | 4.68 | 22.71 | 7.63 | 7.53 | 3.65 | 4.12 | 4.03 | 9.92 | 30.07 | | | 3.33 | 0.00 |
| Days to 80% maturity | 75.97 | 80.32 | 34.26 | 80.64 | 39.7 | 80.14 | 83.72 | 85.67 | 80.12 | 69.39 | | | 12.13 | 0.00 |
| 100 seed weight (g) | 7.25 | 7.32 | 5.68 | 7.51 | 7.77 | 5.96 | 10.67 | 8.81 | 5.6 | 4.06 | | | 12.01 | 0.00 |
| Seed yield plant$^{-1}$ (g) | 103.2 | 56.82 | 98.91 | 38.67 | 82.42 | 107.75 | 23.49 | 40.1 | 86.43 | 324.67 | | | 3.55 | 0.00 |

TABLE 6

Trait-specific accessions for seven quantitative traits from 2000 germplasm accessions of soybean

| Characters | Accessions with lowest value | Mean value | Accessions with highest value | Mean value |
|---|---|---|---|---|
| Days to 50% flowering | SQL 32 | 44 | UPSV 45 | 77 |
| | EC 308327 | 44 | JS 82-780 | 77 |
| | TGX 844-313E | 44 | UPSL 28 | 77 |
| | EC 456650 | 44 | UPSL 254 | 77 |
| | IC 501637 | 44 | UPSM 858 | 77 |
| | JS 335 (Check) | 47.54 | | |
| Plant height (cm) | N 928 | 33.02 | GP 519 | 84.328 |
| | EC 39376 | 35.052 | GC-60115-8 | 82.804 |
| | CAT 2086 A | 35.052 | JS 99-76 | 81.28 |
| | VP 1156 | 35.052 | TGX 560-200 | 80.264 |
| | TGX 86-24-6F | 35.052 | HIMSO 1597 | 79.756 |
| | JS 335 (Check) | 39.67 | | |
| Number of secondary branches plant$^{-1}$ | SEHORE 1 | 3.4 | WT 89 | 7 |
| | UPSL 54 | 3.4 | PS 1337 | 7 |
| | UPSL 750 A | 3.4 | PS 1347 | 7 |
| | EC 381884 | 3.4 | EC 245986 | 7 |
| | UPSM 42 | 3.4 | TGX 352-3D | 6.8 |
| | JS 335 (Check) | 5.86 | | |
| Number of pods plant$^{-1}$ | NRC 2755 | 22.4 | JS 99-76 | 93.4 |
| | EC 457181 | 22.4 | MACS 693 | 91.6 |
| | JS 80-39 | 23 | TGX 825-3D | 86.2 |
| | DT-21 | 23 | V 31 | 84.4 |
| | LEE 75 | 23 | GP-434 | 82.4 |
| | JS 335 (Check) | 54.36 | | |
| Days to 80% maturity | AGS-116 | 95 | EC 39508 | 138 |
| | UPSL-77 | 95 | UPSL 736 | 138 |
| | PS-1336 | 95 | KB 19 | 138 |
| | NB 208 | 95 | UPSL 758 | 138 |
| | EC 572126 | 95 | UPSL 750 A | 138 |
| | JS 335 (Check) | 103.5 | | |
| 100 seed weight (g) | EC 251356 | 6 | TGX 1016-19 F | 23.3 |
| | EC 250601 | 6 | B 160-3 | 22.2 |
| | MACS 57 | 6.3 | JS 20-82 | 21.59 |
| | JS 79-82 | 6.3 | SQL 7 | 21.38 |
| | EC 572087 | 6.3 | EC 25196 | 21.3 |
| | JS 335 (Check) | 15.19 | | |
| Seed yield plant$^{-1}$ (g) | EC 457181 | 36.84 | JS 99-76 | 295 |
| | IC 501785 | 37.04 | MACS 693 | 292 |
| | EC 457211 | 42 | TGX 825-3D | 274.1 |
| | DT-21 | 42.7 | V 31 | 268.1 |
| | IC 501785 | 42.75 | GP-434 | 266.5 |
| | JS 335 (Check) | 118.09 | | |

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## Traits-Specific Accessions

Exploitation of natural genetic variability aim to meet short-term objectives as very often breeders are forced to meet immediate requirement of the farmers, consumers and end-users. Continued crop genetic improvement to meet medium - and / long-term requirements requires availability of variability induced through deliberately planned crosses among the genotypes *harbouring* desired combination of traits. Evaluation of germplasm provides information about the accessions / genotypes with desired combination of traits.

TABLE 7

Superior accessions for multiple traits

| Accessions | Number of pods plant$^{-1}$ | Seed yield plant$^{-1}$ (g) |
|---|---|---|
| TGX 825-3D | 86.2 | 274.1 |
| V 31 | 84.4 | 268.1 |
| GP-434 | 82.4 | 266.5 |
| JS 335 (Check) | 54.36 | 118.09 |

Some of the germplasm accessions were superior to the check JS 335 for 7 quantitative traits and the top five accessions for these traits along with contrasting lines are listed in Table 6. Three lines among the top performing accessions exhibited superiority for multiple traits and is listed in Table 7.

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