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RESEARCH ARTICLE

Evaluation of Soybean [*Glycine max* (L.) Merrill] Germplasm for Yield and Attributing Traits for Rabi Season in the Southern Indian Zone

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Abstract

The present study was undertaken to assess the genetic variability and character associations for seed yield and component characters in 481soybean (*Glycine max*, L.) germplasm accessions and identification of lines suitable for Rabi season cultivation. These lines were raised in an augmented block design in four blocks with five replicated checks during 2018. The analysis of variance revealed the presence of sufficient genetic variability in the gene pool. High PCV and high GCV were recorded for grain yield plot per plant, number of pods per plant and plant height. High heritability coupled with high genetic advance were observed for grain yield, followed by pods per plant, 100-seed weight and plant height, indicating the predominance of additive gene action in controlling the trait. Correlation and regression analysis indicated a significant positive effect of pods per plant, branches per plant and plant height on grain yield. Genetic diversity analysis grouped all germplasm accessions into 4 clusters. PCA revealed the first two principal components to explain 62.84% of total variation, mostly contributed by grain yield, seed size and number of pods. The agronomical variability and its genetic nature revealed from this study may be useful in present and future soybean breeding programmes. The promising accessions identified from the present study will help in strengthening the breeding program.

Keywords: Correlation, Genetic variability, Germplasm diversity, Off-season, Soybean.

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Introduction

Soybean (*Glycine max* L. Merril) is the world's most important seed legume, which contributes to about one-fourth of the global edible oil and about two-thirds of the world's protein concentrate for livestock feeding (Agarwal *et al.*, 2013). It is considered to be nature's highest yielding usable protein source of plant origin, as three times more usable protein per unit area than other important food grains, i.e., rice, wheat, or maize (Kumar, 2005). Soybean is widely used in the preparation of diversified food and food ingredients, including full-fat soy flour, milk, cheese, curd, ice cream, sprouted and roasted snacks, soy fortified bakery, soy protein concentrate, dietary fiber, single-cell protein, citric acid, margarine, etc. (Kumar, 2005). It also has a spectrum of industrial and pharmaceutical applications in the manufacturing of soap, cosmetics, crayons, resins, plastics, inks, solvents and clothing. The crop further improves soil fertility by fixing atmospheric nitrogen through symbiotic association with soil bacteria *Bradyrhizobium japonicum*. Owing to its diverse and quintessential utility, the soybean has been christened as 'miracle bean' (Orf, 2010).

Soybean is a leading oilseed crop, accounting for the production of 358.77 million metric tons in 2018–19 (USDA, 2019). In India, it grows annually as rain rain-fed crop with a production of 11.50 million metric tons in 2018–19 (USDA, 2019). In India, soybean growing regions have been divided into six zones, i.e., Central, Northern plain, Northern Hills, Eastern Zone, North eastern Hill Zone and Southern Zones. However, it is mainly grown in the Central Zone and the Southern Zone (AICRP 2019). Bangalore location in the Southern Zone is chosen to carry out the present experiment because of its congenial environment throughout the year for growing soybean germplasm multiplication and characterization. The Bangalore location is also being utilized in offseason generation advancement of segregation breeding material.

Remarkable progress made in plant genetic resource management in recent years 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*).* In India, ICAR- Indian Institute of Soybean Research, made an effort to bring core collection from USDA and more than 2500 accessions are being brought to Indian through ICAR-NBPGR, New Delhi (ICAR-IISR Annual Report 2019. Germplasm accessions collected from different states of India and introduced from overseas have been conserved in the national gene bank under long-term storage at NBPGR, New Delhi and medium-term storage (MTS) at ICAR-IISR, Indore. Soybean germplasm has been evaluated and characterized for different traits by in large experiments at Indore location (Central Zone) (Agarwal and Bhawsar 2013; Gireesh *et al.,* 2015; Nataraj *et al.,* 2020). However, we need to test the germplasm expression for various traits at Bengaluru station (Southern Zone), as no single report about germplasm evaluation.

Evaluation of germplasm at a particular location helps to identify the adapted genotypes with desired traits. The abundance of genetic diversity present in any genetic material indicates the scope for further improvement of the particular crop (Baig *et al*., 2018). The knowledge of genetic variability existing within the different parameters associated with yield is an important criterion for yield enhancement, but in highly self-pollinated crops like soybean, where natural variation results limited scope for selection opportunity (Jain *et al*., 2015). Similarly, understanding the nature of associations between yield and its attributes and their direct and indirect contributions to seed yield is necessary for efficient selection (Kumar *et al*., 2018). Therefore, the present study was carried out to evaluate the nature and magnitude of genetic diversity available in the soybean gene pool and find out associations between seed yield and its component characters in soybean germplasm accessions, which would help in the selection of efficient genotypes for further utilization in the breeding programme.

Materials and Methods

Plant material

The germplasm material used in this study comprised 481 Soybean (*Glycine max* (L.) Merrill) accessions collected and conserved between 1986-2018 at an active germplasm site (ICAR-IISR, Indore) from different soybean growing states of India and different countries of the world, which were imported between 1970-2018 (Supplementary Table S1). Five morphological data on the germplasm accessions were recorded in the experimental fields at AICRP center of Soybean, UAS, GKVK, Bengaluru, during December 2018-March 2019. This experimental site is located at 12° 51′ 17.75′′ N and 77° 35′ 40.42′′ E and an elevation of 926.59 m above sea level. The soil of the experimental farm is sandy loam inclined more towards a skeletal nature, dry, shallow and moderately rich in organic matter. Average rainfall is 32.1 mm during the months from December to March. Therefore, the plants were given drip irrigation as and when required. Mean minimum and maximum temperature ranges between 13.1- and 33.7°C. The soybean crop was sown in one row of 4 m length with 45 cm row-to-row spacing and harvested. Standard cultivation practices recommended for the Southern zone were followed (ICAR-IISR, 2019). The trial was conducted in an Augmented Block Design (ABD) along with five checks, *viz.* DSb 21, JS 335, JS 93-05, KBS 23 and RKS 18 to estimate phenotype variation attributing to genetic factors with respect to the germplasm panel studied and five checks were repeated once in each block.

Plant characters and data observations

The data on six quantitative traits on these 476 germplasm accessions and five checks were recorded. Days to 50% flowering, plant height (cm), number of branches, number of pods, grain yield (g)/plot and 100 seed weight (g) were recorded using standard methods (IBPGR, 1984). Each genotype, at its R8 stage, was harvested and grain yield per plot was recorded. Three random samples of a hundred seeds of respective accession were taken for weighing to record the 100 seed weight. Plot yield (kg) was converted into yield per hectare (q/ha) using the formula (plot yield/1.8) ×10,000.

Statistical analysis

Adjusted means for all six traits under consideration of 476 accessions were estimated by using the R package ‘augmented RCBD’ (Aravind *et al.,* 2018). Before undertaking statistical analysis on the basis of adjusted mean values, homogeneity of variance was tested as per Levene (1960). Frequency distribution graphs were obtained for the traits and the traits were further analysed for various descriptive statistical parameters, viz., mean, range, variance, etc., by using the R package ‘augmentedRCBD’. Correlation analysis was performed by using the R function cor(), and linear regression analysis was performed using the R function lm(). Correlation plots were obtained by using the R packages ‘corrplot’ (Wei and Simko, 2017) and PCA was performed by using the R packages ‘corrplot’ (Wei and Simko, 2017), ‘factoextra’ (Kassambara and Mundt, 2017) and ‘FactoMineR’

(Lê *et al.*, 2008). The K-means cluster analysis was carried out R package 'factoextra' (Kassambara and Mundt, 2017).

Results

Variability and genetic parameters

The analysis of variance illustrated the existence of a remarkable amount of genetic variability among the soybean germplasm accessions for yield and yield-related parameters under study (Table 1). Analysis of variance for an augmented randomized block design revealed that mean squares of all six traits were significant for different sources of variations except mean squares due to blocks, ignoring the treatments & due to genotypes vs. checks for the trait of number of branches per plant. The mean, range, variance, coefficient of variance, heritability and genetic advance for all six agro-morphological characters are presented in Table 2. Among the traits, grain yield, 100-seed weight and number of pods per plant were found to have more variations than other traits. The mean value of grain yield per plot was recorded as 419.18 g with a range of 47.1 g (EC 100804) - 951.5 g (Shilajeet). The 100 seed weight ranged from 6.7 g (EC 172577) to 27.69 g (AGS 174) with an average value of 13.67 g. Grain yield per plot (41.03/39.38), plant height (37.82/36.28), number of pods per plant (32.28/29.81) and number of branches per plant (31.18/27.41) were found to have high PCV and GCV (Table 1). The heritability was highest for seed index (98.63%), days to 50% flowering (98.62%), grain yield (92.09%), and plant height (92.02%), and the lowest heritability was recorded for the number of branches (77.26%). Genetic advance as percent mean was recorded high for the traits *viz*., grain yield (77.95%), plant height (71.8%) and number of pods (56.81%), and it was lowest for days to 50% flowering (20.45%).

Frequency distribution of quantitative traits

Frequency distribution showed that around 10% of the accessions produced grain yield per plot of more than 650 g and around 20% of lines produced grain yield of 500 to 650 g/plot (data not shown). The number of pods also showed a large variation and 25% of the accessions were found to have pods per plant in the range of 60 to 111. The trait 100-seed weight also showed a good amount of variability, where 30% of the lines produced 15 to 27 g seed. The frequency distribution of six quantitative traits is shown in Fig. 1.

Identification of promising accessions

Promising germplasm accessions were identified based on the best check values and critical difference (CD) value at the 5% level of significance. Accessions such as Shilajeet (951.5g) EC 481571(860.2 g), EC 550828 (852.8 g), EC 333924 (847.4 g), M 1059 (845.2 g), AGS 170 (829.6 g), MAUS-142 (825.2 g), EC 241650 (803.8 g), EC 251416 (792.6 g), EC 467282 (791.8 g) were found promising for grain yield per plot. Germplasm lines i.e.EC 291400 (111.1), EC 241778 (110.6), EC 550828 (106.1), EC 481571 (105.1) and EC 389164 (101.3) were found superior for number of pods per plant while genotypes EC 100804 (113.2 cm), NRC 2396 (113.1 cm), EC 390981 (113.0 cm), Bragg (111.7 cm) and EC 389164 (111.2 cm) found promising for good plant height. For high seed weight, accessions such as AGS 174, MACS 1034, EC 251432, EC 15553 and JSM245 were found promising among the germplasm accessions.

Correlation and regression

The correlation matrix showed significant positive correlation of grain yield with pods per plant (0.72), plant height (0.42), branches per plant (0.27) and days to 50% flowering (0.27); however, 100-seed weight showed a negative correlation (-0.09). 100-seed weight was found to be negatively correlated with all other yield-attributing traits. All traits except 100-seed weight were found to be positively correlated with each other. (Fig. 2). Simple linear regression analysis performed for grain yield versus other traits showed that pods per plant had the highest direct effect on 100-seed weight, followed by plant height and days to 50% flowering and branches per plant (data not presented).

Genetic diversity and principal component analysis

Multivariate analysis among the germplasm lines was performed using genetic divergence and principal component analyses. All the 481 germplasm accessions,

Table 1: Statistical parameters of genetic variability in gene pool under study

Trait	*Mean + SE*	*Variance*	*Variance*	*Range*	*PCV (%)*	*GCV (%)*	*Heritability*	*Genetic advance as*
		(P)	*(G)*					*% of mean*
Days to flowering	54.03 ± 0.26	29.51	29.1	33.25–64.35	10.05	9.98	98.62	20.45
No. of branches per plant	4.08 ± 0.06	1.62	1.25	0.83–12.88	31.18	27.41	77.26	49.71
Plant height (cm)	55.5 ± 0.96	440.54	405.37	13–113.2	37.82	36.28	92.02	71.8
No of pods per plot	51.29 ± 0.75	274.04	233.8	10.42–111.1	32.28	29.81	85.31	56.81
100-seed weight (g)	13.67 ± 0.14	9.42	9.29	6.7–27.6	22.45	22.29	98.63	45.68
Grain yield per plot (g)	419.18 ± 7.8	29583.2	27242.5	47.1–951.5	41.03	39.38	92.09	77.95

Table 2: Analysis of variance of six quantitative traits

Source	*DF*	*Grain yield per plot (g)*	*100 seed weight (g)*	*No. of pods per plant*	*No. of branches per plant*	*Days to flowering*	*Plant height (cm)*
Block (ignoring Treatments)	3	38788.7***	38.96***	692.63***	0.99^{ns}	27.68***	426.55***
Treatment (eliminating Blocks)	480	29528.48***	9.24***	270.06***	1.6**	40.4***	446.03***
Treatment: Check	4	15286.3**	12.01***	367.65**	0.55^{ns}	98.18***	288.73**
Treatment: Test and Test vs. Check	476	29648.16***	9.22***	269.24***	1.61**	39.92***	447.35***
Residuals	12	2340.67	0.13	40.24	0.37	0.41	35.17

ns-P > 0.05; * - P <= 0.05; **-P <= 0.01; **- P <= 0.001

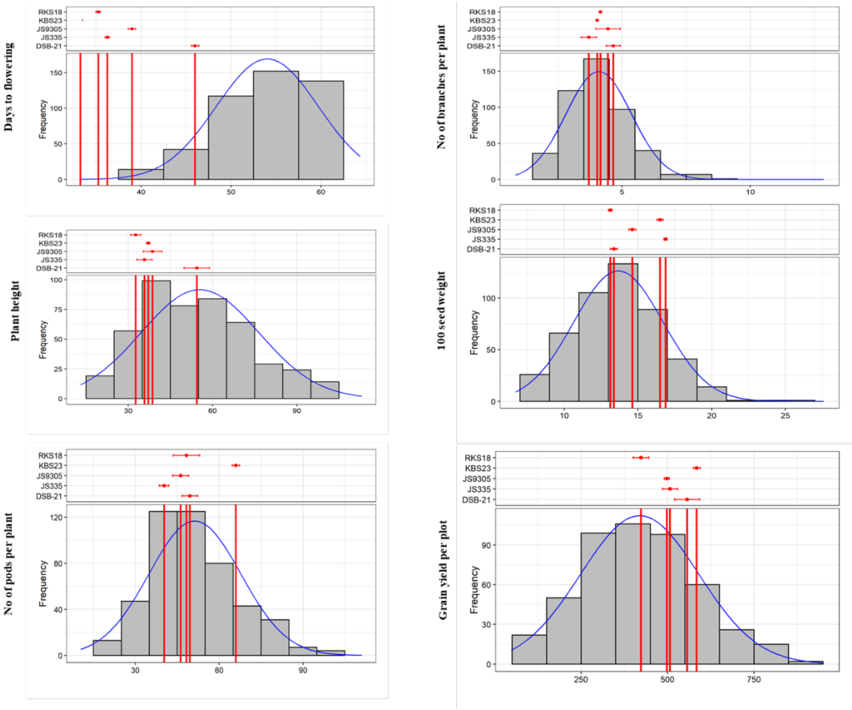

Fig. 1: Frequency distribution of traits under study

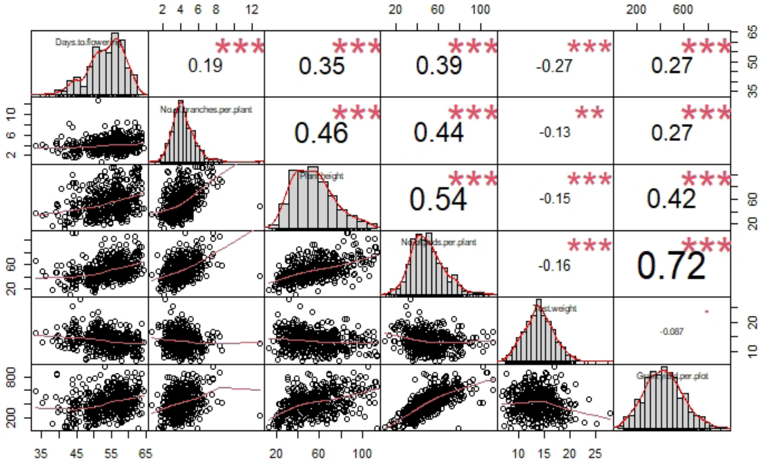

Fig. 2: Graphical depiction of correlation among the quantitative traits in germplasm accessions

Table 3: K-means clustering of genotypes under study

Cluster	*No of genotypes*	*Genotype code*
Cluster 1	79	3, 14, 18, 26, 27, 32, 45, 52, 59, 65, 67, 70, 75, 77, 85, 86, 88, 89, 102, 118, 122, 126, 130, 131, 145, 148, 149, 151, 156, 157, 158, 169, 176, 181, 182, 183, 185, 197, 199, 205, 207, 219, 220, 238, 242, 250, 251, 259, 264, 266, 267, 272, 274, 284, 291, 295, 296, 303, 328, 329, 357, 358, 381, 388, 392, 412, 416, 424, 444, 445, 446, 448, 450, 456, 464, 467, 473, 475 and 476
Cluster 2	165	2, 4, 5, 10, 11, 12, 20, 28, 29, 34, 36, 39, 48, 49, 55, 56, 61, 62, 64, 68, 71, 7, 81, 83, 87, 98, 99, 101, 103, 107, 110, 112, 113, 116, 120, 134, 137, 138, 140, 154, 155, 159, 160, 162, 164, 165, 168, 172, 174, 177, 178, 180, 184, 187, 189, 196, 201, 202, 203, 206, 209, 212, 217, 221, 224, 227, 229, 232, 233, 236, 239, 240, 247, 249, 254, 255, 256, 257, 263, 268, 277, 280, 281, 288, 290, 299, 302, 304, 308, 314, 315, 316, 317, 318, 319, 320, 323, 326, 330, 331, 332, 333, 336, 337, 338, 340, 341, 343, 348, 353, 354, 355, 359, 360, 361, 362, 369, 373, 374, 375, 376, 383, 389, 391, 398, 399, 400, 402, 404, 408, 411, 413, 414, 418, 419, 423, 428, 429, 430, 431, 434, 436, 437, 439, 440, 441, 442, 449, 451, 452, 453, 454, 458, 460, 462, 463, 466, 470, C1, C2. C3. C4 and C5
Cluster 3	73	8, 19, 21, 22, 23, 24, 31, 42, 46, 47, 51, 53, 57, 60, 74, 92, 93, 95, 100, 105, 106, 121, 135, 139, 142, 143, 163, 167, 179, 194, 195, 204, 211, 214, 215, 223, 228, 230, 243, 244, 245, 252, 265, 270, 271, 278, 289, 293, 294, 298, 312, 321, 335, 345, 347, 349, 386, 387, 390, 396, 405, 415, 421, 425, 426, 427, 455, 465 and 472
Cluster 4	164	6, 7, 9, 13, 15, 16, 17, 30, 33, 35, 37, 38, 40, 41, 43, 44, 50, 54, 58, 63, 66, 69, 73, 76, 78, 79, 80, 82, 84, 91, 90, 96, 104, 108, 109, 111, 114, 115, 117, 119, 123, 124, 125, 127, 128, 129, 132, 133, 136, 141, 144, 146, 147, 152, 170, 171, 173, 175, 186, 190, 191, 192, 193, 198, 200, 210, 216, 218, 222, 225, 226, 234, 235, 237, 241, 246, 253, 258, 260, 261, 262, 269, 273, 276, 279, 282, 283, 285, 286, 287, 292, 297, 300, 301, 305, 306, 307, 310, 311, 313, 322, 324, 325, 327, 334, 342, 344, 346, 350, 351, 352, 356, 363, 364, 365, 366, 367, 368, 370, 371, 372, 377, 378, 379, 380, 382, 384, 385, 393, 394, 395, 397, 401, 406, 407, 409, 410, 417, 420, 422, 432, 433, 435, 443, 447, 457, 459, 461, 471 and 474

including checks, were grouped into 4 clusters using k-means clustering. Cluster 1 (C1), cluster 2 (C2), cluster 3 (C3) and cluster 4 (C4) were found to have 79, 165, 73 and 164 accessions respectively (Table 3 and Fig. 3). The mean value of accessions grouped into each cluster (Supplementary Table S2) showed that accessions in C1 and C2 produced high grain yield per plot and pods per plant whereas cluster 3 was found to have the highest 100-seed weight. Plant height, number of branches and days to 50% flowering reported maximum mean in cluster 1, whereas minimum mean in cluster 3 (Table 4).

Table 4: Cluster means for different traits under study

Cluster variables	*C1*	*C2*	*C3*	*C4*
Days to flowering	56.25	54.79	50.44	53.79
Plant height	72.7	56.07	43.31	52.05
No. of branches	4.639	4.195	3.695	3.87
No. of pods	69.97	56.99	34.05	44.21
Seed index	13.62	13.41	14.45	13.62
Grain yield	686.62	491.17	163.37	331.79

PCA revealed that all six quantitatively measured traits have been loaded on six components; however, a major portion of variance (~63%) in germplasm accessions is explained by the first two components with eigenvalue>1 (Table 5). The first component (PC1) accounted for 45.54% of variation largely through grain yield, number of pods and plant height, while PC2 contributed 17.30% through 100-seed weight and days to 50% flowering. PC3, PC4, PC5 and PC 6 contributed 13.56, 11.36, 8.10 and 4.14% of total variation, respectively. Biplotting of PC1 and PC2 indicated 100-seed weight (44.73%) contributed the highest to the first two principal components, followed by number of pods (19.35%) and grain yield (18.14%) (Figure 4).

Discussion

Soybeans are one of the most important oilseeds in the international market, being the fourth most produced and consumed crop worldwide (Gesteira *et al.*, 2018). It has been studied and enhanced for most of its economically important traits, i.e., yield and attributing traits. Yield is considered a complex trait, governed by many genes and the particular environment and their interaction. Development of adapted varieties for a particular location necessitates the deployment of well-adapted high-yielding genotypes in hybridization programmes. Characterization and evaluation of germplasm accessions is the most important activity of any plant gene bank. This is also a bottleneck between the genetic diversity conserved in a gene bank and its utilization in breeding programmes of a particular area. Therefore, most of the soybean breeding programmes are based on very few trait-specific parental lines, which have resulted in poor genetic gains and cause for the creation of a narrow genetic base in the released cultivar. Modern soybean varieties, which account for the major share of total soybean production in India, have been developed exploiting only a small spectrum of soybean variability. Therefore, the limited variability within the modern cultivars has become a restrictive factor for yield increase and increased incidence of many biotic and abiotic stresses. However, this study shows that the soybean (*Glycine max*) gene pool has a great amount

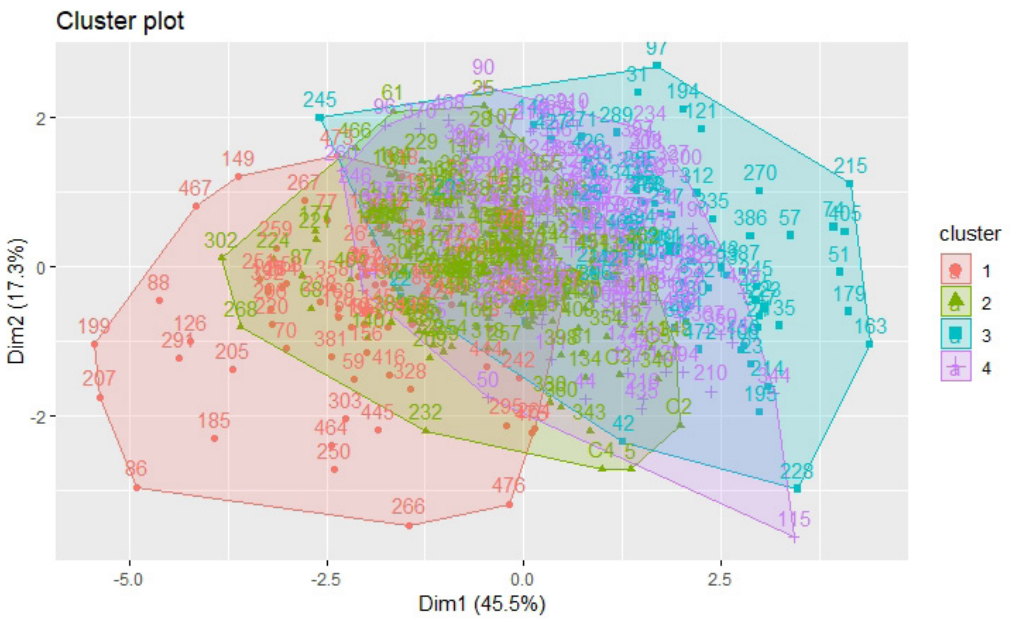

Fig. 3: Biplot of germplasm accessions into different clusters

Fig. 4: Principal Component Analysis of different traits under study

of useful variability for yield-attributing traits.

In this study, ANOVA represented variability for all traits except for the number of branches. Similar results were also reported by Kumar *et al*. (2018) for the number of branches and Bhartiya and Aditya (2016) for the number of pods per plant, indicating sufficient genetic diversity for all traits except the number of branches. High PCV and GCV were recorded for grain yield, plant height and number of pods/plant. High heritability coupled with high genetic advance were observed for plant height, 100-seed weight, number of pods per plant and seed yield per plot, indicating governance of additive gene action for these traits. Similar results have been reported by Kumar *et al*. (2015) for plant height and 100-seed weight, for seed yield per plant, Ekka and Gabrial (2016),) for plant height Kumar *et al*. (2018), for 100-seed weight and seed yield per plant Shivakumar *et al*. (2019) for number of nodes and plant height in soybean nested association mapping population.

Table 5: Eigen values, variance contribution (%), variables coordinates and percent contribution of each variable on the individual five principal components of germplasm accessions

		Days to flowering	*Plant height*	*100 seed weight*	*No. of branches*	*No. of pods*	*Grain yield (g)*	*Eigen values*	*Variance (%)*
PC1	Coordinates	0.58	0.76	-0.32	0.63	0.87	0.75	2.73	45.54
	Contribution (%)	12.49	21.22	3.86	14.46	27.43	20.54		
PC2	Coordinates	-0.44	0.08	0.83	0.14	0.18	0.29	1.04	17.3
	Contribution (%)	18.83	0.68	67.15	1.79	3.29	8.24		
PC3	Coordinates	0.3	-0.23	0.11	-0.68	0.19	0.4	0.81	13.56
	Contribution (%)	11.37	6.56	1.59	56.47	4.24	19.77		
PC4	Coordinates	0.57	0.22	0.42	0.02	-0.16	-0.31	0.68	11.36
	Contribution (%)	48.29	6.8	26.41	0.09	3.88	14.53		
PC5	Coordinates	0.2	-0.56	0.07	0.35	0.08	0.05	0.49	8.1
	Contribution (%)	8.12	64.23	0.93	24.64	1.47	0.6		

Correlation studies revealed that traits such as number of pods and plant height had the highest significant positive effect on grain yield; similar kinds of trends were also observed by Gireesh *et al.* (2015), Yashpal *et al.* (2019) and Shivakumar *et al.* (2019). Grain yield was positively correlated with the number of pods in other legumes like Mung Bean [*Vigna radiata* (L.) Wilezek] (Dar *et al.*, 2025). In the current study, 100-seed weight was found to be negatively correlated with other yield attributes, and has also been reported by Iqbal *et al.* (2010) and Kumar *et al.* (2018). PCA can evaluate the relative contribution of different elements to the total divergence together with the nature of forces operating at intra- and inter-cluster levels (Sharma *et al.*, 2009). In the current study, the first three components (PCs) explained >75% of the total variation. In the first two PCs, the maximum percent of variation is contributed by grain yield, 100-seed weight and number of pods. Therefore, these traits are important in explaining the genetic variation in the germplasm accessions. The results are in agreement with various other studies that reported the maximum contribution of grain yield in soybean (Dubey *et al.*, 2018; Maranna *et al.*, 2019). The PCA was also employed in studying variability in other legumes like Horse Gram [*Macrotyloma uniflorum* (Lam.) Verdc.] (Kumari *et al.*, 2025). Cluster analysis grouped the 481 accessions into 4 clusters, with cluster C4 comprising the maximum number of germplasm lines, indicating close relatedness of these genotypes. A similar way of grouping for yield traits of 900 NAM RILs of soybean into 10 clusters was reported by Shivakumar *et al.* (2019). Genotypes having the highest grain yield per plant, plant height and number of pods fall under cluster C1, whereas the lowest days to 50% flowering and the largest seed-sized germplasm accessions fall under cluster C3. This study identified a number of promising accessions that can be further utilized in soybean hybridization programmes for improving the yield potential of new varieties.

Conclusion

Progress in breeding high-yielding varieties of soybean has been reserved and one of the constraints shown by many soybean breeders is the narrow genetic base present in the released varieties. Given this limitation, plant breeders require genetically diverse germplasm not only for yield but also for its contributing traits. In this direction, this study generated information on a large number of soybean germplasm accessions evaluated in the southern region of India. From this study, it is evident that a wide range of genetic variability for different yield attributes and several diverse and promising germplasm accessions were identified for future use in the hybridization program to create new breeding material with a broad genetic base.

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Supplementary Tables

Table S1: Details of the genotypes evaluated in the current study

Code	*Name*	*Code*	*Name*	*Code*	*Name*	*Code*	*Name*
C1	DSb-21	117	EC 274683	238	EC 589400	359	JS 80-21
C2	JS335	118	EC 457464	239	EC 572019	360	JS 93-05
C3	JS9305	119	EC 467282	240	EC 391172	361	SQL 3
C4	KBS23	120	EC 615160	241	EC 309537	362	SQL-40
C5	RKS18	121	EC 550828	242	EC 389399	363	SQL -12
1	AGS 218	122	EC 251817	243	EC 456556	364	SQL-98
2	AGS 166	123	EC 251378	244	EC 538828	365	SQL 11
3	AGS 108	124	EC 572086	245	TGX 802-150D	366	SQL-5
4	AGS 128	125	EC 175321	246	TGX 86-34	367	SQL-81
5	AGS 174	126	EC 93601	247	TGX 702-4-8	368	SQL 93
6	AGS 156	127	EC 287754	248	TGX 298-7D	369	SQL-106
7	AGS 116	128	EC 481571	249	TGX 899-285D	370	SQL 83
8	ABL-1	129	EC 250591	250	ABL-14	371	SQL -31
9	AGS 143	130	EC 34060	251	TGX 722-110E	372	PK 722
10	AGS 190	131	EC 095297	252	TGX 825-1E	373	SQL 97
11	AGS 230	132	EC 39511	253	TGX 824-35	374	PK 474
12	AGS 38	133	EC 113770	254	TGX 814-148D	375	PK 1284
13	AGS 205	134	EC 175329	255	TGX 863-26F	376	P 318
14	AGS 83	135	EC 250588	256	TGX 849-309A	377	SQL 18
15	AGS110	136	EC 241650	257	TGX 849-47F	378	PK 566
16	AGS 158	137	EC 274701	258	TGX 803-99E	379	PK1225
17	AGS 02	138	EC 100778	259	TGX 854-42D	380	SPL-4
18	AGS 105	139	EC 615187	260	TGX 863-2C	381	PLSO-79
19	ABL-2	140	EC 251498	261	TGX 722-155F	382	P-318
20	AGS102	141	EC 232275	262	TGX 814-78D	383	PS 1029
21	AGS 193	142	EC 41319	263	TGX 539-2D-7	384	SL 142
22	AGS 166	143	EC 18672	264	TGX 822--10E	385	K 53
23	AGS 157	144	EC 602288	265	TGX 984-18A	386	L 129
24	AGS 42	145	EC 309522	266	TGX 849-309F	387	KB 249
25	AGS 153	146	EC 325102	267	TGX 849-294D	388	B-160-3
26	AGS 186	147	EC 103334	268	TGX 885-44E	389	T-49
27	AGS 170	148	EC 291399	269	TGX 1070-F6	390	VLS-63
28	AGS 150	149	EC 250577	270	TGX 802-150E	391	WT 169
29	AGS 41	150	EC 241756	271	TGX 849-207 D	392	GP 493
30	AGS 142	151	EC 274712	272	TGX 854-71E	393	VLS 75
31	AMSS34	152	EC 241995	273	TGX 1016-5F	394	V 55
32	AKSS 65	153	EC 251402	274	TGX 854-60A	395	EC 538814
33	AK 887	154	EC 171536	275	TGX 860-11D	396	HAL
34	AKSS 143	155	EC 25082	276	TGX 855-53D	397	WT 150

35	ACC 1026	156	EC 95815	277	TGX 814-148F	398	HARDEE
36	AKSS 63	157	EC 251446	278	TGX 996-5F	399	LESOY 273
37	AGS 104	158	EC 39177	279	TGX 984-18E	400	GC 12
38	B 1666	159	EC 45732	280	TGX 855-44G	401	ELGIN(S)
39	B 471	160	EC 172663	281	TGX 803-99D	402	HIMSO-175
40	B 252	161	EC 100772	282	TGX 1016-19F	403	NANKING
41	BR 10	162	EC 18673	283	TGX 85B-48	404	SEHORE-1
42	B 1665	163	EC 100804	284	TGX854-429	405	INDORE-2
43	BRG 1	164	EC 457052	285	TGX 702-4-2	406	NRC -1
44	DS 366	165	EC 39376	286	TGX 844-313-B	407	NRC 37
45	BRG 12	166	EC 24200	287	TGX 713-1F	408	NRC 57
46	DS 321	167	EC 241310	288	TGX 293-65E	409	NRC 2396
47	BR 15	168	EC 172577	289	TGX 854-77D	410	NRC 105
48	DE 201	169	EC 241778	290	TGX -813-14D	411	NRC 2346
49	B 1667	170	EC 18593	291	TGX -855-32E	412	NRC 2007-1-3
50	DS 205	171	EC 251886	292	ABL-15	413	NRC 86
51	EC 333908	172	EC 325113	293	TGX B-1435E	414	NRC 2320
52	AGS 74	173	EC 291453	294	TGX -312-012F	415	N 928
53	AGS 74A	174	EC 242091	295	TGX -8116-21D	416	M-1085
54	EC 341822	175	EC 30968	296	TGX -825-3D	417	M-1052
55	EC 343310	176	EC 528620	297	TGX 802-100F	418	M-1059
56	EC 333924	177	EC 76759	298	TGX 317-37E	419	MAUS-142
57	EC 343312	178	EC 589409	299	TGX 298-7E	420	MACS-150B(VG)
58	EC 242108	179	EC 287469	300	TGX 573-209	421	MAUS 47
59	EC 114527	180	EC 393231	301	TGX 239-43D	422	MACS 1034
60	EC 333940	181	EC 389173	302	TGX 849-D 13-4	423	MAUS 41
61	EC 481571	182	EC 289161	303	TGX 573-219D	424	MACS 227
62	EC 308328	183	EC 538801	304	TGX560-20D	425	MACS 250
63	EC 241712	184	EC 396067	305	TGX 416-06C	426	MACS 708
64	EC 251529	185	EC 393224	306	TGX 297-16F	427	MACS 1028
65	EC 333859	186	EC 15553	307	TGX 849-14-3D	428	MACS 58(S)
66	EC 241761	187	EC 572108	308	TGX 330-325D	429	MACS 330
67	EC 251405	188	EC 396065	309	TGX 854-420-1	430	IC 24532A
68	EC 251388	189	EC 93413	310	ABL-16	431	IC 0596790
69	EC 313974	190	EC 572130	311	TGX 302A-68D	432	IC 16821
70	EC 245988	191	EC 391181	312	ABL-17	433	IC 13051
71	EC 528623	192	EC 391346	313	TGX 780-5A	434	PI 283327
72	EC 287464	193	EC 572187	314	ABL-18	435	PI 340900
73	EC 2206 B	194	EC 251456	315	TGX 849-813	436	PI 200465
74	EC 309513	195	EC389156	316	TGX 825-17E	437	IC 4882
75	EC 287460	196	ABL-8	317	TGX 854-4F	438	ICS84/86-858-41
76	EC 251413	197	EC 13054	318	TGX 576-21-9	439	ICAL 122
77	ABL-3	198	EC 389167	319	TGX 814-13E	440	EC 287457

78	EC 581521	199	EC 389148	320	TGX 802-100D	441	EC 333870
79	EC 34115	200	EC 389166	321	TGX 442-20D	442	EC 280129
80	EC 343311	201	EC 538802	322	TGX 311-59E	443	EC 389153
81	EC 34079 B	202	EC 572160	323	TGX 573-97D	444	EC 457161
82	EC 389152	203	EC 380522	324	TGX 342-376	445	RAUS -5
83	EC 37104	204	ABL-9	325	TGX 297	446	ALANKAR
84	EC 241715	205	EC 457280	326	TGX 86-24-10	447	MONETTA
85	EC 100027	206	EC 289099	327	TGX 293-47E	448	PALAM SOYA
86	EC 251514	207	EC 572035	328	TGX 86-24-6E	449	IMPROVED PLICAN
87	EC 274713	208	EC 389165	329	TGX 293-46E	450	INDRA SOYA9
88	EC 389154	209	EC 644409	330	TGX 996-4F6	451	KHSb2
89	EC 325104	210	EC 572071	331	JSM 288	452	PS 1347
90	EC 357998	211	EC 389179	332	JSM 258	453	PUSA 22
91	EC 341115	212	EC 592195	333	JSM 302	454	ADT-1
92	EC 389164	213	EC 390979	334	JS 82	455	PK 308
93	EC 333880	214	EC 390981	335	JS 355	456	ANKUR
94	EC 274711	215	EC 456574	336	JS (SH) 2001-64	457	CO-SOYA-2
95	EC 250601	216	ABL-10	337	JS 94-52	458	GUJARAT SOYBEEN-1
96	EC 291400	217	EC 309529	338	JS 20-49	459	CO-1
97	EC 289091	218	EC 251416	339	JS 95-52	460	KALILAR
98	EC 333876	219	EC 333899	340	JS 20-37	461	SL-295
99	EC 309541	220	EC 357990	341	ABL-21	462	SHIAJEET
100	EC 329157	221	EC 389391	342	JS 20-76	463	LEE
101	EC 309543	222	EC 333872	343	JS 20-38	464	BNAGG
102	EC 251401	223	EC 589407	344	JS 98-02	465	SHIVATIK
103	ABL-4	224	EC 528622	345	JS 94-67	466	DURGA
104	EC 309511	225	EC 572127	346	JS 79-82	467	PUNJAB
105	EC 389160	226	EC 546881	347	JS 20-86	468	PUSA 16
106	EC 242003	227	ABL-11	348	JS 97-52	469	PS 1024
107	EC 251432	228	ABL-12	349	JS(SH)99-02	470	PK 472
108	ABL-5	229	EC 18673	350	JS 20-73	471	PK 262
109	EC 2579	230	EC 606917	351	TGX 802-265D	472	MACS -13
110	ABL-6	231	EC 538807	352	TGX 311-101F	473	MACS 450
111	ABL-7	232	EC 389178	353	TGX 239-6D	474	MACS 58
112	EC 547464	233	EC 39573	354	TGX 573-209-23	475	ABL-19
113	EC 23003	234	ABL-13	355	TGX 328-049	476	ABL-20
114	EC 245986	235	EC 389163	356	TGX 536-1009		
115	EC 291397	236	EC 528666	357	JSM 245		
116	EC467282	237	EC 542431	358	JS 20-72		